Pradip Kumar Sahu

Applied Statistics for Agriculture, Veterinary, Fishery, Dairy and Allied Fields

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To
Kenchu, Mechu, Venpu and Khnako

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Preface

Statistics is now recognized and universally accepted a discipline of science. With the advent of computer technologies, the use of statistics has increased manifold. One can hardly find any area where there is no use of statistics. In the field of Biological Sciences, the use of statistics is also keeping pace with other disciplines. In fact development of many statistical theories has their roots in biological sciences, in particular agricultural sciences. This has led to ever increasing areas of its application in diversified fields. Newer and varieties of problems are being tackled by the subject. Like other branches of science, statistics is being extensively used in agricultural/animal/fishery/dairy and other fields in explaining various basic as well as applied problems. Availability of wide range of statistical techniques suited for various problems has made it possible for its wider application. Everyday type of problem is getting increased and more and more tools or techniques need to be developed to solve various specific problems. Development and/or selection of appropriate statistical technique for a given problem is mostly warranted for getting meaningful explanation of the problems under consideration.

Students/teachers/researchers/practitioners from agriculture and allied fields are to deal with various factors like living flora and fauna, soil, air, water, nutrients, etc. along with socio-economic and behavioral aspects of plant and animal beings for successful research and development. Understanding of the theory and essence of both the agricultural science and the theory of statistics is a must for getting and explaining the problem under consideration in a meaningful way. It is felt increasingly that a user in any field should have well understanding of the logic behind any experimentation as well as the specific statistical tools (during planning, designing, executing, collecting information/data, analytical methods and drawing inference from the results) to be used to draw meaningful conclusion from the experiment.

Statistics is a mathematical science in association with uncertainty. There is a large section of students/teachers/researchers/practitioner who do not have enough mathematical orientation and as such are scares of using statistics, in spite of its wider acceptability. To reach to these huge users remains a challenging task to the statisticians, particularly the biostatisticians. Statistics must reach to the users particularly to these types of user in their terms/manners and language. Biological sciences have moved

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on from mostly simple qualitative description to concepts founded on numerical measurements and counts. In order to have proper understanding of phenomena, correct and efficient handling of these measurements is needed and actually done by statistics. Understanding of basic statistics is essential for planning measurement programs and for analyzing and interpreting data but frequently it has been observed that many users lack in good comprehension of statistics, moreover do not feel comfortable while making simple statistics based decisions. A number of books are available, which deal with various aspects of statistics. The need for the present book has been crept in to the mind of the author during his teaching experience. In India only, there are more than hundred colleges where agriculture, veterinary, fishery, dairy and home science are taught at graduation and post-graduation levels as per the syllabi of the Indian Council of Agricultural Research. Outside India, millions of students are there in these wings. A textbook to cater the need of these types of students with a guide to handle their data using easily available statistical software is mostly needed. An attempt has been made in this book to present the theories of statistics in such a way that the students and researchers from biological/agricultural/animal/fishery/dairy and allied field find it easy to handle and use in addressing many real life problems of their respective fields.

This book starts with an introduction to the subject which does not require any previous knowledge about the subject. The ultimate aim of the book is to make it self-instructional textbook, which can be helpful to the users in solving their problems using statistical tools also with the help of simple and easily available computer software like MSEXCEL. It is expected that thousands of students of biological/agricultural/animal/fishery/dairy and allied fields would be benefitted from this book. In each chapter, theories have been discussed with the help of example(s) from real life situations, followed by worked out examples. Simple easily available packages like MSEXCEL, SPSS, etc. have been used to demonstrate the steps of calculation for various statistical problems. Statistical packages used for demonstration of analytical techniques are gratefully acknowledged. Attempts have been made to familiarize the problems with examples on each topic in lucid manner. Each chapter is followed by a number of solved problems (more than 165) which will help the students in gaining confidence on solving those problems. Due care has been taken on solving varied problems of biological/agricultural/animal/fishery/dairy and allied fields and the examination need of the students. It has got 13 chapters. The first chapter is to address and explain the subject statistics, its usefulness and application with particular reference to biological/agricultural/animal/fishery/dairy and allied fields. A brief narration on statistics, highlighting its use, scope, steps in statistical procedure and limitations along with example, has been provided in Chap. 1. Main ingredient of statistics is the varied range of information or data; in second chapter, attempts have been made to explain different types of information/data from relevant fields. In this chapter, discussion has been made on collection, scrutinisation and presentation of data in different forms so as to have first-hand idea about the data. The third chapter deals with measures of central tendency and measures of dispersion along with

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skewness and kurtosis. Different measures of central tendencies and dispersion along with their uses, merits and demerits have been discussed. Measures of skewness and kurtosis have also been discussed. The theory of probability has been dealt in Chap. 4. Utmost care has been taken to present the theory of probability in its simplest form, starting from the set theory to the application of different laws of probability. Quite a good number of examples on probability theory and random variable are the special features of this chapter. A few discrete and continuous probability distributions like Binomial, Poisson, Normal, χ^2, t and F have been discussed in brief. Introductory ideas about population, types of population, sample, sampling techniques used under different situations, comparison of sample survey techniques and census have been discussed in Chap. 5. Statistical inference has been discussed in Chap. 6. Starting with the introduction of statistical inference, both statistical estimation and testing of hypothesis have been discussed in this chapter. Tests based on distributions mentioned in Chap. 4 have been discussed. Discussions on different non-parametric tests included in this chapter hope to find their applications in various agriculture and allied fields. These tests have been designed with an objective to cater the need of the students of agriculture/animal science/dairy/fishery and allied fields as per the syllabi of the Indian Council of Agricultural Research. Chapter 7 is devoted to the study of correlation. Starting with the idea of bivariate data, bivariate frequency distribution and covariance, this chapter has described the idea of simple correlation and its properties, significance and rank correlation. The idea of regression, need, estimation of parameters of both simple and multiple regression, meaning and interpretations of parameters, test of significance of the parameters, matrix approach of estimation of parameters, partitioning of total variance, coefficient of determination, game of maximization of R^2, adjusted R^2, significance test for R^2, problem of multicollinearity, regression vs. causality, part and partial correlation are discussed in Chap. 8. Discussion on properties and examples are the special features of the correlation and regression chapters. Starting with general idea, the analysis of variance technique has been discussed in Chap. 9. Extensive discussion has been made on assumptions, one-way analysis of variance (with equal and unequal observations), two-way analysis of variance (with one or more than one observations per cell), violation of the assumptions of ANOVA vis-a-vis transformation of data, effect of change in origin and scale on analysis of variance with worked-out examples. Chapter 10 is devoted to basics of experimental design and basic experimental designs. This chapter discusses on experiment, types of experiments, treatment, experimental unit, experimental reliability, precision, efficiency, principles of design of field experiments – replication, randomization, local control, lay out, uniformity trial and steps in designing field experiments. In this chapter, elaborate discussion has been made on completely randomized design, randomized block design and latin square design along with missing plot techniques.

Efforts have been made to explain the basic principles and procedures of factorial experiments in Chap. 11. Factorial experiments, their merits and demerits, types of factorial experiments, two factor factorial (symmetrical and asymmetrical) CRD, two factor factorial (symmetrical and

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asymmetrical) RBD, three factor factorial (symmetrical and asymmetrical) CRD, three factor factorial (symmetrical and asymmetrical) CRD, split plot and strip plot designs are discussed in this chapter. Some special types of experimental designs which are useful to the students, teachers, researchers and other users in agriculture and allied fields have been discussed in Chap. 12. In this chapter, attempt has been made to discuss on augmented CRD and RBD, augmented designs with single control treatment in factorial set up, analysis of combined experiments, analysis of data recoded over times and experiments at farmers fields. Computer has come in a great way to help the experimenter not only in analysis of experimental data but also in different ways. But there has been a tendency of using computer software without providing due consideration to 'what for', 'where to use', 'which tool is to use' and so on. In last chapter of this book, an attempt has been made, by taking example, to show how computer technology can be misused without having knowledge of appropriate statistical tools.

A great number of books and articles in different national and international journals have been consulted during preparation of this book which provided in reference section. An inquisitive reader will find more material from these references. The need of the students/teachers/researchers/practitioners in biological/agricultural/animal/fishery/dairy and allied fields remained the prime consideration during the preparation of this book.

I express my sincere gratitude to everyone who has helped during the preparation of the manuscripts for the book. The anonymous international reviewers who have critically examined the book proposal and put forwarded their valuable suggestions for improvement of the book need to be acknowledged from the core of my heart. My PhD research students, especially Mr Vishawajith K P, Ms Dhekale Bhagyasree, Md Noman, L Narsimaiah and others, who helped a lot during analysis of the examples based on real life data and need to be acknowledged. Taking the help of MSEXCELL, SPSS and SAS softwares various problems have been solved as examples in this book; the author gratefully acknowledges the same. My departmental colleagues and our teachers at BCKV always remained inspiration to such book projects, thanks to them. My sincere thanks to the team of Springer India in taking responsibility of publishing this book and continued monitoring during the publication process. Most importantly my family members, who have always remained constructive and inspirational for such projects need to be thanked; without their help and co-operation it would have not been possible to write such a book. All these will have a better success if this book is well accepted by the students, teachers, researchers and other users for whom this book is meant for. I have the strong conviction that like other books written by the author, this book will also be received by the readers and will be helpful to everyone. Sincere effort are there to make the book error free, however any omissions/mistake pointed out, along with constructive suggestions for improvement will be highly appreciated and acknowledged.

Mohanpur, India
26th January 2016

Pradip Kumar Sahu

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Introduction to Statistics and Biostatistics 1

1.1 Introduction

Knowingly or unknowingly, people use "statistics." In ancient days, people generally used the term statistics to understand the political state. German scholar Gottfried Achenwall most probably used the word "statistics." In any case, the word statistics is being used knowingly or unknowingly since time immemorial. The word statistics is being used in two different forms: (a) in *singular sense*, it is the body of science, which deals with principles, techniques, collections, scrutiny, analysis, and drawing inference on a subject of interest, and (b) in *plural sense*, it refers to *data*, i.e., presentations of facts and figures or information. Year-wise food grain production figures of different provinces of the United States of America may constitute a data set – food grain production statistics – whereas the problem of identifying, analyzing, and establishing the differences between two herds of cows to facilitate breeding improvement program may be the subject matter of the subject statistics. Given a set of data, one can explain it to some extent, but beyond a certain level, it becomes difficult to unearth the hidden information from the data. Data require analysis, theoretical, and computational treatment to speak for itself. Thus, the "subject statistics" is being used to "data statistics" to unearth the so long-hidden information in a set of data for the benefit of humanity.

Inquisitiveness is the mother of all inventions. Human instinct is to study, characterize, and explain the things which so long remained unknown or unexplained; in other words, to study population behavior, characterize it and explain it. In statistics, a *population is a collection of well-defined entities, i.e., individuals having common characteristics*. Often it becomes very difficult to study each and every individual/unit of the population, maybe because of time, resource, or feasibility constraints. In all these cases, the subject statistics plays additional role in characterizing population under consideration.

Statistical tools/methods applied to biological phenomenon are generally known as biostatistics. Biological phenomena are characterized by the resultant of interaction between the genetic architecture and the environmental factors under which lives exist. Thus, one must be careful in taking into consideration of all these factors while inferring about any biological phenomenon. So the understanding of the mechanism of existence of life and also the statistical methods required for specific real-life problem is of utmost importance to a biostatistician.

1.2 Use and Scope of Statistics

In every sphere of modern life, one can notice the application of statistics. In agriculture, fishery,

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veterinary, dairy, education, economics, business, management, medical, engineering, psychology, environment, space, and everywhere, one can find the application of statistics – both data and subject statistics. Not only in daily life, statistics has got multifarious roles in research concerning the abovementioned and other fields also.

1.3 Subject Matter of Statistics

Human instinct is to study the population – a group of entities/objects having common characteristics. In doing so, we are mostly interested in knowing the overall picture of the population under study, rather than a particular individual of the population. The subject matter of statistics is to study the population rather than the individual unit of the population. If the interest of study be the study of economic status of the fishermen of a particular country, then the study should be interested in getting the average income, the range of income, their average expenditure, average family structure, variation in income/expenditure, etc. of the population of the fishermen rather than attempting to the information of particular fisherman. Thus, statistics deals with aggregated information on a subject of interest in which there is a little scope for an individual item to be recognized.

The subject statistics plays a great role in situations particularly where there is little scope to study the whole population, i.e., it is difficult to study each and every element of the population toward explaining the population behavior. A population can be characterized by studying each and every element/unit of the population. As we know, a population may be finite (constituted of definite number of units) or infinite (constituted of indefinite number of units). Time and resource (money, personals, facilities, etc.) required to study the huge number of individual elements of the population may not be available. If available at all, by the time the information are unearthed, these might have lost relevance due to time lapse or otherwise. Sometimes, it may not be possible to have access to each and every element of the population. Let us take some examples. *Hilsa hilsa* is a famous fish for favorite dishes of a section of nonvegetarian people. Now the question is how to know the availability of the quantum of *hilsa* during a particular season in a particular country. It is very difficult to have an idea about the number of *hilsa* that would be available, their weights, etc. But the study has a number of impacts on food habit, business, and economy of the concerned area. Statistics plays a vital role in these situations. How to assess the possible food grain production of a particular country for assured food supply to its population? Taking information from each and every farmer after crop harvest and assessing the same may take considerable time and may come across with shortage of resources and feasibility problem. Both the statistics, singular (subject) and plural (data), play important role.

In most of the cases, a part of the population (sample) is studied and characterized, and inference(s) is/are drawn about that part (sample), in the first step. And in the next step, statistical theories are applied on sample information to judge how far the sample information are applicable for the whole population of interest or otherwise. All the above are accomplished following different steps. In the following section, we shall see the different steps in statistical procedure for the practitioners/users; but one thing should be kept in mind, that neither the steps are exhaustive nor every step is essential and in order. Depending upon the problem, steps and order may change.

1.4 Steps in Statistical Procedure

Data are one of the basic inputs on which statistical theories are applied to make these informative or which otherwise remain hidden. The subject statistics starts with the formation of objective and proceeds to planning for collection of data, care of data, scrutinization and summarization of data, application of statistical theories and rules, and lastly drawing inference.

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(a) *Objective and planning*: At the first outset, an investigator should clearly delineate the objective of the problem encountered. Well-defined objectives are the foundations for proper planning and application of different statistical procedures so as to make the data more informative and conclusive. Depending upon the objective of the study, data needed, type of data needed, source of data, etc. are guided. For example, if one wants to have a comparison on the average performance of different newly developed breeds of milch cows for milk production, he/she has to plan for an experiment from which the information on the performance of these breeds can be compared under identical situations. Similarly, if one wants to compare the economic conditions of the people of different agroecological zones of a country, he/she has to plan for collection of data either from primary or secondary sources. In order to study the growth and yield behavior of different varieties of a particular crop, one needs to set up experiments in such away so as to generate required data to fulfill the objectives. Thus, depending upon the objective of the study, the procedure of collection of information will have to be fixed.

(b) *Collection of data*: Having fixed the objectives, the next task is to collect or collate the relevant data. Data can be collated from the existing sources, or these can be generated from experiments conducted for the purpose adopting (i) complete enumeration and (ii) sampling technique. In complete enumeration technique (census), data are collected from each and every individual unit of the targeted population. As has already been pointed out, in many situations, it may not be possible or feasible (because of time, financial, accessibility, or other constraints) to study each and every individual element of interest, resulting in the selection of a representative part (sample) of the study objects (population) using appropriate sampling technique. For the purpose, a sampling frame is needed to be worked out (discussed in Chap. 5) befitting to the data requirement and nature of the population. Data collection/collation should be made holistically with utmost sincerity and always keeping in mind the objectives for which these are being collected/collated.

(c) *Scrutinization of data*: Once the data are collected, these need to be checked for correctness at the first instance. In a study dealing with the yield potentials of different wheat varieties, if records show an observation 90 t/ha yield under the northern plains of India, one has to check for the particular data point for its correctness. Thus, data sets collected (raw data) should be put under rigorous checking before these are subjected to further presentation or analysis.

(d) *Tabulation of data*: Upon collection/collation of the data following a definite procedure of collection/collation from the population, having specific objectives in mind, and on being scrutinized, it is required to be processed in such a way that it gives a firsthand information at a glance about the data collected. Thus, for example, the following data are collected about the acreages (in '000 ha) of wheat for different wheat-growing provinces in India during the period 2011–2012 from the Directorate of Wheat Research in India: AP 8, Assam 53, Bihar 2142, Chhattisgarh 109, Gujarat 1351, Haryana 2522, HP 357, J&K 296, Jharkhand 159, Karnataka 225, MP 4889, Maharashtra 843, Odisha 1.46, Punjab 3528, Rajasthan 2935, UP 9731, Uttarakhand 369, WB 316, and others 92, with a total for the whole of India 29,865. One can hardly get a comprehensive picture. For getting a firsthand idea, this data can be presented in tabular form as given below:

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States	AP	Assam	Bihar	Chhattisgarh	Gujarat	Haryana	HP	J&K	Jharkhand	Karnataka
Area ('000 ha)	8	53	2142	109	1351	2522	357	296	159	225
States	MP	Maharashtra	Odisha	Punjab	Rajasthan	UP	Uttarakhand	WB	Others	India
Area ('000 ha)	4889	843	1.46	3528	2935	9731	369	316	92	29,865

From data collated on areas under wheat in different states of India, if presented in tabular form, one can have better idea than the previous one. The above presentation can be modified or made in an order as follows:

States	Odisha	AP	Assam	Others	Chhattisgarh	Jharkhand	Karnataka	J&K	WB	HP
Area ('000 ha)	1.46	8	53	92	109	159	225	296	316	357
States	Uttarakhand	Maharashtra	Gujarat	Bihar	Haryana	Rajasthan	Punjab	MP	UP	India
Area ('000 ha)	369	843	1351	2142	2522	2935	3528	4889	9731	29,865

Now, the investigator is far better placed to explain wheat acreage scenario in India; it is possible to get the states having minimum and maximum area under wheat and also the relative position of the states. Explanatory power of the investigator is increased. Thus, tabulation process also helps in getting insight into the data. Data may also be processed or presented in different forms to obtain firsthand information, and these are discussed in details in Chap. 2.

(e) *Statistical treatment on collected data*: Different statistical measures/tools are now applied on the data thus generated, scrutinized, and processed/tabulated to extract or to answer the queries fixed in step (a), i.e., objective of the study. Data are subjected to different statistical tools/techniques to get various statistical measures of central tendency, measures of dispersion, association, probability distribution, testing of hypothesis, modeling, and other analyses so as to answer the queries or to fulfill the objectives of the study.

(f) *Inference*: Based on the results as revealed from the analysis of data, statistical implications vis-à-vis practical inferences are drawn about the objectives of the study framed earlier. Though data used may be pertaining to sample(s), through the use of statistical theories, conclusions, in most of the cases, are drawn about the population from which the samples have been drawn.

With the help of the following example, let us try to have a glimpse of the steps involved in statistical procedure. *The procedure and steps followed here are neither unique nor exhaustive and may be adjusted according to the situation, objective, etc. of the study.*

Example 1.1 In an Indian village, Jersey cows (an exotic breed) have been introduced and acclimatized. An investigator wants to test whether the milk yield performance of the cows are as expected or not. It is believed that Jersey cows generally yield 3000 kg of milk per lactation.

(a) *Objective*: To find out whether the average milk production of acclimatized Jersey cows is 3000 kg/lactation or not.
The whole problem can be accomplished with the help of the following specific steps:
  (i) To determine or estimate the average milk production
  (ii) To find the interval for the average milk at a given probability level

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(iii) To test whether the population average $\mu = 3000$kg or not, with respect to milk production per lactation

(b) *Planning and collection of data*: In order to have proper execution of the study to fulfill the objectives, one needs to have idea about the population under study, resources available for the study, and also the acquaintance of the investigator with appropriate statistical tools.

Here the population is the Jersey milch cows in a particular village. Thus, the population is finite, and the number of units in the population may be obtained. If resources, viz., time, manpower, money, etc. are sufficiently available, then one can go for studying each and every cow of the village. But it may not be possible under the limited resource condition. So one can go for drawing sample of cows following appropriate sampling technique (discussed in Chap. 5) and calculate the average milk production per lactation. In the next step, a confidence interval may be set up and tested for equality of sample average with population-assumed average.

(c) *Collection of data*: Let us suppose one has drawn a sample of 100 Jersey cows following simple random sampling without replacement and the following yields in kilograms are recorded.

2490	3265	2973	3135	3120	3184	3029
2495	3268	2978	3115	2750	2960	3225
2505	3269	2979	3117	3140	3149	3016
3232	2510	2995	3139	3131	3146	3014
2525	3032	3015	3135	3127	3155	3047
2520	3245	3017	3137	2950	3159	3125
3262	2525	3012	3118	3142	3250	3028
2527	3274	3011	3137	3151	3172	3200
2501	3256	3010	3128	3161	3155	3016
2607	3145	3006	3139	3143	3135	3045
2510	3278	3039	3140	3050	3144	
2813	3285	3015	3135	3098	2960	
2514	3291	2995	3118	3087	3122	
2470	3050	3006	3136	3089	2890	
2480	3221	3025	3108	3090	3132	

From the above, one can hardly get any idea about the data and the distribution of amount of milk per lactation for Jersey cows in the village concerned. For the purpose, one can arrange the data either in ascending or descending order and also check for validity of the data points, i.e., scrutinization of data. Let us arrange the above data in ascending order.

(d) *Processing and scrutiny of data:*

2470	2750	3011	3047	3125	3140	3184	2495
2480	2813	3012	3050	3127	3140	3200	3221
2490	2890	3014	3050	3128	3142	3290	
3285	2950	3015	3087	3131	3143	3225	
2501	2960	3015	3089	3132	3144	3232	
2505	2960	3016	3090	3135	3145	3245	
2510	2973	3016	3098	3135	3146	3250	
2510	2978	3017	3108	3135	3149	3256	
2514	2979	3025	3115	3135	3151	3262	
2520	2995	3028	3117	3136	3155	3265	
2525	2995	3029	3118	3137	3155	3268	
2525	3006	3032	3118	3137	3159	3269	
2527	3006	3039	3120	3139	3161	3274	
2607	3010	3045	3122	3139	3172	3278	

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(i) From the above table, one can have an idea that the milk yield per cow per lactation ranges between 2477 and 3291 kg. Also, none of the data point is found to be doubtful.

(ii) Same amounts of milk per lactation are provided by more than one cow in many cases. Thus, depending upon the amount of milk produced, 100 Jersey cows can be arranged into the following tabular form:

Milk yield	No. of cows	Milk yield	No. of cows	Milk yield	No. of cows	Milk yield	No. of cows	Milk yield	No. of cows	Milk yield	No. of cows
2470	1	2890	1	3017	1	3115	1	3140	2	3221	1
2480	1	2950	1	3025	1	3117	1	3142	1	3225	1
2490	1	2960	2	3028	1	3118	2	3143	1	3232	1
2495	1	2973	1	3029	1	3120	1	3144	1	3245	1
2501	1	2978	1	3032	1	3122	1	3145	1	3250	1
2505	1	2979	1	3039	1	3125	1	3146	1	3256	1
2510	2	2995	2	3045	1	3127	1	3149	1	3262	1
2514	1	3006	2	3047	1	3128	1	3151	1	3265	1
2520	1	3010	1	3050	2	3131	1	3155	2	3268	1
2525	2	3011	1	3087	1	3132	1	3159	1	3269	1
2527	1	3012	1	3089	1	3135	4	3161	1	3274	1
2607	1	3014	1	3090	1	3136	1	3172	1	3278	1
2750	1	3015	2	3098	1	3137	2	3184	1	3285	1
2813	1	3016	2	3108	1	3139	2	3200	1	3290	1

From the above table, one can have the idea that most of the cows have different yields, whereas two cows each have produced 2510 and 2525 kg of milk and so on. A maximum of four cows have produced the same 3135 kg of milk each.

To have a more in-depth idea and to facilitate further statistical treatments/calculations, one can form a frequency distribution table placing 100 cows in 10 different classes:

Frequency distribution	
Class	No. of cows
2470–2552	13
2552–2634	1
2634–2716	0
2716–2798	1
2798–2880	1
2880–2962	4
2962–3044	21
3044–3126	16
3126–3208	29
3208–3290	14

Details of formation of frequency distribution table are discussed in Chap. 2.

(e) *Application of statistical tools*: From the above frequency distribution table, one can work out different measures of central tendency, dispersion, etc. (discussed in Chap. 3). To fulfill the objectives, one needs to calculate arithmetic mean and standard deviation from the sample observations.

Frequency distribution					
Class		Mid-value (x)	Frequency (f)	$f.x$	$f.x^2$
2470	2552	2511	13	32,643	81,966,573
2552	2634	2593	1	2593	6,723,649
2634	2716	2675	0	0	0
2716	2798	2757	1	2757	7,601,049
2798	2880	2839	1	2839	8,059,921
2880	2962	2921	4	11,684	34,128,964
2962	3044	3003	21	63,063	189,378,189
3044	3126	3085	16	49,360	152,275,600
3126	3208	3167	29	91,843	290,866,781
3208	3290	3249	14	45,486	147,784,014
Total			100	302,268	918,784,740

Now we use the formulae for arithmetic mean and standard deviation, respectively, as

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$$\bar{x} = \frac{1}{\sum_{i=1}^{n} f_i} \sum_{i=1}^{n} f_i x_i = \frac{1}{\sum_{i=1}^{8} f_i} \sum_{i=1}^{8} f_i x_i$$
$$= \frac{1}{100} 302268 = 3022.7\,\text{Kg}$$

and

$$S_x = \sqrt{\frac{1}{\sum_{i=1}^{n} f_i} \sum_{i=1}^{n} f_i x_i^2 - \bar{x}^2}$$
$$= \sqrt{\frac{1}{\sum_{i=1}^{8} f_i} \sum_{i=1}^{8} f_i x_i^2 - \bar{x}^2}$$
$$= \sqrt{\frac{1}{100} 918784740 - (3022.7)^2}$$
$$= 226.39\,\text{Kg}$$

Interval Estimation The interval in which the true value of the population mean (i.e., average milk production) is expected to lie is given by

$$P\left[\bar{x} - t_{\alpha/2,n-1}\frac{s}{\sqrt{n}} < \mu < \bar{x} + t_{\alpha/2,n-1}\frac{s}{\sqrt{n}}\right] = 1 - \alpha$$

Hence, the confidence interval for average milk production at 5 % level of significance is

$$\left[3022.7 - 1.98 \times \frac{226.39}{10} < \mu < 3022.7 + 1.98 \times \frac{226.39}{10}\right] = [2977.87 < \mu < 3067.52]$$

where $t_{\alpha/2,n-1}$ and $t_{1-\alpha/2,n-1}$ are, respectively, the upper and lower $\frac{\alpha}{2}$ points of t-distribution with $(n-1)$ d.f.

Thus, the average milk production of Jersey cows, as evident from data for 100 cows, is expected to be between 2978 and 3068 kg per lactation.

Testing of Hypothesis For the above problem, the null hypothesis is H_0 $\mu = 3000$kg against H_1 $\mu \neq 3000$ kg, where μ is the population mean, i.e., average milk produced per lactation.

The test statistics is $Z = \frac{\bar{x}-\mu_0}{s/\sqrt{n}}$ where n is the sample size (100). Z follows a standard normal distribution.

The calculated value of $Z = \frac{3022.7-3000}{226.39/10} = \frac{22.7}{22.64} = 1.002$

From the normal probability table and for two-tailed (both-sided) test, the critical values of Z are 1.96 (at $\alpha = 0.05$) and 2.576 (at $\alpha = 0.01$), respectively. For the above problem, $|Z| < 1.96$. So we cannot reject the null hypothesis at 5 % level of significance.

(f) *Conclusion*: We conclude that average milk production of Jersey cows in the studied village can be taken as 3000 kg per lactation with range of 2978 to 3068 kg. That means the performance of the Jersey cows is in the tune of the expectation.

The above problem is nothing but an example to sketch the steps involved in statistical procedures but not a unique one. Depending upon the nature of the problem, appropriate steps are followed.

1.5 Limitation of Statistics

In spite of its tremendous importance and huge applicability, statistics is also not free from limitations. One should be well aware about the limitations, applicability, and suitability of statistical tools before a particular tool is being put to use for drawing inference.

(i) As has been mentioned, one of the ingredients of statistics is data/information. A well-framed objective associated with carelessly framed experiment followed by bad quality of data may lead to bias or worthless conclusion irrespective of the use of appropriate sophisticated statistical tools. On the contrary, in spite of having a good quality of data, unacceptable or useless conclusions are drawn because of the use of incompetent/inadequate/inappropriate statistical tools. Thus, for efficient use

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of statistics for the betterment of humanity, there should be an organic linkage between the objective of the study and the knowledge of statistics. A user should have acquaintance with the subject statistics up to a reasonable level; if not, consultation with a statistician is required. At the same time, the statistician should have some sorts of acquaintance about the field of study under consideration. Under this situation, only a meaningful extraction of the hidden truth could be possible.

(ii) Statistics deals with totality of the population; it is least interested in providing an explanation why an individual member of the population is performing exceedingly good or bad. Statistics deals with population rather than individual.

(iii) Statistical laws or rules are not exact in the sense that statistical inferences are in terms of probability or chances. To each and every conclusion, based on statistical analysis, a chance (probability) factor is associated.

(iv) Statistics can be used to draw inferences as per the choice of the users. Showing a piece of broken chalk, one can say "three fourths of a chalk" or "a one fourth exhausted chalk." Eighty percent of the people who take alcohol regularly suffer from liver problem. Apparently, this statement seems to be true. But this is partly true because one does not know the percentage of people suffering from liver problem who do not take alcohol or one does not know the percentage of alcohol takers in the population. It depends upon the choice of the user how he/she is going to use statistics. It has rightly been said that statistics is like a molded clay one can make devil or God out of it.

(v) Because of reasons stated above, there is every possibility that statistics is being misused. Computers have made the use of sophisticated statistics more easy vis-à-vis its increased acceptability and interest and at the same time has created tremendous problem in the form of misuse of statistics. Without providing due importance, reasons and area of applicability for statistical tools, these are being used indiscriminately to draw inferences with the help of computer programs. Knowledge of subject statistics and also the subject where the statistical theories are to be used and also the particular program among different options, to be used in solving a particular problem, are essential for the best use.

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Data–Information and Its Presentation 2

2.1 Data

While making curry, one needs to have vegetables, spices, and methodology for preparation of particular curry. Using the same ingredient, rice, vegetables, butter and oil, spices etc., one can make *veg-rice* or *veg fried rice*, *byriani*, or other preparation like *pulao*, *chitranna*, etc., depending upon the method used and the intention of the cook. Similarly, for explaining a phenomenon through the extraction of otherwise hidden information from it, one needs to have data. Statistical theories/tools are applied on data to make these informative and hence extraction of information toward explaining a phenomenon under consideration. Thus, the ingredient of statistics is data. Data are known/generated things/facts/figures from which conclusive information are attempted to be drawn. Data requires to be analyzed so that it becomes more and more informative. Data can be obtained from hearsay to results from well-defined and designed research program or investigation. To have objective decision on any phenomenon, it must be based on unbiased and reliable data/information. *Reliability of data generally refers to the quality of data that can be documented, evaluated, and believed*. If any of these factors is missing, the reliability vis-à-vis the confidence in decision making is reduced. *A good quality data should have quantitative accuracy and should be representative, complete, and comparable*; all these can be checked only through peer reviewing. Data can be categorized into different groups/types depending upon its source, type, etc.

2.1.1. Data can be classified into *natural* or *experimental*. Natural data are found to occur in nature. On the other hand, experimental data are obtained through well-planned and designed experiments to fulfill the specific objectives the experimenter has in his or her mind.

2.1.2. Data can be *primary* or *secondary* depending upon the source of its collection/generation or collation. *Primary data are generated by the investigator/experimenter through a well-planned program for specific purpose*. Primary data may be obtained through survey or conduction of field experiments etc. Thus, primary data are generated by the user for specific purpose. Example of primary data may be the data collected on egg-laying capacity of particular poultry breed under particular management practice from different growers in particular area. Example of primary data may be the yield data obtained for five different varieties of rice following specific management practice under experimental setup with an objective to compare the average performance of the varieties under given condition. On the other hand, *secondary data*

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are those data used by the experimenter or user, which are collated from other sources. For example, weather data are recorded by the department of meteorology, one of their primary objectives or mandates; but many agencies like the airport authority, agriculture department, disaster management department, and the experimenters/researchers in biological sciences use these weather data collating from the meteorology department in order to explain more meaningful way the phenomenon under their considerations. Thus, weather data, market data, etc. are used by various users but are generated/recorded by specific agencies. As such, weather data, market data, etc. are primary data to the department concerned which is involved in generating or recording these data as one of their primary responsibilities, but when these data are used by other agencies/experimenters, these become secondary to the users. Data generated by different national and international agencies like the Central Statistics Organization (CSO), National Sample Survey Office (NSSO), State Planning Board (SPB), Food and Agriculture Organization (FAO), World Health Organization (WHO), etc. are used by various researchers or users; to the users these data are secondary data. Secondary data are required to pass through rigorous reviewing for its methodology of collection, correctness, etc. before these are put to use by the users.

2.1.3. Data can be *cross-sectional data* or *time series data*. A set of observations recorded on a particular phenomenon at a particular time frame is termed as *cross-sectional data*. Milk production of different states/provinces of a country during the year 2012–2013, the market prices of poultry eggs at different markets of a county during 2012–2013, inland fish production of different countries at a particular time frame constitute cross-sectional data. On the other hand, when the data are recorded on a particular phenomenon over different periods, then it becomes *time series data*. Milk production or inland fish production of country over the period 2001–2013 constitutes time series data. Thus, cross-sectional data generally have spatial variation at a particular period, whereas time series data have got variation over time. A time series data may be constituted of secular trend, cyclical, seasonal, and irregular components. Overall movement of the time series data is known as secular trend. Periodic movement of the time series data, with period of movement being more than a year, is known as cyclical component, whereas periodic movement of the time series data, with period of movement being less than a year, is known as seasonal component. Portion of the time series data which cannot be ascribed to any of the above three movements is termed as irregular component. Detailed discussion on time series data is left out; an inquisitive reader may consult *Agriculture and Applied Statistics – II* by this author.

In Table 2.1, data pertaining to production of milk is a cross-sectional data as it relates to production figures of different states at a particular point of time, i.e., the year 2011–2012. On the other hand, the information given in table B, C, and D are time series data because in all the cases, the figures relate to realization of the variables "capture fisher production," "population of cattle," and "milk production" at different points of time, arranged chronologically.

2.1.4. A special type of data, combination of both cross-sectional and time series data with the introduction of multiple dimensions, is known as *panel data*. Panel data consist of observations of multiple phenomena/characters at different time periods over the same elements/individuals, etc. It is also known as

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Table 2.1 Cross-sectional and time series data

A. Cross-sectional data

Estimated state-wise milk production (million tones) in India during 2011–2012

State	Production	State	Production
AP	12,088	Manipur	79
Arunachal	22	Meghalaya	80
Assam	796	Mizoram	14
Bihar	6643	Nagaland	78
Goa	60	Orissa	1721
Gujarat	9817	Punjab	9551
Haryana	6661	Rajasthan	13,512
HP	1120	Sikkim	45
J&K	1614	TN	5968
Karnataka	5447	Tripura	111
Kerala	2716	UP	22,556
MP	8149	WB	4672
Maharashtra	8469	India	127,904

B. Time series data

World inland capture fishery production

Year	Production (million tonnes)
2006	9.8
2007	10
2008	10.2
2009	10.4
2010	11.2
2011	11.5

Source: The State of World Fisheries and Aquaculture, FAO-2012

C. Time series data

Year-wise cattle population (million) in India

Year	Cattle
1951	155.3
1956	158.7
1961	175.6
1966	176.2
1972	178.3
1977	180.0
1982	192.5
1987	199.7
1992	204.6
1997	198.9
2003	185.2

D. Time series data

Year-wise milk production (million tonnes) in India

Year	Production	Year	Production
1991–1992	55.6	2001–2002	84.4
1992–1993	58.0	2002–2003	86.2
1993–1994	60.6	2003–2004	88.1
1994–1995	63.8	2004–2005	92.5
1995–1996	66.2	2005–2006	97.1
1996–1997	69.1	2006–2007	102.6
1997–1998	72.1	2007–2008	107.9
1998–1999	75.4	2008–2009	112.2
1999–2000	78.3	2009–2010	116.4
2000–2001	80.6	2010–2011	121.8

Source: National Dairy Development Board

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Table 2.2 Panel data

Year	State	Milk production	[a]AI('000 nos.)
2007–2008	AP	8925	3982
	Arunachal	32	1
	Assam	752	144
	Bihar	5783	251
2008–2009	AP	9570	4780
	Arunachal	24	1
	Assam	753	134
	Bihar	5934	514
2009–2010	AP	10,429	5039
	Arunachal	26	1
	Assam	756	204
	Bihar	6124	950
2010–2011	AP	11,203	5183
	Arunachal	28	2
	Assam	790	204
	Bihar	6517	1948

Source: National Dairy Development Board, India, 2013
[a]AI – artificial insemination

longitudinal data in biostatistics. Example of panel data may be the state-wise milk production and artificial insemination data of different states in India as given in (Table 2.2).

2.2 Character

Data are collected/collated for different characteristics of the elements of the population/sample under consideration. Characters can broadly be categorized into (a) *qualitative character* and (b) *quantitative character*. Religion (viz., Hindu, Muslim, Christian, Jains, Buddhist, etc.), gender (male/female, boys/girls), color (viz., violet, indigo, blue, red, green, etc.), and complexion (bad, good, fair, etc.) are the examples of qualitative character. Thus, characters which cannot be quantified exactly but can be categorized/grouped/ranked are known as qualitative characters. Qualitative characters are also known as *attributes*. On the contrary, characters which can be quantified and measured are known as quantitative characters. Examples of quantitative characters are height, weight, age, income, expenditure, production, disease severity, percent disease index, etc.

2.3 Variable and Constant

Values of the characters (physical quantities) generally vary over situations (viz., over individuals, time, space, etc.); but there are certain physical quantities which do not vary, i.e., which do not change their values over situations. Thus, characters (physical quantities) may be categorized into *variable* and *constant*. *A constant is a physical quantity which does not vary over situations*. For example, universal gravitational constant (G), acceleration due to gravity (g), etc. are well-known constants. Again, in spite of being a constant, the value of the acceleration due to gravity on the surface of the earth, on the top of a mountain, or on the surface of the moon is not same. The value of acceleration due to gravity is restricted for a particular situation; as such constant like acceleration due to gravity is termed as *restricted constant*. Whereas, constants like universal gravitational constant, Avogadro's number, etc. always remain constant under any situation; as such these are termed as *unrestricted constant*.

We have already defined that a character (physical quantity) which varies over individual, time, space, etc. is known as variable; milk production varies between the breeds, egg-laying

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capacity of chicks varies over the breeds, length and weights of fishes vary over species, ages, etc. Thus, milk production, number of eggs laid by chicks, length of fishes, weights of fishes, etc. are examples of variable. There are certain variables like length, height, etc. which can take any value within a given range; these variables are known as *continuous* variable. On the other hand, variables like number of eggs laid by a chick, number of insects per plant or number of parasites per cattle, number of calves per cattle, etc. can take only the integer values within a given ranges; these variables are called *discrete* variables. If we say that per day milk production of Jersey cows varies between 8 and 10 kg under Indian condition, that means if one records milk production from any Jersey cow under Indian condition, its value will lie between 8 and 10 kg; it can be 8.750 or 9.256 kg or any value within the given range. That is why milk production per day is a continuous variable. Let us suppose that while netting in a pond, the number of fish catch per netting varies between 6 and 78. This means in any netting, one can expect any whole number of fishes between 6 and 78. The number of fishes in netting cannot be a fraction; it should always be whole number within the range. Thus, the number of fishes per net, number of insects per plant, number of calves per cattle, etc. are the examples of discrete variable.

We have already come to know that statistics is a mathematical science associated with uncertainty. Now only we have discussed that values of the variable vary over the situations. If we take into account both uncertainty and possible values of the variable under different situations, then we come across with the idea of *variate*; there are chances in realizing each and every value or range of value of a particular variable. That means a chance factor is associated with each and every variable and realization of its different values or range of values. Thus, the variable *associated with chance factor is known as the variate,* and in statistics we are more concerned about the variate instead of the variable.

2.4 Processing of Data

What firsthand information/data the user gets, either through primary sources or secondary sources, are known as raw data. Raw data hardly speaks anything about the data quality and or information contained in it. In order to judge its suitability/correctness, it must go through a series of steps outlined below. Data collected or collated at the initial stage must be arranged. Let us take the example of weights of 60 broiler poultry birds at the age of 50 days recorded through a primary survey as given in Table 2.3.

Table 2.3 Weights of 60 poultry birds

Bird no.	Weight (g)	Bird no.	Weight (g)	Bird no.	Weight (g)	Bird no.	Weight (g)
1	1703	16	1726	31	1640	46	1124
2	1823	17	1850	32	1682	47	1438
3	2235	18	2124	33	1476	48	1476
4	2433	19	1823	34	2124	49	1593
5	2434	20	1682	35	1573	50	1341
6	2177	21	1300	36	1300	51	1476
7	2446	22	2399	37	2047	52	2434
8	2520	23	1573	38	1438	53	2508
9	1915	24	1213	39	1865	54	2124
10	1713	25	1865	40	1213	55	1444
11	2124	26	1788	41	1976	56	1924
12	2054	27	2124	42	1300	57	1405
13	1847	28	1823	43	1439	58	2434
14	2205	29	2434	44	1300	59	2124
15	1183	30	1682	45	1442	60	2398

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It is very difficult either to scrutinize the data or to have any idea about the data from the above table. Data requires to be sorted in order. In Table 2.2 raw data are sorted in ascending order. From Table 2.4 one can easily get idea about some aspects of the data set. Following observations can be made from the above table: (a) weights of broiler chicks vary between 1124 and 2520 g and (b) values are consistent with the knowledge that means no broiler weight is found to be doubtful. Hence further presentation and analysis can be made taking this information (Table 2.4).

Arrangement of Data

From this data we can either comment on how many birds are there having average weight, weights below average, weights above average, etc. It is also found that some birds have registered identical weights; we need to be concise with these information. So one makes a frequency distribution table on the basis of the bird weight. *Frequency is defined as the number of occurrence of a particular value in a set of given data*, i.e., how many times a particular value is repeated in the given set of data (Table 2.5).

Table 2.4 Sorted weights of 60 poultry birds

Bird no	Weight (gm)	Bird no	Weight (gm)	Bird no	Weight (gm)	Bird no	Weight (gm)
46	1124	33	1476	19	1823	54	2124
15	1183	48	1476	28	1823	59	2124
24	1213	51	1476	13	1847	6	2177
40	1213	23	1573	17	1850	14	2205
21	1300	35	1573	25	1865	3	2235
36	1300	49	1593	39	1865	60	2398
42	1300	31	1640	9	1915	22	2399
44	1300	20	1682	56	1924	4	2433
50	1341	30	1682	41	1976	5	2434
57	1405	32	1682	37	2047	29	2434
38	1438	1	1703	12	2054	52	2434
47	1438	10	1713	11	2124	58	2434
43	1439	16	1726	18	2124	7	2446
45	1442	26	1788	27	2124	53	2508
55	1444	2	1823	34	2124	8	2520

Table 2.5 Frequency distribution of body weights of 60 poultry birds

Weight (g)	Frequency	Weight (g)	Frequency	Weight (g)	Frequency
1124	1	1640	1	2047	1
1183	1	1682	3	2054	1
1213	2	1703	1	2124	6
1300	4	1713	1	2177	1
1341	1	1726	1	2205	1
1405	1	1788	1	2235	1
1438	2	1823	3	2398	1
1439	1	1847	1	2399	1
1442	1	1850	1	2433	1
1444	1	1865	2	2434	4
1476	3	1915	1	2446	1
1573	2	1924	1	2508	1
1593	1	1976	1	2520	1

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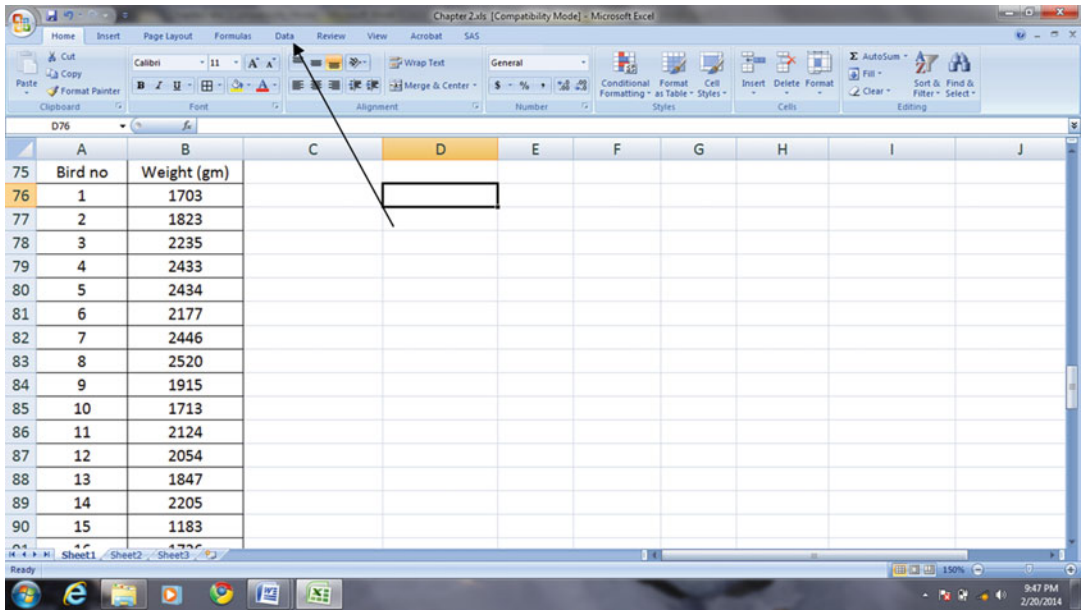
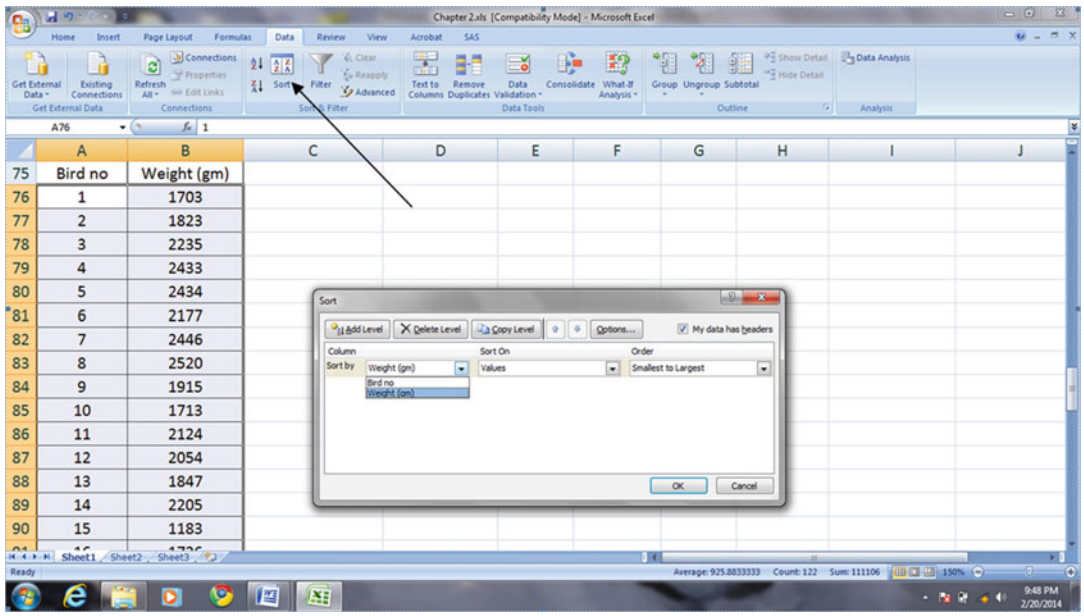
With the help of the MS Excel, one can perform the same using the steps mentioned in following slides (Slides 2.1, 2.2, 2.3, and 2.4).

As because we are dealing with only 60 data points (observations), it is relatively easy to understand the data characters. But when dealing with a huge number of data points, then we are to think for further processing of data. So the next objective will be to study the feasibility of forming groups/classes of elements (birds) which are more or less homogeneous in nature with respect to body weight.



Slide 2.1 Data entered in the Excel sheet



Slide 2.2 Data selected for sorting on the basis of weight, from smallest to largest

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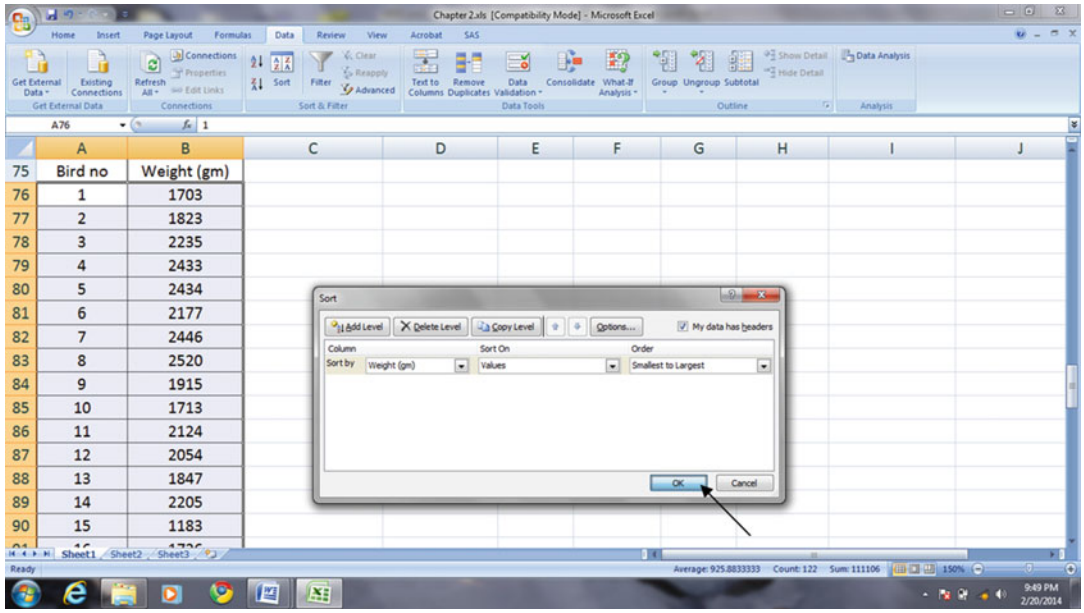
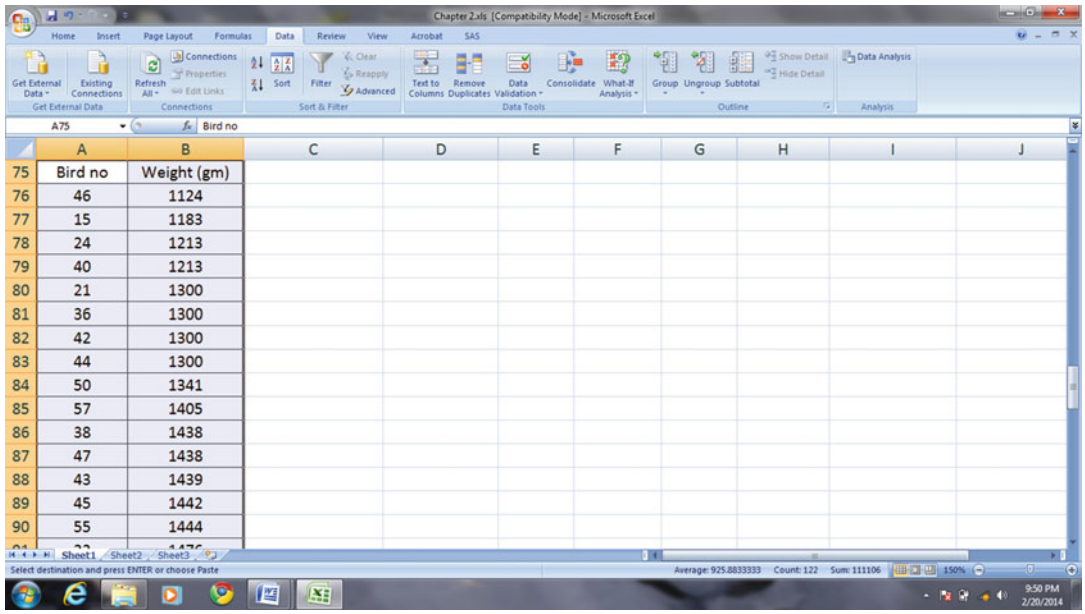


	A	B
75	Bird no	Weight (gm)
76	1	1703
77	2	1823
78	3	2235
79	4	2433
80	5	2434
81	6	2177
82	7	2446
83	8	2520
84	9	1915
85	10	1713
86	11	2124
87	12	2054
88	13	1847
89	14	2205
90	15	1183

Slide 2.3 Instruction to sort the data set



	A	B
75	Bird no	Weight (gm)
76	46	1124
77	15	1183
78	24	1213
79	40	1213
80	21	1300
81	36	1300
82	42	1300
83	44	1300
84	50	1341
85	57	1405
86	38	1438
87	47	1438
88	43	1439
89	45	1442
90	55	1444

Slide 2.4 Data sorted on the basis of body weight from smallest to largest

2.5 Classification/Grouping

Classification refers to grouping of large number of observations into relatively fewer groups so that an instant idea is obtained seeing the groups. The first question in classification that comes into mind is how many classes one should form. The guideline for the formation of classes is that within group variability should be minimum and between groups variability should be

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maximum. Problem is how to know under which classification the above guideline is obeyed! One has to go for trial and error method, which has got its own limitations. However, a good classification or grouping should have the following features:

(i) Classes should be well defined and exhaustive.
(ii) Classes should not be overlapping.
(iii) Classes should be of equal width as far as possible.
(iv) Number of classes should not be too few or too many.
(v) Classes should be devoid of open-ended limit.
(vi) Classes should be framed in such a way that each and every class should have some observation.

There are two rules to guide in fixing the number of classes, viz., *Yule formula* and *Sturges formula*. Fortunately both the methods yield almost similar number of classes for a given set of observations. According to Yule, $k = 2.5 \times n^{1/4}$, *and* the formula given by Sturges for the same purpose is $k = 1 + 3.322 \log_{10} n$, where n is the number of observations and k is the number of classes.

Let us take the example of weights of 60 broiler poultry birds at the age of 50 days as obtained from a primary survey and as given in Table 2.3. There are number of sixty birds, which are required to be grouped into suitable number of groups abiding the above guideline. According to Yule formula, the number of classes comes out to be $2.5 \times (60)^{1/4} = 6.96 \sim 7.00$, and due to Sturges formula it is $1 + 3.322 \log_{10} 60 = 6.91 \sim 7.00$. Thus, one can go for formation of 7 classes with 60 observations. The lowest value is 1124 and the highest value is 2520; hence, the range 2520–1124 = 1396 is to be distributed over seven classes; thereby making the class interval 199.43. It is advisable to make the class interval a round figure (whole number) instead of compound fraction. Thus, in this case one can take class interval as 200 and adjust the lowest and highest values of the data set accordingly as given below:

1119–1319
1320–1520
1521–1721
1722–1922
1923–2123
2124–2324
2325–2525

One can see that adjustment has been made on both the ends of the data set. So we are having seven classes with class width 200 in every case: 1119, 1320, 1521, 1722, 1923, 2124, and 2325 are the *lower class limits* and 1319, 1520, 1721, 1922, 2123, 2324, and 2525 are the *upper class limits*, respectively, for respective classes. One can find that though weights of chicks are a continuous character, during classification we have not considered the continuity, as one can find the gap of one gram between the upper limit of any class and the lower limit of the subsequent class. In doing so we invite two problems: (a) if any chick is found to have body weight in between upper limit of a class and the lower limit of the following class, say 1520.5 g, then there is no way to include the same in the present classification; (b) different measures like average weight, median weight, etc. may not come out to be whole number. As such, depending upon the nature of the character (discrete/continuous), data are advised to be presented in continuous form, so that each and every data point within the given range, irrespective of its value, gets a unique class. This is done by subtracting $d/2$ from the lower class limit of any class and adding "$d/2$" to the upper class limit, where "d" is the difference between the upper limit of any class and the lower limit of the following class; in this case $d = 1$, and thus constructed class limits are known as *lower class boundary* and *upper class boundary*, respectively, in the case of continuous distribution. Class width is defined as the difference between the upper boundary and the lower boundary of the respective class, and mid value of the class is defined as the average of the two boundaries. Readers may note that there is

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no change in the mid values of different classes with the change of classes from discrete to continuous. Now, with the help of these classes, let us frame the following frequency distribution table (Table 2.6).

2.5.1 Method of Classification

Once after forming continuous classes, we come across with typical problem of allocation of items in different classes. For example, if any value is there like 1319.5, then in which class, class one (1118.5–1319.5) or class two (1319.5–1520.5), should the observation be included? When both the lower boundary and upper boundary of a particular class are included in the class, it is known as *inclusive* method of classification, while in other method, one of the limits is excluded from the respective class and the method is known as *exclusive* method of classification. Clearly, one cannot have inclusive method of classification with continuous data set: it is applicable for discrete character only.

2.5.2 Cumulative Frequency

It is simply the accumulation of observation up to certain level in arranged data. Cumulative frequency divides the entire range of data set into different component as per the requirement of the investigator. Cumulative frequency is of two types: *cumulative frequency less than type and cumulative frequency greater than type*. *Cumulative frequency less than type is the total number of observations below a particular value*; it generally corresponds to the upper boundary of different classes. Thus cumulative frequency less than type of the class 1520.5–1721.5 is 27; it means there are 27 chicks whose weights are below 1721.5 g. On the other hand, *cumulative frequency greater than type is the total number of observations equals to or above a particular value*; it generally corresponds to the lower boundary of different classes. For example, in the above frequency distribution table, the cumulative frequency greater than type of the class 1520.5–1721.5 is 42; it means there are 42 chicks whose weights are equal to or more than1520.5 g. Cumulative frequency helps in getting immediate idea about the percent distribution or partition values of the data set.

2.5.3 Relative Frequency

Relative frequency gives an idea about the concentration of observations in different classes with respect to total frequency and is defined as the proportion of observation in a particular class to total number of observations. Thus, the relative frequency of the class 1520.5–1721.5 is $9/60 = 0.15$. Relative frequency may also be expressed in percentage.

2.5.4 Frequency Density

Using the same idea of density, one can define frequency density as the frequency per unit of class width, i.e., $fd = f_i/h$, where f_i is the frequency of the ith class and h is the class width of the respective class. Thus for first class, frequency density is $8/201 = 0.0398$. Frequency density gives an idea about the relative concentration of observation with respect per unit of class width.

One can find that with the processing of data at different stages, the investigator finds himself or herself in better and better position to explain the data on hand about the objective of the study.

In the following slides, demonstrations have been made on how to frame frequency distribution table along with the syntax for getting cumulative frequency, relative frequency, and frequency density. Readers may please note the formulae for calculations of these measures in the slides to follow (Slides 2.5, 2.6, 2.7, and 2.8):

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Table 2.6 Frequency distribution for body weights of 60 poultry birds (grouped data)

Discrete class	Lower limit	Upper limit	Mid value (x)	Continuous class	Lower boundary	Upper boundary	Mid value (x)	Frequency (f)	Cumulative frequency<	Cumulative frequency≥	Relative frequency	Frequency density
1119–1319	1119	1319	1219	1118.5–1319.5	1118.5	1319.5	1219	8	8	60	0.133	0.0398
1320–1520	1320	1520	1420	1319.5–1520.5	1319.5	1520.5	1420	10	18	52	0.167	0.0498
1521–1721	1521	1721	1621	1520.5–1721.5	1520.5	1721.5	1621	9	27	42	0.150	0.0448
1722–1922	1722	1922	1822	1721.5–1922.5	1721.5	1922.5	1822	10	37	33	0.167	0.0498
1923–2123	1923	2123	2023	1922.5–2123.5	1922.5	2123.5	2023	4	41	23	0.067	0.0199
2124–2324	2124	2324	2224	2123.5–2324.5	2123.5	2324.5	2224	9	50	19	0.150	0.0448
2325–2525	2325	2525	2425	2324.5–2525.5	2324.5	2525.5	2425	10	60	10	0.167	0.0498
Total								**60**			**1.000**	**0.2985**

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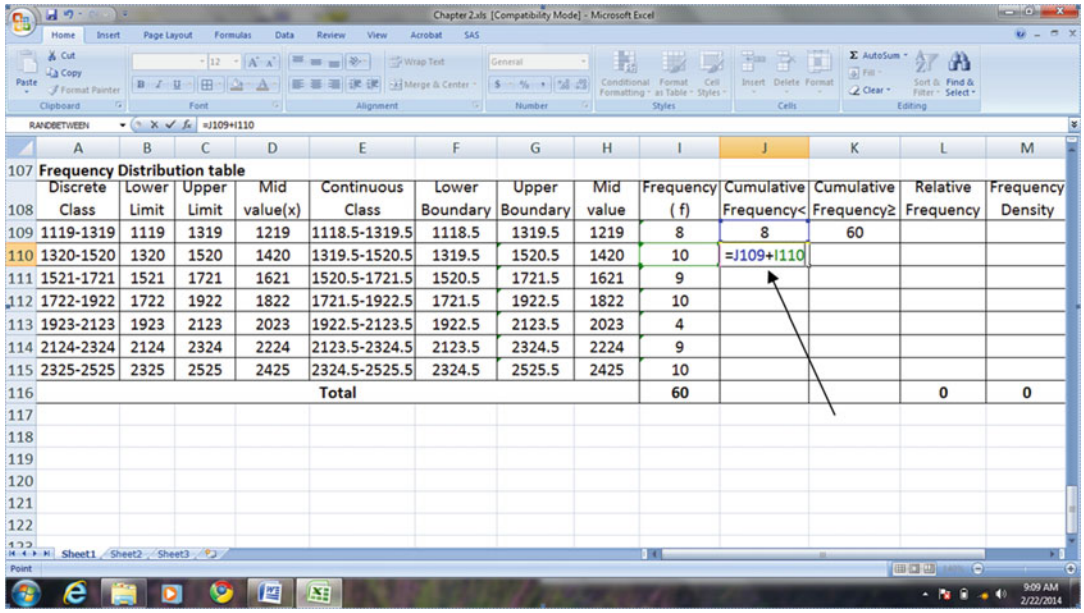
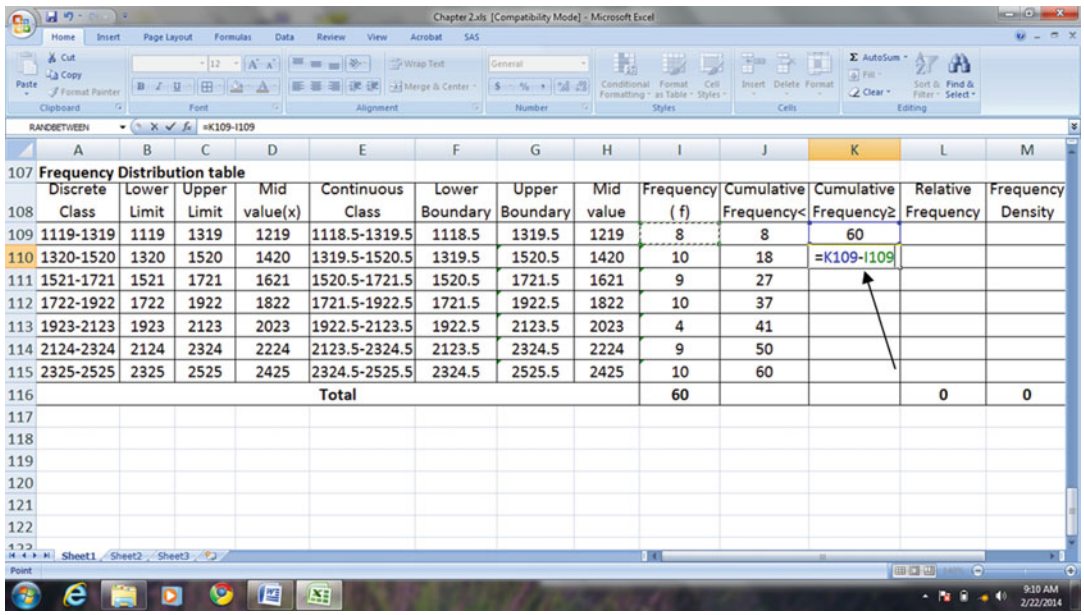


Slide 2.5 Calculation of less than type cumulative frequency



Slide 2.6 Calculation of greater than or equals to type cumulative frequency

2.6 Presentation of Data

At every stage of processing of data, the investigator becomes more and more equipped to explain the phenomenon under consideration and thereby feels the urgency of presenting the information extracted from the data on hand. There are different methods and techniques for presentation of data; among these the *textual, tabular, and diagrammatic forms* are widely used.

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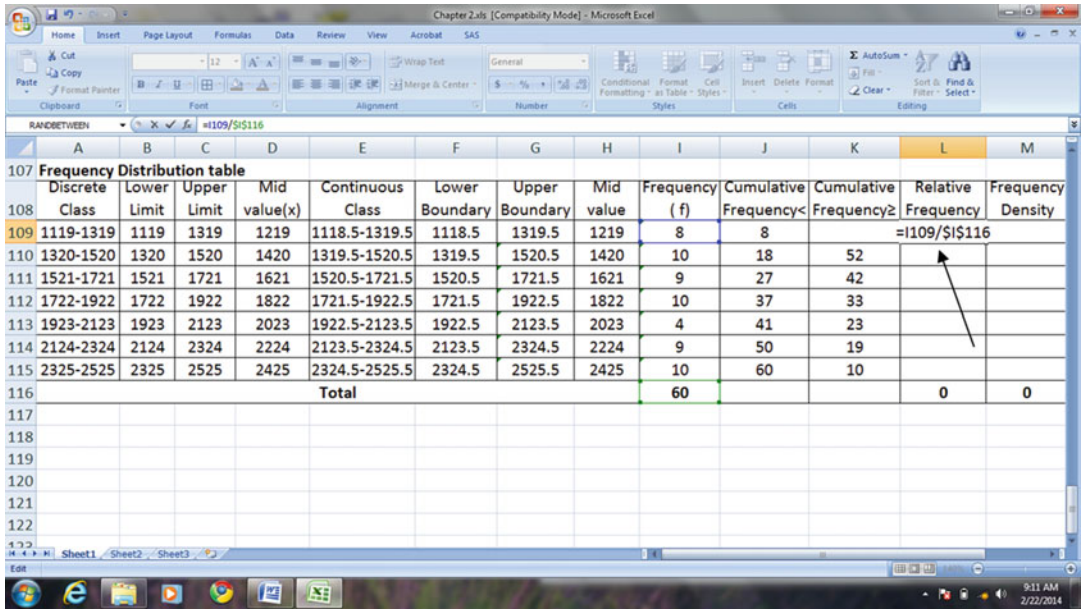
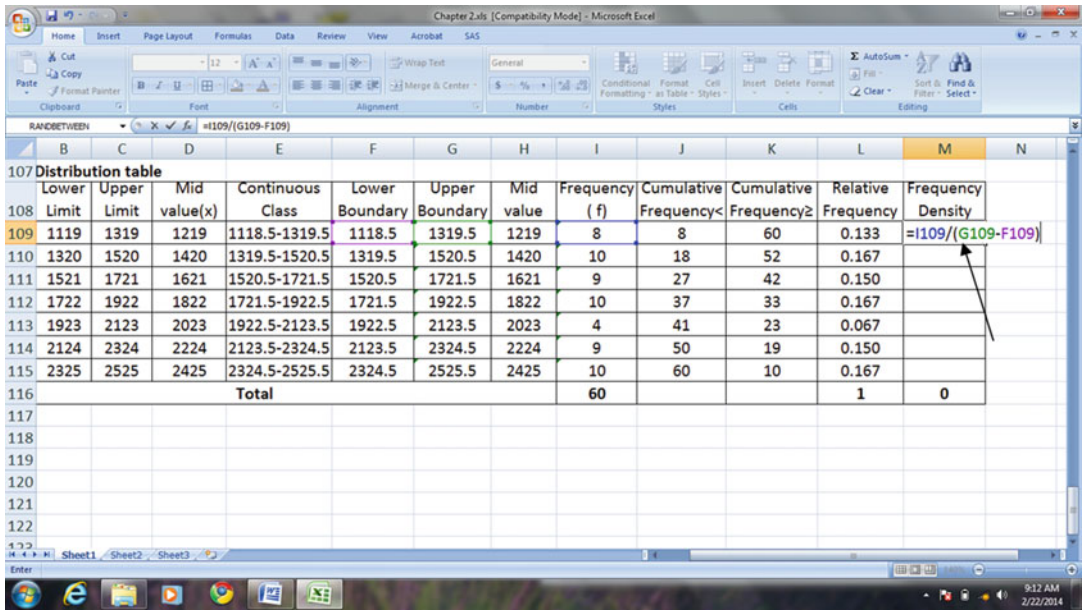


	A	B	C	D	E	F	G	H	I	J	K	L	M
107	Frequency Distribution table												
108	Discrete Class	Lower Limit	Upper Limit	Mid value(x)	Continuous Class	Lower Boundary	Upper Boundary	Mid value	Frequency (f)	Cumulative Frequency<	Cumulative Frequency≥	Relative Frequency	Frequency Density
109	1119-1319	1119	1319	1219	1118.5-1319.5	1118.5	1319.5	1219	8	8		=I109/I116	
110	1320-1520	1320	1520	1420	1319.5-1520.5	1319.5	1520.5	1420	10	18	52		
111	1521-1721	1521	1721	1621	1520.5-1721.5	1520.5	1721.5	1621	9	27	42		
112	1722-1922	1722	1922	1822	1721.5-1922.5	1721.5	1922.5	1822	10	37	33		
113	1923-2123	1923	2123	2023	1922.5-2123.5	1922.5	2123.5	2023	4	41	23		
114	2124-2324	2124	2324	2224	2123.5-2324.5	2123.5	2324.5	2224	9	50	19		
115	2325-2525	2325	2525	2425	2324.5-2525.5	2324.5	2525.5	2425	10	60	10		
116					Total				60			0	0

Slide 2.7 Calculation of relative frequency



	B	C	D	E	F	G	H	I	J	K	L	M	N
107	Distribution table												
108	Lower Limit	Upper Limit	Mid value(x)	Continuous Class	Lower Boundary	Upper Boundary	Mid value	Frequency (f)	Cumulative Frequency<	Cumulative Frequency≥	Relative Frequency	Frequency Density	
109	1119	1319	1219	1118.5-1319.5	1118.5	1319.5	1219	8	8	60	0.133	=I109/(G109-F109)	
110	1320	1520	1420	1319.5-1520.5	1319.5	1520.5	1420	10	18	52	0.167		
111	1521	1721	1621	1520.5-1721.5	1520.5	1721.5	1621	9	27	42	0.150		
112	1722	1922	1822	1721.5-1922.5	1721.5	1922.5	1822	10	37	33	0.167		
113	1923	2123	2023	1922.5-2123.5	1922.5	2123.5	2023	4	41	23	0.067		
114	2124	2324	2224	2123.5-2324.5	2123.5	2324.5	2224	9	50	19	0.150		
115	2325	2525	2425	2324.5-2525.5	2324.5	2525.5	2425	10	60	10	0.167		
116				Total				60			1	0	

Slide 2.8 Calculation of frequency density

2.6.1 Textual Form

In textual form of presentation, information is presented in the form of a text paragraph. While discussing the findings of the research, this method is adopted for explanation of research papers or articles. Before presenting the general budget, the Finance Minister presents a survey of the economic condition, achievements, lacunae, etc. in a book, viz., the Economic Survey. In this economic survey, the minister discusses the economic situation of the country with facts, figures, and data in

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the form of paragraphs or several pages. The above information on weights of 60 chicks can very well be presented in textual form as follows:

Weights of 60 birds of 50 days old are taken to have an idea about the growth of the particular breed of chicks. It is found that the chick weights vary between 1124 g and as high as 2520 g in the same village. Though variations in weights among the birds are recorded, quite a good number of birds are found to have recorded similar weights. More than 50% birds (37 in exact) are found to have less than1922.5 g body weight, while comparatively less number of birds are found to have higher body weight and so on.

Any literate person can have idea about the results on chick weight by studying the paragraph. This form of presentation of data is not suited for illiterate persons; moreover when a huge amount of data is to be presented, then this form of presentation may not be suitable because of monotony in reading a big paragraph or even a good number of paragraphs and pages.

2.6.2 Tabular Form

As has already been discussed during the formation of frequency distribution table, a huge number of data can be presented in a very concise form in a table. At the same time, it can extract out some of the essential features of the data which were hidden in the raw data set. This is one of the most widely used forms of presentation of data. Research findings are generally presented in the form of tables followed by discussion. A table is consisting of rows and columns. In general a table has *(a) title, (b) stub, (c) caption, (d) body, and (e) footnote*. *Title* gives a brief idea about the content or subject matter presented in table. Generally the title should be as short as possible and at the same time should be lucrative in drawing attention of the readers. *Stub* of a table describes the contents of the rows of a table. In the frequency distribution table, the stub describes the different weight classes, viz., 1118.5–1319.5, 1319.5–1520.5, and so on. Thus with the help of the stub, one can extract the features of the rows. For example, there are ten chicks which have gotten a body weight in between 1319.5 and 1520.5, there are 18 chicks which have weight less than 1520.5 g, and there are 52 chicks which have a body weight equal to or greater than 1319.5 g and so on.

Caption informs the readers about the content of each and every column. Thus, "mid value," "frequency," cumulative frequency less than type, cumulative frequency greater than or equals to type, relative frequency, and frequency density are the captions of the frequency distribution table. Relevant information corresponding to different row–column combination are provided in the *body* of the table. In the frequency distribution table, the data pertaining to different classes and columns constitute the body of the table.

Footnotes are generally used to indicate the source of information or to explain special notation (if any) used in the table. Footnotes are not essential but optional to a table, depending upon the requirement of the situation in explaining the phenomenon under consideration. Information presented in tables are more appealing than information presented in textual form. But likewise to that of textual form, tables are also useful for literate persons only.

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Discrete class	Lower limit	Upper limit	Mid value(x)	Continuous class	Lower boundary	Upper boundary	Mid value (x)	Frequency (f)	Cumulative frequency$<$	Cumulative frequency$\geq$	Relative frequency	Frequency Density
1119–1319	1119	1319	1219	1118.5–1319.5	1118.5	1319.5	1219	8	8	60	0.133	0.0398
1320–1520	1320	1520	1420	1319.5–1520.5	1319.5	1520.5	1420	10	18	52	0.167	0.0498
1521–1721	1521	1721	1621	1520.5–1721.5	1520.5	1721.5	1621	9	27	42	0.150	0.0448
1722–1922	1722	1922	1822	1721.5–1922.5	1721.5	1922.5	1822	10	37	33	0.167	0.0498
1923–2123	1923	2123	2023	1922.5–2123.5	1922.5	2123.5	2023	4	41	23	0.067	0.0199
2124–2324	2124	2324	2224	2123.5–2324.5	2123.5	2324.5	2224	9	50	19	0.150	0.0448
2325–2525	2325	2525	2425	2324.5–2525.5	2324.5	2525.5	2425	10	60	10	0.167	0.0498
Total								**60**			**1.000**	**0.2985**

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2.6.3 Diagrammatic Form

Diagrammatic forms of presentations are more appealing and especially useful to the illiterate persons. Seeing the graphs, one can have idea about the nature of the data under study. Among the different diagrammatic forms of presentation, *(i) line diagram*, *(ii) bar diagram*, *(iii) histogram*, *(iv) frequency polygon*, *(v) cumulative frequency curve or ogive*, *(vi) pie charts*, *(vii) stem and leaf*,, *(viii) pictorial diagrams*, etc. are widely used.

(i) *Line diagrams* are the two-dimensional presentations of data in X-Y axes with X axis generally presenting the category or classes and the corresponding values are presented along Y axis. Frequencies, cumulative frequencies, relative frequencies, etc. can be presented in the form of line diagrams (Figs. 2.1, 2.2, and 2.3).

How to draw the line diagrams using MS Excel is shown in the following slide (Slide 2.9):

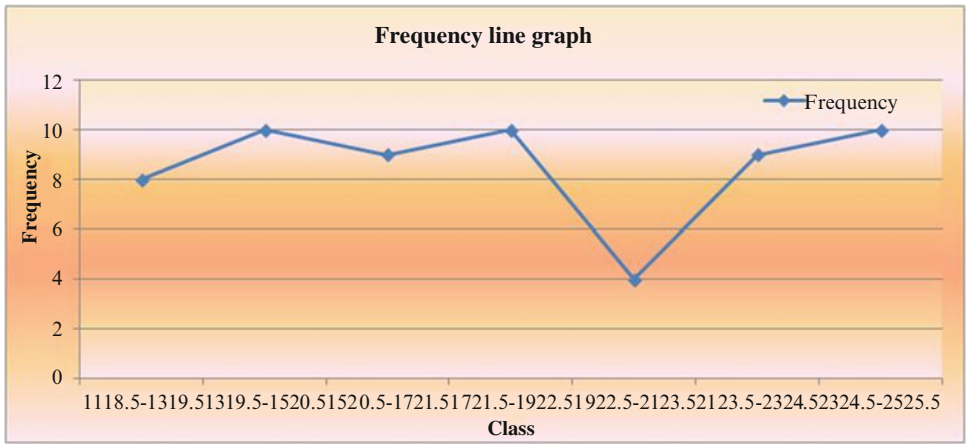

Fig. 2.1 Frequency line graphs

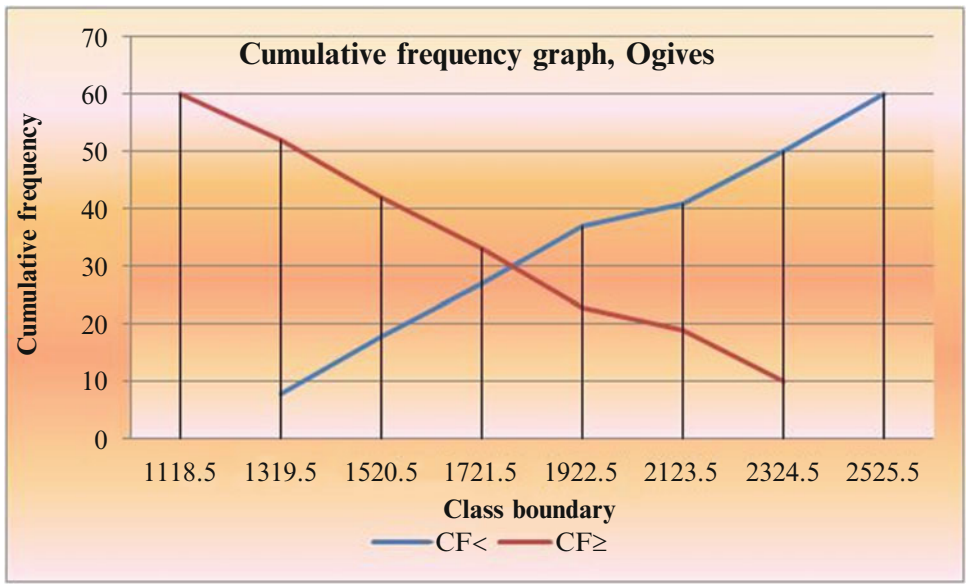

Fig. 2.2 Line graphs of cumulative frequency $<$ and cumulative frequency $\geq$

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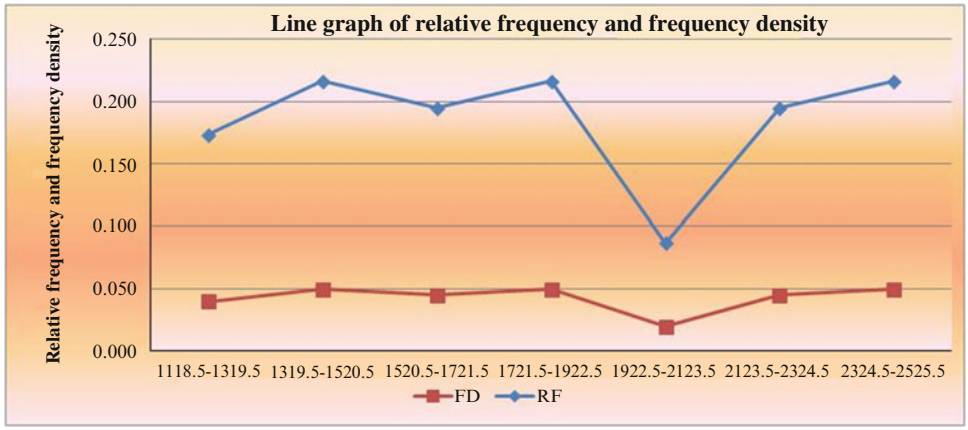
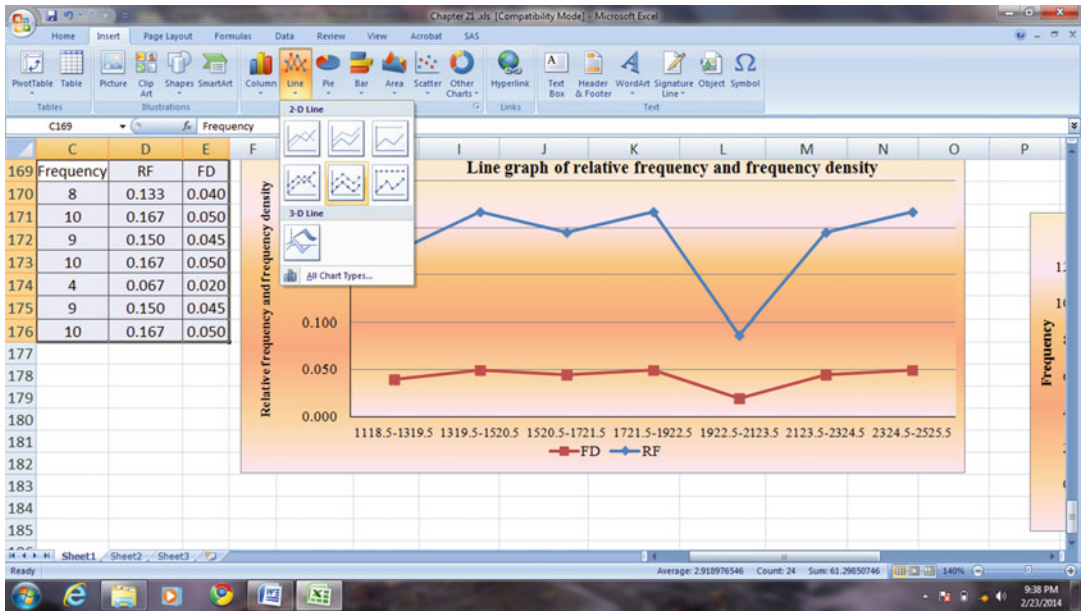


Fig. 2.3 Line graphs of relative frequency and frequency density



Slide 2.9 Slide showing the drawing of line graphs using MS Excel

(ii) *Bar diagrams* are two-dimensional presentations of data in X-Y axis. For example, frequencies corresponding to discrete classes can be represented graphically by drawing bars/ordinates equal to the frequency on a convenient scale at the various values of the variable class. Figure 2.4 corresponds to Table 2.6. The tops of the ordinate may be joined by straight bars.

Drawing of bar diagram using MS Excel is presented in the following slide (Slide 2.10):

Now when selecting the appropriate menu in the chart tool, one can modify the chart.

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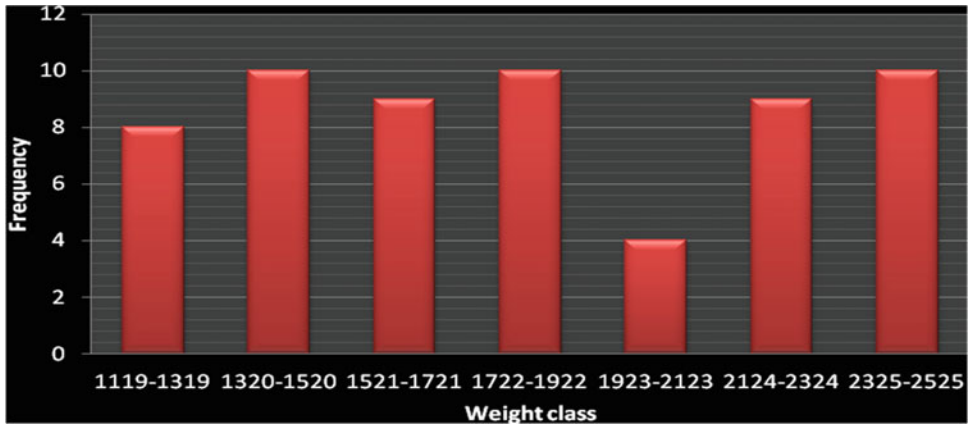
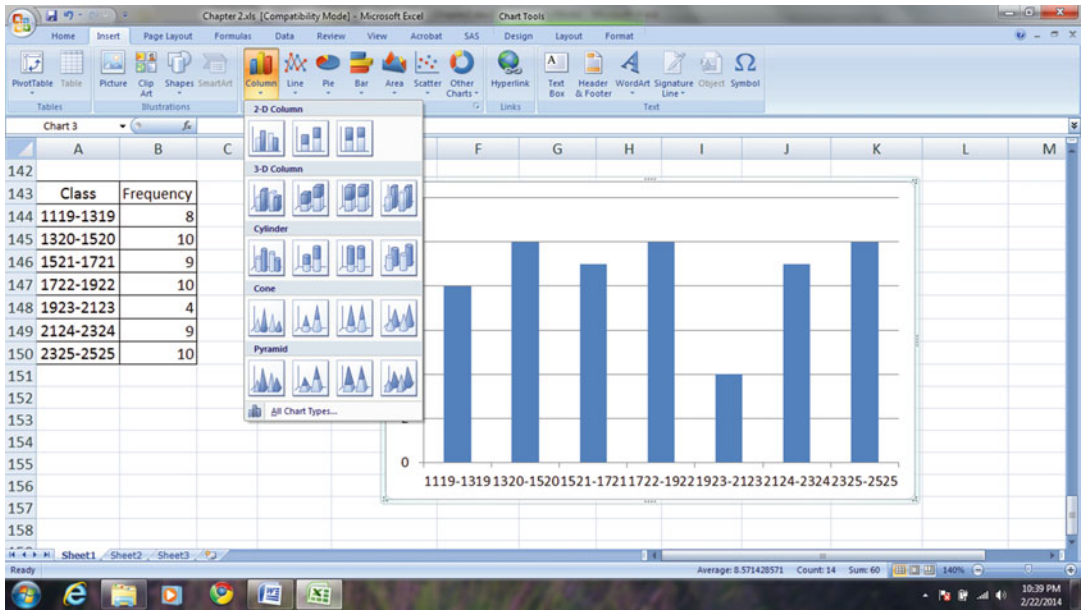


Fig. 2.4 Bar diagram



Slide 2.10 Slide showing drawing of bar diagram using MS Excel

(ii) *Histogram:* Histogram is a bar diagram for continuous data set. Only difference between the bar diagram and the histogram is that in the case of histogram, there is a gap between two consecutive bars; others are as per the bar diagram (Fig. 2.5).

Histogram can be drawn using the technique as shown in the following slide (Slide 2.11):

(iv) *Frequency polygon:* When you join the midpoints of the top of the bars in histogram and then connect both the ends to the

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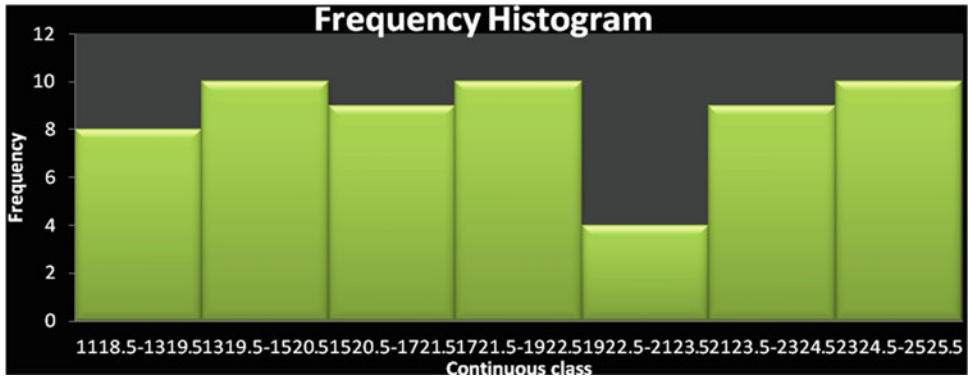
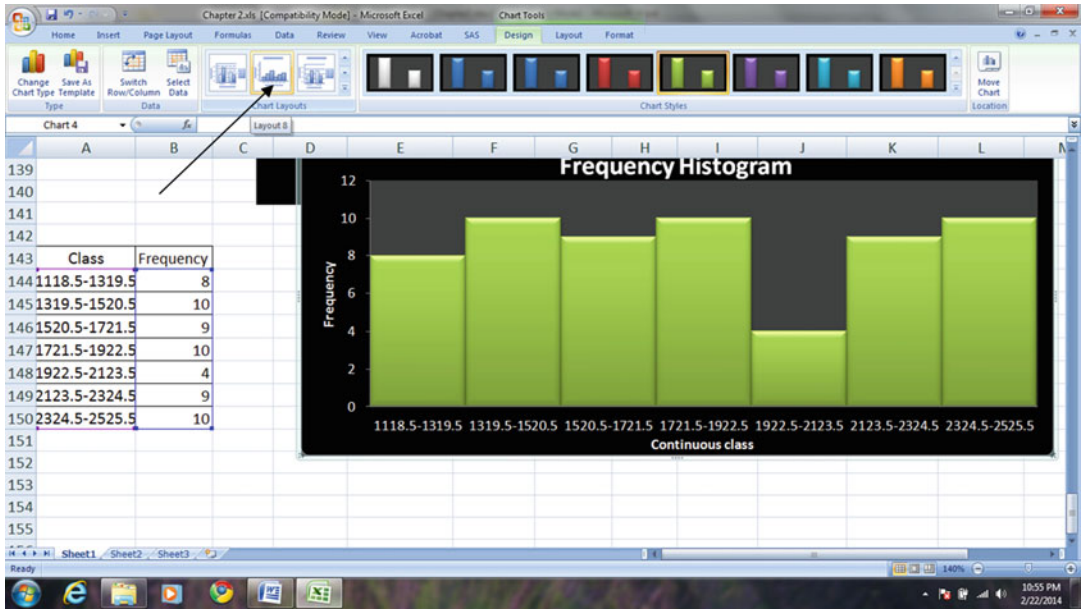


Fig. 2.5 Frequency histogram



Slide 2.11 Drawing of histogram using MS Excel

horizontal axis by straight line segments, then a frequency polygon is obtained. To complete the polygon, it is customary to join the extreme points at each end of the frequency polygon to the midpoints of the next higher and lower hypothetical class intervals on the horizontal line (class axis here). Readers may please note that there were no classes like 917.5–1118.5 and 2525.5–2726.5 in the frequency distribution table; these classes have been assumed with class frequency zero in each case (Fig. 2.6).

If one wants to present more than one parameter/character in the same figure using bar diagram, then one can have the option for *clustered* bar, *stacked* bar, and 100 % *stacked* bar diagram. In clustered bar diagrams, values of same item for different categories are compared. While in stacked columns, proportions of the values across

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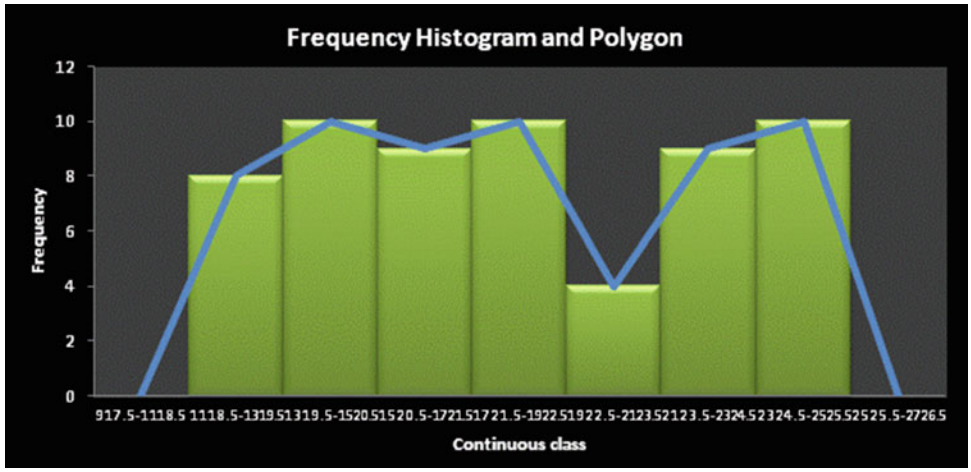

Fig. 2.6 Frequency histogram and/or polygon

Table 2.7 Egg production (million) in major states of India

State	2008–2009	2009–2010	2010–2011
Andhra Pradesh	18,345	19,396	20,128
Haryana	3815	3845	3964
Maharashtra	3550	3864	4225
Punjab	3679	3283	3545
Tamil Nadu	8810	10,848	11,514
West Bengal	3306	3698	3994
Other	14,058	15,334	15,655

the categories are shown. In 100 % stacked bar, comparison of each category is made in such a way so as to make the total bar length to 100 % divided into different categories, one above the other. Let us take the following example of state-wise egg production figures for the years 2008–2009, 2009–2010, and 2010–2011 (Fig. 2.7 and Table 2.7).

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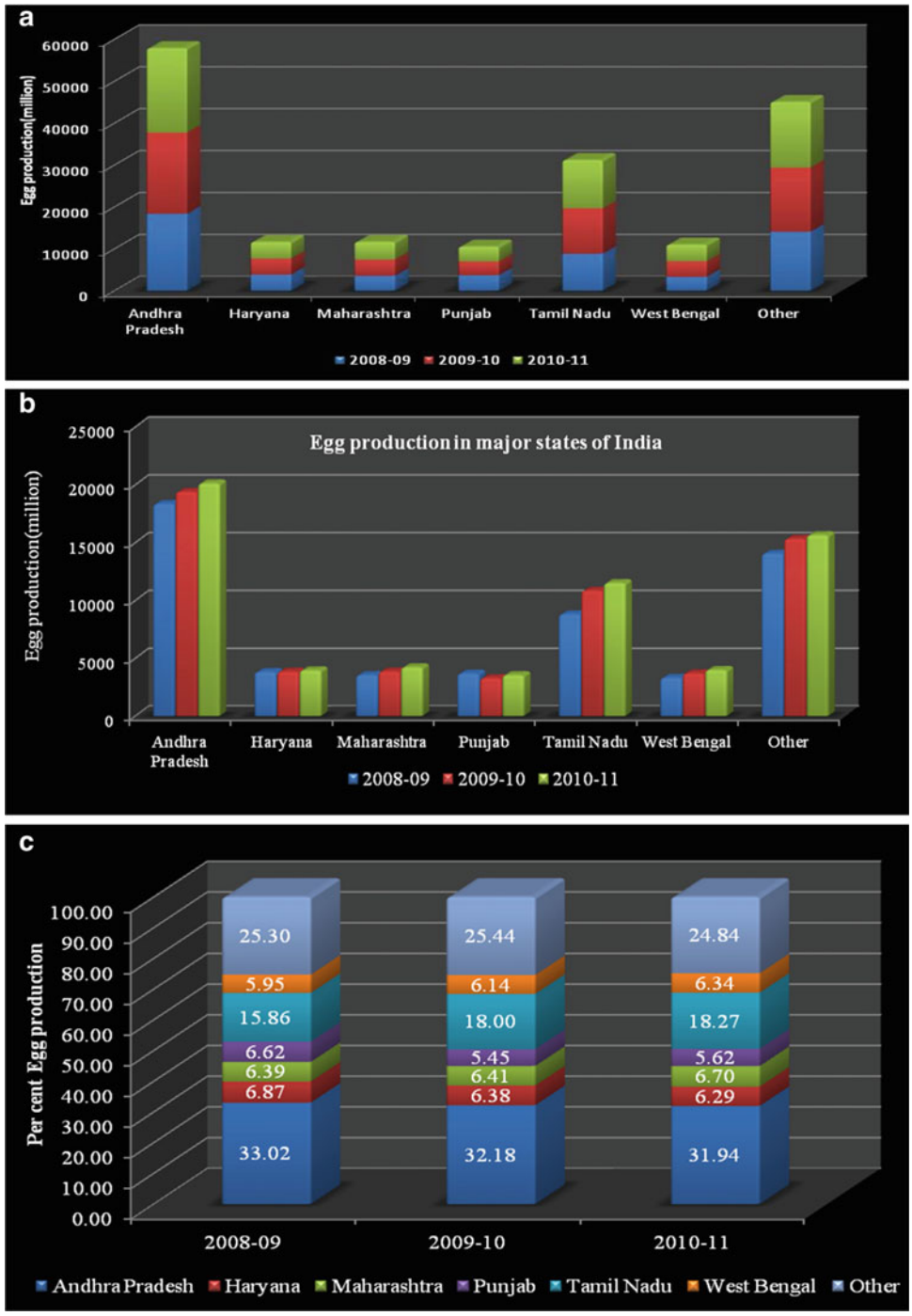

Fig. 2.7 (**a**) Stacked bar diagram of egg production in different states of India from 2008–2009 to 2010–2011 (**b**) Clustered bar diagram of egg production in different states of India from 2008–2009 to 2010–2011 (**c**) 100 % stacked bar diagram of egg production in different states of India

All the above diagrams can be made using MS Excel as demonstrated in the following slide (Slides 2.12, 2.13, and 2.14):

(v) *Pie chart:* The essence of presenting the whole information in the form of pie chart is to assume the total frequencies as 100 %

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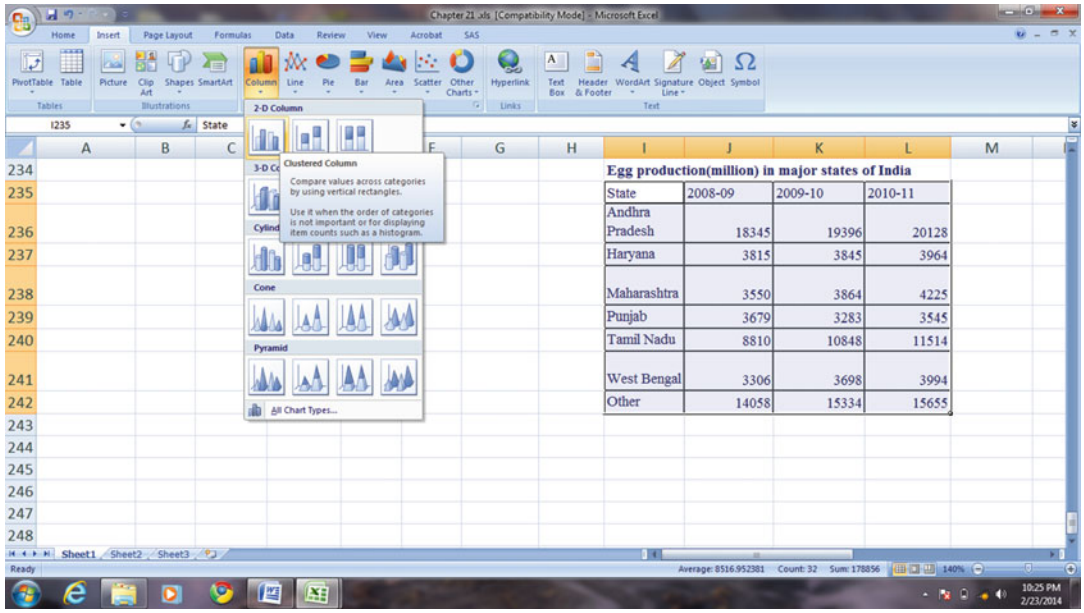
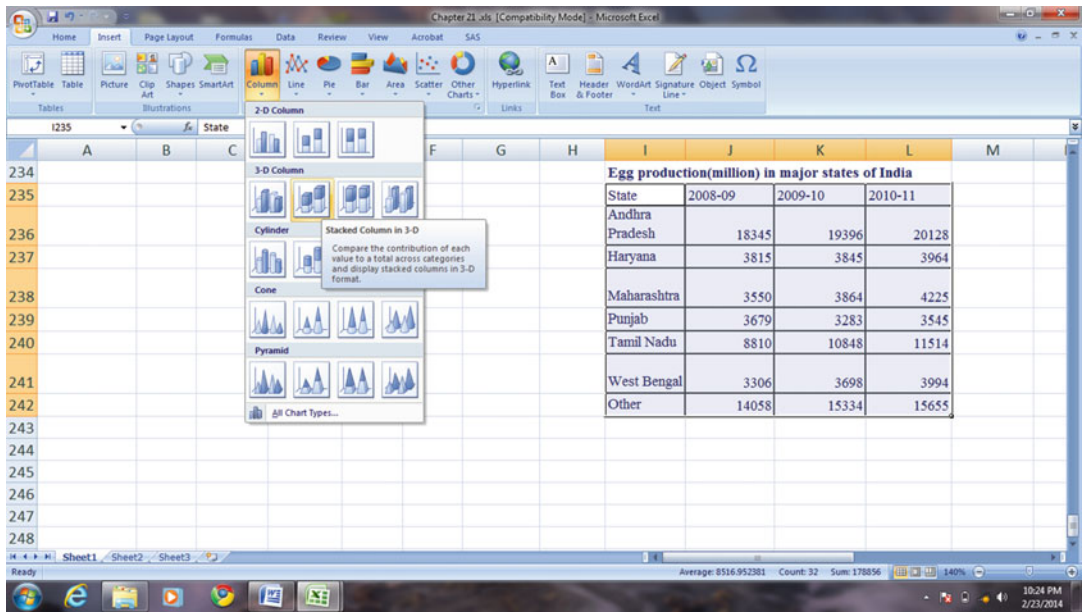


Slide 2.12 Slide showing the options for making cluster bars



Slide 2.13 Slide showing the options for making stacked bars

and present the same in a circle with 360° angle at the center. In the frequency distribution table of body weight of bird, the relative frequency calculated can effectively be used in the form of a pie diagram. The technique behind the calculation during pie diagram is as follows (Fig. 2.8):

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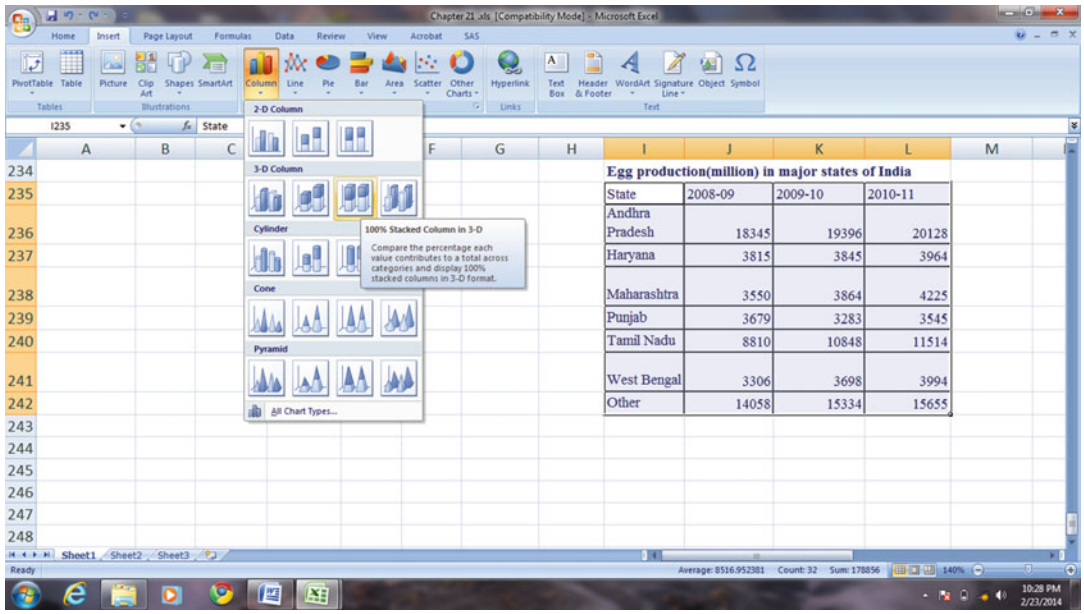

Slide 2.14 Slide showing the options for making 100 % stacked bars

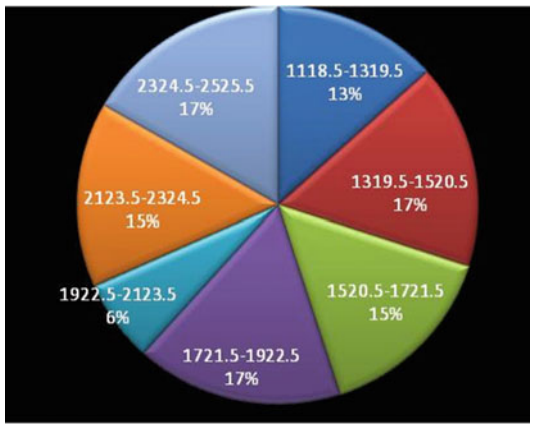

Fig. 2.8 Pie chart

Class	Frequency	RF	%RF	Angle
1118.5–1319.5	8	0.133	13.33	$3.6 \times 13.33 = 48$
1319.5–1520.5	10	0.167	16.67	$3.6 \times 16.67 = 60$
1520.5–1721.5	9	0.150	15.00	$3.6 \times 15.00 = 54$
1721.5–1922.5	10	0.167	16.67	$3.6 \times 16.67 = 60$
1922.5–2123.5	4	0.067	6.67	$3.6 \times 6.67 = 24$
2123.5–2324.5	9	0.150	15.00	$3.6 \times 15.00 = 54$
2324.5–2525.5	10	0.167	16.67	$3.6 \times 16.67 = 60$

(vi) *Stem and leaf diagram:* When the variations in the data set are comparatively less, a well-accepted form of presentation of data is the stem–leaf presentation. In this method, each and every data point is divided into two parts – *stem part and the leaf part*. Generally the stem part consists of higher decimal places for all the data points, and the leaf part consists of the rest of the parts of the data points. For example, if data points are 234, 345, 1324, 987, and so on, then stem part should include 23, 34, 132, and 98, respectively, leaving 4, 5, 6, and 7, respectively, for the leaf part. Data are sorted in ascending or descending order, stem portion is provided in the first column, and the leaf part of each data point is recorded in appropriate row. Let us take the example of body weights of 60 chicks; one can frame the following stem–leaf diagram (Fig. 2.9):

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Stem	Leaf	Stem	Leaf
112	4	182	3,3,3
118	3	184	7
121	3,3	185	0
130	0,0,0,0	186	5,5
134	1	191	5
140	5	192	4
143	8,8,9	197	6
144	2,4	204	7
147	6,6,6	205	4
157	3,3	212	4,4,4,4,4,4
159	3	217	7
164	0	220	5
168	2,2,2	223	5
170	3	239	8,9
171	3	243	3,4,4,4,4
172	6	250	8
178	8	252	0

Fig. 2.9 Stem–leaf diagram of body weight of 60 chicks

Stem	Leaf
23	6,7,7,8,9,9
24	0,0,3,3,5,5,5,6,7,7,7,9
25	0,0,1,1,2,3,6,8
26	1,2,2,2,3,4,5,8
27	0,0,4,4,6,68,8,8
28	0,2,4,5,5,6,7
29	0,0,0,1,2
30	1,1,2,3,4,5,7
31	0,1,1,2,2,4,6,6
32	0,3,3,3,4,5,7,8,9,
33	0,0,1,2,3,6,7,9,9,9,9
34	2,3
35	0,0,1,2,2,2

Fig. 2.10 Stem–leaf diagram of monthly milk production of 100 cows

In the above stem and leaf plot, one can see that corresponding to 143 in stem (seventh row), there are three observations, viz., 1438, 1438, and 1439. Similarly, the third stem observation from the last is 243, which has got 3, 4, 4, 4, and 4 in the leaf column; that means there are four observations and the observations are 2433, 2434, 2434, 2434, and 2434.

Example 2.1

Let us take another example of monthly milk yields (kilogram) of 100 milch cows (Fig. 2.10)

In this stem and leaf plot, one can find that corresponding to the first observation, 23 in the stem column, there are six observations and the observations are 236, 237, 237, 238, 239, and 239. The stem and leaf plot is almost similar to that of the bar diagram with the advantage of knowing the data values along with their concentrations. The only problem with this type of presentation is that if there are large variations among data points, then, under extreme case, the plot will be a huge one and a presentation may not be so useful.

(vii) *Pictorial diagram:* A picture/photograph speaks for itself. Instead of a bar diagram, line diagram, or pie chart, if one uses a relevant picture/photograph to present the data, then it becomes more lively and attractive to the readers. Let us take the following example.

Example 2.2

A study was conducted to investigate the egg-laying capacity of certain breeds of poultry bird. Following data presents, the frequency distribution of the egg-laying groups of the birds. If we represent each egg as equivalent to five observations/frequencies, then one can have the following diagram. From the following picture, any person can understand which breed is having highest egg-laying capacity as well as the distribution of the breeds in accordance with the egg-laying capacity (Fig. 2.11).

This type of pictorial representation is helpful to understand even by the layman and is more eye catching. But the problem with this type of

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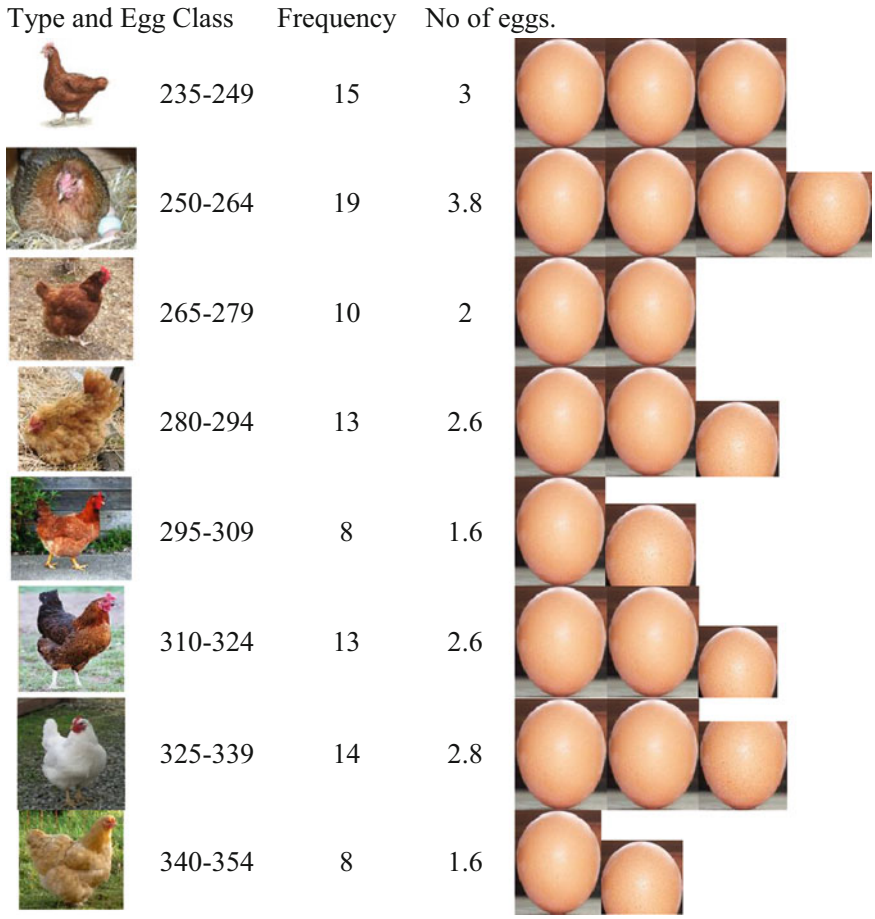

Fig. 2.11 Pictorial diagram

representation is that the frequencies should be divisible by whole number otherwise there would be truncated figures in the presentation like in most of the cases of the above figure excepting the classes one and three. It is very difficult to present the information in true to the scale also.

(viii) *Maps:* Maps are also one of the important and useful tools for summarization and presentation of data. Generally these are used to represent the information on particular parameters like forest area in a country, paddy-producing zone, different mines located at different places in a country, rainfall pattern, population density, temperature zone, agroclimatic zone, etc. The following maps give different zones of two countries, viz., India and Nigeria, based on rainfall distributions (Figs. 2.12 and 2.13).

This type of representation of data is easily conceived by any person but utmost care should be taken to make the statistical map true to the sense and scale.

From the above discussions on different presentation forms of information, it is clear that neither all forms of presentation are suitable every situation nor to all users. Depending upon the nature of the data, need of the situation, and the targeted readers, the appropriate form of presentation is to be decided.

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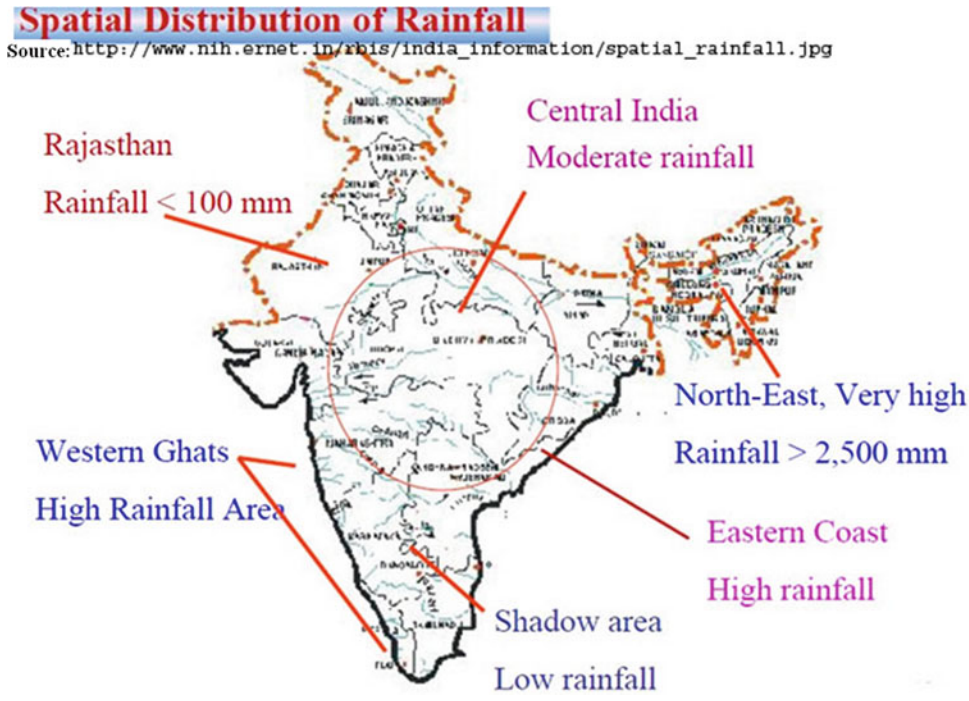

Fig. 2.12 Rainfall distribution map of India

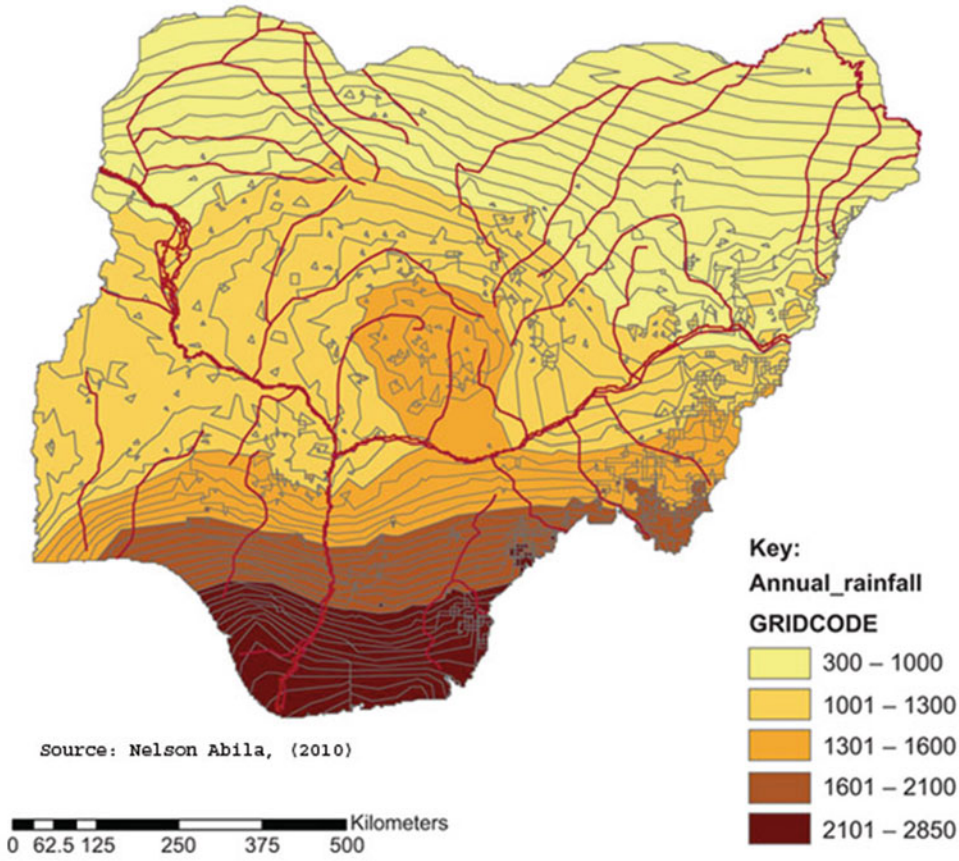

Fig. 2.13 Rainfall distribution map of Nigeria

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Summary Statistics

3

The general instinct of any investigator is to present his/her data with a single value. For example, a breed of poultry bird is known by its average-egg laying capacity, which is obtained from the eggs laid by the individual chick in a group of chicks. At the same time, the investigator may also be interested to know the variations in egg-laying capacity that he or she expects a range with in which a particular breed should lay eggs. Thus, the overall picture, instead of the capacity of the individual chicks, is of utmost interest to the investigator. Let us consider two data sets of weights (pounds) of 20 fishes of a particular breed caught from two different ponds. Our objective is to find the better pond for rearing of that particular breed of fish.

Example 3.1

	Fish weight (lb)																			
Pond A	1.2	0.9	1.5	1.3	2.1	2.0	1.3	1.6	2.0	1.5	1.6	1.7	2.1	1.2	1.3	0.9	1.6	1.4	1.9	1.7
Pond B	0.86	2.0	2.4	1.6	1.09	1.9	1.3	1.8	1.65	1.0	2.1	1.0	2.2	2.2	1.4	0.5	1.2	2.0	0.6	2

That means we need to have certain measures by which one can compare the two ponds with respect to their performance in yielding better weights of fishes. Moreover, human instinct is to find out certain value(s), which can represent the set of information given in a big data set. Let us take another example of run scored by two batsmen in ten different cricket innings which they have played together.

Example 3.2

	Run scored by two batsmen in 10 innings played together									
Player A	12	93	164	16	26	73	178	13	3	8
Player B	46	64	75	45	62	58	106	45	45	40

Now the question is which player is better? How to measure the effectiveness? Thus, in both

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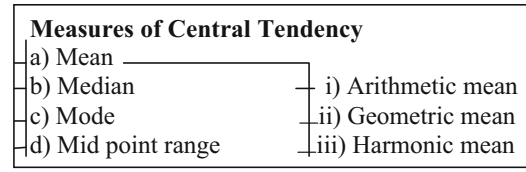
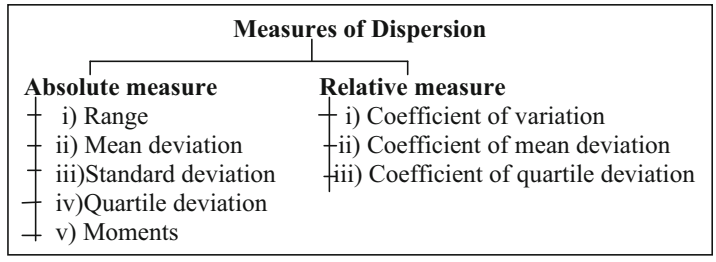
the cases, we are in search of such a measure, which can describe the inherent characteristics of a given set of data so that with the help of this measure, we can compare.

In its preliminary form, the characteristic of a given data set can be visualized with the help of its measure of central tendency and measure of dispersion. What do we mean by central tendency and dispersion? *Tendencies of the values of the observations in a given data set to cluster/center around a particular value are known as central tendency*. On the other hand, *tendencies of the values of the observations in a given data set to remain scattered or dispersed from a particular value are known as dispersion*. Thus, central tendency and dispersion are the two opposite phenomena for a given set of data. How to measure the central tendency or the dispersion? In fact there are different measures of central tendency and also for dispersion. Different measures of central tendency and dispersion are presented below:





In addition to the above measures of central tendency and dispersion, there are certain partitions like quartile, percentile, deciles, etc. which also helps in extracting information and partitioning of data set into different parts. Let us first discuss the measures of central tendency.

Characteristics of Good Measure

As shown above there are different measures for both the central tendency and dispersion, but among these measures, one should try to exploit the best one. That means we are in search of the qualities of good measure. By and large a good measure should be (a) clearly defined, (b) based on all observations, (c) very easy to calculate, (d) very easy to understand, (e) readily amenable to mathematical treatments, and (f) least affected by sampling fluctuations

3.1 Measures of Central Tendency

As we have already come to know, there are different measures of central tendency. Now the question is whether all the measures are equally good or applicable everywhere. For that let us discuss about the characteristics of good measures of central tendency. A good measure of central tendency should be (a) rigidly defined, there should not be any ambiguity in defining the measure, (b) based on all observations, (c) easy to calculate, (d) easy to understand, (e) least affected by sampling fluctuations, and (f) readily acceptable for mathematical treatments.

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3.1.1 Arithmetic Mean

Arithmetic mean is nothing but simple average of a set of observations and is calculated as the sum of the values of the observations divided by the number of observations.

Suppose there are N number of observations $X_1, X_2, X_3,\ldots,X_N$ for variable X, then its arithmetic mean (AM) denoted by $\overline{X}$ is given as $\overline{X} = \frac{\sum_{i=1}^{N} X_i}{N}$

If we take the example of the fish weights (in pound) in pond A of the Example 3.1, then we have

Pond A	1.2	0.9	1.5	1.3	2.1	2.0	1.3	1.6	2.0	1.5	1.6	1.7	2.1	1.2	1.3	0.9	1.6	1.4	1.9	1.7

The AM of the weights of 20 fishes is

$$\overline{X} = \frac{\sum_{i=1}^{N} X_i}{N} = \frac{1.2 + 0.9 + 1.5 + 1.3 + 2.1 + \cdots + 1.9 + 1.7}{20} = 1.54\,\text{lbs}$$

For grouped data, the arithmetic mean is defined as follows:

Arithmetic mean of a set of N number of observations $X_1, X_2, X_3,\ldots,X_N$, grouped into "n" number of classes with mid-values and frequencies of different classes is given as below

Mid-values(x_i)	x_1	x_2	$x_3\ldots,x_i,\ldots x_{n-2}$	x_{n-1}	x_n
Frequency	f_1	f_2	$f_3\ldots f_i,\ldots f_{n-2}$	f_{n-1}	f_n

where $x_1, x_2,\ldots x_i,\ldots x_n$ and $f_1, f_2,\ldots f_i,\ldots f_n$ are the mid-values and frequencies of the respective classes given as $\overline{X} = \frac{\sum_{i=1}^{n} f_i x_i}{\sum_{i=1}^{n} f_i}$

Example 3.3

Let us consider the body weights of 60 poultry birds as given below:

Body weight (g)	Frequency (f)
1118.5–1319.5	8
1319.5–1520.5	10
1520.5–1721.5	9
1721.5–1922.5	10
1922.5–2123.5	4
2123.5–2324.5	9
2324.5–2525.5	10

Body weight (g)	Mid-value (x_i)	Frequency (f_i)	$f_i x_i$
1118.5–1319.5	1219	8	9752
1319.5–1520.5	1420	10	14,200
1520.5–1721.5	1621	9	14,589
1721.5–1922.5	1822	10	18,220
1922.5–2123.5	2023	4	8092
2123.5–2324.5	2224	9	20,016
2324.5–2525.5	2425	10	24,250
Total		60	109,119
AM			1818.65

$$\overline{X} = \frac{\sum_{i=1}^{n} f_i x_i}{\sum_{i=1}^{n} f_i} = \frac{\sum_{i=1}^{7} f_i x_i}{\sum_{i=1}^{7} f_i} = \frac{8 \times 1219 + 10 \times 1420 + \ldots + 9 \times 2224 + 10 \times 2425}{8 + 10 + \ldots + 9 + 10}$$
$$= \frac{9752 + 14200 + \ldots + 24250}{60} = \frac{109119}{60}$$
$$= 1818.65\,\text{g}$$

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Merits and Demerits of Arithmetic Mean AM is clearly defined, easy to calculate and understand, and also based on all observations; so it is following most of the characteristics of good measure of central tendency. But the demerit of AM is that if one of the observations in the given data set is missing, then it cannot be calculated. Moreover, AM is highly susceptible to extreme values; a single large value or a small value can change the AM drastically. Some important properties of AM are discussed below:

(a) Arithmetic mean of a set of "n" number of constants ($X = M$, say) is also the constant, because

$$\sum_{i=1}^{n} X_i = \frac{1}{n}[M + M + M + \ldots + M] = \frac{nM}{n} = M$$

(b) Arithmetic mean depends on both the change of origin and scale:

Let $Y = \frac{X-a}{b}$ where X and Y are variables and both a and b are constants.

Thus, a is the change in origin and b is the change in scale.

Now, we have $X = a + bY$

$\Rightarrow X_i = a + bY_i$, where i stands for i -th observation.

$$\Rightarrow \sum_{i=1}^{N} X_i = \sum_{i=1}^{N} (a + bY_i)$$

$$\Rightarrow \frac{1}{N}\sum_{i=1}^{N} X_i = \frac{1}{N}\sum_{i=1}^{N} (a + bY_i)$$

$$\Rightarrow \overline{X} = \frac{1}{N}\sum_{i=1}^{N} a + \frac{1}{N}\sum_{i=1}^{N} bY_i = \frac{Na}{N} + b\frac{1}{N}\sum_{i=1}^{N} Y_i = a + b\overline{Y}$$

The arithmetic means of two related variables X and Y are also related with change of origin and scale.

This relationship is also true for grouped data

$$\begin{aligned}\overline{X} &= \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i(x_i) \\ &= \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i(a + by_i) \\ &= \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i a + \frac{1}{\sum_{i=1}^{k} f_i}\sum_{i=1}^{n} f_i b y_i \\ &= a + b\overline{Y},\end{aligned}$$

where a and b are change of origin and scale, respectively, x_i are mid-values of i-th class for X and f_i is the frequency of i-th class, and y_i is the transformed value corresponding to xi.

Let us use the same example of body weight of 60 poultry birds and also suppose that we have changed the origin to 1800 g and scale to 200 g for the body weight X, i.e., $Y = \frac{X-1800}{200}$

Now we have the following table for calculation:

Body weight (g)	Mid-value (x)	Frequency (f)	$f_i x_i$	$y_i = \frac{x_i - 1800}{200}$	$f_i y_i$
1118.5–1319.5	1219	8	9752	−2.91	−23.240
1319.5–1520.5	1420	10	14,200	−1.90	−19.000
1520.5–1721.5	1621	9	14,589	−0.90	−8.055
1721.5–1922.5	1822	10	18,220	0.11	1.100
1922.5–2123.5	2023	4	8092	1.12	4.460
2123.5–2324.5	2224	9	20,016	2.12	19.080
2324.5–2525.5	2425	10	24,250	3.13	31.250
Total		60	109,119		5.595
AM			1818.65		0.09325

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We have

$$\bar{y} = \frac{1}{\sum_{i=1}^{n} f_i} \sum_{i=1}^{n} f_i y_i = \frac{1}{60}[-23.24 - 19 - 8.055 + 1.1 + 4.46 + 19.08 + 31.25]$$
$$= 5.595/60 = 0.09325\,\text{g}$$
$$\therefore \bar{x} = 1800 + 200x\bar{y} = 1800 + 200 \times 0.09325 = 1818.65\,\text{g}$$

which is exactly the same value that we got without changing the origin and scale.

One of the important uses of this type change of origin and scale is to reduce the large values into small ones with suitable change of origin and scale.

(c) Composite arithmetic mean of "k" number of samples having arithmetic means $\bar{x}_1, \bar{x}_2, \bar{x}_3, \ldots, \bar{x}_k$ for n_1, n_2, n_3,...., n_k number of observations, respectively, is the weighted average of the arithmetic means of the samples.

Samples	1	2	3	4	5	...	k
No. of observations	n_1	n_2	n_3	n_4	n_5	...	n_k
AM	$\overline{x_1}$	$\overline{x_2}$	$\overline{x_3}$	$\overline{x_4}$	$\overline{x_5}$		$\overline{x_k}$

We have the sum of all observations $n_1\bar{x}_1 + n_2\bar{x}_2 + ... + n_k\bar{x}_k = \sum_{i=1}^{k} n_i\bar{x}_i$

So the average of the above $\sum_{i=1}^{k} n_i = (n_1 + n_2 + n_3 + ... + n_k) = n$ observation is $\frac{\sum_{i=1}^{k} n_i\bar{x}_i}{\sum_{i=1}^{k} n_i} = \bar{x}$

Example 3.4

The following table gives the average body weights (kg) of five groups of goats. Find out the overall average weight of the goats.

Group	1	2	3	4	5
No of Goats	32	40	30	35	13
Average weight (kg)	14.5	16.8	17.5	16.0	18

The overall average weight of 150 goats is given by

$$\bar{x} = \frac{\sum_{i=1}^{k} n_i\bar{x}_i}{\sum_{i=1}^{k} n_i}, \text{ here } k = 5, \text{so}$$
$$\bar{x} = [32 \times 14.5 + 40 \times 16.8 + 30 \times 17.5 + 35 \times 16 + 13 \times 18] \times /150$$
$$= 16.37\,\text{kg}.$$

3.1.2 Geometric Mean

Geometric mean of a set of "N" observations X_1, X_2,X_3,...,X_i,...,X_N is defined as the N-th root of the product of the observations.

Thus, the geometric mean (GM) of X_1,X_2, X_3,...,X_i,...,X_N is given as

$$X_g = \sqrt[N]{X_1.X_2.....X_i.....X_N}$$
$$= (X_1.X_2.....X_i.....X_N)^{1/N}$$
$$= \left(\prod_{i=1}^{N} X_i\right)^{1/N}$$

Now, $X_g = \left(\prod_{i=1}^{N} X_i\right)^{1/N}$

$\Rightarrow \log(X_g) = \frac{1}{N}\log\left(\prod_{i=1}^{N} X_i\right)$

$= \frac{1}{N}.[\log X_1 + \log X_2 + ... + \log X_N]$

$= \frac{1}{N}\sum_{i=1}^{N} \log X_i$ [Arithmetic mean of the logarithms of the observations]

$= \text{GM(say)}$

So, $X_g = \text{Antilog(GM)}$

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Thus geometric mean is the antilogarithm of the arithmetic mean of logarithms of the observations.

The geometric mean for grouped data of a set of "N" observations grouped into "n" number of groups with mid-values and frequencies of the different classes, respectively, given as

Mid-values of different classes (x_i)	x_1	x_2	$x_3 \ldots, x_i, \ldots x_{n-2}$	x_{n-1}	x_n
Class Frequency	f_1	f_2	$f_3 \ldots, f_i, \ldots f_{n-2}$	f_{n-1}	f_n

is given as

$$X_g = \left(\prod x_i^{f_i}\right)^{1/\sum_{i=1}^{n} f_i} = \left(x_1^{f_1} . x_2^{f_2} \ldots x_n^{f_n}\right)^{1/N}$$

Using similar technique, we have

$$X_g = \left(x_1^{f_1} . x_2^{f_2} \ldots x_n^{f_n}\right)^{1/N} = \left(\prod x_i^{f_i}\right)^{1/\sum_{i=1}^{n} f_i}$$

$$\Rightarrow \log(X_g) = \frac{1}{N}\log\left[x_1^{f_1} . x_2^{f_2} \ldots x_n^{f_n}\right]$$
$$= \frac{1}{N}[f_1 \log x_1 + f_2 \log x_2 + \ldots + f_n \log x_n]$$
$$= \frac{1}{N}\sum_{i=1}^{n} f_i \log x_i = \mathrm{AM}'(\text{say})$$

$$\therefore X_g = \mathrm{Alog}(\mathrm{AM}')$$
$$= \text{Antilogarithm of weighted arithmetic mean of the logarithmsof the mid values of different classes.}$$

For grouped frequency data, x_i is taken as the mid-values of the i-th class

With the help of log conversion or scientific calculator, one can easily find out the geometric mean.

Example 3.5

If we go back to the data of fish weight of 20 fishes, then what should be the GM?

Pond A	1.2	0.9	1.5	1.3	2.1	2.0	1.3	1.6	2.0	1.5	1.6	1.7	2.1	1.2	1.3	0.9	1.6	1.4	1.9	1.7

Solution The geometric mean for 20 fishes is given by $G = (1.2 \times 0.9 \times 1.5 \times 1.3 \times \ldots \times 1.9 \times 1.7)^{1/20} = (3202.566)^{1/20} = 1.497$ lb

Example 3.6

Let us find out the geometric mean of body weights of ten chicks at birth using the following data:

Chick No	1	2	3	4	5	6	7	8	9	10
Body weight (g)	42	32	55	27	30	35	45	52	47	40

Solution: Method 1 The geometric mean for ten chicks is given by $G = (42 \times 32 \times 55 \times 27 \times 30 \times 35 \times 45 \times 52 \times 47 \times 40)^{1/10} = (9219104294400000.00)^{1/10} = 39.49$

Method 2: We can calculate geometric mean as the antilogarithm of the arithmetic mean of logarithms of the observations. Thus, we have

$$G = \mathrm{Antilog}[(1/10)(\log 42 + \log 32 + \log 55 + \log 27 + \log 30 + \log 35 + \log 45 + \log 52 + \log 47 + \log 40)]$$
$$= \mathrm{Antilog}[(1/10)\ (1.623 + 1.505 + 1.740 + 1.431 + 1.477 + 1.544 + 1.653 + 1.716 + 1.672 + 1.602)]$$
$$= \mathrm{Antilog}(1.5965) = 39.49$$

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Example 3.7
Let us find out the geometric mean of the body weights of 60 poultry birds from the following frequency distribution:

Body weight (g)	Mid-value (x_i)	Frequency (f)
1118.5–1319.5	1219	8
1319.5–1520.5	1420	10
1520.5–1721.5	1621	9
1721.5–1922.5	1822	10
1922.5–2123.5	2023	4
2123.5–2324.5	2224	9
2324.5–2525.5	2425	10

Solution From the above frequency distribution, we have the geometric mean

$$X_g = \left(x_1^{f_1}.x_2^{f_2}\ldots x_n^{f_n}\right)^{1/\sum_{i=1}^{n} f_i}.$$

$$\begin{aligned}
\mathrm{Log}(X_g) &= \frac{1}{\sum_{i=1}^{n} f_i}\log\left(\prod_{i=1}^{n} x_i^{f_i}\right)\\
&= \frac{1}{60}\log\left(1219^8.1420^{10}.1621^9.....2425^{10}\right)\\
&= \frac{1}{60}[8\log(1219)+10\log(1420)+9\log(1621)+10\log(1822)+4\log(2023)\\
&\quad +9\log(2224)+10\log(2425)]\\
&= \frac{1}{60}[8\times 3.086+10\times 3.1523+9\times 3.2098+10\times 3.2605+4\times 3.3060\\
&\quad +9\times 3.3471\times 10\times 3.3847]\\
&= \frac{1}{60}[194.8998] = 3.2483\\
\therefore X_g &= \mathrm{Alog}(3.2483) = 1771.4516\,\mathrm{g}
\end{aligned}$$

Thus the geometric mean of the above simple frequency distribution is 1771.4516 g.

Merits and Demerits of Geometric Mean
The definition of geometric mean is clear-cut, and there is no ambiguity in defining geometric mean; geometric mean is based on all observations but it is not so easy to calculate or understand the physical significance of GM; mathematical treatments are not so easy as in the case of arithmetic mean. If one of the values in the given data set is zero, then the GM is also zero for the whole data set. Compared to AM, GM is least affected by the inclusion/deletion of extreme value in the data set. Let us discuss some of the important properties of GM.

(a) Let us suppose we have k number of samples; $G_1, G_2, \ldots, G_k$ are the geometric means of the samples, and $n_1, n_2, \ldots, n_k$ are the number of observations of the respective samples; then the combined geometric mean is given by

$$\begin{aligned}
G &= \left(G_1^{n_1}.G_2^{n_2}.....G_k^{n_k}\right)^{1/\sum_{i=1}^{k} n_i}\\
&= \prod_{i=1}^{k} G_i^{1/\sum_{i=1}^{k} n_i}\\
\text{or, } \log G &= \frac{1}{\sum_{i=1}^{1} n_i}\sum_{i=1}^{k} n_i \log[G_i]
\end{aligned}$$

(b) If all the observations are equal to a constant, say M, then the geometric mean is also equal to M.
(c) Likewise to that of AM, GM of a set of observations also depends on change of origin and scale.

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3.1.3 Harmonic Mean

Harmonic mean of a set of "N" observations X_1, X_2,X_3,. . .,X_i,. . .,X_N is defined as the "the reciprocal of the arithmetic mean of the reciprocals of the observations".

Thus, harmonic mean H.M. $= \dfrac{N}{\sum_{i=1}^{N} \dfrac{1}{x_i}}$.

For grouped data of a set of "N" observations grouped into "n" number of groups with mid-values and frequencies of the different classes, respectively, given as

Mid-values of different classes (x_i)	x_1	x_2	x_3. . ., x_i,. . .x_{n-2}	x_{n-1}	x_n
Class frequency	f_1	f_2	f_3. . ., f_i,. . .f_{n-2}	f_{n-1}	f_n

the harmonic mean is given as $\mathrm{H} = \dfrac{\sum_{i=1}^{n} f_i}{\sum_{i=1}^{n} f_i / x_i}$

Example 3.8
Let us take the example of the fish weights (in pound) in pond A of the Example 3.1:

Pond A	1.2	0.9	1.5	1.3	2.1	2.0	1.3	1.6	2.0	1.5	1.6	1.7	2.1	1.2	1.3	0.9	1.6	1.4	1.9	1.7

to find the harmonic mean of the above fish weights.

Solution Here the number of observations is 20. So the harmonic mean of the fish weights (in pound) is given by

$$\mathrm{H.M.} = \frac{20}{\sum_{i=1}^{20} \frac{1}{x_i}}$$

$$= \frac{18}{\frac{1}{1.2}+\frac{1}{0.9}+\frac{1}{1.5}+\frac{1}{1.3}+\frac{1}{2.1}+\frac{1}{2.0}+\frac{1}{1.3}+\frac{1}{1.6}+\frac{1}{2.0}+\frac{1}{1.5}+\frac{1}{1.6}+\frac{1}{1.7}+\frac{1}{2.1}+\frac{1}{1.2}+\frac{1}{1.3}+\frac{1}{0.9}+\frac{1}{1.6}+\frac{1}{1.4}+\frac{1}{1.9}+\frac{1}{1.7}}$$

$$= \frac{20}{13.77437} = 1.4519\,\mathrm{lb}$$

Example 3.9
To find the harmonic mean of milk production (liter) per day from a data of 20 days for a particular cow from the following frequency distribution:

Milk(l/day)	10	12	14	16	18
Frequency	5	7	2	2	4

Solution This is a simple frequency distribution; hence, the formula for getting harmonic mean is

$$\mathrm{H.M} = \frac{\sum_{i=1}^{n} f_i}{\sum_{i=1}^{n} f_i / x_i} = \frac{\sum_{i=1}^{5} f_i}{\sum_{i=1}^{5} f_i / x_i}$$

$$= \frac{5+7+2+2+4}{\frac{5}{10}+\frac{7}{12}+\frac{2}{14}+\frac{2}{16}+\frac{4}{18}}$$

$$= \frac{20}{1.5734} = 12.711$$

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Example 3.10
To find the harmonic mean of the body weights of 60 poultry birds from the following frequency distribution:

Body weight (g)	Mid-value (x_i)	Frequency (f)
1118.5–1319.5	1219	8
1319.5–1520.5	1420	10
1520.5–1721.5	1621	9
1721.5–1922.5	1822	10
1922.5–2123.5	2023	4
2123.5–2324.5	2224	9
2324.5–2525.5	2425	10

Solution From the above frequency distribution, we have harmonic mean

$$\text{H.M} = \frac{\sum_{i=1}^{n} f_i}{\sum_{i=1}^{n} (f_i/x_i)} = \frac{8+10+....+9+10}{\frac{8}{1219}+\frac{10}{1420}+\frac{9}{1621}+\frac{10}{1822}+\frac{4}{2023}+\frac{9}{2224}+\frac{10}{2425}}$$
$$= \frac{60}{0.00656+0.00704+0.00555+0.00549+0.00198+0.00405+0.00412}$$
$$= \frac{60}{0.03479} = 1724.4676\,\text{g}$$

Merit and Demerits of a Harmonic Mean
Like other two means, viz., the arithmetic mean and geometric mean, the harmonic mean is also defined clearly; it is also based on all observations but comparatively complicated in calculation and understanding. Moreover, if one of the observations is zero, then it is difficult to work out the harmonic mean. The harmonic mean of "n" number of constants is the constant. Let there be a set of "N" observations, each having a constant value, say "U," so their harmonic mean $= \frac{N}{\sum_{i=1}^{N} \frac{1}{U}} = \frac{N}{\frac{N}{U}} = U$.

3.1.4 Use of Different Types of Means

If one critically examines the values of three types of means from the same data of 60 poultry birds as given in Examples 3.3, 3.6, and 3.10, one can find that AM > GM > HM (AM = 1818.65 g, GM = 1771.4516 g, HM = 1724.4676 g). In fact the relation among the three types of means is that AM ≥ GM ≥ HM. Thus for a given set of data, HM has the lowest value. This type relationship among the three means raises the question as to which type of mean should be used to represent a particular data set. Arithmetic mean is widely used in most of the situations where the data generally do not follow any definite pattern. It can be used to have an overview of both the discrete as well as continuous characters. Before using one should check for the existence of any extreme value(s) in the data set. Geometric mean is generally used when values of a series of observations change in geometric progression (i.e., values of the observations change in a definite ratio). Average rate of depreciation, compound rate of interest, etc. are the examples of some of the areas where geometric mean can effectively be used. GM is useful in the construction of index numbers. As GM gives greater weights to smaller items, it is useful in economic and socioeconomic data. Though the use of harmonic mean is very restricted, it has got ample uses in practical fields, particularly under changing rate scenario. Let us take the following example:

Example 3.11
Price of petrol changes fortnightly (mostly), and let us assume that a two-wheeler owner has fixed amount of money allocated on fuel from his

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monthly budget. So, the use of petrol is to be managed in such a way that both the conditions are satisfied (monthly expenditure on petrol remains constant and the prices of petrol changes over the fortnights), i.e., the objective is to get average price of petrol per liter, which will fix the amount of average consumption of petrol/month vis-à-vis the mileage he can run the two wheelers.

Solution Let fortnightly expenditure on petrol be Rs and "E" and the prices of petrol for "n" consecutive fortnights be p_1, p_2,. . ., p_n, respectively. Thus the amounts of petrol used in n fortnights are $\frac{E}{p_1}, \frac{E}{p_2}, \ldots, \frac{E}{p_n}$, respectively. Then average fortnightly consumption of petrol is given by

$$= \frac{nE}{\frac{E}{p_1} + \frac{E}{p_2} + \ldots + \frac{E}{p_n}}$$

$$= \frac{nE}{E\left(\frac{1}{p_1} + \frac{1}{p_2} + \ldots + \frac{1}{p_n}\right)}$$

$$= \frac{n}{\sum_{i=1}^{n} 1/p_i} = \text{Harmonic mean of price of petrol}$$

3.1.5 Median

Median of a set of "N" number of observations $X_1, X_2, X_3, \ldots, X_N$ for variable X is defined as the value of the middlemost observation. When we talk about the value of the middlemost observation, then there is a need for arrangement of the data either in ascending or descending order, so that middlemost observation could be identified. One can easily find that the median of a set of observations divides the whole set of data set into two parts; below and above the median there are equal number of observations.

Example 3.12
Number of insects per plant is given as follows: 17, 27, 30, 26, 24, 18, 19, 28, 23, 25, and 20. Find out the median value of number of insects per plant.

Solution Let us arrange the data in ascending order of their values as follows: 17, 18, 19, 20, 23, 24, 25, 26, 27, 28, and 30. Here, we have 11 observations, so the middlemost observation is the (11–1)/2 + 1 = 6th observation and the value of the sixth observation is 24. Hence, the median value of number of insects per plant is 24.

Problem with this definition is that when number of observation is even, then one cannot have a unique middlemost observation; rather there would be two middlemost observations. In this type of situation, median is worked out by taking the average of the values of two middlemost observations. Let us consider the following example;

Example 3.13
Following table gives the fish production figures of 20 Indian states/union territories during 2011–2012. Find out the median fish production of the states.

State/UT	AP	Assam	Bihar	Chhatt-isgarh	Goa	Guja-rat	Hary-ana	Jhark-hand	Karn-ataka	Kerala	MP	Maha-rashtra	Orissa	Pondi-cherry	Punjab	Rajas-than	TN	Tri-pura	UP	WB
Production ('000 t)	1603	229	344	251	90	784	106	92	546	693	75	579	382	42	98	48	611	53	430	1472

Solution Here the number of states is 20, an even number; so the median value would be the average of the values of two middlemost observations, i.e., tenth and 11th observations after the states are arranged in order as follow:

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
State/UT	AP	WB	Guja-rat	Kerala	TN	Maha-rashtra	Karn-ataka	UP	Orissa	Bihar	Chhat-tisgarh	Assam	Haryana	Punjab	Jhark-hand	Goa	MP	Tripura	Rajas-than	Pondi-cherry
Production ('000 t)	1603	1472	784	693	611	579	546	430	382	344	251	229	106	98	92	90	75	53	48	42

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From the above arranged data, one can find that Bihar and Chhattisgarh occupy the middlemost positions. Therefore, the median value of fish production would be (344 + 251)/2 = 297.6 thousand tone.

Thus, calculation of median for even and odd number of observations is different. This situation, however, takes different forms for grouped data.

Steps in Calculation of Median from Raw Data

1. Arrange the raw data, either in ascending or descending order.
2. Locate the middlemost (for odd number of observation) or two middlemost observation (s)(for even number of observations).
3. When the total number of observations is odd, then the value of the middlemost observation would be the median, while the average of the two middlemost observations would be the median for even number of observations.

For grouped data, the median of a set of N number of observations $X_1, X_2, X_3, \ldots, X_N$ for variable X grouped into "n" number of classes as follows is given as

Class	Mid-value (x_i')	Frequency (f_i)	CF<	CF≥
X_1–X_2	x_1'	f_1	F_1	F_1'
X_2–X_3	x_2'	f_2	F_2	F_2'
X_3–X_4	x_3'	f_3	F_3	F_3'
:	:	:	:	:
:	:	:	:	:
:	:	:	:	:
:	:	:	:	:
:	:	:	:	:
X_n–X_{n+1}	x_n'	f_n	F_n	F_n'

$$\text{Me} = X_l + \frac{\frac{N}{2} - F_{me-1}}{f_{me}}.\text{CI}$$

where X_l = is the lower class boundary of the median class

N = total frequency

$F_{\text{me}-1}$ = cumulative frequency (less than type) of the class preceding the median class

f_{me} = frequency of the median class and CI = width of the median class

The first task for getting the median value from a classified data is to find out the median class from the cumulative frequency column of frequency distribution table; that means the class in which the middlemost observation(s) is lying. Then one can use the above formula to get median value. Step by step procedure of getting median from classified data is presented below:

Steps in Calculation of the Median from Grouped Data1

1. Identify the median class (i.e., the class containing N/2th or N/2 + 1th observation) from the cumulative frequency (less than type) column of the frequency distribution table.
2. Identify the lower class boundary (X_l), class width (CI), and the frequency (f_m) of the median class.
3. Identify the cumulative frequency (less than type) of the class preceding the median class (F_{me-1}) and the frequency of the median class, i.e., f_{me}.
4. Use the above values in the formula for median.

Example 3.14

Once again let us take the classified data for body weight of 60 poultry birds. Find out the median value of body weights from following frequency distribution table.

Body weight (g)	Mid-value (x_i)	Frequency (f)	CF<
1118.5–1319.5	1219	8	8
1319.5–1520.5	1420	10	18
1520.5–1721.5	1621	9	27
1721.5–1922.5	1822	10	37
1922.5–2123.5	2023	4	41
2123.5–2324.5	2224	9	50
2324.5–2525.5	2425	10	60

Solution From the above table, we have total number of observation, 60, an even number. Therefore, the median would be the average of

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the values of the two middlemost observations (viz., 30th and 31st observations). From the column of cumulative frequency, one can find that 30th and 31st observations are lying in class 1721.5–1922.5.

Lower boundary (X_l) of the median class = 1721.5.

Frequency of the median class = 10.

Cumulative frequency of the class preceding the median class = 27.

Class interval/width = 201.

Therefore the median $\text{Me} = X_l + \frac{\frac{N}{2} - F_{me-1}}{f_{me}}$.

$\text{CI} = 1721.5 + \frac{\frac{60}{2} - 27}{10} \times 201 = 1721.5 + 60.3 = 1781.8\,\text{g}$.

Note

1. For even number of observations in classified data, two middlemost observations may lie in two consecutive classes. In that case, one would have two median classes, and two medians are to be worked out using the above procedure as usual. Ultimately the median of the set of given data would be the average of the two median values worked out.
2. Median can also be worked from the intersection point of the two cumulative frequency (less than and more that type) curves.

Merits and Demerits of Median Median is easy to calculate and understand; it can also be used for qualitative data. But median is not defined rigidly as one could find for AM, GM, or HM. The median is also not based on all observation, to the median, one needs to have information on middlemost observations/classes. The median cannot be put under mathematical treatment easily. The median is comparatively more affected by sampling fluctuations.

Uses of the Median The median has got various uses in agriculture and allied fields as well as in industry. As this is basically a partition value, divide the whole population into two equal parts; it is used as an indicator stratifying the population. Most important use of median is found in qualitative data sets where the numerical measures of central tendency may not work suitably. The formula for median can very well be improvised in getting different partition values.

3.1.6 Partition Values (Percentiles, Deciles, and Quartiles)

Sometimes it becomes of interest to partition the whole population into different parts. For example, one may be interested to know the income level below which there are 90 % or 3/4th or 60 % of the people in a particular area. One may be interested in knowing the number of insects per plant below which 25 % or 1/4th, 70 %, or 90 % of the plants exist in a particular field. Thus, we are interested in partitioning the whole population into different quarters, different deciles, different percentiles, etc. Knowing these values one can take decision on different aspects of practical utility. The economic injury level population of different pests in different crops have been identified by the scientists. Knowledge of the percentage or deciles of plant populating below or above the corresponding economic injury level population will help the farmers in taking decision whether to go for chemical control measure or otherwise. It has already been discussed that median divides the whole population into two equal halves; below and above which there are 50 % observations; thus median can be thought of as fifth decile or second quartile in any set of data. One can work out different percentiles, deciles, or quartiles from the frequency distribution improvising the formula of median. The formula for median can be modified to work out different percentile/decile/quartile values by substituting "Np/100," "Nd/10," or "Nq/4" and the corresponding cumulative frequencies (less than type) in place of "N/2" in median formula; where "p," "d," and "q" denote for p-th percentile, d-th decile, and q-th quartile, respectively.

Thus, the formulae for percentiles, deciles, or quartiles are as follows:

$$30\text{th percentile or } P_{30} = X_l + \frac{\frac{30N}{100} - Fp_{30-1}}{fp_{30}}.\text{CI}$$

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X_l = is the lower class boundary of the 30th percentile class.
N = total frequency.
Fp_{30-1} = cumulative frequency (less than type) of the class preceding the 30th percentile class.
fp_{30} = frequency of the 30th percentile class.
CI = width of the 30th percentile class.

$$\text{6th decile or } D_6 = X_l + \frac{\frac{6N}{10} - Fd_{6-1}}{fd_6}.\text{CI}$$

X_l = is the lower class boundary of the sixth decile class.
N = total frequency.
$Fd_{_{6-1}}$ = cumulative frequency (less than type) of the class preceding the sixth deciles class.
fd_6 = frequency of the sixth decile class.
CI = width of the sixth decile class.

$$\text{3rd quartile or } Q_3 = X_l + \frac{\frac{3N}{4} - Fq_{3-1}}{fq_3}.\text{CI}$$

X_l = is the lower boundary of the third quartile class.
n = total frequency.
Fq_{3-1} = cumulative frequency (less than type) of the class preceding the third quartile class.
fq_3 = frequency of the third quartile class.
CI = width of the third quartile class.

Example 3.15

Let us take the example of body weight of 60 poultry birds once again and try to find out the body weights below which 40 %, 8/10 parts, and 3/4th birds exist. We have the following frequency distribution table:

Body weight (g)	Mid-value (x_i)	Frequency (f)	CF<
1118.5–1319.5	1219	8	8
1319.5–1520.5	1420	10	18
1520.5–1721.5	1621	9	27
1721.5–1922.5	1822	10	37
1922.5–2123.5	2023	4	41
2123.5–2324.5	2224	9	50
2324.5–2525.5	2425	10	60

Solution Thus the problem is to find out 40th percentile, eighth decile, and third quartile values for body weight of 60 poultry birds.

(a) *Calculation of 40th percentile value, i.e., P_{40}*

We have $N = 60$, P_{40} is the value of the $\frac{60\times40}{100} =$ 24th observation, and the 24th observation is lying in the third class, i.e., in 1520.5–1721.5 class.

$$\begin{aligned}\therefore P40 &= X_l + \frac{\frac{40N}{100} - FP_{40-1}}{fP_{40}}.\text{CI} \\ &= 1520.5 + \frac{\frac{40.60}{100} - 18}{9}.201 \\ &= 1520.5 + 134 = 1654.5\,\text{g}\end{aligned}$$

∴ There are 40 % (=24) poultry birds out of total 60 birds which have body weight 1654.5 g or less, and 60 % (=36) birds are having body weight above 1654.5 g.

(b) *Calculation of eighth decile value, i.e., D_8*

We have $N = 60$, D_8 is the value of the $\frac{60\times8}{10} =$ 48th observation and the 48th observation is lying in sixth class, i.e., in 2123.5–2324.5 class.

$$\begin{aligned}D_8 &= X_l + \frac{\frac{8N}{10} - Fd_{8-1}}{fd_8}.\text{CI} \\ &= 2123.5 + \frac{\frac{8.60}{10} - 41}{9}.201 \\ &= 2123.5 + 156.33 = 2279.83\,\text{g}\end{aligned}$$

∴ There are 8/10 parts(=48) poultry birds out of total 60 birds which have body weight 2279.83 g or less, and 2/8th (=12) birds are having body weight above 2279.83 g

(c) *Calculation of third quartile value, i.e., Q_3*

We have $N = 60$, Q_3 is the value of the $\frac{60\times3}{4}$ = 45th observation, and the 45th observation is lying in sixth class, i.e., in 2123.5–2324.5 class.

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$$Q_3 = X_l + \frac{\frac{3N}{4} - Fq_{3-1}}{fq_3}.\text{CI} = 2123.5 + \frac{\frac{3.60}{4} - 41}{9}.201 = 2123.5 + 89.33 = 2212.83\,\text{g}$$

Thus, there are 3/4th(=45) poultry birds out of total 60 birds which have body weight 2212.83 g or less, and 1/4th (=15) birds are having body weight above 2212.83 g.

3.1.7 Mode

It is not necessary that all the observations or all the classes in a given set of data have got equal frequency. One might be interested in knowing the observation or the value which is having maximum occurrence in a given data set, for the purpose mode is defined. Mode of a set of given data is defined as the value of the observation having maximum frequency.

Example 3.16
Let us suppose the following data are pertaining to the of panicle per plant (hill) in a paddy field: 12, 13, 15, 8, 6, 9, 15, 12, 10, 8, 7, 15, 10, 10, 8, 9, 10, 9, 13, and 10. Find out the mode of the number of panicle per plant.

No. of panicle/plant	6	7	8	9	10	12	13	15
Frequency	1	1	3	3	5	2	2	3

Thus, modal value of number of panicle per plant of paddy from the above data is found to be 10, as this value has maximum (5) frequency among all other values.

For grouped data mode of a set of N number of observations $X_1, X_2, X_3, \ldots, X_N$ for variable X is grouped into "n" number of classes as follows:

Class	Mid-value (x_i')	Frequency (f_i)
x_1-x_2	x_1'	f_1
X_2-x_3	x_2'	f_2
X_3-x_4	x_3'	f_3
:	:	:
:	:	:
X_n-x_{n+1}	x_n'	f_n

Now mode of the above data set is given as

$$\text{Mo} = X_l + \frac{f_{mo} - f_{mo-1}}{(f_{mo} - f_{mo-1}) + (f_{mo} - f_{mo+1})}.\text{CI}$$

where X_1 = the lower class boundary of the modal class.
f_{mo-1} = frequency of the class preceding the modal class.
f_{mo} = frequency of the modal class.
f_{mo+1} = frequency of the class following the modal class.
CI = width of the modal class.

The first step for getting modal value from a classified data is to find out the modal class from the frequency column of frequency distribution table; that means to identify the class in which maximum number of observations is lying. Then one can use the above formula to get modal value. Step by step procedure of getting mode from classified data is presented below:

Steps in Calculation of Mode from Grouped Data

1. Identify the modal class, i.e., the class having maximum frequency.
2. Identify the lower class boundary (X_l), class width (CI), and the frequency (f_m) of the modal class.
3. Identify the frequencies of the class preceding and following the modal classes, respectively (i.e., f_{mo-1} and f_{mo+1}).
4. Use the above values in the formula for mode.

Example 3.17
Let us take the example of body weight of 60 poultry birds once again to find out the mode of body weights birds. We have the following frequency distribution table:

Body weight (g)	Mid-value (x_i)	Frequency (f)
1118.5–1319.5	1219	8
1319.5–1520.5	1420	10
1520.5–1721.5	1621	9
1721.5–1922.5	1822	10
1922.5–2123.5	2023	4
2123.5–2324.5	2224	9
2324.5–2525.5	2425	10

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Solution Total number of observation (birds) = 60

From the frequency distribution table one can find that there are three classes, viz., second (1319.5–1520.5), fourth (1721.5–1922.5), and seventh (2324.5–2525.5), having same highest frequency, i.e., 10. Thus we are coming across with multimodal frequency distribution. A critical examination reveals that there is no problem in working out the modal values from the second and fourth classes, but getting a modal value from the seventh class, the last class of the frequency distribution, is not possible using the above formula for calculation of mode.

Let us try to find out the mode from the second class:

1. Modal class is 1319.5–1520.5.
2. Lower class boundary (X_l) =1319.5, class width (CI) = 201, and the frequency (f_m) = 10 of the modal class.
3. Frequency of the class preceding the modal class ($f_{m\text{-}1}$) = 8 and frequency of the class following the modal class (f_{m+1}) = 9.

So the mode

$$\begin{aligned}\text{Mo} &= X_l + \frac{f_{mo} - f_{mo-1}}{(fmo - fmo - 1) + (fmo - fmo + 1)}.\text{CI} \\ &= 1319.5 + \frac{10 - 8}{(10 - 9) + (10 - 8)}.201 \\ &= 1319.5 + 134.00 = 1453.50\,\text{g}\end{aligned}$$

Similarly one can also find out the mode corresponding to the fourth class.

Merits and Demerits of Mode Mode is easy to calculate and understand; it can also be used qualitative data. But mode is not defined rigidly like AM, GM, or HM. For a given set of data, one can have only one AM, GM, HM, and median values, respectively, but there might be more than one mode for some distributions like in Example 3.17. Mode is also not based on all observations, like median; to know the mode one need not know the information on observations at the beginning or at the end of the data set; one needs to have information on modal class and its preceding and following classes; information on rest of the classes are of least importance as far as calculation of modal value is concerned. If mode happens to lie in the last class of the frequency distribution, then it poses problem in its calculation. Mode cannot be put under mathematical treatment easily. Like median, mode also is comparatively more affected by sampling fluctuations.

Uses of Mode Mode has got various uses in agriculture and allied fields as well as in industry. As this is basically gives importance on concentration of observations, it plays vital role in qualitative data analysis. Mode is best used when number of observations is huge.

Relationship of the Mean, Median, and Mode No exact relationship among the arithmetic mean, median, and mode could be found. But for a moderately skewed (a dispersion property discussed in the next chapter) unimodal distribution, the following approximate relation holds good: *Mean – Mode = 3(Mean – Median)*. This can be used for approximate value of any one of the three if the other two are given. Moreover for symmetric distributions like normal distribution, *Mean = Median = Mode*.

3.1.8 Midpoint Range

Midpoint range of a set of "*N*" number of observations $X_1, X_2, X_3, \ldots, X_N$ for variable X is defined as the average of the maximum and minimum values of a given set of data. If "*M*" and "*m*" are the maximum and minimum values of a given set of data, respectively, the midpoint range is $(M + m)/2$. Thus, to get midpoint range of given set of data, may it be ungrouped or grouped data, one needs to know only the maximum and minimum values of the data set. Though very simple and easy to understand, as this measure is based on only two extreme values, it does not satisfy the criteria of good measure. As such it is affected by the extreme values in the data set and also by the sampling fluctuation.

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3.1.9 Selection of Proper Measure of Central Tendency

From the above discussions on different measures of central tendency, it is clear that all measures are not suitable to be used in every set of data. Selection of a particular measure mainly depends on the (a) type of data, (b) objective of the study, and (c) merits and demerits of the measures on hand. Though three types of means are based on all observation, these have their own merits and demerits and restrictive nature in use. Moreover, median and mode, though are useful measure for qualitative data, are not based on all observation for quantitative data. If the objective of the study is to find out the point or region of highest concentration of occurrence of the observations, then one can very well use mode. On the other hand, if one is interested in dissection of the population, then partition values may provide useful information. Thus, while selecting a measure, one should be very careful and should have thorough knowledge about the measures.

Trimmed Mean In many cases the arithmetic mean is affected by the presence of outlier (values are supposed to be different from the rest of the values of a given data set; thus outliers are generally high or low values compared to other values in a data set). On the other hand, the median is least affected by the presence of outlier in a data set compared to arithmetic mean. But arithmetic mean has got other advantages over median. To overcome the drawback of arithmetic mean in presence of outlier, trimmed mean has been advocated. *Trimmed mean is the arithmetic mean of the ordered data set after deleting a percentage of data points from both the ends of the ordered data set*. On the other hand, *trimming percentage is the percentage of data points at each end not considered for calculation of arithmetic mean*. Thus 10 % trimmed mean means 10 % data points from each end is not considered for calculation of mean; that means altogether 80 % middle observation are being included during calculation of trimmed mean.

Example 3.18
The following data are pertaining to the milk yield (kg/day) of ten different cows of particular breed. Find out the arithmetic mean and the 10% trimmed mean from the data, and conclude the arithmetic mean, trimmed mean, and median in describing the central tendency of the data.

5.6	15.6	35.6	12.5	14.5	14.6	15	16.5	13.4	15.9

Solution The arithmetic mean is calculated to be 5.6 + 15.6 + . . .13.4 + 15.9/10 = 15.92 kg/day.

The ordered data would be:

5.6	12.5	13.4	14.5	14.6	15	15.6	15.9	16.5	35.6

We have ten observations; hence, 10 % trimmed means were calculated, the mean leaving aside one observation at each end. Thus the arithmetic mean of 12.5, 13.4,.....16.5 would 12.5 + 13.4 +. . . + 15.9 + 16.5/8 = 14.75 kg/day

Now the median calculated from ordered data would be the average value of 14.6 and 15, i.e., 14.8 kg/day. Clearly due to the presence of two too low(5.6) and too high (35.6), the arithmetic mean was overestimated. On the other hand, the 10 % trimmed mean and the median result in same average of 14.75 and 14.8 kg/day, respectively. Thus, one can conclude that median and 10 % trimmed means are the better measure (least affected by the presence of outlier) of central tendency.

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3.2 Dispersion and Its Measures

We have already defined that *tendencies of the values of the observations in a given data set to remain scattered or dispersed from a particular value(observation) are known as dispersion.*

Example 3.19
Let us suppose that the run scored by two batsmen in ten different innings are:

Batsman A:	10	60	0	5	120	98	15	75	85	12
Batsman B:	35	45	52	47	62	56	37	40	65	41

A critical analysis reveals that both the batsmen have scored equal total runs, viz., 480 in ten innings, but the run scored by the batsman A varies between 0 and 120 while that of the batsman B is in between 35 and 65. Thus the scoring patterns of the two batsmen are not same; the batsman A has the tendency to score around the 48, the average score, whereas the batsman B has the tendency of scoring pattern to remain scattered from the average value 48. Thus, the run scored by the batsmen in different innings has same central tendency, but they differ in dispersion. So to know the nature of the data, or to explain the information hidden within a set of data, measure of central tendency only is not sufficient: one should explore the measure of dispersion also.

In this chapter we have seen that there are two types of measures of dispersions, viz., the absolute measures of dispersions and the relative measures of dispersion. Now the question is whether all the measures are applicable in every situation or are equally effective. To get answers to these queries, one should have clear-cut idea about the characteristics of good measures of dispersion. Ideally a good measure of dispersion should have the following characteristics:

(a) *A good measure of dispersion should be rigidly defined-,there should not be any ambiguity in defining the measure.*
(b) *A good measure of dispersion should be based on all observations.*
(c) *A good measure of dispersion should be easy to calculate.*
(d) *A good measure of dispersion should be easy to understand.*
(e) *A good measure of dispersion should be least affected by sampling fluctuations*
(f) *A good measure of dispersion should be readily acceptable for mathematical treatments.*
(g) *A good measure of dispersion should be least affected by the extreme values.*

In order to reflect the true nature of the data, a good measure should be based on all observations and must be defined without any ambiguity. To be applicable by varied range of users, a good measure of dispersion should be easy to understand and explain. For further application of a measure, it should be responsive to mathematical treatments and must be least affected either by sampling fluctuations or by extreme values in the data set.

With the above knowledge, let us now examine the different measures and their important properties:

3.2.1 Absolute Measures of Dispersion

The range, mean deviation, variance, standard deviation, quartile deviation, and moments are the prominent absolute measures. In the following sections, we shall discuss the measures:

3.2.1.1 Range

Range of a set of N observations $X_1, X_2, X_3, \ldots, X_N$ is defined as the difference between the

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maximum value and the minimum value of a set of data, i.e., $X_{max} - X_{min.}$ This is the simplest of all the measures of dispersion. Thus, to get range in a set of data, one need not to put the data under any rigorous processing, excepting to find out the two extreme values (the maximum and the minimum) in the given data set.

Example 3.20

Find out the range of egg-laying capacity of 100 birds from the following data.

Bird no	Egg/Year	Bird no	Egg/Year	Bird no	Egg/Year	Bird no	Egg/Year
1	170	26	173	51	164	76	122
2	182	27	185	52	168	77	154
3	224	28	212	53	148	78	158
4	243	29	182	54	212	79	169
5	243	30	168	55	157	80	144
6	218	31	130	56	130	81	158
7	245	32	240	57	205	82	253
8	252	33	157	58	144	83	261
9	192	34	121	59	187	84	222
10	171	35	187	60	117	85	154
11	212	36	179	61	198	86	202
12	205	37	212	62	130	87	151
13	185	38	182	63	144	88	253
14	221	39	243	64	130	89	222
15	118	40	168	65	144	90	250
16	138	41	218	66	159	91	259
17	158	42	223	67	174	92	268
18	178	43	228	68	189	93	277
19	198	44	233	69	204	94	286
20	218	45	238	70	219	95	295
21	238	46	243	71	234	96	304
22	258	47	248	72	249	97	313
23	278	48	253	73	264	98	322
24	298	49	258	74	279	99	331
25	318	50	263	75	294	100	340

From the above data, it is clear that the variable egg-laying capacity (X) has maximum value 340 (X_{max}) and minimum value 117 (X_{min}). Therefore, the range of egg-laying capacity of 100 poultry birds is $(X_{max} - X_{min}) = 340–117 = 223$ eggs/year.

Example 3.21

Following table gives the milk yield (kilogram/month) of 100 cows in certain village. Find out the range of monthly milk yield from the given data.

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Cow no	MM*	Cow no	MM*	Cow no	MM*	Cow no	MM*
1	275	26	250	51	256	76	224
2	287	27	262	52	260	77	256
3	329	28	289	53	240	78	260
4	348	29	259	54	304	79	271
5	348	30	245	55	249	80	246
6	323	31	207	56	222	81	260
7	350	32	317	57	297	82	355
8	357	33	234	58	236	83	363
9	297	34	200	59	279	84	324
10	276	35	264	60	213	85	256
11	317	36	256	61	290	86	304
12	310	37	289	62	222	87	253
13	290	38	259	63	236	88	355
14	326	39	320	64	222	89	324
15	223	40	245	65	236	90	352
16	243	41	295	66	251	91	361
17	263	42	300	67	266	92	370
18	283	43	305	68	281	93	379
19	303	44	310	69	296	94	388
20	323	45	315	70	311	95	397
21	343	46	320	71	326	96	406
22	363	47	325	72	341	97	315
23	383	48	330	73	356	98	325
24	403	49	335	74	371	99	285
25	424	50	340	75	386	100	242

Note: MM* = Milk yield(kg) per month

Milk yield among the given 100 cows has the maximum (X_{max}) and minimum (X_{min}) values 424 kg and 200 kg, respectively. Therefore, the range of monthly milk yield of 100 cows is $Rx = X_{max} - X_{min} = 424 - 200 = 224$ kg per month.

Merits and Demerits of Range

1. Range is rigidly defined and can be calculated easily.
2. It is easy to understand and also convincing.
3. Though, to find out range in a given data set, all the observations are required to be examined, its calculation is based on only two values in the given entire data set.
4. Range cannot be worked out if there are missing value(s).
5. Range is difference between the two extreme values in a given data set, so it is very much affected by sampling fluctuation.

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Uses of Range In spite of all these drawbacks, range is being used in many occasions only because of its simplicity and to have a firsthand information on variation of the data. Range can be used in any type of continuous or discrete variables. It is easy to calculate so an ordinary person can also use it. It is hard to find any field of study where range has not been used to get firsthand information about a given data set.

3.2.1.2 Mean Deviation

Mean deviation of a set of N observations $X_1, X_2, X_3, \ldots, X_N$ of a variable "X" about any arbitrary point "A" is defined as the mean of the absolute deviation of different values of the variable from the arbitrary point "A" and may be denoted as

$$\mathrm{MD}_A = \frac{1}{N}\sum_{i=1}^{N}|X_i - A|$$

For grouped data mean deviation about an arbitrary point A of a set of N number of observations $X_1, X_2, X_3, \ldots, X_N$, of the variable X grouped into "n" number of classes with mid-values and frequencies of different classes given as below:

Mid-values(x_i)	x_1	x_2	$x_3 \ldots, x_i, \ldots x_{n-2}$	x_{n-1}	x_n
Frequency	f_1	f_2	$f_3 \ldots, f_i, \ldots f_{n-2}$	f_{n-1}	f_n

$$\mathrm{MD}_A = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i|x_i - A|$$

The deviation from arbitrary point can suitably be replaced by the arithmetic mean ($\overline{X}$), median (M_e), or mode (M_o) to get mean deviation from arithmetic mean or median or mode, respectively, and the respective formula is given below:

Mean deviation from	Ungrouped data	Grouped data
AM	$\frac{1}{N}\sum_{i=1}^{N}\lvert Xi - \overline{X}\rvert$	$\frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i\lvert xi - \overline{X}\rvert$
Median	$\frac{1}{N}\sum_{i=1}^{N}\lvert Xi - M_e\rvert$	$\frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i\lvert xi - M_e\rvert$
Mode	$\frac{1}{N}\sum_{i=1}^{N}\lvert Xi - M_o\rvert$	$\frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i\lvert xi - M_o\rvert$

Example 3.22

Following table gives the average meat weight (kg) from ten different Indian breeds of sheep. Find out the mean deviations from arbitrary value 18 kg, arithmetic mean, median, and mode.

Breed of sheep	Meat (kg) at 12 month age
Gaddi	14
Rampur Bushair	18
Chokla	18
Nali	18
Marwari	21
Magra	28
Malpura	21
Sonadi	19
Patanwadi	22
Muzaffarnagari	25

As we are dealing with ungrouped data, there would be no change in arithmetic mean and mode if we arrange the data in order. On the other hand, this arrangement will facilitate to find out the median. Thus, using the arranged data, one can find that the (a) arithmetic mean of the given data set is $\overline{X} = \frac{1}{10}[14 + 18 + 18 + \ldots + 25 + 28] = 20\,\mathrm{kg}$; (b) median is average value of the fifth and sixth observations, i.e., (19 + 21)/2 = 20 kg, and (c) mode of the given data set is 18 kg. Now using these information, one can frame the following table:

Breed of sheep	Meat (kg) at 12 month age (X_i)	$\lvert X_i - 18\rvert$	$\lvert X_i - \overline{X}\rvert$	$\lvert X_i - M_e\rvert$	$\lvert X_i - M_o\rvert$
Gaddi	14	4	6	6	4
Nali	18	0	2	2	0
Rampur Bushair	18	0	2	2	0
Chokla	18	0	2	2	0
Sonadi	19	1	1	1	1

(continued)

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Breed of sheep	Meat (kg) at 12 month age (X_i)	$\lvert X_i - 18\rvert$	$\lvert X_i - \overline{X}\rvert$	$\lvert X_i - M_e\rvert$	$\lvert X_i - M_o\rvert$
Malpura	21	3	1	1	3
Marwari	21	3	1	1	3
Patanwadi	22	4	2	2	4
Muzaffarnagari	25	7	5	5	7
Magra	28	10	8	8	10
Average	**20**	**3.2**	**3**	**3**	**3.2**

Thus, we have

$$\begin{aligned}\mathrm{MD}_{18} &= \frac{1}{10}\big[|14-18| + |18-18| + \ldots\ldots \\ &\qquad + |25-18| + |28-18|\big] \\ &= \frac{1}{10}[4 + 0 + \ldots\ldots + 7 + 10] \\ &= \frac{32}{10} = 3.2\,\mathrm{kg}.\end{aligned}$$

$$\begin{aligned}\mathrm{MD} &= \frac{1}{10}[|14-20| + |18-20| + \ldots\ldots \\ &\qquad + |25-20| + |28-20|] \\ &= \frac{1}{10}[6 + 2 + \ldots\ldots + 5 + 8] \\ &= \frac{30}{10} = 3.0\,\mathrm{kg}.\end{aligned}$$

$$\begin{aligned}\mathrm{MD}_{Me} &= \frac{1}{10}[|14-20| + |18-20| + \ldots\ldots \\ &\qquad + |25-20| + |28-20|] \\ &= \frac{1}{10}[6 + 2 + \ldots\ldots + 5 + 8] \\ &= \frac{30}{10} = 3.0\,\mathrm{kg}.\end{aligned}$$

$$\begin{aligned}\mathrm{MD}_{Mo} &= \frac{1}{10}[|14-18| + |18-18| + \ldots\ldots \\ &\qquad + |25-18| + |28-18|] \\ &= \frac{1}{10}[4 + 0 + \ldots\ldots + 7 + 10] \\ &= \frac{32}{10} = 3.2\,\mathrm{kg}.\end{aligned}$$

For a frequency distribution, the above formulae for calculation of mean deviation from an arbitrary point "A," mean, median, and mode may be calculated using the following formulae:

1. $$\mathrm{MD}_A = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i |x_i - A|$$

2. $$\mathrm{MD} = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i \left|x_i - \overline{X}\right|$$

3. $$\mathrm{MD}_{Me} = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{\mathrm{n}} f_i |x_i - Me|$$

4. $$\mathrm{MD}_{Mo} = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{\mathrm{n}} f_i |x_i - Mo|$$

For a grouped frequency, distribution x_i is taken as the mid-value of the i-th class.

Example 3.23
Following table gives the frequency distribution for 100 poultry birds with respect to their egg-laying capacity per year. Using the data, find out the mean deviation from 200, mean, median, and mode.

Egg class	117–144	145–172	173–200	201–228	229–256	257–284	285–312	313–340
Frequency	5	10	14	31	20	10	7	3

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From the above information, let us make following frequency table:

Class	Frequency (f)	x_i	CF<	$f_i x_i$	$\lvert x_i - 200\rvert$	$f_i \lvert x_i - 200\rvert$	$\lvert x_i - \overline{X}\rvert$	$f_i \lvert x_i - \overline{X}\rvert$	$\lvert x_i - Me\rvert$	$f_i \lvert x_i - Me\rvert$	$\lvert x_i - Mo\rvert$	$f_i \lvert x_i - Mo\rvert$
117–144	5	130.5	5	652.5	69.5	347.5	90.72	453.60	88.79	443.95	86.89	434.45
145–172	10	158.5	15	1585.0	41.5	415.0	62.72	627.20	60.79	607.90	58.89	588.90
173–200	14	186.5	29	2611.0	13.5	189.0	34.72	486.08	32.79	459.06	30.89	432.46
201–228	31	214.5	60	6649.5	14.5	449.5	6.72	208.32	4.79	148.49	2.89	89.59
229–256	20	242.5	80	4850.0	42.5	850.0	21.28	425.60	23.21	464.20	25.11	502.20
257–284	10	270.5	90	2705.0	70.5	705.0	49.28	492.80	51.21	512.10	53.11	531.10
285–312	7	298.5	97	2089.5	98.5	689.5	77.28	540.96	79.21	554.47	81.11	567.77
313–340	3	326.5	100	979.5	126.5	379.5	105.28	315.84	107.21	321.63	109.11	327.33
Total		1828		22,122		4025		3550.40		3511.80		3473.80
Average				221.22		40.25		35.50		35.12		34.74

The arithmetic mean is calculated as per the formula given in and found to be 221.22.

From the cumulative frequency (less than type), it is found that the median class is the fourth class, i.e., the class 201–228. Using the formula for calculation of median from grouped data (vido Example 3.14), the median of the distribution is calculated to be 219.29.

Mode of the distribution is lying within the class 201–228 and using the formula for calculation of mode from grouped data (vido Example 3.17), we have mode of the distribution as 217.39.

Using the above values for mean, median, and mode, respective mean deviations are worked out.

$$\mathrm{MD}_{200} = \frac{1}{\sum_{i=1}^{n} f_i} \sum_{i=1}^{n} f_i |x_i - 200|$$

$$= \frac{1}{100}[5 \times |130.5 - 200| + 15 \times |130.5 - 200| + \ldots + 7 \times |298.5 - 200| + 3 \times |326.5 - 200|]$$

$$= \frac{4025}{100} = 40.25\,\mathrm{no}$$

1. $$\mathrm{MD} = \frac{1}{\sum_{i=1}^{n} f_i} \sum_{i=1}^{n} f_i |x_i - \overline{X}|$$

$$= \frac{1}{100}[5 \times |130.5 - 221.22| + 15 \times |130.5 - 221.22| + \ldots + 7 \times |298.5 - 221.22| + 3 \times |326.5 - 221.22|]$$

$$= \frac{3550.45}{100} = 35.504 no.$$

2. MD_{Me}

$$\mathrm{MD}_{\mathrm{Me}} = \frac{1}{\sum_{i=1}^{n} f_i} \sum_{i=1}^{n} |x_i - \mathrm{Me}|$$

$$= \frac{1}{100}[5 \times |130.5 - 219.29| + 15 \times |130.5 - 219.29| + \ldots + 7 \times |298.5 - 219.29| + 3 \times |326.5 - 219.29|]$$

$$= \frac{3511.80}{100} = 35.118 no.$$

3. $\mathrm{MD}_{\mathrm{Mo}}$

$$MD_{\mathrm{Mo}} = \frac{1}{\sum_{i=1}^{n} f_i} \sum_{i=1}^{n} |x_i - \mathrm{Mo}|$$

$$= \frac{1}{100}[5 \times |130.5 - 217.39| + 15 \times |130.5 - 217.39| + \ldots + 7 \times |298.5 - 217.39| + 3 \times |326.5 - 217.39|]$$

$$= \frac{3473.80}{100} = 34.738 no.$$

Mean deviations are good measures of dispersion, but these are defined only for absolute values of the deviations. In fact, because of wide acceptability and easy comprehension, mean deviation from mean is widely used over other measures.

Example 3.24

Let us take the problem of milk yield per month for 100 cows as given in the following table. Find

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out the mean deviation from arbitrary point 300, arithmetic mean, median, and mode.

Milk class	220–228	228–256	256–284	284–312	312–340	340–368	368–396	396–424
Frequency	8	14	21	18	16	13	6	4

Solution This is an example of continuous variable, milk yield per month in kilogram. From the given information and using the formulae for calculation of arithmetic mean, median, and mode, one can have the following measures:

AM = 298.84 kg, median = 294.889 kg, and mode = 275.6 kg.

Class	Frequency (f)	x_i	CF<	$f_i x_i$	$\lvert x_i - 300\rvert$	$f_i\lvert x_i - 300\rvert$	$\lvert x_i - \overline{X}\rvert$	$f_i\lvert x_i - \overline{X}\rvert$	$\lvert x_i - Me\rvert$	$f_i\lvert x_i - Me\rvert$	$\lvert x_i - Mo\rvert$	$f_i\lvert x_i - Mo\rvert$
220–228	8	214	8	1712	86	688	84.84	678.72	81	648	62	496
228–256	14	242	22	3388	58	812	56.84	795.76	53	742	34	476
256–284	21	270	43	5670	30	630	28.84	605.64	25	525	6	126
284–312	18	298	61	5364	2	36	0.84	15.12	3	54	22	396
312–340	16	326	77	5216	26	416	27.16	434.56	31	496	50	800
340–368	13	354	90	4602	54	702	55.16	717.08	59	767	78	1014
368–396	6	382	96	2292	82	492	83.16	498.96	87	522	106	636
396–424	4	410	100	1640	110	440	111.16	444.64	115	460	134	536
Total	100			29,884		4216		4190.48		4214		4480
Average				298.84		42.16		41.90		42.14		44.80

Using the above values for mean, median, and mode, respective mean deviations are worked out.

$$\begin{aligned}\mathrm{MD}_{300} &= \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i|x_i - 300| \\ &= \frac{1}{100}[8 \times |214 - 300| + 14\times \\ &\quad |242 - 300| + \ldots + 7 \times |382 - 300| \\ &\quad + 3 \times |410 - 300|] \\ &= \frac{4216}{100} = 42.16\,\mathrm{kg}\end{aligned}$$

4. $$\begin{aligned}\mathrm{MD} &= \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i\left|x_i - \overline{X}\right| \\ &= \frac{1}{100}[8 \times |214 - 298.84| + 14\times \\ &\quad |242 - 298.84| + \ldots + 7\times \\ &\quad |382 - 298.84| + 3 \times |410 - 298.84|] \\ &= \frac{4190.48}{100} = 41.90\,\mathrm{kg}\end{aligned}$$

5. $$\begin{aligned}\mathrm{MD}_{Me} &= \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i|x_i - Me| \\ &= \frac{1}{100}[8 \times |214 - 294.89| + 14\times \\ &\quad |242 - 294.89| + \ldots + 7\times \\ &\quad |382 - 294.89| + 3 \times |410 - 294.89|] \\ &= \frac{4214}{100} = 42.14\,\mathrm{kg}\end{aligned}$$

$$\begin{aligned}\mathrm{MD}_{Mo} &= \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i|x_i - Mo| \\ &= \frac{1}{100}[8 \times |214 - 275.60| + 14 \\ &\quad \times |242 - 275.60| + \cdots + 7\times \\ &\quad |382 - 275.60| + 3 \times |410 - 275.60|] \\ &= \frac{4480}{100} = 44.80\,\mathrm{kg}\end{aligned}$$

3.2.1.3 Standard Deviation

To avoid the criticism of taking only absolute values of the deviations in case of mean

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deviation, a measure known as *variance* has been proposed by taking mean of the squared deviations from arithmetic mean. And the positive square root of the variance is termed as standard deviation. Thus we have for N number of observations $X_1, X_2, X_3,\ldots,X_N$ for variable X the variance as $\sigma_X^2 = \frac{1}{N}\sum_{i=1}^{N}\left(X_i - \overline{X}\right)^2$, where $\overline{X}$ is the arithmetic mean of the variable X based on $X_1, X_2, X_3,\ldots,X_N$. Therefore, standard deviation is given as $\sigma_X = +\sqrt{\frac{1}{N}\sum_{i=1}^{N}\left(X_i - \overline{X}\right)^2}$

For grouped data variance is defined as follows:

For a set of N number of observations $X_1, X_2, X_3,\ldots,X_N$, grouped in "n" number of classes with mid-values and frequencies of different classes as given below

Mid-values(x_i)	x_1	x_2	$x_3\ldots,x_i,\ldots x_{n-2}$	x_{n-1}	x_n
Frequency	f_1	f_2	$f_3\ldots,f_i,\ldots f_{n-2}$	f_{n-1}	f_n

Variance is given as $\sigma_X^2 = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i\left(x_i - \overline{X}\right)^2$ and the standard deviation as $\sigma_X = +\sqrt{\frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i\left(x_i - \overline{X}\right)^2}$

Variance can also be written as:

1. *Ungrouped data*

$$\sigma^2{}_X = \frac{1}{N}\sum_{i=1}^{N}\left(X_i - \overline{X}\right)^2 = \frac{1}{N}\sum_{i=1}^{N}\left(X_i{}^2 + \overline{X}^2 - 2X_i.\overline{X}\right)$$
$$= \frac{1}{N}\sum_{i=1}^{N}X_i{}^2 - 2\overline{X}\frac{1}{N}\sum_{i=1}^{N}X_i + \frac{1}{N}\sum_{i=1}^{N}\overline{X}^2$$
$$= \frac{1}{N}\sum_{i=1}^{N}X_i^2 - 2\overline{X}^2 + \overline{X}^2 = \frac{1}{N}\sum_{i=1}^{N}X_i^2 - \overline{X}^2$$

2. *Similarly for grouped data*

$$\sigma_X^2 = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i\left(x_i - \overline{X}\right)^2 = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i\left(x_i{}^2 + \overline{X}^2 - 2x_i.\overline{X}\right)$$
$$= \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i x_i{}^2 - 2\overline{X}\frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i x_i + \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i\overline{X}^2$$
$$= \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i x_i{}^2 - 2\overline{X}^2 + \overline{X}^2 = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i x_i{}^2 - \overline{X}^2$$

where f_i and x_i are the frequency and mid-value of the i-th class.

Example 3.25

Find the variance of meat weight (kg) of ten different breeds of sheep from the following data.

Breed of sheep	*Gaddi*	*Rampur Bushair*	*Chokla*	*Nali*	*Marwari*	*Magra*	*Malpura*	*Sonadi*	*Patanwadi*	*Muzaffarnagari*
Meat (kg) at 12 month age	14	18	18	18	21	28	21	19	22	25

Method 1: Using the $\sigma_X^2 = \frac{1}{N}\sum_{i=1}^{N}\left(X_i - \overline{X}\right)^2$

Let us construct the following table and get the totals and average of each column. From the first column we get arithmetic mean as 20.4 kg.

Breed of sheep	Meat (kg) at 12 month age (x_i)	$\left(X_i - \overline{X}\right)^2$
Gaddi	14	40.96
Rampur Bushair	18	5.76
Chokla	18	5.76
Nali	18	5.76

(continued)

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Breed of sheep	Meat (kg) at 12 month age (x_i)	$(X_i - \overline{X})^2$
Marwari	21	0.36
Magra	28	57.76
Malpura	21	0.36
Sonadi	19	1.96
Patanwadi	22	2.56
Muzaffarnagari	25	21.16
Total	**204**	**142.4**
Mean	**20.4**	**14.24**

Now using this value of arithmetic mean, one can have $\sigma_X^2 = \frac{1}{N}\sum_{i=1}^{N}(x_i - \overline{X})^2 = \frac{142.4}{10} = 14.24\,\text{kg}^2$

Method 2 Using the formula $\sigma_X^2 = \frac{1}{N}\sum_{i=1}^{N} X_i^2 - \overline{X}^2$

Let us construct the following table and get the totals and average of each column. Using the arithmetic mean from first column in the above formula for variance, we have:

Breed of Sheep	Meat (kg) at 12 month age (x_i)	X_i^2
Gaddi	14	196
Rampur Bushair	18	324
Chokla	18	324
Nali	18	324
Marwari	21	441
Magra	28	784
Malpura	21	441
Sonadi	19	361
Patanwadi	22	484
Muzaffarnagari	25	625
Total	**204**	**4304**
Mean	**20.4**	**430.4**

$$\sigma_X^2 = \frac{1}{N}\sum_{i=1}^{N} X_i^2 - \overline{X}^2 = 430.4 - 20.4^2 = 14.24\,\text{kg}^2$$

For calculation of variance from frequency distribution, let us take the following example:

Example 3.26
Using the table of frequency distribution for 100 poultry birds with respect to their egg-laying capacity per year, find out the variance.

Egg class	117–144	145–172	173–200	201–228	229–256	257–284	285–312	313–340
Frequency	5	10	14	31	20	10	7	3

Class	Frequency	x_i	$f_i x_i$	x_i-AM	$(x_i\text{-AM})^2$	$f_i(x_i\text{-AM})^2$
117–144	5	130.50	652.50	90.72	8230.1184	41150.59
145–172	10	158.50	1585.00	62.72	3933.7984	39337.98
173–200	14	186.50	2611.00	34.72	1205.4784	16876.70
201–228	31	214.50	6650.00	6.72	45.1584	1399.91
229–256	20	242.50	4850.00	21.28	452.8384	9056.77
257–284	10	270.50	2705.00	49.28	2428.5184	24285.18
285–312	7	298.50	2090.00	77.28	5972.1984	41805.39
313–340	3	326.50	979.50	105.28	11083.8784	33251.64
Total		1828.00	22122.00			207164.20
Average			221.20			2071.642

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From the above data, mean is calculated to be 27.585 cm, and using method 1 $\sigma_X^2 = \frac{1}{\sum_{i=1}^{n} f_i} \sum_{i=1}^{n} f_i (x_i - \overline{X})^2 = \frac{1}{100} \times 207164.2 = 2071.64$

Class	Frequency	x_i	$f_i x_i$	${x_i}^2$	$f_i {x_i}^2$
117–144	5	130.5	652.5	17030.25	85151.25
145–172	10	158.5	1585	25122.25	251222.5
173–200	14	186.5	2611	34782.25	486951.5
201–228	31	214.5	6649.5	46010.25	1426317.75
229–256	20	242.5	4850	58806.25	1,176,125
257–284	10	270.5	2705	73170.25	731702.5
285–312	7	298.5	2089.5	89102.25	623715.75
313–340	3	326.5	979.5	106602.25	319806.75
Total	100	1828	22,122		5100993.000
Average			221.22		51009.93

and using method 2 $\sigma_X^2 = \frac{1}{\sum_{i=1}^{n} f_i} \sum_{i=1}^{n} f_i {x_i}^2 - \overline{X}^2 = 51009.93 - 221.22^2 = 2071.64$

Thus, both the methods' result same variance.

Standard deviation worked out from the variance is $+\sqrt{\text{Variance}} = +\sqrt{2071.64} = 45.52 no.$

Variance is the squared quantity of standard deviation, as such properties of standard deviation and variance are same; moreover variance is easier to handle than standard deviation because of no question of taking square root. In the following sections, we shall discuss the important merits and demerits of variance.

Merits and Demerits of Variance

Variance is a good measure of dispersion as it is defined clearly, is based on all observations, is easy to understand, is easy to put under mathematical treatments, ranges between zero to infinity, and is least affected by sampling fluctuations or extreme values. Let us examine some of the important properties of variance.

(i) *Variance for a set of constant is zero.*

Intuitively, variance measures the variability among the values of the observations; if there is no variability among the values of the observations (as all are same), question of measuring the variability does not arise at al.

Mathematically, $\sigma_X^2 = \frac{1}{\sum_{i=1}^{n} f_i} \sum_{i=1}^{n} f_i (x_i - \overline{X})^2$; now for the present situation, $x_i = c$ (say) for all observations, and as a result the arithmetic mean of the constants "c" is also "c," i.e., $\sigma_X^2 = \frac{1}{\sum_{i=1}^{n} f_i} \sum_{i=1}^{n} f_i (c - c)^2 = \frac{1}{\sum_{i=1}^{n} f_i} \sum_{i=1}^{n} f_i 0^2 = 0$

(ii) *Variance does not depend on change of origin but depends on change of scale.*

Let us suppose a variable Q is changed to P, such that $P = a + bQ$, where a and b are constants. If $\overline{Q}$ and σ_Q^2 are the arithmetic mean and variance, respectively, for the variable Q, then what could be the variance for P?

We know that $\sigma_P^2 = \frac{1}{\sum_{i=1}^{n} f_i} \sum_{i=1}^{n} f_i (P_i - \overline{P})^2$

$= \frac{1}{\sum_{i=1}^{n} f_i} \sum_{i=1}^{n} f_i (a + bQ_i - a - b\overline{Q})^2$

$= \frac{1}{\sum_{i=1}^{n} f_i} \sum_{i=1}^{n} b^2 f_i (Q_i - \overline{Q})^2 = b^2 \sigma_Q^2$

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Thus, the variance of P depends only on change in scale "b," not on change in origin. Similarly, $\sigma_y = \text{s.d}(P) = |b|\sigma_Q = |b|\text{s.d.}(Q)$

Example 3.27
If the relation between weight (Y) and length (X) of fish is given as $Y = 5 + 0.5X$ and the ${\sigma_X}^2 = 10.2$ then find the standard deviation of Y.

Solution We know that $\sigma_Y^2 = b^2\sigma_X^2$; here $b = 0.5$, so $\sigma_Y^2 = (0.5)^2 \times 10.2 = 2.55$.

Standard deviation $\sigma_Y = +\sqrt{(2.55)} = 1.596$

(iii) Composite variance of "k" number of samples having arithmetic means $\overline{x}_1, \overline{x}_2, \overline{x}_3, \ldots, \overline{x}_k$, variances ${\sigma_1}^2\ {\sigma_2}^2\ {\sigma_3}^2$..... ${\sigma_i}^2$.... ${\sigma_k}^2$ with $n_1, n_2, n_3, \ldots, n_k$ number of observations, respectively, is

Samples	1	2	3	4...	i	...	K
No. of observations	n_1	n_2	n_3	n_4	n_i	...	N_k
AM	$\overline{x_1}$	$\overline{x_2}$	$\overline{x_3}$	$\overline{x_4}$	$\overline{x_i}$		$\overline{x_k}$
Variance	${\sigma_1}^2$	${\sigma_2}^2$	${\sigma_3}^2$	${\sigma_4}^2$	${\sigma_i}^2$		${\sigma_k}^2$

$$\sigma^2 = \frac{1}{\sum_{i=1}^{k} n_i}\left[\sum_{i=1}^{k} n_i\sigma_i^2 + \sum_{i=1}^{k} n_i d_i^2\right], \text{ where } {\sigma_i}^2 \text{ is}$$

the variance of i-th sample with "n_i" observations, and $d_i = \overline{x}_i - \overline{X}$, where $\overline{X}$ is the combined arithmetic mean of all the samples.

Let us put $k = 2$, the composite variance

$$\begin{aligned}
\sigma^2 &= \frac{1}{n_1+n_2}\left[n_1\sigma_1^2 + n_2\sigma_2^2 + n_1(\overline{x}_1 - \overline{x})^2 + n_2(\overline{x}_2 - \overline{x})^2\right], \text{where}, \overline{x} = \frac{n_1\overline{x}_1 + n_2\overline{x}_2}{n_1+n_2} \\
&= \frac{1}{n_1+n_2}\left[n_1\sigma_1^2 + n_2\sigma_2^2 + n_1\left(\overline{x}_1 - \frac{n_1\overline{x}_1 + n_2\overline{x}_2}{n_1+n_2}\right)^2 + n_2\left(\overline{x}_2 - \frac{n_1\overline{x}_1 + n_2\overline{x}_2}{n_1+n_2}\right)^2\right. \\
&= \frac{1}{n_1+n_2}\left[n_1\sigma_1^2 + n_2\sigma_2^2 + n_1\left(\frac{n_1\overline{x}_1 + n_2\overline{x}_1 - n_1\overline{x}_1 - n_2\overline{x}_2}{n_1+n_2}\right)^2 + n_2\left(\frac{n_1\overline{x}_2 + n_2\overline{x}_2 - n_1\overline{x}_1 - n_2\overline{x}_2}{n_1+n_2}\right)^2\right. \\
&= \frac{1}{n_1+n_2}\left[n_1\sigma_1^2 + n_2\sigma_2^2 + n_1\left(\frac{n_2\overline{x}_1 - n_2\overline{x}_2}{n_1+n_2}\right)^2 + n_2\left(\frac{n_1\overline{x}_2 - n_1\overline{x}_1}{n_1+n_2}\right)^2\right] \\
&= \frac{1}{n_1+n_2}\left[n_1\sigma_1^2 + n_2\sigma_2^2 + n_1n_2^2\left(\frac{\overline{x}_1 - \overline{x}_2}{n_1+n_2}\right)^2 + n_1^2n_2\left(\frac{\overline{x}_2 - \overline{x}_1}{n_1+n_2}\right)^2\right] \\
&= \frac{1}{n_1+n_2}\left[n_1\sigma_1^2 + n_2\sigma_2^2 + \frac{n_1n_2(\overline{x}_1 - \overline{x}_2)^2(n_2+n_1)}{(n_1+n_2)^2}\right] \\
&= \frac{1}{n_1+n_2}\left[n_1\sigma_1^2 + n_2\sigma_2^2 + \frac{n_1n_2(\overline{x}_1 - \overline{x}_2)^2}{(n_1+n_2)}\right]
\end{aligned}$$

Thus, for two samples, one need not to calculate composite mean also to get composite variance.

Example 3.28
Following data gives the no. of cobs per plant in two samples of maize. Find out the composite variance of maize plants.

Characteristics	Sample 1	Sample 2
Sample size	40	45
Average number of cobs/plant	12	15
Sample variance	4.2	2.5

Solution Combined variance of two sample is given as

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$$\sigma^2 = \frac{1}{n_1+n_2}\left[n_1\sigma_1^2 + n_2\sigma_2^2 + \frac{n_1 n_2(\bar{x}_1-\bar{x}_2)^2}{(n_1+n_2)}\right]$$
$$= \frac{1}{40+45}\left[40\times 4.2 + 45\times 2.5 + \frac{40\times 45(12-15)^2}{(40+45)}\right]$$
$$= \frac{1}{85}\left[168 + 112.5 + \frac{1800(-3)^2}{85}\right]$$
$$= \frac{1}{85}[168 + 112.5 + 190.588]$$
$$= \frac{1}{85}[471.088]$$
$$= 5.542$$

3.2.1.4 Quartile Deviation

Quartile deviation is defined as the half of the difference between the third and first quartile values of a given set of data; as such it is also known as semi-interquartile range and is calculated as $QD = \frac{Q_3-Q_1}{2}$. The usual procedure is to calculate the quartile values from the given raw data or frequency distribution and get the quartile deviation value. It is clear from the definitions of quartiles as well as the quartile deviation that this measure may not be based on all observations; rather a few observations or groups are considered during calculation of quartile deviation. But it is easy to understand and better than the range.

3.2.2 Moments

A more general type of measures to describe the nature of a given set of data is given by moments. It can be easily verified that the measures like arithmetic mean, mean deviations, variances, etc. can very well be expressed in terms of moments. The r-th moment of a set of N number of observations $X_1, X_2, X_3,\ldots,X_N$ for variable X about an arbitrary point A is defined as the mean of the r-th power of the deviations of the observations from the arbitrary point A and is expressed as

$$\mu_r(A) = \frac{1}{N}\sum_{i=1}^{N}(X_i - A)^r,\ r = 0,1,2,3\ldots$$

For grouped data the r-th moment of a set of N number of observations $X_1, X_2, X_3,\ldots,X_N$ for variable X grouped into "n" number of classes with mid-values and frequencies of different classes as given below

Mid-values(x_i)	x_1	x_2	$x_3\ldots,x_i,\ldots x_{n-2}$	x_{n-1}	x_n
Frequency	f_1	f_2	$f_3\ldots,f_i,\ldots f_{n-2}$	f_{n-1}	f_n

about an arbitrary point A is given as $\mu_r(A) = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i(x_i - A)^r$.

Let us take $A = 0$, then we have

$\mu_r(0) = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i x_i^r$ and in particular

$\mu_1(0) = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i x_i = \text{AM}$

putting $A = \overline{X}$, we have

$\frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i(x_i - \overline{X})^r$, the $r$thmoment about mean, known as rth central moment and is denoted as m_r.

Henceforth, we shall denote the raw moments and central moments with "μ" and "m," respectively.

It can be noted that

$\mu_0(A) = m_0 = 1$ and $\mu_1(0) = \overline{X}$, $m_1 = 0$, $m_2 = \sigma^2$

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Now putting $r = 1,2.3.4$ we have

Raw data	Grouped data
$\mu_1(A) = \frac{1}{N}\sum_{i=1}^{N}(X_i - A) = \frac{1}{N}\sum_{i=1}^{N}X_i - A = \overline{X} - A$	$\mu_1(A) = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i(x_i - A) = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i x_i - A = \overline{x} - A$
$\mu_2(A) = \frac{1}{N}\sum_{i=1}^{N}(X_i - A)^2$	$\mu_2(A) = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i(x_i - A)^2$
$\mu_3(A) = \frac{1}{N}\sum_{i=1}^{N}(X_i - A)^3$	$\mu_3(A) = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i(x_i - A)^3$
$\mu_4(A) = \frac{1}{N}\sum_{i=1}^{N}(X_i - A)^4$	$\mu_4(A) = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i(x_i - A)^4$

Similarly for central moments,

Raw data	Grouped data
$m_1 = \frac{1}{N}\sum_{i=1}^{N}(X_i - \overline{X}) = \frac{1}{N}\sum_{i=1}^{N}X_i - \overline{X} = \overline{X} - \overline{X} = 0$	$m_1 = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i(x_i - \overline{X}) = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i x_i - \overline{X} = \overline{X} - \overline{X} = 0$
$m_2 = \frac{1}{N}\sum_{i=1}^{N}(X_i - \overline{X})^2 =$ Variance	$m_2 = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i(x_i - \overline{X})^2 =$ Variance
$m_3 = \frac{1}{N}\sum_{i=1}^{N}(X_i - \overline{X})^3$	$m_3 = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i(x_i - \overline{X})^3$
$m_4 = \frac{1}{N}\sum_{i=1}^{N}(X_i - \overline{X})^4$	$m_4 = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i(x_i - \overline{X})^4$

Central Moment Does Not Depend on Change of Origin but on Scale

Let us suppose a variable Q is changed to P, such that $P = a + bQ$, where a and b are constants.

$$
\begin{aligned}
m_r(P) &= \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i(P_i - \overline{P})^r \\
&= \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i(a + bQ_i - a - b\overline{Q})^r = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i(bQ_i - b\overline{Q})^r \\
&\frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} b^r f_i(Q_i - \overline{Q})^r = b^r\frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i(Q_i - \overline{Q})^r = b^r m_r(Q)
\end{aligned}
$$

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Conversion of Moments

1. *Conversion of central moments to raw moments about an arbitrary origin.*

Let us suppose we have the mid-values of different classes of the variable X denoted by x_i and that the mean of variable is denoted by $\overline{x}$; the arbitrary origin is "A."

$$\therefore \quad m_r = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i (x_i - \overline{x})^r = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i (x_i - A - \overline{x} + A)^r$$

$$= \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i ((x_i - A) - (\overline{x} - A))^r$$

$$= \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i \left[(x_i - A)^r - \binom{r}{1}(x_i - A)^{r-1}(\overline{x} - A) + \binom{r}{2}(x_i - A)^{r-2}(\overline{x} - A)^2 - \ldots \right.$$

$$\left. + (-1)^{r-1}\binom{r}{r-1}(x_i - A)(\overline{x} - A)^{r-1} + (-1)^r \binom{r}{r}(x_i - A)^0 (\overline{x} - A)^r \right]$$

$$= \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i (x_i - A)^r - \binom{r}{1}\frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i (x_i - A)^{r-1}(\overline{x} - A) + \binom{r}{2}\frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i (x_i - A)^{r-2}(\overline{x} - A)^2 - \ldots$$

$$+ (-1)^{r-1}\binom{r}{r-1}\frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i (x_i - A)(\overline{x} - A)^{r-1} + (-1)^r \binom{r}{r}\frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i (\overline{x} - A)^r$$

$$= \mu_r - \binom{r}{1}\mu_{r-1}\mu_1 + \binom{r}{2}\mu_{r-2}\mu_1^2 + \ldots + (-1)^{r-1}\binom{r}{r-1}\mu_1 \mu_1^{r-1} + (-1)^r \binom{r}{r}\mu_1^r$$

$$\left[\because \mu_1 = \frac{1}{N}\sum_{i=1}^{n} f_i (x_i - A) = \frac{1}{N}\sum_{i=1}^{n} f_i (x_i - A) = \overline{x} - A\right]$$

Using the above relationship and putting r =1,2,3,4, one can find out

$$m_1 = 0$$

$$m_2 = \mu_2 - \binom{2}{1}\mu_{2-1}\mu_1 + \binom{2}{2}\mu_{2-2}\mu_1^2$$
$$= \mu_2 - 2\mu_1\mu_1 + \mu_1^2$$
$$= \mu_2 - \mu_1^2$$

$$m_3 = \mu_3 - \binom{3}{1}\mu_{3-1}\mu_1 + \binom{3}{2}\mu_{3-2}\mu_1^2 - \binom{3}{3}\mu_{3-3}\mu_1^3$$
$$= \mu_3 - 3\mu_2\mu_1 + 3\mu_1\mu_1^2 - \mu_1^3$$
$$= \mu_3 - 3\mu_2\mu_1 + 2\mu_1^3$$

$$m_4 = \mu_4 - \binom{4}{1}\mu_{4-1}\mu_1 + \binom{4}{2}\mu_{4-2}\mu_1^2 - \binom{4}{3}\mu_{4-3}\mu_1^3 + \binom{4}{4}\mu_{4-4}\mu_1^4$$
$$= \mu_4 - 4\mu_3\mu_1 + 6\mu_2\mu_1^2 - 4\mu_1\mu_1^3 + \mu_1^4$$
$$= \mu_4 - 4\mu_3\mu_1 + 6\mu_2\mu_1^2 - 3\mu_1^4$$

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2. *Conversion of raw moments about an arbitrary origin to central moments.*

Let us suppose we have the mid-values of different classes of the variable X denoted by x_i and that the mean of variable is denoted by $\bar{x}$; also the arbitrary origin is "A."

Let us suppose the arbitrary origin is "A."

$$\therefore \mu_r = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i (x_i - A)^r = \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i (x_i - \bar{x} - A + \bar{x})^r$$

$$= \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i ((x_i - \bar{x}) + (\bar{x} - A))^r$$

$$= \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i \left[(x_i - \bar{x})^r + \binom{r}{1}(x_i - \bar{x})^{r-1}(\bar{x} - A)\right.$$

$$\left. + \binom{r}{2}(x_i - \bar{x})^{r-2}(\bar{x} - A)^2 - \ldots + \binom{r}{r-1}(x_i - \bar{x})(\bar{x} - A) + \binom{r}{r}(x_i - \bar{x})^0 (\bar{x} - A)^r\right]$$

$$= \frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i (x_i - \bar{x})^r + \binom{r}{1}\frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i (x_i - \bar{x})^{r-1}(\bar{x} - A)$$

$$+ \binom{r}{2}\frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i (x_i - \bar{x})^{r-2}(\bar{x} - A)^2 + \ldots + \binom{r}{r-1}\frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i (x_i - \bar{x})(\bar{x} - A)^{r-1} + \binom{r}{r}\frac{1}{\sum_{i=1}^{n} f_i}\sum_{i=1}^{n} f_i (\bar{x} - A)^r$$

$$= m_r + \binom{r}{1} m_{r-1}\mu_1 + \binom{r}{2} m_{r-2}\mu_1^2 + \ldots + \binom{r}{r-1} m_1 \mu_1^{r-1} + \binom{r}{r}\mu_1^r \qquad [\because \mu_1 = \bar{x} - A]$$

Using the above relationship and putting $r = 1, 2, 3, 4$, one can find out

$$\mu_1 = m_1 + \binom{2}{1} m_{1-1}\mu_1 = 0 + \mu_1$$

$$\mu_2 = m_2 + \binom{2}{1} m_{2-1}\mu_1 + \binom{2}{2} m_{2-2}\mu_1^2$$
$$= m_2 + 2m_1\mu_1 + \mu_1^2$$
$$= m_2 + \mu_1^2$$

$$\mu_3 = m_3 + \binom{3}{1} m_{3-1}\mu_1 + \binom{3}{2} m_{3-2}\mu_1^2 + \binom{3}{3} m_{3-3}\mu_1^3$$
$$= m_3 + 3m_2\mu_1 + 3m_1\mu_1^2 + \mu_1^3$$
$$= m_3 + 3m_2\mu_1 + 3 \times 0\mu_1^2 + \mu_1^3$$
$$= m_3 + 3m_2\mu_1 + \mu_1^3$$

$$\mu_4 = m_3 + \binom{4}{1} m_{4-1}\mu_1 + \binom{4}{2} m_{4-2}\mu_1^2$$
$$+ \binom{4}{3} m_{4-3}\mu_1^3 + \binom{4}{4} m_{4-4}\mu_1^4$$
$$= m_3 + 4m_3\mu_1 + 6m_2\mu_1^2 + 4m_1\mu_1^3 + \mu_1^4$$
$$= m_3 + 4m_3\mu_1 + 6m_2\mu_1^2 + \mu_1^4 \quad [\because m_1 = 0]$$

Sheppard's Correction for Moments

During calculation of moments from grouped data, we assume that in any class, all the observations are equal to the mid-value (class mark) of the particular class. Actually, this may not be true; the values within a class also vary among themselves. Because of this assumption, error is automatically introduced; this error is known as *error due to grouping*. To correct these errors due to grouping for different moments, Sheppard's correction is introduced. Corrections adopted for first four raw and central moments are given below:

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Raw moments	Central moments
$\mu_1(\text{corrected}) =$ No correction needed	$m_1 = 0$
$\mu_2(\text{corrected}) = \mu_2(\text{uncorrected}) - \frac{h^2}{12}$	$m_2(\text{corrected}) = m_2(\text{uncorrected}) - \frac{h^2}{12}$
$\mu_3(\text{corrected}) = \mu_3(\text{uncorrected}) - \frac{h^2}{4}\mu_1$	$m_3 =$ no correction needed
$\mu_4(\text{corrected}) = \mu_4(\text{uncorrected}) - \frac{h^2}{2}\mu_2(\text{uncorrected}) + \frac{7}{240}h^4$	$m_4(\text{corrected}) = m_4(\text{uncorrected}) - \frac{h^2}{2}m_2(\text{uncorrected}) + \frac{7}{240}h^4$

where "h" is the class width.

Sheppard's correction should be used when (i) total frequency should be very large, preferably > 1000; (ii) no. of classes is not too many, preferably <20; (iii) only the frequency at both the ends of the distribution approaches to zero values; and (iv) the frequency distribution is moderately skewed (discussed later in this chapter).

Merits and Demerits of Moments

Moments are clearly defined and based on all observations. Moments are more general class of measures than the measures of central tendency and dispersion; these take care of both the central tendency and dispersion. In the subsequent section, we shall see that moments have got further uses in measuring the horizontal as well as vertical departure of the frequency distributions.

Example 3.29

Compute the first four raw moments about the value 20 and the four central moments from the following data on fruits per plant from 1045 plants of ladies' finger (*okra*/*bhindi*). Use Sheppard's correction for moments for the following distribution.

Fruit no./plant	4–6	7–9	10–12	13–15	16–18	19–21	22–24	25–27	28–30	31–33	34–36	37–39	40–42	43–45
Frequency	54	67	83	94	111	157	104	91	74	66	52	45	32	15

(a) **Method 1**: Let us make the following table:

Fruit no./plant	Frequency (f_i)	Class mark x_i	$(x_i - 20)$	$f_i(x_i - 20)$	$(x_i - 20)^2$	$f_i(x_i - 20)^2$	$(x_i - 20)^3$	$f_i(x_i - 20)^3$	$(x_i - 20)^4$	$f_i(x_i - 20)^4$
4–6	54	5	−15	−810	225.00	12,150	−3375.00	−182250.00	50625.00	2733750.00
7–9	67	8	−12	−804	144.00	9648	−1728.00	−115776.00	20736.00	1389312.00
10–12	83	11	−9	−747	81.00	6723	−729.00	−60507.00	6561.00	544563.00
13–15	94	14	−6	−564	36.00	3384	−216.00	−20304.00	1296.00	121824.00
16–18	111	17	−3	−333	9.00	999	−27.00	−2997.00	81.00	8991.00
19–21	157	20	0	0	0.00	0	0.00	0.00	0.00	0.00
22–24	104	23	3	312	9.00	936	27.00	2808.00	81.00	8424.00
25–27	91	26	6	546	36.00	3276	216.00	19656.00	1296.00	117936.00
28–30	74	29	9	666	81.00	5994	729.00	53946.00	6561.00	485514.00
31–33	66	32	12	792	144.00	9504	1728.00	114048.00	20736.00	1368576.00
34–36	52	35	15	780	225.00	11,700	3375.00	175500.00	50625.00	2632500.00
37–39	45	38	18	810	324.00	14,580	5832.00	262440.00	104976.00	4723920.00
40–42	32	41	21	672	441.00	14,112	9261.00	296352.00	194481.00	6223392.00
43–45	15	44	24	360	576.00	8640	13824.00	207360.00	331776.00	4976640.00
Total	**1045**			**1680**		**101,646**		**750,276**		**25,335,342**
Average				**1.608**		**97.269**		**717.967**		**24244.346**

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Thus, from the above table, we have the raw moments about 20 as

$\mu_1 = 1.608$
$\mu_2 = 97.269$
$\mu_3 = 717.967$
$\mu_4 = 24244.346$

Using the above raw moments and the relationship for conversions of raw moments to central moments, one can have the following central moments:

$$
\begin{aligned}
m_1 &= 0 \\
m_2 &= \mu_2 - \mu_1^2 = 97.269 - 1.608^2 = 97.269 - 2.586 = 94.683 \\
m_3 &= \mu_3 - 3\mu_2\mu_1 + 2\mu_1^3 = 717.967 - 3x97.269x1.608 + 2x1.608^3 \\
&= 717.967 - 469.226 + 8.315 \\
&= 1195.508 \\
m_4 &= \mu_4 - 4\mu_3\mu_1 + 6\mu_2\mu_1^2 - 3\mu_1^4 \\
&= 24244.346 - 4x717.967 \times 1.608 + 6x97.269 \times 1.608^2 - 3x1.608^4 \\
&= 24244.346 - 4617.964 + 1509.0297 - 20.0057 \\
&= 21115.406
\end{aligned}
$$

So the arithmetic mean and standard deviation of the number of fruits per plant are:

We have $\mu_1 = \overline{x} - A \Rightarrow \overline{x} = \mu_1 + A$

$$
\begin{aligned}
\text{Arithmetic mean } \overline{x} &= 20 + \mu_1 = 20 + 1.608 \\
&= 21.608 \text{ and} \\
\text{Standard deviation sd} &= +\sqrt{94.683} = 9.7305
\end{aligned}
$$

(b) **Method 2**: Instead of using this relationship between raw and central moments, one can directly use the formulae for calculation of different central moments. For the purpose, let us make the following table:

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Fruit no./ plant	Frequency (f_i)	x_i	$f_i x_i$	$(x_i - 21.608)$	$f_i(x_i - 21.608)$	$(x_i - 21.608)^2$	$f_i(x_i - 21.608)^2$	$(x_i - 21.608)^3$	$f_i(x_i - 21.608)^3$	$(x_i - 21.608)^4$	$f_i(x_i - 21.608)^4$
4–6	54	5	270	−16.608	−896.832	275.83	14894.59	−4580.91	−247369.28	76079.80	4108309.03
7–9	67	8	536	−13.608	−911.736	185.18	12406.9	−2519.90	−168833.14	34290.77	2297481.41
10–12	83	11	913	−10.608	−880.464	112.53	9339.962	−1193.71	−99078.32	12662.93	1051022.80
13–15	94	14	1316	−7.608	−715.152	57.88	5440.876	−440.36	−41394.19	3350.29	314926.98
16–18	111	17	1887	−4.608	−511.488	21.23	2356.937	−97.84	−10860.76	450.87	50046.40
19–21	157	20	3140	−1.608	−252.456	2.59	405.9492	−4.16	−652.77	6.69	1049.65
22–24	104	23	2392	1.392	144.768	1.94	201.5171	2.70	280.51	3.75	390.47
25–27	91	26	2366	4.392	399.672	19.29	1755.359	84.72	7709.54	372.09	33860.29
28–30	74	29	2146	7.392	547.008	54.64	4043.483	403.91	29889.43	2985.71	220942.65
31–33	66	32	2112	10.392	685.872	107.99	7127.582	1122.27	74069.83	11662.63	769733.68
34–36	52	35	1820	13.392	696.384	179.35	9325.975	2401.80	124893.45	32164.87	1672573.09
37–39	45	38	1710	16.392	737.64	268.70	12091.39	4404.49	198202.14	72198.43	3248929.56
40–42	32	41	1312	19.392	620.544	376.05	12033.59	7292.36	233355.36	141413.35	4525227.19
43–45	15	44	660	22.392	335.88	501.40	7521.025	11227.39	168410.79	251403.63	3771054.43
Total	**1045**		**22,580**	**40.488**	**−0.36**	**2164.59**	**98945.1**	**18102.7**	**268622.6**	**639045.8**	**22065547.6**
Average			**21.608**	**0.039**	**0.000**	**2.071**	**94.684**	**17.323**	**257.055**	**611.527**	**21115.357**

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From the above table, one can easily verify that AM = 21.608, $m_1 = 0$, and $m_2 = 94.684$, and these are exactly the same as what we got using the relationship between the central and raw moments.

Now using the formulae for correction of moments as per Sheppard's correction, one can have the following corrected moments:

Raw moments	Central moments
$\mu_1(\text{corrected}) =$ No correction needed $= 1.608$	$m_1 = 0$
$\mu_2(\text{corrected}) = \mu_2(\text{uncorrected}) - \frac{h^2}{12}$ $= 97.269 - \frac{2^2}{12} = 96.936$	$m_2(\text{corrected}) = m_2(\text{uncorrected}) - \frac{h^2}{12}$ $= 94.684 - \frac{2^2}{12} = 94.351$
$\mu_3(\text{corrected}) = \mu_3(\text{uncorrected}) - \frac{h^2}{4}\mu_1$ $= 717.967 - 1.608 = 716.359$	$m_3 =$ no correction needed
$\mu_4(\text{corrected}) = \mu_4(\text{uncorrected}) - \frac{h^2}{2}\mu_2(\text{uncorrected}) + \frac{7}{240}h^4$ $= 24244.346 - 2 \times 97.269 + 0.029 \times 16$ $= 24244.813 - 194.538$ $= 24050.275$	$m_4(\text{corrected}) = m_4(\text{uncorrected}) - \frac{h^2}{2}m_2(\text{uncorrected}) + \frac{7}{240}h^4$ $= 21115.357 - 2 \times 94.684 + 0.029 \times 16$ $= 21115.357 - 189.368 + 0.464$ $= 20926.453$

3.2.3 Relative Measures of Dispersion

The absolute measures discussed in the previous section are not unit-free; as such if one wants to compare the dispersions of different variables, it is not possible because different variables are measured in different units. Relative measures of dispersions are mainly the coefficients based on the absolute measures. As such these do not have any definite units; these can be used to compare the dispersions of different variables measured in different units. In literature, based on almost all the absolute measures of dispersion, one can find different coefficients of dispersions developed. In the following section, let us discuss those coefficients of dispersion.

(i) *Based on range*: Coefficient of dispersion based on range is defined as $\frac{X_{\max} - X_{\min}}{X_{\max} + X_{\min}}$, where $X_{\max}$ and $X_{\min}$ are the maximum and minimum values of the variable "X."

(ii) *Based on quartile deviation*: Coefficient of dispersion based on quartiles is defined as $\frac{\frac{Q_3 - Q_1}{2}}{\frac{Q_3 + Q_1}{2}} = \frac{Q_3 - Q_1}{Q_3 + Q_1}$

(iii) *Based on mean deviation*: Coefficient of dispersion based on mean deviation from mean/median/mode is given by $\frac{\text{MD mean/median/mode etc.}}{\text{Mean/Median/Mode}}$

(iv) *Based on standard deviation*: Coefficient of dispersion based on standard deviation is defined as $\frac{\sigma_X}{\overline{X}}$, where σ_X and $\overline{X}$ are, respectively, the standard deviation and arithmetic mean of the variable "X." This measure takes care of two most widely used absolute measures of central tendency (arithmetic mean) and dispersion (standard deviation) and is termed as "*coefficient of variation* (CV)." Most widely used form of coefficient of variation is to express it in percentage form, *i.e.*, $\frac{\sigma_X}{\overline{X}} \times 100$.

Example 3.30

Let us take the problem of milk yield per month for 100 cows as given in the following table. Find out the different relative measures of dispersion.

Milk class	200–228	228–256	256–284	284–312	312–340	340–368	368–396	396–424
Frequency	8	14	21	18	16	13	6	4

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Solution From the given information, the following table is prepared, and using the formulae for calculation of arithmetic mean, median, mode, and standard deviations are calculated.

Class	Frequency (f)	x_i	CF<	$f_i x_i$	$f_i x_i^2$	$\lvert x_i - \overline{X}\rvert$	$f_i \lvert x_i - \overline{X}\rvert$	$\lvert x_i - Me\rvert$	$f_i \lvert x_i - Me\rvert$	$\lvert x_i - Mo\rvert$	$f_i \lvert x_i - Mo\rvert$
200–228	8	214	8	1712	366,368	84.84	678.72	81	648	62	496
228–256	14	242	22	3388	819,896	56.84	795.76	53	742	34	476
256–284	21	270	43	5670	1,530,900	28.84	605.64	25	525	6	126
284–312	18	298	61	5364	1,598,472	0.84	15.12	3	54	22	396
312–340	16	326	77	5216	1,700,416	27.16	434.56	31	496	50	800
340–368	13	354	90	4602	1,629,108	55.16	717.08	59	767	78	1014
368–396	6	382	96	2292	875,544	83.16	498.96	87	522	106	636
396–424	4	410	100	1640	672,400	111.16	444.64	115	460	134	536
Total	100	–	–	29,884	9,193,104		4190.48	–	4214	–	4480
Average	–	–	–	298.84	91,931		41.90	–	42.14	–	44.80

AM = 298.84 kg, median = 294.889 kg, mode = 275.6 kg, Q1 = 260, Q3 = 336.5, and standard deviation = 51.24 kg

From the above table, we have MD (300) = 42.16, MD = 41.90, MD_{Me} = 42.14, and MD_{Mo} = 44.80.

Thus, the Coefficient of Dispersion Is Based on

(a) Range: $\dfrac{X_{\max} - X_{\min}}{X_{\max} + X_{\min}} = \dfrac{424 - 220}{424 + 220} = \dfrac{204}{644} = 0.3167$

(b) Quartile deviation: $\dfrac{\frac{Q_3 - Q_1}{2}}{\frac{Q_3 + Q_1}{2}} = \dfrac{Q_3 - Q_1}{Q_3 + Q_1} = \dfrac{336.5 - 260}{336.5 + 260} = \dfrac{76.5}{596.5} = 0.128$

(c) Mean deviation about:

(i) $\dfrac{\text{MD mean}}{\text{Mean}} = \dfrac{41.90}{298.84} = 0.140$

(ii) $\dfrac{\text{MD median}}{\text{Median}} = \dfrac{42.14}{294.889} = 0.143$

(iii) $\dfrac{\text{MD mode}}{\text{Mode}} = \dfrac{44.80}{275.6} = 0.163$

(d) Standard deviation = coefficient of variation (CV) $= \frac{SD_X}{\overline{X}} = \frac{51.24}{298.84} = 0.1714$ or in percentage form CV% $= \frac{SD_X}{\overline{X}} \text{x} 100 = \frac{51.24}{298.84} \text{x} 100 = 17.14\%$

3.3 Skewness and Kurtosis

With the introduction of relative measures of dispersion in the previous section, it is now clear that neither the measure of central tendency nor the measure of dispersion alone is sufficient to extract the inherent characteristics of a given set of data. We need to combine both these measures together. We can come across with a situation where two frequency distributions have same measures of central tendency as well as measure of dispersion, but they differ widely in their nature. Let us take the following example where we can see that both the frequency distributions have almost same arithmetic mean and standard deviation, yet the nature of these two distributions is different.

Example 3.31

Given below are the two frequency distributions for panicle length (mm) of 175 panicles in each case. Calculation of data indicates that the two distributions have got means (AM1 = 127.371 and AM2 = 127.171) and standard deviations (sd1 = 34.234 and sd2 = 34.428) almost same. Thus, both the distributions have almost same measure of central tendency as well as measure of dispersion. But a close look at the graphs, drawn for two frequency distributions, shows that they differ widely in nature.

Frequency distribution (A)		Frequency distribution (B)	
Class	Frequency	Class	Frequency
112.5–117.5	9	112.5–117.5	9
117.5–122.5	25	117.5–122.5	23

(continued)

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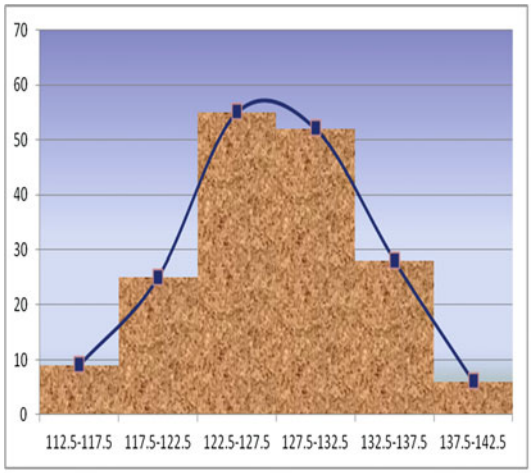
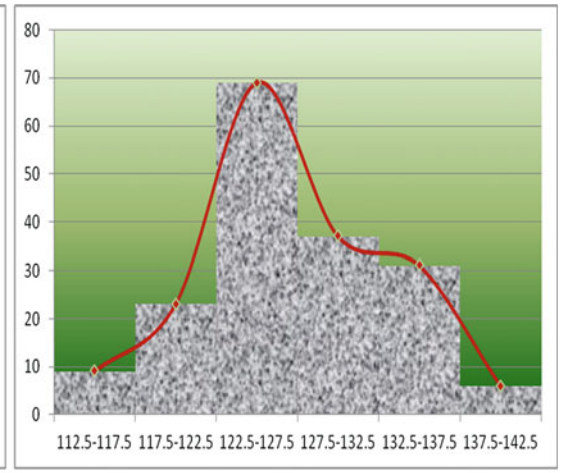
Frequency distribution (A)		Frequency distribution (B)	
Class	Frequency	Class	Frequency
122.5–127.5	55	122.5–127.5	69
127.5–132.5	52	127.5–132.5	37
132.5–137.5	28	132.5–137.5	31
137.5–142.5	6	137.5–142.5	6
AM	127.371	AM	127.171
Variance	34.234	Variance	34.428



Frequency Distribution (A)



Frequency Distribution(B)

Thus, either the measure of central tendency or the measure of dispersion in isolation or in combination may not always speak about the nature of the data. So, along with the measures of dispersion and central tendency, one needs to have other techniques/measures to extract the original nature of the given set of data. *Skewness* and *kurtosis* provide additional information about the nature of the data set in this regard.

3.3.1 Skewness

Skewness of a frequency distribution is the departure of the frequency distribution from symmetry. Based on the skewness, a distribution is either symmetric or asymmetric. A frequency distribution of a discrete variable X is said to be symmetric about X', a value of the variable if the frequency of the variable in $X' - \delta$ is same as the frequency of the variable in $X' + \delta$, for different values of δ. Similarly a frequency distribution of a continuous variable X is said to be symmetric about X', a value of the variable, if the frequency density of the variable in $X' - \delta$ is same as the frequency density of the variable in $X' + \delta$, for different values of δ.

Again an asymmetric/skewed distribution may be positively skewed or negatively skewed depending upon the longer tail on higher or lower values, respectively.

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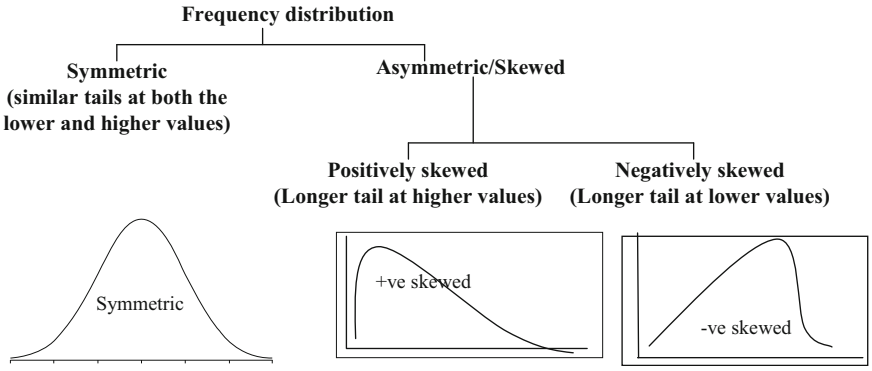

Given a frequency distribution, how should one know whether it is symmetric or asymmetric distribution? In fact in literature, there are different measures of skewness; among these Pearsonian measures, Bowley's measure, measures based on moments, etc. are widely used.

Measures of Skewness

(a) *Based on the relative position of mean, median, and mode,* the frequency distribution is
   (i) Symmetric if mean = median = mode.
   (ii) Positively skewed if mean > median > mode.
   (iii) Negatively skewed if mean < median < mode.Problem with this measure is that if uniform trend is not found among the AM, median, and mode, then it is difficult to use the same measure.

(b) *Pearsonian type I measure*: According to this measure $\text{Skewness} = \frac{(\text{Mean}-\text{Mode})}{\text{Standard deviation}}$, This measure assumes that there exists only one mode for the frequency distribution. But in a frequency distribution, mode may not exist or may have more than one mode, in these cases this definition does not work properly. To overcome these problems, Pearsonian type II measure has been proposed.

(c) *Pearsonian type II measure*: According to this measure $\text{Skewness} = \frac{3(\text{Mean}-\text{Median})}{\text{Standard deviation}}$. In this measure instead of using mode like in type I measure, median has been used based on the empirical relationship (mean-mode) = 3(mean-median). But this relationship is true for moderately skewed distribution, so moderate skewness of the distribution is assumed, which may not always hold true.

(d) *Bowley's measure:* According to this measure, $\text{Skewness} = \frac{(Q_3-Q_2)-(Q_2-Q_1)}{(Q_3-Q_2)+(Q_2-Q_1)}$, thus the measure is entirely dependent on quartile values and as such criticized for not considering all the values/observations of a given data set.

(e) *Measure based on moments:* According to this measure skewness $\gamma_1 = \sqrt{\beta}_1 = \frac{m_3}{\sqrt{m^3{}_2}} = \frac{m_3}{\text{sd}^3}$, where m_3 and m_2 are the third and second central moments, respectively. This type of measure is widely used. The sign of $\sqrt{\beta}_1$ depends on the sign of m_3. Limiting value of the above measure is theoretically $-\infty$ to $+\infty$. It may be noted that all the measures of skewness have no units; these are pure numbers and equal to zero when the distribution is symmetric.

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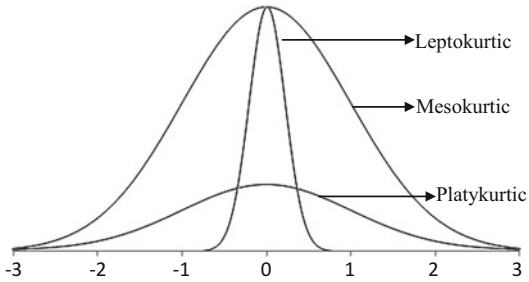
3.3.2 Kurtosis

Inspite of having same measure of central tendency (AM), dispersion (variance), and skewness, two frequency distributions may vary in their nature; these may differ in peakedness. *Peakedness of frequency distribution is termed as kurtosis*. Kurtosis is measured in terms of $\beta_2 - 3 = \frac{m_4}{m_2^2} - 3 = \gamma_2$, where m_4 and m_2 are the fourth and second central moments, respectively. Depending upon the value γ_2, a frequency distribution is termed *leptokurtic* $(\gamma_2 > 0)$, *platykurtic* $(\gamma_2 < 0)$, *or mesokurtic* $(\gamma_2 = 0)$.

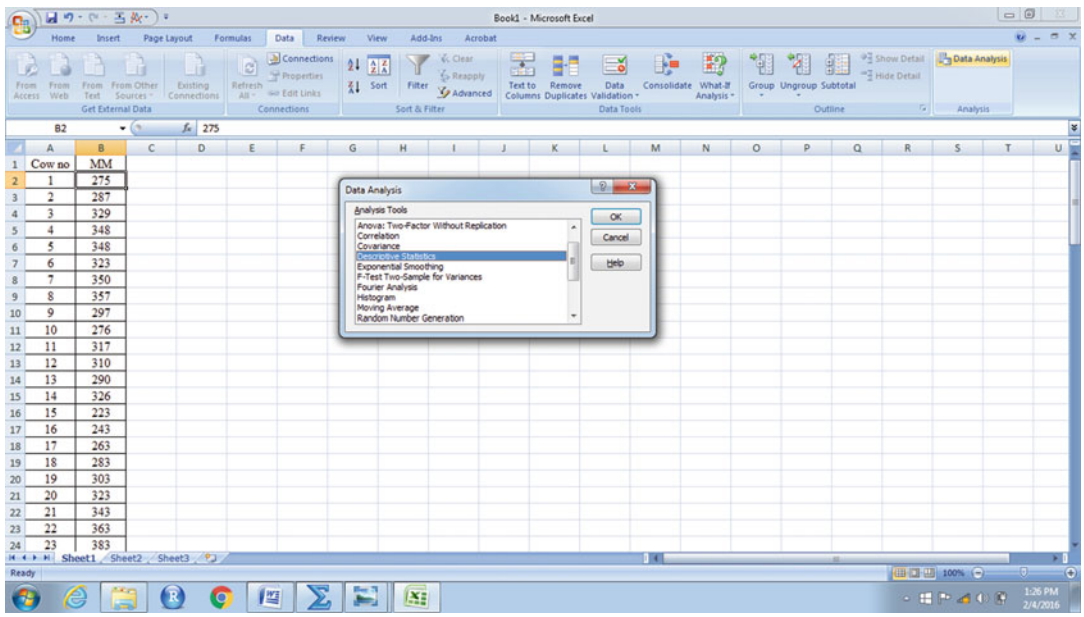


Both the skewness and kurtosis have got great practical significance. These two picturize the concentration of the observation in different ranges for a given set of data.

Thus, to know the nature of data, measures of central tendency and measures of dispersion along with skewness and kurtosis of the frequency distribution are essential.

Calculation of Descriptive Statistics Through MS Excel

Step 1: Go to Data Analysis submenu of Data in MS Excel. Select the Descriptive Statistics as shown below:



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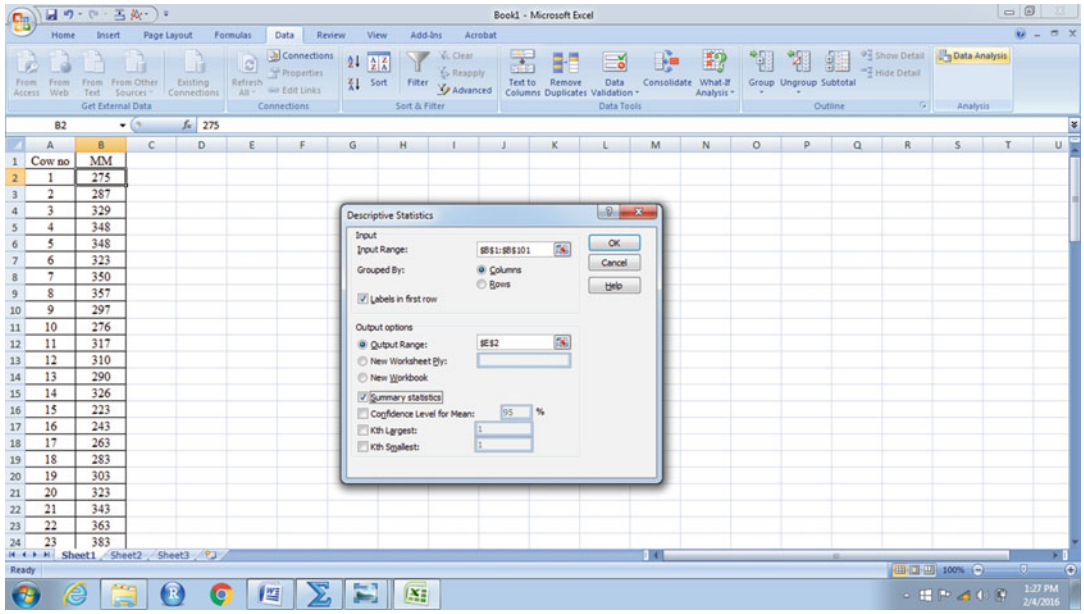
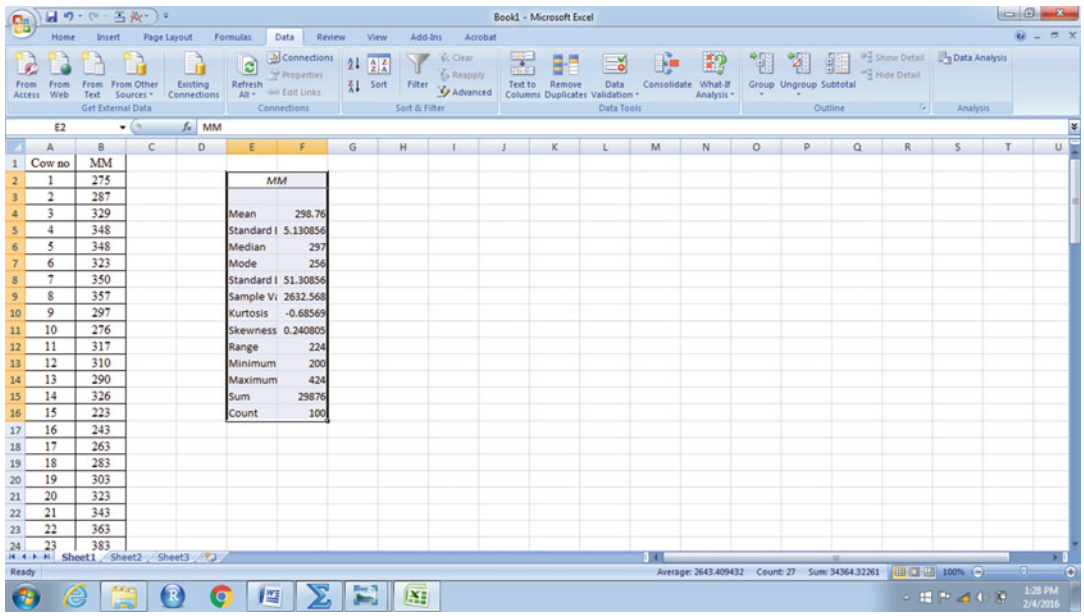
Step 2: Provide the input range and the output range (where the output is to be placed upon analysis), and tick on to Summary Statistics as show below:



Step 3: Click on OK to get the windows as given below containing the output.



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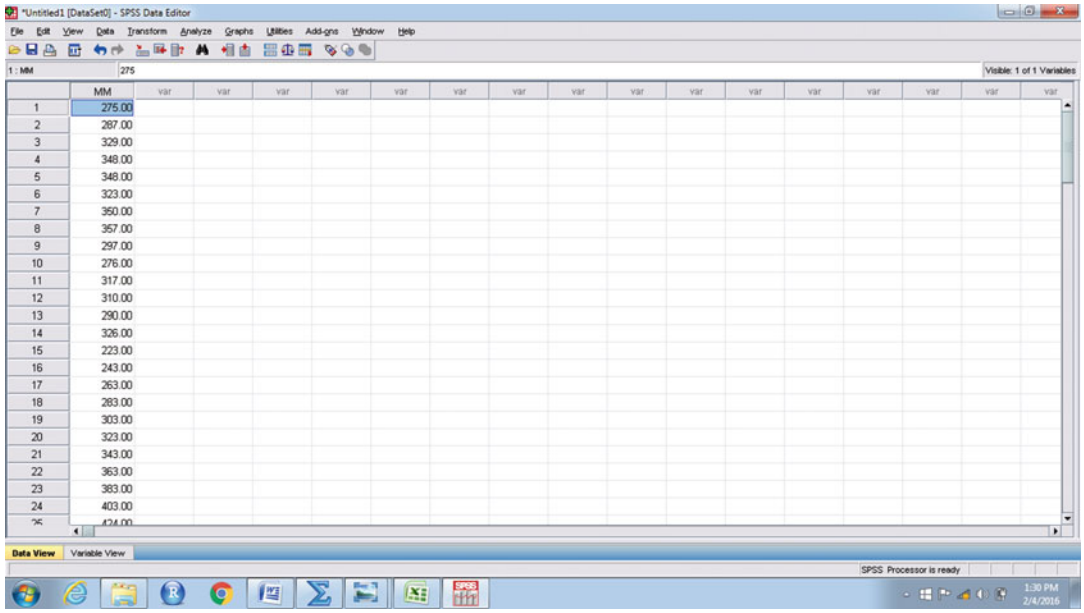
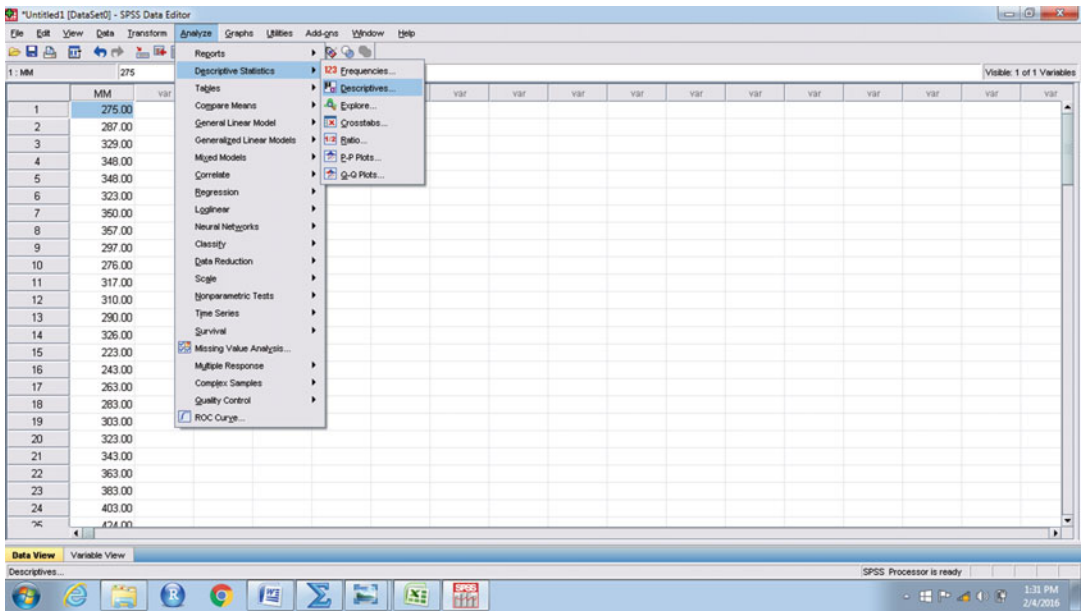
Calculation of Descriptive Statistics Through SPSS

Step 1: When these data are transformed to SPSS. Data editor, either copying from the sources or importing, looks like the following slide.



Step 2: Go to analysis menu followed by Descriptive Statistics and Descriptive as shown below.



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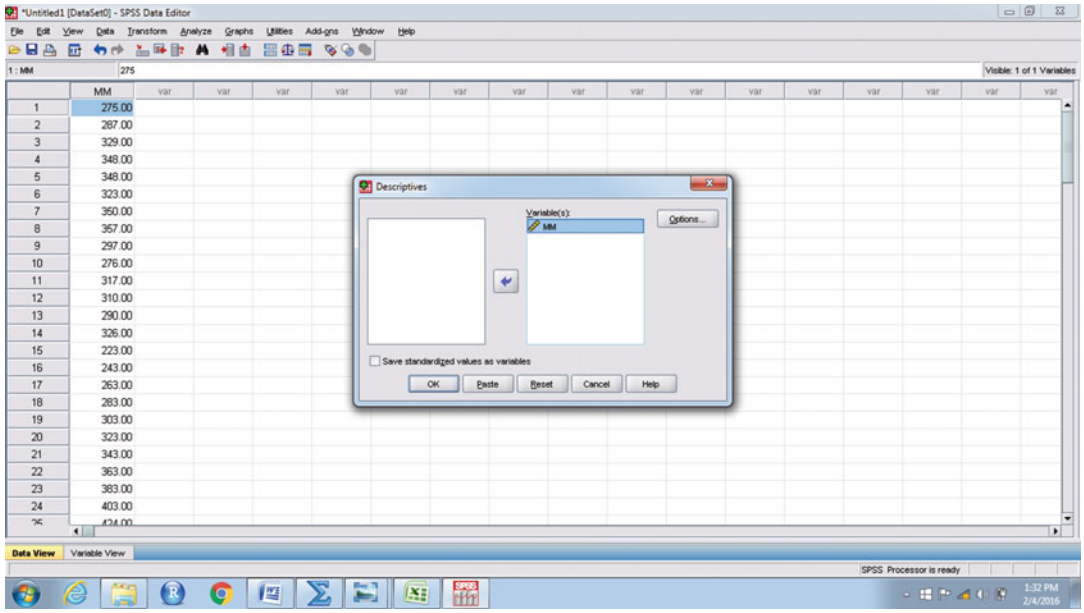
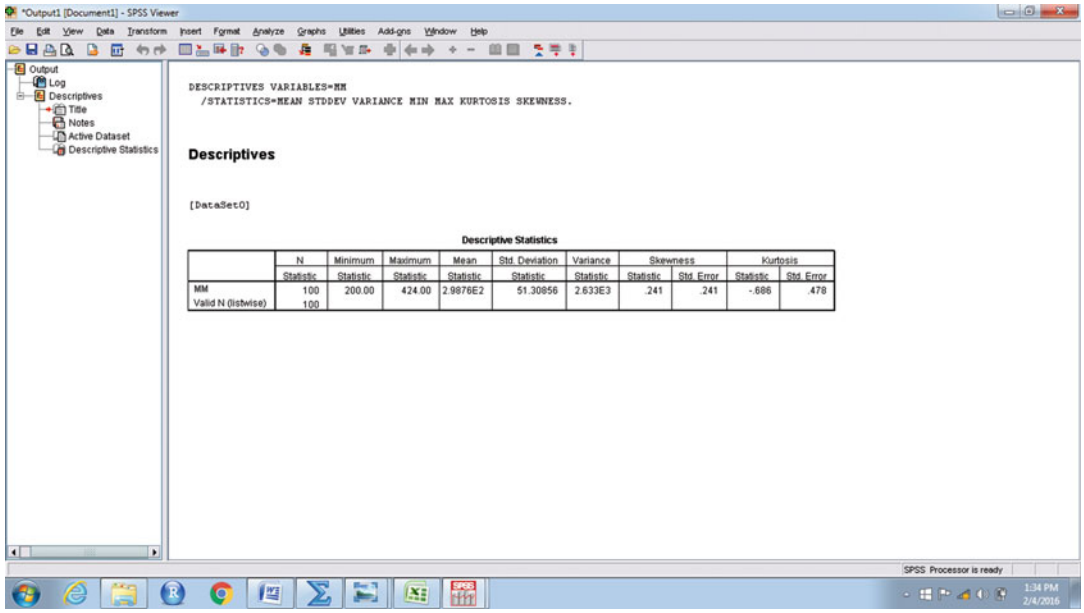
Step 3: Select the variable for which one wants the Descriptive statistics and then click on to Option menu as shown below.



Step 4: From the options, select the required measures as shown below, and click on to continue and then OK to get output as below.



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Probability Theory and Its Application 4

4.1 Introduction

In our daily life, we are experienced about the fact that occurrence or nonoccurrence of any event/phenomenon is associated with a chance/uncertainty factor. We are always in search of likelihood of happening or nonhappening of event/phenomenon. The farmers who want to have plant protectional spray on a particular day will be interested to know the likelihood of raining before and after spray so that the effect of spray is not washed out by the occurrence rain. A fish farm will be interested to spend money on a particular type of feed only knowing after likelihood of increasing body weight of fishes by the new feed. In statistics, the likelihood of happening or nonhappening of an event is generally known as probability. Probability is a mathematical construction that determines the likelihood of occurrence or nonoccurrence of events that are subjected to chance factor. Thus the farmers are interested to know the probability of occurrence rain before and after spraying. As we have already discussed, the subject matter of statistics is concerned with drawing inference about the population based on observations recorded, mostly from sample. In this regard probability plays a great role. Noting a particular character (say percentage of cancer patients or percentage of disease affected area in a field), in a sample the experimenter wants to infer about the (percentage of cancer) population or percentage of disease-affected area as a whole, with a probability. Greater is the probability of drawing accurate inference about the population; better is the inference about the population.

Before dealing with the theory of probability, it is useful to have some knowledge of set theory. Knowledge of set theory and its laws will help us in understanding probability theory. In the next section, we shall discuss the set theory in brief.

Set *A set is accumulation or aggregation of well-defined objects/entities having some specific and common characteristics*. For example, the fishes in a pond, fishes of weight greater than 1 lb in a pond, fishes with scales in a pond, and fishes without scales in a pond, all these constitute set of fishes in the pond, set fishes greater 1 lb in the pond, set of scaled fishes in the pond, and set fishes without scales in the pond, respectively. The individual member of set is called its element/member/point of the set. If x is a member of a set "X," then we denote it as $x \in X$ that means x belongs to or is an element of the set X, and if x does not belong to a set X or x is not a member of the set, then it is denoted as $x \notin X$.

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4.2 Types of Set

Finite Set Finite set is a set having finite number of elements/members, e.g., ripe mangoes in a tree, integers beween 1 and 100, etc.

Infinite Set A set consisting of infinite number of elements/member/units is called infinite set. Infinite set again is of two types: (*a) countably infinite and (b) uncountably infinite*. A set consists of infinite number of elements but these can be ordered and is known as countably infinite set, e.g., the set of all integers, i.e., $X = \{x$: all integers$\} = \{1, 2, 3, 4, 5,\ldots\}$. On the other hand, an uncountably infinite set is a set of elements which can neither be counted nor be ordered, e.g., the set of numbers in between 0 and 1, i.e., $A = \{x: 0 < x < 1\}$.

Equal Set Two sets "*A*" and "*B*" are said to be equal if every element of the set "*A*" is also an element of the set "*B*" and vice versa and is denoted as $A = B$. Thus, if $A = \{1,2,3\}$ and $B = \{2,3,1\}$, $A = B$.

Null Set A set having no element is called an empty set or null set and is denoted by ϕ. The set of negative integers between 2 and 3, i.e., $A = \{x$:2 < all negative numbers < 3$\}$. The set $A = \{0\}$ is not a null set as it contains an element zero. Null set is a subset of every set.

Subset A set "*A*" is said to be a subset of a set "*B*" if all the elements of the set *A* are included in the set *B* and we write $A \subseteq B$.

Suppose we have two sets $A = \{x: 0 < x$ (integer) $\leq 3\} = \{1,2,3\}$ and $B = \{x: 0 \leq x$ (all numbers) $\leq 3\} = \{0, 0.1, 0.2,\ldots1,\ldots2,\ldots,3\}$, then $A \subseteq B$.

It is to be noted that if a set has n elements, then it has 2^n subsets.

Mainly there are three types of fertilizers, viz., inorganic, organic, and bio-fertilizers. So each of the set of inorganic, organic, or bio-fertilizers are individually the subsets of the set of fertilizers.

Power Set A set of all the subset of a set *A* including the null set is called the power set of *A*. In tossing a coin, the set of outcomes would be {H, T}, {H}, and {T}, then the set $[[\phi, \{H\}, \{T\}, \{H, T\}]$ is the power set *A*.

Universal Set Suppose all the sets under consideration are the subsets of a certain set *A*, then this set *A* is called the universal set or the whole set, and it is generally denoted by *U*.

If $A = \{x$: all the fertilizers$\}$
$B = \{x$: all inorganic fertilizers$\}$
$C = \{x$: all the organic fertilizers$\}$
$D = \{x$: all the bio-fertilizers$\}$

Therefore, *A* is the universal set for all the sets *B*, *C*, and *D*.

Union Set A set *A* is said to be the union of two sets *B* and *C* if it contains all the elements belonging to either set *B* or set *C* or both, but no repetition is allowed and is denoted as $A = B \cup C$. The idea of union can very well be extended to more than two sets also. Thus, $B \cup C = \{x : x \in B \text{ or } x \in C\}$. Similarly for more than two sets B_i $(i = 1, 2, 3\ldots n)$, $\bigcup_{i=1}^{n} B_i = x : x \in B_i$, for at least one i, $i = 1, 2, 3\ldots n\}$.

Example 4.1 In throwing a dice, let *A* be the set of all odd faces and *B* be the set of all even faces. Find out the union set for *A* and *B*.

Solution Thus,

$A = \{x$: all odd faces of the dice$\} = \{1,3,5\}$
$B = \{x$: all even faces of the dice$\} = \{2,4,6\}$
$A \cup B = \{$x: all faces of the dice$\} = \{1, 2, 3, 4, 5, 6\}$

Complement The complement of a set *A* is the set containing the elements except the elements of the set *A* and is denoted by $A'/A^c/\bar{A}$. Thus, a set and its complement divide the universal set

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into two distinct sets. In throwing a dice, the set of odd faces of the dice is the complement of the set of all even faces. All elements belonging to the universal set U but not belonging to A constitute A^c. Thus a set $A'/A^c/\bar{A}$ is the complement of the set A if it is constituted of all the elements of the universal set which are not members of the set A.

Example 4.2
$U = \{x$: all faces of dice$\} = \{1, 2, 3, 4, 5, 6\}$.
Now if $A = \{x$: all odd faces of dice$\} = \{1, 3, 5\}$ then
$\Rightarrow A^c = \{x$: all even faces of dice$\} = \{2, 4, 6\}$

Example 4.3 If the universal set $U = \{x$: all fertilizers$\}$ and

if $A = \{x$: all inorganic fertilizers$\}$, then
$A'/A^c/\bar{A} = \{x$: all fertilizers excepting inorganic fertilizers$\}$

Intersection The intersection set of two or more sets is the set of all elements common to all the component sets. Thus the intersection of two sets A and B is the set of all elements contained in both the sets and is denoted as $A \cap B$. Similarly, for more than two sets A_i $(i = 1, 2, 3 \ldots n)$, $\bigcap_{i=1}^{n} A_i = x : x \in A_i$, for all i, $i = 1, 2, 3 \ldots n\}$.

If there is no common element in both the sets, then $A \cap B = \phi$ (null set).

Example 4.4 In throwing a dice, let A be set of all faces multiple of three, i.e.,
$A = \{x$: all faces multiple of three of dice$\} = \{3,6\}$, and B be a set of all even faces, i.e., $B = \{x$: all even faces of dice$\} = \{2,4,6\}$

$$\therefore A \cap B = \{6\}.$$

Disjoint Set When there exists no common element among two or more sets, then the sets are known as disjoint; as such $\bigcap_{i=1}^{n} A_i = \phi$, where A_i denotes i-th set.

Example 4.5 Let $A = \{x$: all inorganic fertilizers$\}$, $B = \{x$: all organic fertilizers$\}$, then $A \cap B = \phi$ and we call set A and set B as disjoint.

Difference A set consisting of all elements contained in set A but not in set B is said to be the difference set of A and B and is denoted as $A-B$.

$$A - B = \{x : x \in A, \text{but} x \notin B\}$$

Similarly $B - A = \{x : x \in B, \text{but} x \notin A\}$ is the set of all elements belonging to the set B but not in A. It may be noted that a difference set is the subset of the set from which difference of other set is being taken, i.e., $A - B \subseteq A, B - A \subseteq B$. Moreover, it should also be noted that $A-B \neq B-A$

Example 4.6 Let

$A = \{x$: all fertilizers, i.e., inorganic, organic, and bio-fertilizers$\}$
$B = \{x$: all inorganic and organic fertilizers$\}$
$\Rightarrow A-B = \{x$: all bio-fertilizers$\}$

4.3 Properties of Sets

The above mentioned sets follow some important properties. Let us state some of the important properties without going into those details.

(i) *Commutative law for union:* If A and B are two sets, then $A \cup B = B \cup A$
(ii) *Commutative law for intersection:* If A and B are two sets, then $A \cap B = B \cap A$.
(iii) *Distributive law of union:* If A, B, and C are three sets, then $A \cup (B \cap C) = (A \cup B) \cap (A \cup C)$.
(iv) *Distributive law of intersection:* If A, B, and C are three sets, then $A \cap (B \cup C) = (A \cap B) \cup (A \cap C)$.
(v) *Associative law:* If A, B, and C are three sets, then $A \cup (B \cup C) = (A \cup B) \cup C$ and $A \cap (B \cap C) = (A \cap B) \cap C$.

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(vi) *Difference law:* If A and B are two sets, then (i) $A - B = A \cap B^c$ and (ii) $A - B = A - (A \cap B) = (A \cup B) - B$.

(vii) *Complementary laws:* (a) $U^c = \phi$ and $\phi^c = U$, (b) $A \cup U = U$, (c) $A \cap U = A$, (d) $A \cap A^c = \phi$, (e) $A \cup \phi = A$, (f) $A \cap \phi = \phi$, (g) $A \cup A^c = U$, and (h) $(A^c)^c = A$.

(viii) *De Morgan's law:* (a) $(A \cup B)^c = A^c \cap B^c$, (b) $(A \cap B)^c = A^c \cup B^c$.

4.4 Experiment

So long we have tried to establish probability in terms of chances or likelihood of occurrence of events. Such events may be thought of as outcome of experiments. Now the question is what do we mean by an experiment? What are its types? What are its components? In the following section, we shall try to discuss in brief about experiment and related terminologies.

(i) *Experiment and random experiment:* An experiment is a systematic process or activity which leads to collection of information and its analysis on certain objects to answer to the objectives that the researcher has already in mind. An experiment may be regarded as an act which can be repeated essentially under the same condition. A random experiment is an experiment whose results cannot be predicted in advance or whose results depend on chance factor. For example, in throwing a dice, any one face out of six faces, viz., 1, 2, 3, 4, 5, and 6, can appear, but nobody knows which face will appear in any particular throw. The results of any random experiment are called *outcome* of the experiment. In throwing a dice having six faces, the possible outcomes are 1, 2, 3, 4, 5, or 6. Thus any outcome of any random experiment is always associated with chance factor. For an unbiased dice, each face has got 1/6 chance to appear in any draw.

(ii) *Event:* One or more outcomes of a random experiment constitute event. Event is almost synonymous to outcome of a random experiment; actually events are set of certain specified outcomes of random experiment; on the other hand, outcomes or the elementary events are the ultimate results of any random experiment which cannot be disaggregated further.

Example 4.7 In the experiment of throwing a dice, appearance of 1, 2, 3, 4, 5, or 6 in any throw is the outcome of the experiment, but the three outcomes 1, 3, and 5 or 2, 4, and 6 constitute two events, viz., event of odd faces and event of even faces, respectively. Both the events of odd faces and the even faces can further be disaggregated into the outcomes of 1, 3, and 5 or 2, 4, and 6, respectively. Again take the example of tossing an unbiased coin: the outcomes are head (H) or tail (T). Thus head and tail both are outcomes as well as elementary events for the experiment of throwing an unbiased coin.

(iii) *Compound event:* When an event is obtained by combining together two or more events, then it is known as compound event. For example, in throwing dice getting multiple of three is a compound event because this will occur if either or both of the elementary events 3 and 6 occur.

(iv) *Trial:* When an experiment is repeated essentially under the same/identical condition, instead of providing unique result, provide one of the possible outcomes, then it is called a trial. In other words, each performance of a random experiment is called a trial, and all the trials conducted under the same condition form a random experiment. In the example of throwing coins, each time we throw the coin, it results in one of the outcomes, head or tail – thus it is known as trial. When this trial of throwing coin is repeated, and

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other conditions remain constant, then these constitute a random experiment of throwing coin. Take another example: before releasing any variety, the same is put under experimentation along with some check varieties at different situations (may be locations) under the same experimental protocol; we call these as multilocational trials. All these multilocational trials constitute the varietal experiment.

(v) *Mutually exclusive events:* Two events are mutually exclusive or incompatible if the occurrence or nonoccurrence of one event precludes the occurrence or nonoccurrence of the other event. Let us take the example of throwing an unbiased coin: if head appears in any throw, this means tail cannot appear and vice versa. Thus appearance of head in any throw precludes/cancels the appearance of tail and vice versa. More than two events may also be mutually exclusive. For example, in throwing a dice, any one of the six faces will appear and other five faces cannot appear. Thus appearance of one face precludes/nullifies/cancels the occurrence of other faces.

(vi) *Exhaustive events:* Exhaustive event is the set of all possible outcomes of any random experiment. For example, in case of throwing a dice, the set of all the possible outcomes, viz., 1, 2, 3, 4, 5, and 6, constitutes exhaustive events for the experiment.

(vii) *Independent events:* Two or more events are said to be *independent* if the occurrence or nonoccurrence of an event is not affected by the occurrence or nonoccurrence of other events. In throwing an unbiased coin, the outcome does not have anything to do with the outcomes of its previous or subsequent throws. Similarly in throwing a dice, the result of the second throw does not depend on the result of the first, third, fourth, or subsequent throws.

(viii) *Equally likely events:* Two or more events of any random experiment are equally likely when one cannot have any reason to prefer one event rather than the others. In tossing coin, there is no reason to prefer head over tail, because both the faces of the coin have same chances to appear in any throw. So the events head and tail are equally likely.

(ix) *Sample space:* A sample space is related with an experiment; more specifically it is related with the outcomes of the experiment. Actually a sample space is the set of all possible outcomes of any random experiment, and each element of the sample space is known as the sample point or simply point. Sample space may be finite or infinite. For example, in throwing dice the sample space is $S = \{1,2,3,4,5,6\}$, a finite sample space. Now if we are conducting an experiment in the form of tossing a coin such that the coin is tossed till a head appears or a specific number of head appears; in this case the sample space may be $S = [\{H\}, \{T,H\}, \{T,T,H\}, \{T,T,T,H\}\ldots]$. Thus the time or duration of telephonic talk per day from a particular number in a particular telephone exchange is also an example of infinite continuous sample space, which may be written as $S = \{x{:}0 < t < 24\ \text{h}\}$.

(x) *Favorable event:* By favorable event we mean the number of outcomes or events, which entails the happening of an event in a trial. For example, in throwing an unbiased coin, the number of cases/event favorable of getting head out of two alternatives H/T is one, as such either head or tail is the favorable event.

(xi) *Œ (sigma) field:* It is the class of events or set of all subsets of sample space "*S*."

4.5 Probability Defined

In its simplest form, probability is a way to measure the chances of uncertainty. Probability can be a priori or a posteriori. If a day is cloudy,

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our general knowledge says that there might be rain. If the weather conditions are cloudy and humid, then there is probability of late blight of potato. Thus, such probabilities come from the logical deduction of the past experience and are known as a priori probability. On the other hand, an a posteriori probability is to be ascertained by conducting planned experiment. For example, tuition helps in getting better grade by the students can be established only after placing a group of students under tuition and recording their grades with certain probability.

Probability can be explained and defined in different approaches: (*i) the classical or mathematical approach, (ii) the statistical/empirical approach, and (iii) the axiomatic approach.*

According to *mathematical or classical approach*, probability of an event A is defined as $P(A) = \frac{\text{Number of favourable cases for } A}{\text{Total number of cases}} = \frac{m}{n}$ where the random experiment has resulted in "n" exhaustive, mutually exclusive, equally likely events and out of which "m" is favorable to a particular event "A" with $m \geq 0, n > 0$, and $m \leq n$. Thus, according to the conditions above, $0 \leq P(A) \leq 1$. In spite of its simplicity and easy to understand nature, this definition suffers from the fact that in many cases, the cases or event may not be equally likely. Moreover when the sample space or the number of exhaustive cases is not finite, then it is difficult to define the probability.

Example 4.8 Suppose in a throwing coin experiment, out of ten tosses, head has appeared six times. Hence the probability of the event head in the above experiment is 6/10 = 0.6.

According to *statistical approach* probability of an event, A is defined as $P(A) = \lim_{n\to\infty} \frac{m}{n}$, under the condition that the experiment has been repeated a great number of times under the same condition where "m" is the number of times in which the event A happens in a series of "n" trials and the above limit exists. This definition also suffers from the fact that it is not easy to get the limit always and sometimes limit does not provide a unique value; also as we increase the number trials to a great number, it is very difficult to maintain the identical experimental condition.

The *axiomatic approach of probability* has an intention to overcome the limitations of the other two definitions. In this approach any function "P" defined on a Œ (sigma) field satisfying the following axioms is called probability function or simply probability.

Axiom I: For any event $P(A) \geq 0; A \in Œ$
Axiom II: $P(S) = 1$ (S = sample space)
Axiom III: For any countably infinite number of mutually exclusive events $A_1, A_2 \ldots$ each belonging to Œ-field $P(A_1 \cup A_2 \cup A_3 \ldots.) = P(A_1) + P(A_2) + P(A_3) + \ldots.$, i.e., $P\left(\cup_{i=1}^{\infty} A_i\right) = \sum_{i=1}^{\infty} P(A_i)$

In the following section, we shall state some of the important results of probability without going details in to their proofs.

4.5.1 Important Results in Probability

(i) $P(\phi) = 0$
(ii) *If $A_1, A_2, A_3, \ldots A_n$ are n disjoint events each belonging to Œ-field, then*

$$P\left(\bigcup_{i=1}^{n} A_i\right) = \sum_{i=1}^{n} P(A_i)$$

Example 4.9 In throwing a coin, there two mutually exclusive equally likely outcomes/events, head and tail, each with probability 1/2 and 1/2. Hence, $P(H \cup T) = P(H) + P(T) = 1/2 + 1/2 = 1$.

(iii) *If A is an event in Œ-field, then $P(A^c) = 1 - P(A)$.*

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Example 4.10 In the above Example 4.9, the complement of head is the tail. Hence $P(T) = 1 - P(H) = 1/2$.

(iv) *If A_1 and A_2 are two events in Œ-field and $A_1 \subset A_2$, then $P(A_1) \leq P(A_2)$.*

Example 4.11 Suppose there are two events, A: {x:1,2,3,4,5}, and B:{2,3,4}, in a sample space S: {1,2,3,4,5,6}, clearly $B \subset A$. Now $P(A) = 5/6$ and $P(B) = 3/6$, so $P(B) < P(A)$.

(v) *For any two events A and B in the Œ-field, $P(A \cup B) = P(A) + P(B) - P(A \cap B)$.*

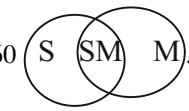
The above result can also be extended for any "n" events as follows:

$$P\left(\bigcup_{i=1}^{n} A_i\right) = \sum_{i=1}^{n} P(A_i) - \sum_{1 \leq i \angle j \leq n} \sum P\left(A_i \bigcap A_j\right)$$
$$+ \sum_{1 \leq i < j < k \leq n} \sum \sum \left(A_i \bigcap A_j \bigcap A_k\right) - \ldots\ldots$$
$$\ldots\ldots + (-1)^{(n-1)} P\left(A1 \bigcap A2 \bigcap A3 \ldots\ldots\ldots \bigcap An\right)$$

Example 4.12 In an examination out of 100 students, 70 passed in statistics, 80 in mathematics, and 60 in both. Then how many students passed either in statistics or mathematics or both?

Thus we have $P(S)$ = probability of passing in statistics = 70/100 = 0.70,

$P(M)$ = probability of passing in mathematics = 80/100 = 0.80, and

$P(S \cap M)$ = probability of passing both the subjects = 60/100 = 0.60 

$$\therefore P(S \cup M) = P(S) + P(M) - P(S \cap M)$$
$$= 0.70 + 0.80 - 0.60 = 0.90$$

(vi) *Boole's inequality*: For any three events A_1, A_2, and A_3:

(a) $P(A_1 \cup A_2 \cup A_3) \leq \sum_{i=1}^{3} P(A_i)$

(b) $P(A_1 \cap A_2 \cap A_3) \geq \sum_{i=1}^{3} P(A_i) \sum_{i=1}^{3} P(A_i) - 2$

(vii) *Conditional probability:* Two events A_1 and A_2 are such that neither $P(A_1)$ nor $P(A_2)$ equals to zero, then probability of happening "A_1" fully knowing that "B" has already happened is known as the conditional probability of "A_1" given that "A_2" has already occurred and is given as $P(A_1/A_2) = P(A_1 \cap A_2)/P(A_2)$. Similarly, the conditional probability of "A_2" given that "A_1" has already occurred is given by $P(A_2/A_1) = P(A_1 \cap A_2)/P(A_1)$.

Example 4.13 In a paddy field, 50 % is affected by BPH (brown plant hopper), 70 % by GLH (green leafhopper), and 40 % by both BPH and GLH. Find the probability of (i) area affected by either of the pests, and (ii) find the probability of any area affected by BPH when it is already affected by GLH and vice versa.

The first problem is related with union of probabilities (fifth important results in probability 4.5.1.V) and the second one is with the conditional probability of one happening even when the other event has already occurred (i.e., 4.5.1.VII). Let us first find out the probabilities:

Probability of an area affected by BPH = P (BPH) = 50/100 = 0.50.

Probability of an area affected by GLH = P (GLH) = 70/100 = 0.70.

Probability of an area affected by both BPH and GLH

GLH = P(BPH ∩ GLH) = 40/100 = 0.40.

(i) So the probability of an area affected by either BPH/GLH/both is the union of the two probabilities

$$\therefore P(\text{BPH} \cup \text{GLH}) = P(\text{BPH}) + P(\text{GLH}) - P(\text{BPH} \cap \text{GLH})$$
$$= 0.50 + 0.70 - 0.40$$
$$= 0.80$$

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(ii) Conditional probability of an area affected by GLH when the area is already affected by

$$\text{BPH is } P(\text{GLH}/\text{BPH}) = \frac{P(\text{BPH} \cap \text{GLH})}{P(\text{BPH})} = \frac{0.40}{0.50} = 0.80$$

and the conditional probability of an area affected by BPH when the area is already affected by BPH is $P(\text{BPH}/\text{GLH}) = \frac{P(\text{BPH} \cap \text{GLH})}{P(\text{GLH})} = \frac{0.40}{0.70} = 0.57.$

(ix) *Independent events:* Two events A and B are said to be independent if the probability of happening of the event A does not depend on the happening or nonhappening of the other event B. Thus using the formula of conditional probability of two events A and B, for two independent events A and B, we have $P(A/B) = P(A)$ and $P(B/A) = P(B)$.

So when two events A and B are independent, then using compound law of probability, we have $P(A \cap B) = P(A)P(B)$.

For three or more events $A_1, A_2, A_3 \ldots A_n$ to be independent, we have

$$\left.\begin{aligned} P(A_1 \cap A_2) &= P(A_1).P(A_2) \\ P(A_1 \cap A_3) &= P(A_1).P(A_3) \\ P(A_2 \cap A_3) &= P(A_2)P(A_3) \end{aligned}\right\} \ldots\ldots\ldots(1)$$
$$P(A_1 \cap A_2 \cap A_3) = P(A_1).P(A_2).P(A_3)$$

If only the condition (1) is satisfied, then A_1, A_2, and A_3 are pair-wise independent. The idea of three events can be extended to n events A_1, A_2, $A_3, \ldots, A_n$ and, we shall have

$$P(A_1 \cap A_4) = P(A_1).P(A_4)$$
$$\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots$$
$$\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots$$
$$P(A_1 \cap A_2 \cap \ldots\ldots\ldots\ldots \cap A_n) = P(A_1).P(A_2).P(A_3)\ldots\ldots\ldots\ldots\ldots\ldots P(A_n)$$

(x) *Bayes' theorem:* Suppose E is an arbitrary event such that $P(E) \neq 0$ and also suppose that let $A_1, A_2, \ldots, A_n$ are "n" mutually exclusive events whose union is the sample space S such that $P(A_i) > 0$ for each I, then

$$P(A_i/E) = \frac{P(A_i)P(E/A_i)}{\sum_{i=1}^{n} P(A_i)P(E/A_i)}, i = 1, 2, 3, \ldots\ldots n$$

In this context one should note that (i) $P(A_i)$ s are the priori probabilities, (ii) $P(A_i/E)$s are posterior probabilities, and (iii) $P(E/A_i)$s are likelihood probabilities.

Example 4.14 In an experiment of fruit setting in pointed gourd, three different methods of pollination were used in 30 %, 40 %, and 30 % plots, respectively, knowing fully that the success rates of three types of pollination are 50 %, 85 %, and 90 %, respectively. What is the probability that a particular plot has been pollinated by the method two?

Solution Let A_1, A_2, and A_3 denote the three methods of pollination, respectively, and E be the event of pollination. Now as per the information $P(A_1) = 0.3$, $P(A_2) = 0.4$, and $P(A_3) = 0.3$, also $P(E/A_1) = 0.5$, $P(E/A_2) = 0.85$, and $P(E/A_3) = 0.90$.

$$\therefore P(A_2/E) = \frac{P(A_2 \cap E)}{P(E)} = \frac{P(A_2)P(E/A_2)}{P(A_1)P(E/A_1) + P(A_2)P(E/A_2) + P(A_3)P(E/A_3)}$$
$$= \frac{(0.4)(0.85)}{(0.3)(0.5) + (0.4)(0.85) + (0.3)(0.9)} = \frac{0.340}{0.15 + 0.34 + 0.27} = \frac{0.34}{0.76} = 0.447$$

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Thus the probability of the plants of a particular plot being pollinated by method two is 0.447.

Similarly the probability of the plants of a particular plot being pollinated by the method one will be

$$\therefore P(A_1/E) = \frac{P(A_1 \cap E)}{P(E)} = \frac{P(A_1)P(E/A_1)}{P(A_1)P(E/A_1) + P(A_2)P(E/A_2) + P(A_3)P(E/A_3)}$$
$$= \frac{(0.3)(0.5)}{(0.3)(0.5) + (0.4)(0.85) + (0.3)(0.9)} = \frac{0.15}{0.15 + 0.34 + 0.27} = \frac{0.15}{0.76} = 0.197$$

and the probability of the plants of a particular plot being pollinated by the method three will be

$$\therefore P(A_3/E) = \frac{P(A_3 \cap E)}{P(E)} = \frac{P(A_3)P(E/A_3)}{P(A_1)P(E/A_1) + P(A_2)P(E/A_2) + P(A_3)P(E/A_3)}$$
$$= \frac{(0.3)(0.9)}{(0.3)(0.5) + (0.4)(0.85) + (0.3)(0.9)} = \frac{0.27}{0.15 + 0.34 + 0.27} = \frac{0.27}{0.76} = 0.355$$

4.6 Random Variables and Their Probability Distributions

We have described the random experiment and the events arising out of the random experiment. In this section we shall define random variable and its properties. For each elementary event in the sample space of a random experiment, one can associate a real number or a range of real numbers according to certain rule or following certain functional form. Here we define a random variable as a rule or function that assigns numerical values which varies randomly to observations. Thus, it takes different values for different observations at random in a random experiment. *Given a random experiment with sample space S, a function X which assigns to each element $w \in S$ one and only one real number X(w) = x is called a random variable*. The space of X is the set of real numbers $R = \{x : x = X(w), w \in S\}$.

Suppose X is a random variable and x_1, x_2, x_3..... are the values which it assumes, the aggregate of all sample points on which X assumes the fixed values x_i forms the event that $X = x_i$; its probability is denoted by $P[X = x_i] = f(x_i)$, where $i = 1,2,3, \ldots$.is called the probability distribution of the random variable X. Clearly, $f(x_i) \geq 0$ and $\sum_i f(x_i) = 1$.

Example 4.15 Suppose a coin is tossed two times, then its sample space will be HH, HT, TH, and TT. Thus, the number of heads (X) to be observed in tossing the unbiased coin two times, we have

$X = x$	:	2	1	0
Events favorable	:	1	2	1
$P(X = x)$	:	1/4	2/4	1/8

This is the probability distribution of the random variable X (number of heads)

Distribution Function Random variables can be discrete or continuous. *A continuous random variable can take any value in an interval of real numbers, whereas a discrete random variable can take particular values, mostly the integer values, in the given interval*. For example, plant height of paddy at particular growth stage can take any value within the interval [$h1$,$h2$], where

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$h1$ and $h2$ are the shortest and tallest height values of the interval, respectively; so paddy plant height is an example of continuous random variable. On the other hand, the number of grains per panicle of particular paddy variety is an example of discrete random variable. Thus each value of the random variable or the each range of the random variable can be treated as event and as such occurs with certain probability following certain probability law. *Presentation of probabilities corresponding to different values of the discrete random variable or corresponding to the ranges of values of the random variable can be presented in the form of table/graph/formula which is known as probability distribution*. When the cases are finite, for a discrete random variable the probability distribution corresponds to the frequency distribution as per the classical definition of probability. *Function that provide the probability distribution corresponding to a random variable is known as probability function. The discrete probability function is known as probability mass function (pmf), whereas the continuous probability function is known as probability density function (pdf)*. If a function "P" is the pmf for a random variable X within a range of $[a, b]$, then $P(X = x) \geq 0$ and $\sum_a^b P(x) = 1$. On the other hand, if a function "f" is the pdf of the random variable X within a range $[a, b]$, then $f(X = x) \geq 0$ and $\int_a^b f(x)dx = 1$.

4.7 Mean, Variance, and Moments of Random Variable

Analogous to that of measures of central tendency, dispersion as discussed for variables, for random variables also these can be worked out using its probability distribution. In this section we shall discuss the mean, variance, and moments of random variables.

Expectation of Random Variables

We have already discussed that the measure of central tendency particularly the average value of any phenomenon is of utmost importance in our daily life. Given a data set, we always want to know mean/average so that we can have an idea about its expected value in the population. Thus, in all sphere of data handling, the major aim is to have an expected value of the random variable. Given the probability distribution of a random variable, its expectation is given as follows:

(i) For discrete random variable X, if $P(x)$ is the probability mass function, then $E(X) = \sum_x xP(x)$.

(ii) For a continuous random variable "X" within a range $a \leq x \leq b$ with pdf $f(x)$, $E(X) = \int_a^b xf(x)dx$ (provided the integration is convergent).

Example 4.16 Suppose an experiment is conducted with two unbiased coins. Now the experiment is repeated 50 times, and the number of times of occurrence of each event is given as follows. Find out the expected occurrence of head.

HH	HT	TH	TT
12	**15**	**14**	**9**

Solution The favorable event for the above experiment is occurrence of head.

So the probability distribution of occurrence of head is:

Event	HH	HT	TH	TT
Prob.	1/4	1/4	1/4	1/4

$\Rightarrow$

Event	2H	1H	2 T
Prob.	1/4	1/2	1/4

Two heads – 1/4, one head = 1/4 + 1/4 = 2/4 = 1/2, and 0 head = 1/4. So the occurrence of head in the above experiment of tossing two coins is a random variable, and it takes the values 0, 1, and 2 with probabilities 1/4, 1/2, and 1/4 respectively.

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No. of heads	0	1	2
Probability	0.25	0.5	0.25
Frequency	9	29	12

So for getting the expected value of head out 50 trial is $1/4\times9 + 1/2\times29 + 1/4\times12 = 19.75$

Properties of Expectation

(a) Expectation of a constant "c" is $E(c) = c$.
(b) If $Y = a + X$ then $E(Y) = a + E(X)$, where a is a constant.
(c) If $Y = a + bX$, then $E(Y) = a + b\ E(X)$, where both a and b are constants.
(d) $E(X + Y) = E(X) + E(Y)$, where both X and Y are random variables.
(e) If "X" is random variable such that $X \geq 0$, then $E(X) \geq 0$.
(f) Expectation of a random variable serves as the average or the arithmetic mean of the random variable.

The geometric mean, harmonic mean, median, mode quartile values, percentile value, etc. of discrete random variable can be calculated from the probability distribution of the random variable using the following formulae, respectively:

Geometric mean	$\text{Log}(G) = \sum_{i=1}^{n} \log(x_i).P(x_i)$, where n is number of observations
Harmonic mean	$\sum_{i=1}^{n} \frac{1}{x_i} P(x_i)$, where n is number of observations
Median	$\sum_{i=1}^{m} P(x_i) = \sum_{i=m+1}^{n} P(x_i) = \frac{1}{2}$, where n is number of observations and m is the halfway point
Mode	$P(r-1) \leq P(r) \geq P(r+1)$, where r is the r-th event
Q1 and Q3	$Q_1 = \sum_{i=1}^{Q1} P(x_i) = \frac{1}{4}$ and $Q_3 = \sum_{i=1}^{Q3} P(x_i) = \frac{3}{4}$
i-th percentile	$p_i = \sum_{i=1}^{pi} P(x_i) = \frac{i}{100}$

If the random variable X is continuous, then the corresponding expectation, geometric mean, harmonic mean, median, mode quartile values, percentile value, etc. of the random variable can be calculated from the probability distribution of the random variable using the following formulae, respectively:

Expectation	$\int_a^b xf(x)dx$
Geometric mean	$\log(G) = \int_a^b \log x.f(x)dx$
Harmonic mean	$\int_a^b \frac{1}{x} f(x)dx$
Median	$\int_a^m f(x)dx = \int_m^b f(x)dx = \frac{1}{2}$
Mode	For mode $f'(x) = 0$ and $f''(x) < 0$ within the range of $x = [a,b]$

Variance of a Random Variable

One of the of the most important measures of dispersion is the variance, and variance of a random variable is a measure of the variation/dispersion of the random variable about its expectation (mean). The variance of a random variable is given as $V(X) = E\{X - E(X)\}^2$

$$= E\left[X^2 + \{E(X)\}^2 - 2X.E(X)\right]$$
$$= E(X^2) + \{E(X)\}^2 - 2\,E(X).E(X)$$
$$= E(X^2) - \{E(X)\}^2$$

Properties of Variance of Random Variable

Most of the properties of variance for a variable discussed in Chap. 3 hold good for variance of random variable. Thus,

(a) $V(c) = 0$, where "c" is a constant.
(b) Variance of random variable does not depend on change of origin but depends on change of scale. Thus $V(c + X) = V(X), V(cX) = c^2V(X)$ and $V(b + cX) = c^2V(X)$.
(c) $V(X + Y) = V(X) + V(Y) + 2\text{Cov}(X, Y)$, where X and Y are two random variables.
(d) $\text{Cov}(X, Y) = E(XY) - E(X)E(Y)$.

Moments

(a) If X is a discrete random variable, then:
  (i) The r-th raw moment about origin is defined by $\upsilon_r = E(X^r) \sum_{i=1}^{n} x_i^r P(x_i)$,

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provided $E|X^r| < \infty$. Clearly, $\upsilon_1 = E(X) = \mu$ and $\upsilon_0 = 1$.

(ii) The r-th central moment about its expectation is defined as

$$m_r = E(X - E(X))^r = \sum_{i=1}^{n} (X_i - E(X))^r P(x_i)$$

provided it exists.

The other measures of dispersion like mean deviation about mean, r-th raw moment about any arbitrary point A are given as follows:

Mean deviation about the mean	$\sum_x \lvert x - E(X)\rvert P(x)$
$\mu_r^{'}$ (about point A)	$\sum_{i=1}^{n} (x_i - A)^r P(x_i)$

(b) If X is continuous random variable, then the mean deviation about mean, r-th moment about origin, r-th moment about any arbitrary point A, and r-th moment about mean, quartiles, and percentiles can be calculated using the following formulae, respectively:

Mean deviation about the mean	$\int_a^b \lvert x - E(X)\rvert f(x)dx$
υ_r (about origin)	$\int_a^b x^r f(x)dx$
$\mu_r^{'}$ (about point A)	$\int_a^b (x - A)^r f(x)dx$
m_r (about mean)	$\int_a^b (x - E(X))^r f(x)dx$
Q1 and Q3	$\int_a^{Q1} f(x)dx = \frac{1}{4}$ and $\int_a^{Q3} f(x)dx = \frac{3}{4}$
i-th percentile	$p_i = \int_a^{pi} f(x)dx = \frac{i}{100}$

Distribution Function If X is a random variable defined on $(S, Œ, P)$ then the function $F_x(x) = P(X \le x) = P(w{:}X(w) \le x)$ is known as the distribution function of the random variable X. It should be noted that $F(-\infty) = 0, F(+\infty) = 1$, and $0 \le F(x) \le 1$.

Example 4.17 The fish length of certain breed of fish at the age of 6 months is supposed to be within the range of 12–24inches. If the probability density function of length of fish is given as k $(x-3x + 2)$:

(a) Find the value of "k."
(b) Work out the cumulative distribution function of the variable fish length (X).
(c) Find the probability of fishes having length less than $1.5'$ and $1.75'$.

Solution

(a) We know that a function f is a density function of certain continuous random variable $\int_R f(x)dx = 1$. For this function to be a density function

$$\int_1^2 1k\left(x^2 - 3x + 2\right)dx = 1$$

$$\therefore \frac{x^3}{3} - 3\frac{x^2}{2} + 2x\Big]_1^2 = 1/k$$

$$\text{Or, } \left(\frac{2^3}{3} - 3\frac{2^2}{2} + 2.2\right) - \left(\frac{1^3}{3} - 3\frac{1^2}{2} + 2.1\right) = 1/k$$

$$\text{Or, } (8/3 - 6 + 4) - (1/3 - 3/2 + 2) = 1/k$$

$$\text{Or, } 2/3 - 5/6 = 1/k$$

$$\text{Or, } -1/6 = 1/k$$

$$\text{or, } k = -6.$$

So the pdf. of the random variable plant height (X) is

$$k(x^2 - 3x + 2) = (-6)x^2 - 3(-6)x + 2 = -6x^2 + 18x - 12.$$

(b) The cumulative density function $F(x)$ is given by

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$$F(x) = \int_1^x (-6t^2 + 18t - 12)dt$$
$$= \frac{-6t^3}{3} + 18\frac{t^2}{2} + 2t\Big]\Big|_1^x$$
$$= \frac{-6x^3}{3} + 9x^2 - 2x - (-2 + 9 - 12)$$
$$= -2x^3 + 9x^2 - 12x + 5$$

(c) The probability of fishes having length less than $1.5' = P(X < 1.5') = P(X \leq 1.5') = F(1.5')$

$$F(x) = -2x^3 + 9x^2 - 12x + 5$$
$$\therefore F(x) = 5 - 12 \times 1.5 + 9 \times 1.5^2 - 2 \times 1.5^3$$
$$= 5 - 18 + 20.25 - 6.75$$
$$= 0.50$$

Similarly the probability of fish length less than 1.75 m is given by $P(X \leq 1.75)$.

Now $P(X \leq 1.75) = F(1.75)$

$$F(x) = -2x^3 + 9x^2 - 12x + 5$$
$$\therefore F(x) = 5 - 12 \times 1.75 + 9 \times 1.75^2 - 2 \times 1.75^3$$
$$= 5 - 21 + 27.56 - 10.72$$
$$= 32.56 - 31.72$$
$$= 0.84$$

So the probability that the fish length lies between $1.5'$ and $1.75'$ is given by $P(1.5 \leq X \leq 1.75) = F(1.75) - F(1.5) = 0.84 - 0.50 = 0.34$

4.8 Moment-Generating Function

Already we have come to know that with the help of moments, important characteristics like mean, median, mode, variance, skewness, kurtosis, etc. can be presented. Thus with the help of the moments, one can characterize distribution of a random variable also. In this section, we are interested to know whether there exists any function like probability function which can provide different moments. In fact in literature, one can find such functions called moment generating function (mgf) which generates different moments corresponding to probability function of random variables.

The moment generating function (mgf) of a random variable "X" is defined by $M_x(t) = E[e^{tx}]$
$= \int_R e^{tx} f(x)dx$, for continuous random variable
$\sum e^{tx} P(x)$, for discrete random variable

Thus, $Mx(t) = E[e^{tx}]$
$$= E\left[1 + t(x) + \frac{t^2}{\underline{|2}}(x)^2 + \ldots\ldots\ldots + t^r \underline{|r}(x)^r + \ldots\ldots\ldots\right]$$
$$= 1 + tE(x) + \frac{t^2}{\underline{|2}}E\left\{(x)^2\right\} + \ldots\ldots\ldots + \frac{t^r}{\underline{|r}}E\{(x)^r\} + \ldots\ldots$$
$$= 1 + t\upsilon_1 + \frac{t^2}{\underline{|2}}\upsilon_2 + \ldots\ldots\ldots + \frac{t^r}{\underline{|r}}\upsilon_r + \ldots\ldots\ldots,$$

where υ_r is the moment of ored r about the origin or simply rth raw moment.

Thus, the coefficient of $\frac{t^r}{\underline{|r}}$ in $M_x(t)$ gives υ_r the r-th moment about origin. The function $M_x(t)$ is called the mgf since it generates the moments. When a distribution is specified by its mgf, then its r-th raw moment can be obtained by taking r-th derivative with respect to t, i.e.,

$$\upsilon_r = \frac{d^r M_x(t)}{dt^r}\Big|_{t=0} = \frac{d^r E[e^{tx}]}{dt^r} = \frac{d^r E\left[1 + t(x) + \frac{t^2}{\underline{|2}}(x)^2 + \ldots\ldots\ldots + \frac{t^r}{\underline{|r}}(x)^r + \ldots\ldots\ldots\right]}{dt^r}$$

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Thus,

$$\upsilon_1 = \frac{dM_x(t)}{dt}\Big]_{t=0} = E(X)$$

$$\upsilon_2 = \frac{d^2M_x(t)}{dt^2}\Big]_{t=0} = E(X^2)$$

$$\upsilon_3 = \frac{d^3M_x(t)}{dt^3}\Big]_{t=0} = E(X^3)$$

$$\upsilon_4 = \frac{d^4M_x(t)}{dt^4}\Big]_{t=0} = E(X^4)$$

.....

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.....

Similarly the central moments can be obtained by taking deviations from mean (μ) of the distribution, i.e.,

Thus, $M_{x-\mu}(t) = E\left[e^{t\,(x-\mu)}\right]$

$$= E\left[1 + t(x-\mu) + \frac{t^2}{\underline{|2}}(x-\mu)^2 + \ldots\ldots\ldots + \frac{t^r}{\underline{|r}}(x-\mu)^r + \ldots\ldots\ldots\right]$$

$$= 1 + tE(x-\mu) + \frac{t^2}{\underline{|2}}E\left\{(x-\mu)^2\right\} + \ldots\ldots\ldots + \frac{t^r}{\underline{|r}}E\{(x-\mu)^r\} + \ldots\ldots$$

$$= 1 + tm_1 + \frac{t^2}{\underline{|2}}m_2 + \ldots\ldots\ldots + \frac{t^r}{\underline{|r}}m_r + \ldots\ldots\ldots,$$

where, m_r is the central moment of order r or simply rth central moment.

Central moments can also be worked out by differentiating the mgf about AM of different orders and equating to zero as follows:

$$m_r = \frac{d^rM_{x\text{-}\mu}(t)}{dt^r}\Big|_{t=0} = \frac{d^rE\left[e^{t\,(x-\mu)}\right]}{dt^r}$$

$$= \frac{d^rE\left[1 + t(x-\mu) + \frac{t^2}{\underline{|2}}(x-\mu)^2 + \ldots\ldots\ldots + \frac{t^r}{\underline{|r}}(x-\mu)^r + \ldots\ldots\ldots\right]}{dt^r}$$

Thus

$$m_1 = \frac{dM_{x-\mu}(t)}{dt}\Big]_{t=0} = E(X-\mu) = E(X) - \mu$$

$$= \mu - \mu = 0$$

$$m_2 = \frac{d^2M_{x-\mu}(t)}{dt^2}\Big]_{t=0} = E(X-\mu)^2$$

$$m_3 = \frac{d^3M_{x-\mu}(t)}{dt^3}\Big]_{t=0} = E(X-\mu)^3$$

$$m_4 = \frac{d^4M_{x-\mu}(t)}{dt^4}\Big]_{t=0} = E(X-\mu)^4$$

.....

.....

.....

Properties of Moment Generating Function

(i) For a random variable X, if $Mx(t)$ is its mgf, then the mgf of the random variable bX is $M_{bx}(t) = M_x(bt)$.

(ii) Let $Y = a + bX$ where both X and Y are random variables and the mgf of X is $Mx(t)$, then the mgf of Y is $M_Y(t) = e^{at}.M_X(bt)$, a and b being constants.

(iii) Let $X_1, X_2, X_3, \ldots X_n$ be n independent random variables with $Mx_1(t)$, $Mx_2(t)$, $Mx_3(t)\ldots Mx_n(t)$ being their respective moment generating functions. If $Y = \sum_{i=1}^{n} X_i$ then

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$$M_Y(t) = \prod_{i=1}^{n} M_{xi}(t)$$
$$= M_{x1}(t).M_{x2}(t).M_{x3}(t).....M_{xn}(t).$$

(iv) Let two random variables X_1 and X_2 having respective mgf $Mx_1(t)$ and $Mx_2(t)$ such that $Mx_1(t) = Mx_2(t)$, then the two random variables have got the same probability distribution.

4.9 Theoretical Probability Distributions

The probability distributions of random variables play great roles in our daily lives. Many of our real-life activities can be presented by some well-known theoretical probability distribution, hence the importance of studying the probability distributions of random variables. Depending upon the involvement of number of variables, probability distributions are univariate, bivariate, or multivariate. In the following sections, we shall consider some of the widely used univariate probability distributions like binomial, Poisson, normal, χ^2, t, and F distribution. Among these theoretical distributions, the first two are discrete while the rest are continuous probability distributions.

4.9.1 Binomial Distribution

Before discussing this distribution, let us have some discussion about the Bernoulli trial. A Bernoulli trial is a trial where one can expect either of only two possible outcomes. For example, in tossing a coin, either head or tail will appear in any tossing, so tossing of coin can be regarded as Bernoulli trial. Similarly, while spraying insecticide in a field of crop, one can expect that either the insect will be controlled or continue to infest the field. Thus in Bernoulli trial, the probability of occurrence of either of the events is 1/2.

Let a random experiment be conducted with "n" (fixed) independent Bernoulli trials each having "success" or "failure" with respective probabilities "p" and "q" in any trial. Then the random variable X, number of successes out of "n" trials, is said to follow binomial distribution if its pmf is given by

$$P(X = x) = P(x) = \left\{ \binom{n}{x} p^x q^{n-x} \right\},$$
$$x = 0, 1, 2, \ldots, n; q = 1 - p.$$
$$= 0 \text{ otherwise}$$

where "n" and "p" are the two parameters of the distribution and the distribution is denoted as $X \sim b(n, p)$, i.e., the random variable follows binomial distribution with parameters "n" and "p."

Thus, $P(x) \geq 0$ and $\sum_{x=0}^{n} P(x) = q^n + \binom{n}{1} q^{n-1} p + \binom{n}{2} q^{n-2} p^2 + ... + p^n = (q + p)^n = 1.$

Moment Generating Function of Binomial Distribution

Moment generating function is given as

$$M_x(t) = E(e^{tx}) = \sum_{x=0}^{n} e^{tx} P(x)$$
$$= \sum_{x=0}^{n} e^{tx} \binom{n}{x} p^x q^{n-x}$$
$$= \sum_{x=0}^{n} \binom{n}{x} (pe^t)^x q^{n-x} = (pe^t + q)^n$$

Moments of Binomial Distribution

(a) *From moment generating function*

We know that $\upsilon_r = \left. \frac{d^r M_x(t)}{dt^r} \right|_{t=0} = \frac{d^r E[e^{tx}]}{dt^r} = \frac{d^r \mathrm{E}\left[1 + \mathrm{t}(x) + \frac{t^2}{\underline{|2}}(x)^2 + ... + \frac{t^r}{\underline{|r}}(x)^r + ...\right]}{dt^r}$

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Thus,

$$\upsilon_1 = \frac{dM_x(t)}{dt}\Big]_{t=0} = npe^t(pe^t+q)^{n-1}\Big]_{t=0} = np$$

$$\upsilon_2 = \frac{d^2M_x(t)}{dt^2}\Big]_{t=0} = n(n-1)p^2e^{2t}(pe^t+q)^{n-2} + npe^t(pe^t+q)^{n-1}\Big]_{t=0} = n(n-1)p^2 + np$$

$$\upsilon_3 = \frac{d^3M_x(t)}{dt^3}\Big]_{t=0} = n(n-1)(n-2)p^3e^{3t}(pe^t+q)^{n-3} + 2n(n-1)p^2e^{2t}(pe^t+q)^{n-2}$$
$$+ n(n-1)p^2e^{2t}(pe^t+q)^{n-2} + npe^t(pe^t+q)^{n-1}\Big]_{t=0}$$
$$= n(n-1)(n-2)p^3 + 2n(n-1)p^2 + np$$

$$\upsilon_4 = \frac{d^4M_x(t)}{dt^4}\Big]_{t=0}$$
$$= n(n-1)(n-2)(n-3)p^4 + 6n(n-1)(n-2)p^3 + 7n(n-1)p^2 + np$$

(b) *Without using moment generating function*

As we know that r-th order raw moment about the origin is given by $\upsilon_r = E(X^r) = \sum_{x=0}^{n} x^r \binom{n}{x} p^x q^{n-x}$, putting $r = 1, 2, 3, \ldots\ldots$ we shall get different moments about origin.

Thus,

$$\upsilon_1 = \sum_{x=0}^{n} x\binom{n}{x}p^xq^{n-x}$$
$$= \sum_{x=0}^{n} x\frac{n!}{x!(n-x)!}p^xq^{n-x}$$
$$= np\sum_{x=1}^{n}\frac{(n-1)!}{(x-1)!\{(n-1)-(x-1)\}!}p^{x-1}.q^{\{(n-1)-(x-1)\}}$$
$$= np\sum_{x=1}^{n}\binom{n-1}{x-1}p^{x-1}q^{(n-1)-(x-1)} = np\sum_{y=0}^{n-1}\binom{n-1}{y}p^yq^{(n-1-y)}[\text{where}, y = x-1]$$
$$= np(q+p)^{n-1} = np$$

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Similarity,

$$\begin{aligned}
\upsilon_2 &= E\left(X^2\right) = E[X(X-1)+X] = E[X(X-1)] + E[X] \\
&= \sum_{x=0}^{n}(x(x-1))\frac{n(n-1)(n-2)!}{x(x-1)(x-2)!(n-x)!}p^x q^{n-x} + E[X] \\
&= \sum_{x=2}^{n}\frac{n(n-1)(n-2)!}{(x-2)!(n-x)!}.p^x q^{n-x} + np \\
&= n(n-1)p^2\sum_{x=2}^{n}\frac{(n-2)!}{(x-2)!(n-x)!}.p^{x-2}q^{n-x} + np \\
&= n(n-1)p^2(q+p)^{n-2} + np \\
&= n(n-1)p^2 + np
\end{aligned}$$

$$\begin{aligned}
\upsilon_3 &= E\left(X^3\right) = E[X(X-1)(X-2) + 3X(X-1) + X] \\
&= E[X(X-1)(X-2)] + 3E[X(X-1)] + E[X] \\
&= \sum_{x=0}^{m}x(x-1)(x-2)\binom{n}{y}p^x q^{n-x} + 3n(n-1)p^2 + np \\
&= n(n-1)(n-2)p^3\sum_{x=3}^{n}\binom{n-3}{x-3}p^{x-3}q^{n-x} + 3n(n-1)p^2 + np \\
&= n(n-1)(n-2)p^3 + 3n(n-1)p^2 + np \\
\upsilon_4 &= E\left(X^4\right) = E[X(X-1)(X-2)(X-3) + 6X(X-1)(X-2) + 7X(X-1) + X] \\
&= n(n-1)(n-2)(n-3)p^4 + 6n(n-1)(n-2)p^3 + 7n(n-1)p^2 + np
\end{aligned}$$

Thus, mean of the binomial distribution is $E(X) = np$.

The second central moment is

$$\begin{aligned}
m_2 &= \upsilon_2 - {\upsilon_1}^2 \\
&= n(n-1)p^2 + np - (np)^2 \\
&= n^2p^2 - np^2 + np - n^2p^2 = np(1-p) \\
&= npq = \text{variance}
\end{aligned}$$

The third central moment is

$$\begin{aligned}
\mathrm{m}_3 &= \upsilon_3 - 3\upsilon_2\upsilon_1 + 2{\upsilon_1}^3 \\
&= n(n-1)(n-2)p^3 + 3n(n-1)p^2 + np \\
&\quad - 3\left\{n(n-1)p^2 + np\right\}np + 2(np)^3 \\
&= npq(q+p-2p) \\
&= npq(q-p)
\end{aligned}$$

The fourth central moment is

$$\begin{aligned}
\mathrm{m}_4 &= \upsilon_4 - 4\upsilon_3\upsilon_1 + 6\upsilon_2{\upsilon_1}^2 - 3{\upsilon_1}^4 \\
&= n(n-1)(n-2)(n-3)p^4 + 6n(n-1)(n-2)p^3 \\
&\quad + 7n(n-1)p^2 + np \\
&\quad - 4[n(n-1)(n-2)p^3 + 2n(n-1)p^2 + np]np \\
&\quad + 6[n(n-1)p^2 + np](np)^2 - 3(np)^4 \\
&= npq[1 + 3(n-2)pq]
\end{aligned}$$

The coefficient of skewness and kurtosis as measured through β_1 and β_2, respectively, is given as follows:

$$\beta_1 = \frac{m_3^2}{m_2^3} = \frac{(1-2p)^2}{npq}$$

Thus the skewness is positive for $p < \frac{1}{2}$, negative for $p > \frac{1}{2}$ and zero for $p = \frac{1}{2}$.

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$$\beta_2 = \frac{m_4}{m^2} = 3 + \frac{1 - 6pq}{npq}.$$

Thus, the distribution is leptokurtic or platykurtic depending upon the value of p.

Recurrence Relation for the Probabilities of Binomial Distribution

We know that

$$\frac{P(x)}{P(x-1)} = \frac{{}^nC_x p^x q^{n-x}}{{}^nC_{(x-1)} p^{x-1} q^{n-x+1}} = \frac{n-x+1}{x}.\frac{p}{q}$$

$$\Rightarrow P(x) = \frac{p}{q}\frac{n-x+1}{x}P(x-1), x = 1, 2, 3.....n$$

Using the above recursion relationship, the probabilities of the individual terms of the binomial distribution can be calculated.

Properties of Binomial Distribution

(i) For a random variable $X \sim b(n,p)$, its mean and variance are np and npq, respectively. As p and q both are fractions (generally), mean is always greater than variance.

(ii) The variance of binomial distribution is maximum when $p = ½$, and the maximum variance is $n/4$.

PROOF: $V(x) = npq = np(1-p)$

$$= -n\left[p^2 - 2\left(\frac{1}{2}\right)p + \frac{1}{4} - \frac{1}{4}\right]$$

$$= -n\left[\left(p - \frac{1}{2}\right)^2 - \frac{1}{4}\right]$$

$$= n\left[\frac{1}{4} - \left(p - \frac{1}{2}\right)^2\right]$$

Thus the variance is maximum when $\left(p - \frac{1}{2}\right)^2$ is zero, and it is possible only when $p = \frac{1}{2}$ and at $p = \frac{1}{2}$, $V(X) = \frac{n}{4}$.

(iii) If $X_1, X_2, \ldots\ldots X_k$ be k independent binormal varietes with parameter (n_i, p) then $\sum_{i=1}^{k} X_i \sim b\left(\sum_{i=1}^{k}, n_i, p\right)$.

The mgf of the binomial distribution is $M_x(t) = (q + pe^t)^n$.

Now the mgf of $Y = X_1 + X_2 + \ldots + X_k$ is

$$\begin{aligned}
M_Y(t) &= E[e^{tY}] \\
&= E\left[e^{t(X_1 + X_2 + \cdots\cdots + X_k)}\right] \\
&= E[e^{tX_1}].E[e^{tX_2}].....E[e^{tX_k}] \cdots\cdots [\because X_1.X_2.....X_k \text{ are independent}] \\
&= M_{X_1}(t)M_{X_2}(t).....M_{X_k}(t) \\
&= (q + pe^t)^{n_1}.(q + pe^t)^{n_2}.....(q + pe^t)^{n_k} \\
&= (q + pe^t)^{n_1 + n_2 + \cdots + n_k}
\end{aligned}$$

which is the mgf of the binomial distribution with parameter $\left(n_1 + n_{2+} \ldots + n_k \left(n_1 + n_{2+} \ldots + n_k = \sum_{i=1}^{k} n_i\right)\right)$ and p.

Example 4.18 It is claimed that 70 % insects will die upon spraying a particular insecticide on cauliflower. Five insects in a jar were subjected to particular insecticide: find out the probability distribution of the number of insect that responded. Also find out the probability (i) that at least three insects will respond and (ii) more than three insects will respond.

Solution Given that the probability of responding to the insecticide is $70/100 = 0.7$ and we assume that the response to the insecticide by the individual insect is independent of other insects; we have $n = 5$.

According to Binomial law of probability, the probability of x insects die is

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$P(x) = P(X = x) = {}^5C_x p^x q^{5-x} = {}^5C_x (0.7)^x (0.3)^{5-x}$, where $p = 0.7, q = 0.3, x = 0, 1, 2, .., 5$

With the help of the above pmf, let us find out the probabilities for different values of X and the cumulative probability distribution as follows:

x	$P(x)$	$F(x)$
0	0.0024	0.0024
1	0.0284	0.0308
2	0.1323	0.1631
3	0.3087	0.4718
4	0.3602	0.8319
5	0.1681	1.0000

Alternatively the probabilities for different values of X could be worked out using the recurrence relationship of Binomial probability, i.e., $P(x) = \frac{p}{q} \frac{n-x+1}{x} P(x-1), x = 1, 2, 3.....n$

The initial probability, i.e., $(X = 0)$ is worked out as $P(x) = P(X = 0) = {}^5C_0 p^0 q^{5-0} = {}^5C_0 (0.7)^0 (0.3)^{5-0} = 1.1.0.00243 = 0.00243$. Now using this initial probability, following probabilities are worked out as follows:

x	$P(x = 0)$	$P(x) = \frac{p}{q} \frac{n-x+1}{x} P(x-1)$, $x = 1, 2, 3, 4, 5$	$F(x)$
0	0.0024	–	0.0024
1	–	0.0284	0.0308
2	–	0.1323	0.1631
3	–	0.3087	0.4718
4	–	0.3602	0.8319
5	–	0.1681	1.0000

(i) To find out the probability that at least three insects will die means we are to add $P(x = 3) + P(x = 4) + P(x = 5) = 1 - F(x = 2) = 1 - 0.1631 = 0.8369$.

(ii) Probability of responding more than three insects, i.e., $P(x = 4) + P(x = 5) = 0.3602 + 0.1681 = 0.5283$.

Example 4.19 An experiment was conducted to know the effect of rotenone chemical to remove the undesirable fishes from the small tank. Rotenone was sprayed to 120 tanks containing seven undesirable fishes each. The following table gives the frequency distribution of number of fishes that died in 120 tanks.

No. of unwanted fishes died	0	1	2	3	4	5	6	7
No. of tanks	0	3	14	24	47	21	7	3

1. Fit binomial distribution with equal probability of dying and living after spraying.
2. With unknown probability of dying or living per tank.

Solution There are two mutually exclusive outcomes of the above experiment:

1. That is, either the fish will die or not die. So this can be treated as Bernoulli trial having binomial distribution. The two events "die" or "not die" have the same probability of 1/2.

   Given that, $n = 7, N = 120$, and the probability $p = 0.5$

   Let us try to construct the following table.

Frequency f	No. of insects dead (x) (1)	$(m-x+1)/x$ (2)	Col.2 x p/q (3)	$P(x) = P(x-1) \times$ Col.3 (4)	Exp. frequency $f^* = N \times$ col.4
0	0	–	–	0.00781	1
3	1	7.00000	7.00000	0.05469	7
14	2	3.00000	3.00000	0.16406	20
25	3	1.66667	1.66667	0.27344	33
47	4	1.00000	1.00000	0.27344	33
21	5	0.60000	0.60000	0.16406	20
7	6	0.33333	0.33333	0.05469	7
3	7	0.14286	0.14286	0.00781	1

* Nearest whole number

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With equal probability of dying and living, a fish sprayed with the rotenone, the ratio of $p/q = 0.5/0.5 = 1$. We have $P(0)$: the probability of zero fish dying per tank is $\binom{n}{x}p^x q^{n-x} = \binom{7}{0}p^0 q^{7-0} = q^7 = \left(\frac{1}{2}\right)^7 = 0.00781$. From the recursion relation of binomial probabilities, we have $P(x) = \frac{n-x+1}{x}.\frac{p}{q}.P(x-1)$ for $x = 1,2,3,\ldots,7$. Using the above relation, the probabilities are calculated and placed in the col. 4 of the above table. Expected frequencies are obtained by multiplying the total frequency (N) with respective probabilities.

2. In this problem to fit binomial distribution, p, the probability of success has to be estimated from the observed distribution.

We know that the mean of the binomial distribution is given by "np." For the given distribution mean is calculated as $\frac{1}{\sum_{i=1}^{k} f_i}\sum_{i=1}^{k} f_i x_i = \frac{1}{\sum_{i=1}^{8} f_i}\sum_{i=1}^{8} f_i x_i = 3.85$ where k is the number of classes.

Thus $np = 3.85$.

$\therefore \hat{p} = \frac{3.85}{8} = 0.48$. So $\hat{q} = 1 - 0.48 = 0.52$.

Thus, $\frac{\hat{p}}{\hat{q}} = 0.923$ and $P(0) = (0.52)^7 = 0.010$.

Using the same procedure used in (1), we make the following table:

Frequency	No. of insects dead (x)	$(m-x+1)/x$	Col.2 $\frac{x\hat{p}}{\hat{q}}$	$P(x) = P(x-1)\times$Col3	Exp. frequency
f	1	2	3	4	$f^* = n \times$ Col. 4
0	0	–	–	0.01028	1
3	1	7.00000	6.46154	0.06643	8
14	2	3.00000	2.76923	0.18396	22
25	3	1.66667	1.53846	0.28301	34
47	4	1.00000	0.92308	0.26124	31
21	5	0.60000	0.55385	0.14469	17
7	6	0.33333	0.30769	0.04452	5
3	7	0.14286	0.13187	0.00587	1

* Nearest whole number

Note: With the change in probability of success and failure, the probabilities as well as the expected frequencies have changed.

4.9.2 Poisson Distribution

There are certain events which occur rarely, for example, the number of accidents at a particular place of highway at a specific interval of time, number of spastic child born per year in a particular hospital, number of mistakes per pages of a book, number of telephone calls received by a person per unit time, number of defective items per lot of item, etc. The probability distribution of such events was discovered by S D Poisson, a French mathematician in 1837. This distribution is applicable when the number of trials is very large but the chances of occurrence of the event is rare, as such the average number of occurrence of the event is moderate. A discrete random variable X is said to have Poisson distribution if its probability mass function is given by

$$P(x) = \frac{e^{-\lambda}\lambda^x}{x!}, x = 0, 1, 2, 3, \ldots\ldots\ldots; \lambda > 0$$

Obviously, $P(x) \geq 0, \forall x$ and

$$\sum_{0}^{\infty} P(x) = e^{-\lambda}\left[1 + \lambda + \frac{\lambda^2}{2!} + \frac{\lambda^3}{3!} + \frac{\lambda^4}{4!} + \frac{\lambda^5}{5!} + \ldots\ldots\ldots\right]$$
$$= e^{-\lambda}e^{\lambda} = e^0 = 1$$

λ is known as a parameter of the distribution and the distribution is denoted as $X \sim P(\lambda)$.

Assumptions

(a) Probability of occurrence of an event at any interval is the same.

(b) The occurrence of the event in any interval is independent of its occurrences in other interval.

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Moment Generating Function

The mgf of the Poisson distribution is given by

$$M_x(t) = E[e^{tx}] = \sum_{x=0}^{\infty} \frac{e^{-\lambda}\lambda^x}{x!} e^{tx}$$
$$= e^{-\lambda} \sum_{x=0}^{\infty} \frac{(e^t\lambda)^x}{x!} = e^{-\lambda}.e^{\lambda e^t} = e^{\lambda(e^t-1)}$$

Differentiating $M_x(t)$ once, twice etc. with respect to 't' and putting $t = 0$ we can get the raw moments.

Moments of Poisson Distribution from Moment Generating Function

We know that $\upsilon_r = \frac{d^r M_x(t)}{dt^r}\Big|_{t=0} = \frac{d^r E[e^{tx}]}{dt^r}$

$$\upsilon_1 = \frac{dM_x(t)}{dt}\Big]_{t=0} = \lambda e^t e^{\lambda(e^t-1)}\Big]_{t=0} = \lambda$$
$$\upsilon_2 = \frac{d^2M_x(t)}{dt^2}\Big]_{t=0} = (\lambda e^t)^2 e^{\lambda(e^t-1)} + \lambda e^t e^{\lambda(e^t-1)}\Big]_{t=0}$$
$$= \lambda^2 + \lambda$$
$$\upsilon_3 = \frac{d^3M_x(t)}{dt^3}\Big]_{t=0} = \lambda^3 e^{-\lambda}e^{\lambda} + 3\lambda^2 + \lambda$$
$$= \lambda^3 + 3\lambda^2 + \lambda$$
$$\upsilon_4 = \frac{d^4M_x(t)}{dt^4}\Big]_{t=0} = \lambda^4 e^{-\lambda}e^{\lambda} + 6\lambda^3 + 7\lambda^2 + \lambda$$
$$= \lambda^4 + 6\lambda^3 + 7\lambda^2 + \lambda$$

Moments of Poisson Distribution Without Using mgf

$$\upsilon_1 = E(X) = \sum_{x=0}^{\infty} xP(x) = \sum_{x=0}^{\infty} x\frac{e^{-\lambda}\lambda^x}{x!}$$
$$= \lambda e^{-\lambda}\left\{\sum_{x=1}^{\infty}\frac{\lambda^{x-1}}{(x-1)!}\right\}$$
$$= \lambda e^{-\lambda}\left(1 + \lambda + \frac{\lambda^2}{2!} + \ldots\ldots\ldots\ldots\right)$$
$$= \lambda e^{-\lambda}e^{\lambda} = \lambda$$

Hence the mean of the Poisson distribution is λ.

$$\upsilon_2 = E(X^2) = E[X(X-1)] + E[X]$$
$$= e^{-\lambda}\sum_{x=0}^{\infty} x(x-1)\frac{\lambda^x}{x!} + \lambda$$
$$= \lambda^2 e^{-\lambda}\left\{\sum_{x=2}^{\infty}\frac{\lambda^{x-2}}{(x-2)!}\right\} + \lambda$$
$$= \lambda^2 e^{-\lambda}e^{\lambda} + \lambda = \lambda^2 + \lambda$$

$$\upsilon_3 = E(X^3) = E[X(X-1)(X-2)] + 3E[X(X-1)] + E[X]$$
$$= e^{-\lambda}\sum_{x=0}^{\infty} x(x-1)(x-2)\frac{e^{-\lambda}\lambda^x}{x!} + 3\lambda^2 + \lambda$$
$$= \lambda^3 e^{-\lambda}\left\{\sum_{x=3}^{\infty}\frac{\lambda^{x-3}}{(x-3)!}\right\} + 3\lambda^2 + \lambda$$
$$= \lambda^3 e^{-\lambda}e^{\lambda} + 3\lambda^2 + \lambda = \lambda^3 + 3\lambda^2 + \lambda$$

$$\upsilon_4 = E(X^4) = E[X(X-1)(X-2)(X-3)] + 6E[X(X-1)(X-2)] + 7E[X(X-1)] + E[X]$$
$$= \lambda^4 e^{-\lambda}\left\{\sum_{x=4}^{\infty}\frac{\lambda^{x-4}}{(x-4)!}\right\} + 6\lambda^3\left\{\sum_{x=3}^{\infty}\frac{\lambda^{x-3}}{(x-3)!}\right\} + 7\lambda^2 + \lambda$$
$$= \lambda^4 e^{-\lambda}e^{\lambda} + 6\lambda^3 + 7\lambda^2 + \lambda = \lambda^4 + 6\lambda^3 + 7\lambda^2 + \lambda$$

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The four central moments of the distribution are as follows:

$$m_1 = \upsilon_1 = \lambda$$
$$m_2 = \upsilon_2 - {\upsilon_1}^2 = \left(\lambda^2 + \lambda\right) - \lambda^2 = \lambda$$
$$\begin{aligned} m_3 &= \upsilon_3 - 3\upsilon_2\upsilon_1 + 2{\upsilon_1}^3 \\ &= \left(\lambda^3 + 3\lambda^2 + \lambda\right) - 3\lambda\left(\lambda^2 + \lambda\right) + 2\lambda^3 \\ &= 3\lambda^3 + 3\lambda^2 + \lambda - 3\lambda^3 - 3\lambda^2 \\ &= \lambda \end{aligned}$$
$$\begin{aligned} m_4 &= \upsilon_4 - 4\upsilon_3\upsilon_1 + 6\upsilon_2{\upsilon_1}^2 - 3{\upsilon_1}^4 \\ &= \left(\lambda^4 + 6\lambda^3 + 7\lambda^2 + \lambda\right) - 4\lambda\left(\lambda^3 + 3\lambda^2 + \lambda\right) \\ &\quad + 6\lambda^2\left(\lambda^2 + \lambda\right) - 3\lambda^4 \\ &= \lambda^4 + 6\lambda^3 + 7\lambda^2 + \lambda - 4\lambda^4 - 12\lambda^3 - 4\lambda^2 \\ &\quad + 6\lambda^4 + 6\lambda^3 - 3\lambda^4 \\ &= 3\lambda^2 + \lambda \end{aligned}$$

Coefficient of skewness and kurtosis is given by

$$\beta_1 = \frac{{m_3}^2}{{m_2}^3} = \frac{\lambda^2}{\lambda^3} = \frac{1}{\lambda}$$

and

$$\beta_2 = \frac{m_4}{{m_2}^2} = 3 + \frac{1}{\lambda}$$
$$\gamma_1 = \sqrt{\beta_1} = \frac{1}{\sqrt{\lambda}}$$

and

$$\gamma_2 = \beta_2 - 3 = \frac{1}{\lambda}$$

Thus, Poisson distribution is positively skewed and leptokurtic in nature.

Recurrence Relation for Probability of Poisson Distribution

$$P(x+1) = \frac{e^{-\lambda}\lambda^{x+1}}{(x+1)!}$$

and

$$P(x) = \frac{e^{-\lambda}\lambda^{x}}{x!}$$

We have

$$\frac{P(x+1)}{P(x)} = \frac{\frac{e^{-\lambda}\lambda^{x+1}}{(x+1)!}}{\frac{e^{-\lambda}\lambda^{x}}{x!}} = \frac{\left(\frac{\lambda}{x+1}\right).P(x)}{P(x)} = \left(\frac{\lambda}{x+1}\right).$$

$$\therefore P(x+1) = \left(\frac{\lambda}{x+1}\right).P(x), x = 0, 1, 2.....$$

Properties of Poisson Distribution

1. Poisson distribution may be looked upon as the limiting form of binomial distribution. If n, the number of trials, tends to be infinitely large, i.e., $n \to \infty$, with constant probability of success, p in each trial is very small i.e., $p \to 0$ and $np = \lambda$ (say) is finite.
2. If $X_1, X_2....., X_k$ be k independent Poisson variates with $\lambda_1, \lambda_2....., \lambda_k$ parameters, respectively, then $\sum_{i=1}^{k} X_i \sim P\left(\sum_{i=1}^{k} \lambda_i\right)$.

Example 4.20 A number of swine death in a rearing yard of equal dimension and capacity are given below.

No. of swine death per yard	0	1	2	3	4	5	6	7
Frequency	6	14	24	28	19	11	3	1

(i) Find out the average swine death per rearing yard.
(ii) Find the probability of having death less than four.
(iii) Find the number of yards having death more than four.

Solution Death in rearing yard may be treated as rare event, and as such it is assumed to follow Poisson distribution. We know that the Poisson distribution is characterized by its only parameter λ = mean = variance and the Poisson probabilities are calculated from its probability mass function, given as $P(x) = \frac{e^{-\lambda}\lambda^{x}}{x!}$. So to get the probabilities corresponding to different values of "x" (no. of swine death per yard), first we are to get the mean of the distribution.

No. of swine death per yard (x_i)	0	1	2	3	4	5	6	7
Frequency (f_i)	6	14	24	28	19	11	3	1
$f_i x_i$	0	14	48	84	76	55	18	7

(i) $Mean = \frac{1}{\sum_i f_i}\sum_i f_i x_i = 302/106 = 2.849 = \lambda.$

Thus the average swine death per yard is 2.849. From the pmf we have

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$$P(0) = \frac{e^{-2.849}2.849^0}{0!} = e^{-2.849} = 0.0579, P(1) = \frac{e^{-2.849}2.849^1}{1!} = 0.1650, P(2) = \frac{e^{-2.849}2.849^2}{2!} = 0.2350$$

$$P(3) = \frac{e^{-2.849}2.849^3}{3!} = 0.2232, P(4) = \frac{e^{-2.849}2.849^4}{4!} = 0.1590, P(5) = \frac{e^{-2.849}2.849^5}{5!} = 0.0906$$

$$P(6) = \frac{e^{-2.849}2.849^6}{6!} = 0.0430, P(7) = \frac{e^{-2.849}2.849^7}{7!} = 0.0175$$

Readers may note that the sum of the probabilities worked out using the pmf in this procedure is not unity, rather it is 0.009 less than the unity. This happens because of approximation in decimal places throughout the calculation. As a customary, the probability of last outcome is taken as 1-sum of the all other previous probabilities. As such the probability of seven deaths per yard should be 1–0.9735 = 0.0265.

Using the recurrence relationship of Poisson probabilities, other probabilities and corresponding cumulative probabilities ($F(x)$) can be worked out as given in the following table:

x	$P(x)$	$P(x+1) = \frac{2.849}{(x+1)}P(x)$	$F(x)$
0	0.0579		0.0579
1		0.1650	0.2229
2		0.2350	0.4578
3		0.2232	0.6810
4		0.1589	0.8399
5		0.0906	0.9305
6		0.0430	0.9735
7		0.0265*	1.0000

* This has been calculated as 1-sum of all other probabilities, i.e., 1–0.9735, as total probability must be equal to unity.

(ii) So the probability that a farm yard has less than four swine deaths is given by $P(0) + P(1) + P(2) + P(3) = 0.0579 + 0.1650 + 0.2350 + 0.2232 = 0.6810$, or $F(X = 3) = 0.6810$.

(iii) The number of yards having more than four swine deaths is given by $N.P(5) + N.P(6) + N.P(7) = 106[0.0906 + 0.0430 + 0.0265] = 106 \times 0.1601 = 16.97 \simeq 17$ (as the number of yards cannot be fraction), where N is the total frequency.

Example 4.21 The number of cow death per month within a distance of 1 km due to accident in particular highway is as given below. Fit Poisson distribution to the given data.

No. of cow death per month	0	1	2	3	4	5	6
Frequency	6	17	19	14	13	9	5

Solution We know that the only parameter for the Poisson distribution is $\lambda =$ mean. In order to fit the data in Poisson distribution, we are to estimate the $\lambda = E(x)$ by $\frac{1}{\sum_i f_i}\sum_i f_i x_i = 2.698$.

We know that for Poisson distribution, the probability is given by $P(x) = \frac{e^{-\lambda}\lambda^x}{x!}$. So the probability of $(x = 0)$ is given by $P(0) = \frac{e^{-2.698}\lambda^0}{0!} = e^{-2.698} = 0.067$. The rest of the probabilities are obtained with the help of the recursion relation for Poisson probabilities, i.e., $P(x+1) = \left(\frac{\lambda}{x+1}\right).P(x), x = 0, 1, 2, 3, 4, 5, 6$. Expected frequencies corresponding to different values of number of cow death per month are obtained by multiplying n =83 with the respective probabilities. The following table summarizes the result of Poisson fitting of the above data with $P(x = 0) = 0.067$.

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No. death (x)	Frequency (f)	$\frac{\lambda}{x+1}$	$P(x+1)=\frac{\lambda}{x+1}P(x)$	Expected freq.* $= NP(x)$
0	6	2.6988		5.5610 $\sim$ 06
1	17	1.3494	0.1816	15.0728 $\sim$ 15
2	19	0.8996	0.2450	20.3350 $\sim$ 20
3	14	0.6747	0.2204	18.2932 $\sim$ 18
4	13	0.5398	0.1487	12.3421 $\sim$ 12
5	9	0.4498	0.0903	7.4949 $\sim$ 08
6	5	0.3855	0.0470	3.9010 $\sim$ 04
	83			**82**

4.9.3 Normal Distribution

Most probably in the history of statistics, formulation of normal distribution is a landmark. Names of three scientists, viz., de Moivre, a French mathematician; P Laplace of France, and Gauss of Germany, are associated with the discovery and applications of this distribution. Most of the data in different fields like agriculture, medical, engineering, economics, social, business, etc. can reasonably be approximated to normal distribution. Discrete distributions like binomial distribution can very well be approximated to normal distribution for large number of observations.

A random variable X is said to follow the normal probability distribution with parameter μ (mean) and σ (standard deviation) if its probability density function is given by the probability law

$$f(x)=\frac{1}{\sqrt{2\pi}\sigma}e^{\left\{-\frac{1}{2}\left(\frac{x-\mu}{\sigma}\right)^2\right\}}\ -\infty<x<\infty,\sigma>0,\pi,$$

and e have their usual values
and is denoted as $X \sim N(\mu, \sigma^2)$.

Clearly, $f(x) > 0 \forall x$

Proof To prove that $f(x)=\frac{1}{\sqrt{2\pi}\sigma}\int_{-\infty}^{\infty}e^{-\frac{1}{2\sigma^2}(x-\mu)^2}dx$ is a pdf

$$\int_{-\infty}^{\infty}f(x)dx=\frac{1}{\sqrt{2\pi}\sigma}\int_{-\infty}^{\infty}e^{-\frac{1}{2\sigma^2}(x-\mu)^2}dx,\ \left[\text{putting } z = \frac{x-\mu}{\sigma}\Rightarrow dz=\frac{dx}{\sigma}\right]$$

$$=\frac{1}{\sqrt{2\pi}}\int_{-\infty}^{\infty}e^{-\frac{1}{2}z^2}dz,\ \left[\text{putting } t=\frac{1}{2}z^2\Rightarrow dt=zdz\right]$$

$$=\frac{2}{\sqrt{2\pi}}\int_{0}^{\infty}e^{-t}\frac{dt}{\sqrt{2t}}$$

$$=\frac{1}{\sqrt{\pi}}\int_{0}^{\infty}e^{-t}t^{\frac{1}{2}-1}dt,\ \left[\because\int_{0}^{\infty}e^{-x}x^{n-1}dx=\Gamma n=(n-1)!\text{ and }\Gamma\left(\frac{1}{2}\right)=\sqrt{\pi}\right.$$

$$=\frac{1}{\sqrt{\pi}}\Gamma\left(\frac{1}{2}\right)=1$$

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If $X \sim N(\mu, \sigma^2)$ then $Z = \frac{X-\mu}{\sigma}$ is known as standardized normal variate.

Now, $E(Z) = E\left[\frac{X-\mu}{\sigma}\right] = \frac{E(X)-E(\mu)}{E(\sigma)} = \frac{\mu-\mu}{\sigma} = 0$ and

$\text{Var}(Z) = E(Z^2) = E\left[\frac{X-\mu}{\sigma}\right]^2 = \frac{E(X-\mu)^2}{E(\sigma^2)} = \frac{\sigma^2}{\sigma^2} = 1$

Thus, Z follows a normal distribution with mean 0 and variance 1, i.e., $Z \sim N(0,1)$.

The pdf of the standard normal distribution can be written as

$$\phi(z) = \frac{1}{\sqrt{2\pi}} e^{-\frac{1}{2}z^2} \cdots\cdots - \infty < z < \infty$$

Subsequently the distribution function is written as

$$\Phi(z) = P(Z \le z) = \int_{-\infty}^{z} \phi(u)du$$
$$= \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{Z} e^{-\frac{u^2}{2}} du$$

Properties of Normal Distribution:

1. $\Phi(-z) = P(Z \le -z) = P(Z \ge z) = 1 - P(Z \le z) = 1 - \Phi(z)$
2. $P(a \le x \le b)$
$= P\left(\frac{a-\mu}{\sigma} \le z \le \frac{b-\mu}{\sigma}\right), z = \frac{x-\mu}{\sigma}$
$= P\left(z \le \frac{b-\mu}{\sigma}\right) - P\left(z \le \frac{a-\mu}{\sigma}\right)$
$= \Phi\left(\frac{b-\mu}{\sigma}\right) - \Phi\left(\frac{a-\mu}{\sigma}\right)$
3. The mean of normal distribution is given by $E(X)$

$$= \int_{-\infty}^{\infty} xf(x)dx = \frac{1}{\sqrt{2\pi}\sigma} \int_{-\infty}^{\infty} xe^{-\frac{1}{2\sigma^2}(x-\mu)^2} dx \quad \left[\text{let } z = \frac{x-\mu}{\sigma}, \text{we have } dz = \frac{dx}{\sigma}\right]$$
$$= \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{\infty} (\mu + \sigma z) e^{-\frac{1}{2}(z)^2} dz$$
$$= \frac{\mu}{\sqrt{2\pi}} \int_{-\infty}^{\infty} e^{-\frac{1}{2}(z)^2} dz + \frac{\sigma}{\sqrt{2\pi}} \int_{-\infty}^{\infty} ze^{-\frac{1}{2}(z)^2} dz$$
$$= \mu + 0 = \mu \qquad \left[\because \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{\infty} e^{-\frac{1}{2}(z)^2} dz = 1, \text{ because } Z \text{ is standard normal variate}\right.$$
$$\left. \text{and the 2nd term is zero because it is an odd function}\right]$$

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4. *Moment generating function:*

The moment generating function of the normal distribution is given by

$$
\begin{aligned}
M_0(t) = E(e^{tx}) &= \int_{-\infty}^{\infty} e^{tx} f(x)dx \\
&= \frac{1}{\sqrt{2\pi}\sigma} \int_{-\infty}^{\infty} e^{tx} e^{-\frac{1(x-\mu)^2}{2\sigma^2}} dx, \ \ putting \ \ z = \frac{(x-\mu)}{\sigma}, \ \ \text{we have } dz = \frac{dx}{\sigma} \\
&= \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{\infty} e^{t(\mu+\sigma z)} e^{-\frac{1z^2}{2}} dz \\
&= \frac{e^{t\mu}}{\sqrt{2\pi}} \int_{-\infty}^{\infty} e^{-\frac{1}{2}\left[z^2 - 2z\sigma t + (\sigma t)^2 - (\sigma t)^2\right]} dz \\
&= \frac{e^{t\mu + \frac{1}{2}t^2\sigma^2}}{\sqrt{2\pi}} \int_{-\infty}^{\infty} e^{-\frac{1}{2}(z-\sigma t)^2} dz \\
&= \frac{e^{t\mu + \frac{1}{2}t^2\sigma^2}}{\sqrt{2\pi}} \int_{-\infty}^{\infty} e^{-\frac{1}{2}y^2} dy, \ [\text{putting } \ y = z - \sigma t, \ \ \text{thus } \ dz = dy] \\
&= e^{t\mu + \frac{1}{2}t^2\sigma^2}
\end{aligned}
$$

Differentiating once, twice, etc. with respect to t and putting $t = 0$, one can get raw moments.

5. *Central moment of normal distribution:*

The odd-order central moments of the normal distribution about the mean (μ) is given by

$$
\begin{aligned}
m_{2r+1} &= \int_{-\infty}^{\infty} (x-\mu)^{2r+1} f(x)dx = \frac{1}{\sqrt{2\pi}\sigma} \int_{-\infty}^{\infty} (x-\mu)^{2r+1} e^{-\frac{1}{2}\left(\frac{x-\mu}{\sigma}\right)^2} dx \\
&= \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{\infty} (\sigma z)^{2r+1} e^{-\frac{z^2}{2}} dz, \text{since} \left[z = \frac{x-\mu}{\sigma}\right] \\
&= \frac{\sigma^{2r+1}}{\sqrt{2\pi}} \int_{-\infty}^{\infty} z^{2r+1} e^{-\frac{z^2}{2}} dz
\end{aligned}
$$

Now $z^{2r+1}e^{-\frac{z^2}{2}}dz$ is an odd function of z so

$$
\int_{-\infty}^{\infty} z^{2r+1} e^{-\frac{z^2}{2}} dz = 0
$$

$$
\therefore m_{2r+1} = 0
$$

Thus all odd-order central moments of normal distribution are zero. The even-order central moment of this distribution is

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$$
\begin{aligned}
m_{2r} &= \int_{-\infty}^{\infty} (x-\mu)^{2r} f(x)\,dx \\
&= \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{\infty} (\sigma z)^{2r} e^{-\left(z^2/2\right)} dz \\
&= \frac{\sigma^{2r}}{\sqrt{2\pi}} \int_{-\infty}^{\infty} (z)^{2r} e^{-\left(z^2/2\right)} dz \\
&= \frac{\sigma^{2r}}{\sqrt{2\pi}} 2\int_{0}^{\infty} (z)^{2r} e^{-\left(z^2/2\right)} dz \\
&= 2\frac{\sigma^{2r}}{\sqrt{2\pi}} \int_{0}^{\infty} (2t)^{r} e^{-t} \frac{dt}{\sqrt{2t}}, \left(t = \frac{z^2}{2}\right) \\
\therefore m_{2r} &= \frac{2^r \sigma^{2r}}{\sqrt{\pi}} \int_{0}^{\infty} e^{-t} t^{\left(r+\frac{1}{2}\right)-1} dt \\
\Rightarrow m_{2r} &= \frac{2^r \sigma^{2r}}{\sqrt{\pi}} \Gamma\left(r+\frac{1}{2}\right)
\end{aligned}
$$

Changing r to $(r-1)$, we get

$$
\begin{aligned}
m_{2r-2} &= \frac{2^{r-1}\sigma^{2(r-1)}}{\sqrt{\pi}} \Gamma\left(r-\frac{1}{2}\right) \\
\therefore \frac{m_{2r}}{m_{2r-2}} &= 2\sigma^2 \frac{\Gamma\left(r+\frac{1}{2}\right)}{\Gamma\left(r-\frac{1}{2}\right)} = 2\sigma^2\left(r-\frac{1}{2}\right) \\
&= \sigma^2(2r-1), \text{since } \left[\Gamma r = (r-1)\Gamma(r-1)\right] \\
\Rightarrow m_{2r} &= \sigma^2(2r-1) m_{2r-2}
\end{aligned}
$$

This gives the recurrence relation for the moments of normal distribution. Putting $r = 1,2$ we have $m_2 = \sigma^2 =$ Variance and $m_4 = 3\sigma^4$. Thus $\beta_1 = 0$ and $\beta_2 = 3$.

6. *Median of the normal distribution is* $\mu =$ Mean.

Let M be the median of the normal distribution, then

$$
\int_{-\infty}^{M} f(x)dx = \int_{M}^{\infty} f(x)dx = \frac{1}{2}
$$

$$
\text{Now, } \frac{1}{\sqrt{2\pi}\sigma} \int_{M}^{\infty} e^{-\frac{1}{2\sigma^2}(x-\mu)^2} dx = \frac{1}{2},
$$

$$
\left[\text{putting z } = \frac{(x-\mu)}{\sigma}, \text{ we have } dz = \frac{dx}{\sigma}\right]
$$

$$
= \frac{1}{\sqrt{2\pi}} \int_{\frac{M-\mu}{\sigma}}^{\infty} e^{-\frac{1}{2}z^2} dz = \frac{1}{2} \tag{1}
$$

We know that $\frac{1}{\sqrt{2\pi}} \int_{-\infty}^{\infty} e^{-\frac{1}{2}z^2} dz = 1$

$$
\Rightarrow \frac{1}{\sqrt{2\pi}} \int_{0}^{\infty} e^{-\frac{1}{2}z^2} dz = \frac{1}{2}. \tag{2}
$$

Comparing (1) and (2) we have $\frac{M-\mu}{\sigma} = 0 \Rightarrow M = \mu$

$\therefore$ The median of the normal distribution is μ

7. *Mode of the normal distribution is* $\mu =$ Mean.

The mode is the value of X for which $f(x)$ is maximum, i.e., the mode is the solution of $f'(x) = 0$ and $f' < 0$. Mode of the normal distribution is obtained as follows:

$$
\begin{aligned}
f'(x) &= \frac{df(x)}{dx} = \frac{1}{\sqrt{2\pi}\sigma} e^{-\frac{1}{2}\left(\frac{x-\mu}{\sigma}\right)^2} \left[-\frac{2}{2}\left(\frac{x-\mu}{\sigma^2}\right)\right] \\
&= \frac{x-\mu}{\sigma^3\sqrt{2\pi}} e^{-\frac{1}{2}\left(\frac{x-\mu}{\sigma}\right)^2} = 0
\end{aligned}
$$

It is possible only when $x = \mu$ $(\because f(x) \neq 0)$

$$
\begin{aligned}
f''(x) &= \frac{d^2 f(x)}{dx^2} \\
&= \frac{(x-\mu)^2}{\sigma^5\sqrt{2\pi}} e^{-\frac{1}{2}\left(\frac{x-\mu}{\sigma}\right)^2} - \frac{1}{\sigma^3\sqrt{2\pi}} e^{-\frac{1}{2}\left(\frac{x-\mu}{\sigma}\right)^2}
\end{aligned}
$$

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Now, $\left.\frac{d^2f(x)}{dx^2}\right|_{x=\mu} < 0$

$\therefore f(x)$ is maximum at $x = \mu$. So mode of the normal distribution is μ.

Thus, mean = median = mode = μ. The normal distribution is symmetrical about the point $x = \mu$, since $f(\mu + u) = f(\mu - u) = \frac{1}{\sqrt{2\pi}\sigma} e^{-\frac{1}{2}u^2}$, whatever u may be.

8. The linear combination of independent normal variate is also a normal variate.

Let $X_1, X_2, \ldots, X_n$ be n independent normal variates with $(\mu_1, \sigma_1^2), (\mu_2, \sigma_2^2), (\mu_3, \sigma_3^2)$ ..... (μ_n, σ_n^2), i.e., if then $\sum_{i=1}^{n} a_i X_i \sim N\left[\sum_{i=1}^{n} a_i\mu_i, \sum_{i=1}^{n} a_i^2\sigma_i^2\right]$

9. Area under normal distribution.

If $X \sim N(\mu, \sigma^2)$, then the

$$P(\mu < X < x_1) = \int_{\mu}^{x_1} f(x)dx = \frac{1}{\sqrt{2\pi}\sigma}\int_{\mu}^{x_1} e^{-\frac{1}{2}\left(\frac{x-\mu}{\sigma}\right)^2} dx$$

Putting $\left(\frac{x-\mu}{\sigma}\right) = z$

$$P(\mu < X < x_1) = P(0 < Z < z_1) = \frac{1}{\sqrt{2\pi}}\int_{0}^{z_1} e^{-\frac{1}{2}(z)^2} dz$$

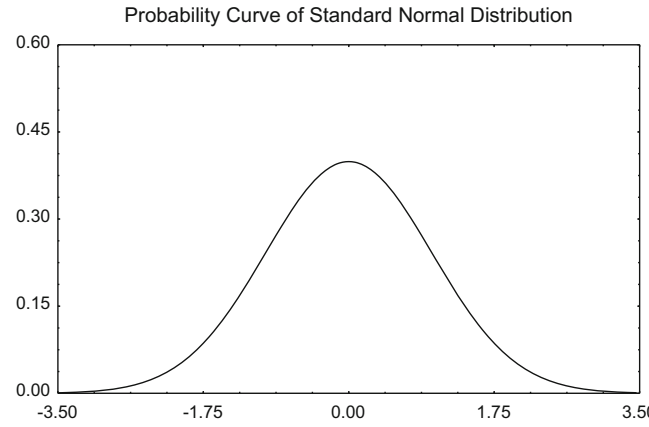
$$= \int_{0}^{z_1} \phi(z)dz = \int_{-\infty}^{z_1} \phi(z)dz - \int_{-\infty}^{0} \phi(z)dz = \Phi(z_1) - 0.5$$

where $\phi(z)$ is the probability function of standard normal variate.

$\int_{0}^{z_1} \phi(z)dz$ gives the area under standard normal curve between $z = 0$ and $z = z_1$.

The area under standard normal curve is shown below

Fitting of normal distribution



Example 4.22 Fit a normal distribution to the frequency distribution for body weight (kg) of chicks reared in a poultry farm.

Body weight (x)	2.00–2.10	2.10–2.20	2.20–2.30	2.30–2.40	2.40–2.50	2.50–2.60	2.60–2.70	2.70–2.80	2.80–2.90	2.90–3.00
Frequency(f)	7	15	17	29	37	34	28	16	14	8

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Solution The first step in fitting any distribution is to estimate the parameters of the concerned distribution. In case of normal distribution, the parameters are the mean μ and the standard deviation σ. The method of moments can give us the estimates $\bar{x}$ and s from the given data for population parameters μ and σ, respectively. From the above data, we have $n = 205$, mean $= 2.50$ kg, and standard deviation $s = 0.222$ kg.

Having worked out these estimates, we can calculate the expected frequencies by using the tables of the standard normal variate given in Table 1 of Chap. 6. The expected frequency of the standard normal variate within an interval $[a,b]$ is given by

$$n\int_a^b \frac{1}{\sqrt{2\pi}s} e^{-\frac{1}{2s^2}(x-\bar{x})^2} dx = n\int_{\frac{a-\bar{x}}{s}}^{\frac{b-\bar{x}}{s}} \phi(\tau)d\tau, \left[\text{where}, \tau = \frac{x-\bar{x}}{s}\right]$$

$$= n\left[\int_{-\infty}^{\frac{b-\bar{x}}{s}} \phi(\tau)d\tau - \int_{-\infty}^{\frac{a-\bar{x}}{s}} \phi(\tau)d\tau\right] = n\left[\Phi\left(\frac{b-\bar{x}}{s}\right) - \Phi\left(\frac{a-\bar{x}}{s}\right)\right]$$

In order to draw the fitted normal curve over the histogram, one should compute the ordinates for different values of x, and x's are taken as class boundaries. The ordinates are computed as follows: $n\frac{1}{\sqrt{2\pi}s} e^{-\frac{1}{2s^2}(x-\bar{x})^2} = \frac{n}{s}\phi(\tau)\left[\text{where}, \tau = \frac{x-\bar{x}}{s}\right]$. The values of $\varphi(\tau)$ and $\Phi(\tau)$ are given in the (Table 6.1) in Chap. 6 corresponding to different values of τ.

With the help of the above information and Table 6.2 given in Chap. 6, we prepare the following table:

Class	Height (cm) (x)	$\tau = \frac{x-\bar{x}}{s}$	$\Phi(\tau)$	probability $= \Delta\Phi(\tau)$	Expected frequency $n.\Delta\Phi(\tau)$	$\phi(\tau)$	ordinate $= \frac{n}{s}\phi(\tau)$
<2.00	2.00	−2.25225	0.01215	0.01215	2	0.031740	29.30918
2.00–2.10	2.10	−1.80180	0.03579	0.02364	5	0.078950	72.90446
2.10–2.20	2.20	−1.35135	0.08829	0.05250	11	0.160383	148.1017
2.20–2.30	2.30	−0.90090	0.18382	0.09553	20	0.266085	245.7093
2.30–2.40	2.40	−0.45045	0.32619	0.14237	29	0.360527	332.9191
2.40–2.50	2.50	0.00000	0.50000	0.17381	36	0.398942	368.3927
2.50–2.60	2.60	0.45045	0.67381	0.17381	36	0.360527	332.9191
2.60–2.70	2.70	0.90090	0.81618	0.14237	29	0.266085	245.7093
2.70–2.80	2.80	1.35135	0.91171	0.09553	20	0.160383	148.1017
2.80–2.90	2.90	1.80180	0.96421	0.05250	11	0.078950	72.90446
2.90–3.00	3.00	2.25225	0.98785	0.02364	5	0.031740	29.30918
>3.00	∞	∞	1.00000	0.01215	2	0.000000	0

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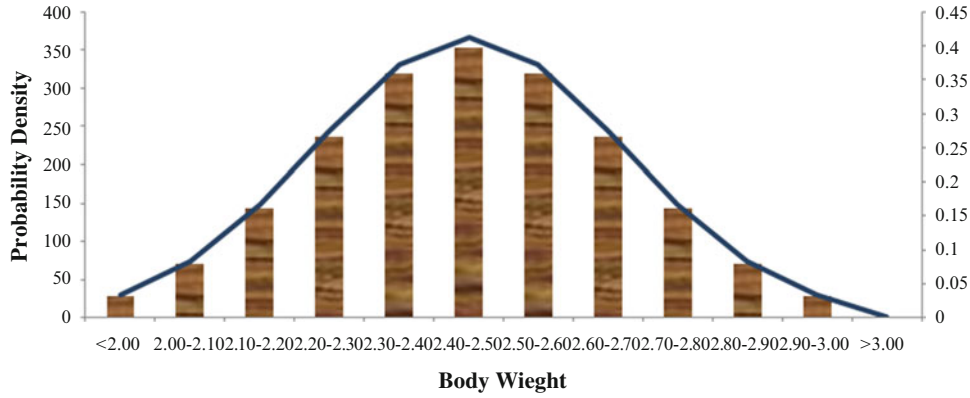

Example 4.23 Egg weight of particularly chick breed is known to follow normal distribution with mean 56 g and sd 5.65 g. Find the probability that (i) $P(X > 60$ g), (ii) $P(X \leq 60$ g), and (iii) $P(40 \leq X \leq 70$ g).

Solution Given that $\mu = 56$ g and $\sigma = 5.65$ g, i.e., $X \sim N(56,31.92)$.

For $X = 60$, we have $Z = \frac{60-56}{5.65} = 0.70$

(i) $P(X > 60) = P(Z \geq 0.70)$
$= 0.50 - P(0 \leq Z \leq 0.70)$
$= 0.5 - 0.2580$
$= 0.242$

(ii) $P(X \leq 60) = 1 - P(X > 60)$
$= 1 - P(Z \geq 0.70)$
$= 1 - 0.242$
$= 0.758$

(iii) $P(40 \leq X \leq 70)$
$= P\left(\frac{40-56}{5.65} \leq \frac{X-56}{5.65} \leq \frac{70-56}{5.65}\right)$
$= P(-2.83 \leq Z \leq 2.477)$
$= P(Z \leq 2.83) - P(Z \leq -2.477)$
$= P(Z \leq 2.83) - (1 - P(Z \leq 2.477))$
$= 0.9976 - (1 - 0.9932)$
$= 0.9976 - 0.0068$
$= 0.9908$

4.10 Central Limit Theorem

Central limit theorem is one of the landmarks in the history of statistics. In majority of the cases, we study the population or infer about the population with its mean μ. In doing so on the basis of the samples, sample mean $\bar{x}$ is taken as estimate of population mean. So one needs to study the sampling behavior of sample mean, i.e., we must study the sampling distribution of sample mean arising out of different samples for different population distributions. It may be noted that not necessarily all the distributions will follow normal distribution and its characteristics. So the means arising out of different types of distributions and different samples need to be studied before it is taken as estimator of population mean. To tackle these varied situations, central limit theorem plays a very important role. Though the central limit theorem (CLT) has been put forwarded in different ways, the simplest one is as follows: under the sufficiently large n (the number of observations), the distribution of $\bar{x}$ is approximately normal with mean μ and standard deviation $\sigma/\sqrt{n}$ irrespective of the nature of population distribution, i.e., $\bar{x} \sim N(\mu, \sigma/\sqrt{n})$ as $n \to \infty$.

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4.11 Sampling Distribution

The main objective of studying statistics is to characterize population, particularly with respect to its different parameters. In doing so, we examine the sample characteristics and try to infer about the population on the basis of the knowledge of sample properties. The process of knowing population characteristics from the knowledge of sample characteristic is known as the *statistical inference*. Sampling distribution plays an important role in statistical inference. Generally we construct different statistics from sample observations to estimate population parameters. Depending upon the parameter(s) and the form of the parameters of the parent population, the statistics are developed. In the following sections, we shall discuss some of the important distributions, used in day-to-day activities in agricultural and allied fields.

4.11.1 χ^2-Distribution

Statistical theory mostly deals with quantitative data, but there are certain tests based on χ^2 distribution which can effectively be used for qualitative data. Tests based on χ^2 distribution have got its application both in parametric and nonparametric statistical inference. χ^2 test is used to test goodness of fit, to test the hypothetical value of population variance, to test the homogeneity of variances, to test the independence of attributes, etc.

Let X_1, X_2, X_3..... X_n be "n" independent standard normal variates with mean zero and variance unity, then the statistic $\sum_{i=1}^{n} {X_i}^2$ is called a chi-square (χ^2) variate with "n" degrees of freedom and is denoted as ${\chi_n}^2$. The pdf of χ^2 distribution is given by $f(\chi^2) = \frac{1}{2^{n/2}\Gamma\frac{n}{2}} e^{-\frac{1}{2}X^2} (\chi^2)^{\frac{n}{2}-1}, 0 \le \chi^2 < \infty$

If X_1, X_2, X_3..... X_n be independent normal variates, instead of standard normal variate, with mean μ_i and variance $\sigma_i^2 (i = 1, 2, 3, \ldots, n)$, then $\chi^2 = \sum_{i=1}^{n} \frac{(X_i - \mu_i)^2}{{\sigma_i}^2}$ is χ^2- variate with n degrees of freedom.

Properties of χ^2 Distribution

1. The moment generating function of the χ^2 distribution is given by $M_{\chi 2}(t) = (1-2t)^{-n/2}, |2t| < 1.$
2. The first four raw moments are

$$
\begin{aligned}
\upsilon_1 &= \left.\frac{dM_{\chi 2}(t)}{dt}\right]_{t=0} = n \\
\upsilon_2 &= \left.\frac{d^2M_{\chi 2}(t)}{dt^2}\right]_{t=0} = n\left[-\left(\tfrac{n}{2}+1\right)\right](1-2t)^{-(n/2+2)}(-2)\Big]_{t=0} \\
&= \left.2n\left(\tfrac{n}{2}+1\right)(1-2t)^{-(n/2+2)}\right]_{t=0} \\
&= \left.n(n+2)(1-2t)^{-(n/2+2)}\right]_{t=0} \\
&= n(n+2) \\
\upsilon_3 &= \left.\frac{d^3M_{\chi 2}(t)}{dt^3}\right]_{t=0} = n(n+2)\left[-\left(\tfrac{n}{2}+2\right)\right](1-2t)^{-(n/2+3)}(-2)\Big]_{t=0} \\
&= \left.2n(n+2)\left(\tfrac{n}{2}+2\right)(1-2t)^{-(n/2+3)}\right]_{t=0} \\
&= \left.n(n+2)(n+4)(1-2t)^{-(n/2+3)}\right]_{t=0} \\
&= n(n+2)(n+4) \\
\upsilon_4 &= \left.\frac{d^4M_{\chi 2}(t)}{dt^4}\right]_{t=0} = n(n+2)(n+4)\left[-\left(\tfrac{n}{2}+3\right)\right](1-2t)^{-(n/2+4)}(-2)\Big]_{t=0} \\
&= \left.2n(n+2)(n+4)\left(\tfrac{n}{2}+3\right)(1-2t)^{-(n/2+4)}\right]_{t=0} \\
&= \left.n(n+2)(n+4)(n+6)(1-2t)^{-(n/2+4)}\right]_{t=0} \\
&= n(n+2)(n+4)(n+6)
\end{aligned}
$$

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3. The first four central moments of χ^2 distribution are:

$$\begin{aligned} m_1 &= \upsilon_1 = n \\ m_2 &= \upsilon_2 - \upsilon_1^2 = n(n+2) - n^2 \\ &= n^2 + 2n - \{n\}^2 \\ &= 2n \\ m_3 &= \upsilon_3 - 3\upsilon_1\upsilon_2 + 2\upsilon_1^3 \\ &= n(n+2)(n+4) - 3n^2(n+2) + 2n^3 \\ &= n^3 + 6n^2 + 8n - 3n^3 - 6n^2 + 2n^3 \\ &= 8n \end{aligned}$$

$$\begin{aligned} m_4 &= \upsilon_4 - 4\upsilon_3\upsilon_1 + 6\upsilon_1^2\upsilon_2 - 3\upsilon_1^4 \\ &= n(n+2)(n+4)(n+6) - 4n(n+2)(n+4)n \\ &\quad + 6n^2n(n+2) - 3n^4 \\ &= n^4 + 12n^3 + 44n^2 + 48n - 4n^4 - 24n^3 \\ &\quad - 32n^2 + 6n^4 + 12n^3 - 3n^4 \\ &= 12n^2 + 48n \\ &= 12n(n+4) \end{aligned}$$

4. $\beta_1 = \dfrac{{m_3}^2}{{m_2}^3} = \dfrac{8}{n}, \beta_2 = \dfrac{m_4}{{m_2}^2} = \dfrac{12}{n} + 3$

   Therefore, n being positive number, χ^2 distribution is positively skewed and leptokurtic in nature.
5. Both skewness and kurtosis are inversely proportional to the degrees of freedom. So as the degrees of freedom increase, the distribution tends to be symmetric.

   That means $n \to \infty$, $\frac{\chi^2 - n}{\sqrt{2n}} \to N(0,1)$.
6. Mode of the ${\chi_n}^2$ distribution is $(n-2)$.
7. If ${\chi_1}^2$ and ${\chi_2}^2$ are independent χ^2 variates with n_1 and n_2 df, then $({\chi_1}^2 + {\chi_2}^2)$ is also a χ^2 variate with $(n_1 + n_2)$ df. This is known as the additive property of the χ^2 distribution.

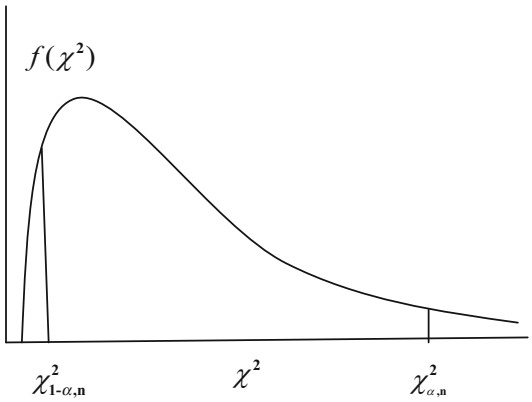

Fig. Percentage points of χ^2 distribution with n d.f.

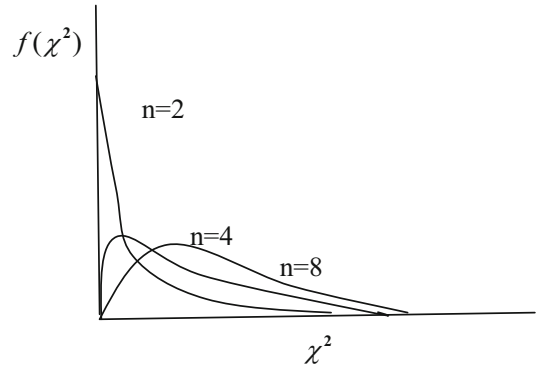

Fig. Shape of the density curve of χ^2

4.11.2 *t*-Distribution

In statistics sometimes we want to test the significant difference between the sample mean and the hypothetical population mean, between two sample means, to test the significance of observed correlation coefficient, regression coefficient, partial correlation coefficient, etc., and in these regards the tests based on *t*-distribution play a vital role. The above tests have been discussed in detail in Chap. 6 of this book. In this section we shall define and examine the properties of *t*-distribution.

Let X be a standard normal variate; now we define t statistic as the ratio of the standard normal variate to the square root of a χ^2 variate divided by its degrees of freedom. Thus $t = \frac{x}{\sqrt{\frac{\chi^2}{n}}}$ with n degrees of freedom where x is a standard normal variate and χ^2 is independent of X. The pdf of *t*-distribution is given as $f(t) = \frac{1}{\sqrt{n}\beta\left(\frac{1}{2},\frac{n}{2}\right)} \cdot \frac{1}{\left(1+\frac{t^2}{n}\right)^{\frac{n+1}{2}}}$, $-\infty < t < \infty$.

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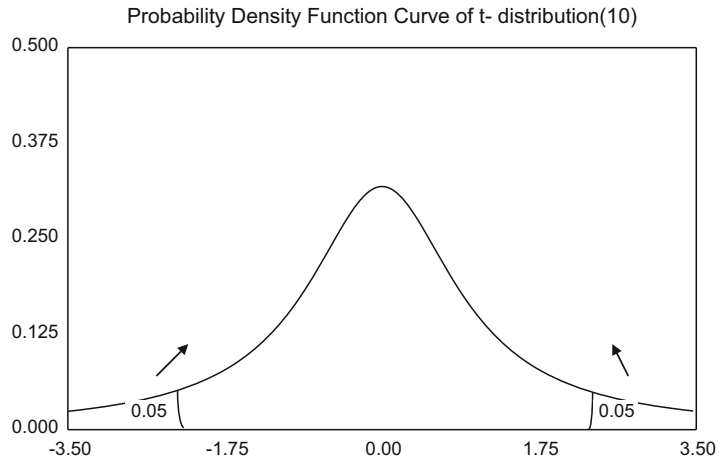
Properties of *t*-Distribution

1. Likewise to that of normal distribution, *t*-distribution is a continuous, symmetric distribution about zero.
2. All odd-order moments about the origin are zero, i.e., $\upsilon_{2r+1} = 0; r = 0, 1, 2, 3.....$ As central moments coincide with the moments about origin, $m_{2r+1} = 0; r = 0, 1, 2, 3.....$
3. The $2r$-th order central moment, i.e., the even-order moment of *t*-distribution is given by $m_{2r} = n^r \frac{(2r-1)(2r-3).....5.3.1}{(n-2)(n-4)(n-6).....(n-2r)}, n > 2r,$ where n is the degrees of freedom. Thus

$$m_2 = \frac{n}{n-2}, n > 2,$$

$$m_4 = \frac{3n^2}{(n-2)(n-4)}, n > 4.$$

4. $\beta_1 = \frac{{m_3}^2}{{m_2}^3} = 0, \beta_2 = \frac{m_4}{{m_2}^2} = 3\frac{n-2}{n-4}$. Thus *t*-distribution is symmetric and leptokurtic. Again as $n \to \infty, \lim_{n\to\infty} 3\left(\frac{1-\frac{2}{n}}{1-\frac{4}{n}}\right) = 3$, thereby the distribution tends to be mesokurtic. As $n \to \infty$, the *t*-distribution approaches to the distribution of standard normal variate.
5. $P[t > t_{\alpha,n}] = \alpha$ and $P[t < t_{1-\alpha,n}] = \alpha$, then $t_{\alpha,n}$ and $t_{1-\alpha,n}$ are the upper and lower α-points, respectively, of *t*-distribution with n degrees of freedom. By symmetry, $t_{1-\alpha,n} = -t_{\alpha,n}$.
6. Using student's *t*-distribution one can work out the Fisher's *t*-distribution also (Ref 4.11.5).



4.11.3 *F* Distribution

Another important sampling distribution is the *F* distribution. Tests based on *F* distribution have varied range of application in statistics, e.g., test for significances of equality of two population variances, multiple correlations, correlation ratio, etc. Tests based on *F* distribution have been discussed in Chap. 6. Another important use of this distribution has been made in comparing several means at a time through the technique of analysis of variance as discussed in Chap. 9.

An *F* statistic is defined as the ratio of two independent χ^2 variates divided by their respective degrees of freedom. Thus, $F = \frac{{\chi_1}^2/n_1}{{\chi_2}^2/n_2}$, where

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χ_1^2 and χ_2^2 are two independent χ^2 variates with n_1 and n_2 degrees of freedom, respectively, i.e., an F variate with (n_1,n_2) degrees of freedom.

The pdf of F distribution is given by

$$f(F) = \frac{\left(\frac{n_1}{n_2}\right)^{n_1/2}}{\beta(n_1/2, n_2/2)} \cdot \frac{F^{\left(\frac{n_1}{2}-1\right)}}{\left(1+\frac{n_1}{n_2}F\right)^{\frac{n_1+n_2}{2}}}, 0 \le F < \infty$$

Properties of F Distribution

1. Unlike normal and t-distribution, F distribution is a continuous but asymmetric distribution.
2. The r-th moment about origin of F distribution is given by

$$\upsilon_r = E(F^r) = \int_0^\infty F^r f(F)dF = \left(\frac{n_2}{n_1}\right)^r \frac{\beta\left(r+\frac{n_1}{2}, \frac{n_2}{2}-r\right)}{\beta\left(\frac{n_1}{2}, \frac{n_2}{2}\right)}, n_2 > 2r$$

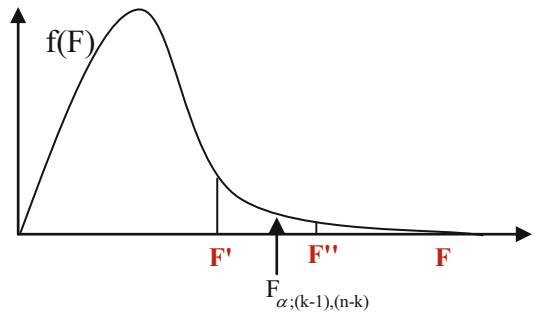
$$= \left(\frac{n_2}{n_1}\right)^r \frac{\Gamma\left(r+\frac{n_1}{2}\right)\Gamma\left(\frac{n_2}{2}-r\right)}{\Gamma\frac{n_1}{2}.\Gamma\frac{n_2}{2}}, \qquad n_2 > 2r$$

Thus mean, $\upsilon_1 = \frac{n_2}{n_2-2}$, $n_2 > 2$, mean depends only on the d.f. of the numerator χ^2 and mean is always greater than unity.

$$\upsilon_2 = \frac{n_2^2}{n_1}\frac{n_1+2}{(n_2-2)(n_2-4)}, \quad n_2 > 4$$

$$\therefore m_2 = \frac{2n_2^2(n_1+n_2-2)}{n_1(n_2-2)^2(n_2-4)}; \quad n_2 > 4.$$

3. The mode of F distribution is given by $\frac{n_2}{n_1}\left(\frac{n_1-2}{n_2+2}\right)$. Thus mode exists only when $n_1 > 2$.
4. The distribution is positively skewed.
5. $$F(n_1, n_2) = \frac{1}{F(n_2, n_1)}.$$
6. If $P\left[F > F_{\alpha;n_1,n_2}\right] = \alpha$ and $P\left[F < F_{1-\alpha;n_1,n_2}\right] = \alpha$ then $F_{\alpha;n_1,n_2}$ and $F_{1\text{-}\alpha;n_1,n_2}$ are the upper and lower α -point of F distribution with (n_1, n_2) d.f. respectively and $F_{1-\alpha;n_1,n_2} = \frac{1}{F_{\alpha;n_2,n_1}}$. As such only upper α -point of F-distribution for different degrees of freedom are given in most of the statistical tables.
7. In case $n_1 = 1$, then $F = \frac{\chi_1^2}{\chi_2^2/n_2}$, where χ_1^2 is just the square of a standard normal variate. Hence $F_{1,n_2} = t^2$ where t has the t distribution with n_2 d.f.
8. If $n_2 \to \infty$, then $\chi^2 = n_1 F$ distribution with n_1 degrees of freedom.



4.11.4 Sampling Distribution of Sample Mean and Sample Mean Square

Let $x_1, x_2, x_3, \ldots x_n$ be a random sample drawn from $N(\mu, \sigma^2)$. Then the sample mean $\bar{x} = \frac{1}{n}\sum_{i=1}^{n} x_i$ also follows normal distribution with mean μ and variance (σ^2/n). Thus the pdf of $\bar{x}$ is given by

$$f(\bar{x}) = \frac{\sqrt{n}}{\sigma\sqrt{2\pi}} e^{-\frac{n}{2\sigma^2}(\bar{x}-\mu)^2}, \quad -\infty < \bar{x} < \infty$$

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We knoen thst $\chi_n^2 = \frac{\sum_{i=1}^{n}(x_i-\mu)^2}{\sigma^2} = \frac{\sum_{i=1}^{n}(x_i-\bar{x})^2}{\sigma^2} + \frac{n(\bar{x}-\mu)^2}{\sigma^2} = \frac{(n-1)s^2}{\sigma^2} + \frac{n(\bar{x}-\mu)^2}{\sigma^2}$

Since $\frac{(\bar{x}-\mu)}{\sigma/\sqrt{n}} \sim N(0,1)$

$$\therefore \frac{n(\bar{x}-\mu)^2}{\sigma^2} \sim \chi_1^2$$

By additive property of χ^2, we have $\frac{(n-1)s^2}{\sigma^2} \sim \chi_{n-1}^2$

Hence the distribution of the sample mean square (s^2) is $\frac{1}{2^{\frac{n-1}{2}}\Gamma\frac{n-1}{2}} e^{-\frac{(n-1)s^2}{2\sigma^2}} \cdot \left(\frac{(n-1)s^2}{\sigma^2}\right)^{\frac{n-1}{2}-1} d\left(\frac{(n-1)s^2}{\sigma^2}\right)$

$$i.e, f(s^2)\frac{(n-1)^{\frac{n-1}{2}}}{(2\sigma^2)^{\frac{n-1}{2}}\Gamma\frac{n-1}{2}} e^{-\frac{(n-1)s^2}{2\sigma^2}} \cdot (s^2)^{\frac{n-3}{2}} ds^2,$$

$0 < s^2 < \infty$

4.11.5 Fisher's *t*-Distribution and Student's *t*-Distribution

We have sample mean and s^2 are distributed independently and since $\bar{x} \sim N(\mu, \sigma^2/n)$

$\therefore z = \frac{\bar{x}-\mu}{\sigma/\sqrt{n}} \sim N(0,1)$ and $\chi^2 = \frac{(n-1)s^2}{\sigma^2} \sim \chi_{n-1}^2$

z and χ^2, both are indepenedent.

Then according to the definition of t, we have $t = \frac{z}{\sqrt{\chi^2/n-1}} = \frac{\frac{\bar{x}-\mu}{\sigma/\sqrt{n}}}{\sqrt{\frac{(n-1)s^2}{\sigma^2(n-1)}}} = \frac{\bar{x}-\mu}{s/\sqrt{n}}$ With (*n*-1) d.f.; this is known as student's *t* statistic.

Let us suppose two independent samples of sizes n_1 and n_2 are drawn randomly from two normal populations and we assume that $\sigma_1^2 = \sigma_2^2 = \sigma^2$.

Thus, $x_1, x_2, x_3, ...x_{n_1} \sim N\left(\mu_1, \sigma_1^2\right) \Rightarrow \bar{x} \sim N(\mu_1, \sigma^2/n_1)$ and

$$y_1, y_2, y_3, ...y_{n_2} \sim N\left(\mu_2, \sigma_2^2\right) \Rightarrow \bar{y} \sim N(\mu_2, \sigma^2/n_2)$$

Thus, $\bar{x} - \bar{y} \sim N\left(\mu_1 - \mu_2, \frac{\sigma^2}{n_1} + \frac{\sigma^2}{n_2}\right)$

$$\Rightarrow z = \frac{\bar{x} - \bar{y} - (\mu_1 - \mu_2)}{\sqrt{\frac{\sigma^2}{n_1} + \frac{\sigma^2}{n_2}}} \sim N(0,1)$$

Again, $\frac{\sum_{i=1}^{n}(x_i-\bar{x})^2}{\sigma^2} = \frac{(n_1-1)s_x^2}{\sigma^2} \sim \chi_{n-1}^2$ and $\frac{\sum_{i=1}^{m}(y_i-\bar{y})^2}{\sigma^2} = \frac{(n_2-1)s_y^2}{\sigma^2} \sim \chi_{m-1}^2$

Thus, $\chi_{n_1-1}^2 + \chi_{n_2-1}^2 = \chi_{n_1+n_2-2}^2 = \frac{(n_1-1)s_x^2}{\sigma^2} + \frac{(n_2-1)s_y^2}{\sigma^2}$

and $t = \frac{z}{\sqrt{\left\{\frac{(n_1-1)s_x^2}{\sigma^2} + \frac{(n_2-1)s_y^2}{\sigma^2}\right\}/(n_1+n_2-2)}}$

$$= \frac{\bar{x} - \bar{y} - (\mu_1 - \mu_2)}{\sqrt{\left\{\frac{(n_1-1)s_x^2 + (n_2-1)s_y^2}{(n_1+n_2-2)}\right\}\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}} = \frac{\bar{x} - \bar{y} - (\mu_1 - \mu_2)}{s\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}},$$

known as Fisher's *t* statistic with $(n_1 + n_2 - 2)$ d.f.

where $s^2 = \frac{(n_1-1)s_x^2 + (n_2-1)s_y^2}{n_1+n_2-2}$

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Population and Sample

5

5.1 Population

The main objective of studying statistics is to characterize population, defined as the collection of well-defined entities having some common characteristics. The observations or entities could refer to anything like persons, plants, animals, and objects (books, pens, pencils, medicines, engines, etc.), and a character is defined on the population. Population may be constituted of persons living in a country, population of goats in a country, population of books in a library, population of fishes in a particular pond, population of farmers in a country, populations of students in a country/state/university, etc. Individual member of the population is known as *element or unit* of the population. *Population size* refers to the number of observations in the population. Depending upon the size of the population, a population may be *finite or infinite*. *A finite population* is a population having fixed number of observations/units/elements, e.g., population of students in a university, germplasms of mango in a mango garden, books in a particular library, population of cattle in a province, and so on. On the other hand, *an infinite population* is a population having infinite number of observations/units/element. For example, fishes in a particular river, stars in a galaxy, population of hairs on a person's head, etc. An infinite population may be infinite or countably infinite.

5.2 Sample

From the above definition and examples of population, it is quite clear that to study a particular population, one has to study each and every element/unit of the population (the *census or complete enumeration* method). But, it may not be possible/feasible to study each and every element/unit of population for various reasons. To study each and every element of a population may not be possible/feasible because of time, labor, and cost involvement. Sometimes, it may not be possible also to identify each and every unit of the population (infinite population). As such in our daily, life we are quite familiar with the word *sample and sample survey* method of data collection. A sample is a *representative part* of the population. If we go to market to buy any commodity, we ask the retailer to show the sample. The retailer shows a handful of the commodity from a stock of huge amount. We check the sample for its quality assuming that the quality of the commodity from which we are supposed to buy (the population) a certain amount of that commodity will be of the same quality as that of the sample shown to us. If the sample shown to the buyer is not a proper representative part of the population, then it may lead to wrong decision with regard to buying of the commodity. In statistics, one studies the sample characteristics and verifies how far the sample behaviors are

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acceptable for the whole population (inference about the population without studying all the elements of particular population), with the help of appropriate statistical theories. The sample and the inference about the population based on its characteristics play important role particularly during the time of disasters, natural calamities, etc. in quick estimating the quantum of losses incurred and thereby helping the policy-makers in taking immediate measures. Sampling technique has been, in fact, use in every sphere of our daily life. The branch of statistical science, in which the technique of sampling for various types of populations and study of the characteristics are dealt with, is coming under sampling theory.

Sampling theory mainly has three major components: (a) *how to select proper sample*, (b) *collection of information from the samples*, and (c) *analysis of sample information* to be utilised during drawing of inferences about the population as a whole. If the sample fails to represent the population adequately, then there is every chance of drawing wrong inference about the population based on such sample because of the fact that it may overestimate or underestimate population characteristics. In fact, one of the major areas of sampling theory is to decide appropriate technique of drawing samples which clearly reflects the nature of the population; in doing so, variability and the nature of the population play a vital role. Before drawing sample from any population, we should have a sampling frame. *A list of all the units in the population to be sampled constitutes sampling frame*. A list of all the blocks in India may constitute the sampling frame in a survey over India. Let us suppose that we want to know the average height of the students of a college. If the college is coeducation college and one draws (i) a sample of either boys or girls only, or (ii) from a particular class, then the sample fails to represent the whole population, i.e., the students of that particular college vis-à-vis the average height obtained from the sample may fail to picturize the true average height of the students of the college (the population). Suppose we want to know the productivity of milking cows in a particular block. While selecting sampling units, one must take into considerations that the milk yield varies depending upon the breed of the cows in the concerned block, age of the cows, rearing conditions of the cows, and so on. All these are to be provided due importance so that each and every category is represented in the sample, and thereby the sample becomes in true to the sense a representative part of the milking cows in the particular block. This will lead to efficient estimation of average productivity of the milking cows in the block; otherwise, this will be misleading. A sample, if fails to represent the parent population, is known *biased sample*, whereas an *unbiased sample* is statistically almost similar to its parent population, and thus inference about population based on this type of sample is more reliable and acceptable than from biased sample. A clear specification of all possible samples of a given type with their corresponding probabilities is said to constitute a *sample* design.

Size (n) of a sample is defined as the number of elements/units with which the sample is constituted of. There is no hard and fast rule, but generally a sample is recognized as *large sample* if the sample size $n \geq 30$, otherwise *small sample*.

Before discussing the sampling techniques in details, let us have a comparative study of the two methods of data/information collection, viz., the *census and the sample survey method*.

A comparative account of the two methods of collection of data is given below:

Sample survey method	Sl no.	Census method
Only a representative part of the population (sample) comes under investigation	1	Every element of the population comes under investigation
Comparatively less accurate, if not done properly	2	Accurate
Economical	3	Costly
Lesser time and resource consuming	4	Time- and resource consuming
Helpful in case of infinite population	5	Not possible for infinite population

(continued)

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Sample survey method	Sl no.	Census method
Helpful for large population	6	Difficult for large population
Having both sampling and non-sampling errors	7	Sampling errors are absent
Nonresponse errors can be solved	8	Difficult to solve nonresponse problem
Parameters are to be estimated and tested	9	Parameters are directly worked out
Used frequently	10	Not used frequently (e.g., human population census, livestock census, etc. are not done frequently)

5.3 Parameter and Statistic

Let us suppose, we have a population Y_1, Y_2, Y_3,. . .,Y_N of size N. Now a *parameter* is defined as a real-valued function of the population values.

For example, population mean $= \overline{Y} = \frac{1}{N}\sum_{i=1}^{N} Y_i$, Population variance $= \sigma_Y^2 = \frac{1}{N}\sum_{i=1}^{N}\left(Y_i - \overline{Y}\right)^2$; Population coefficient of variation $= C_Y = \frac{\sigma_Y}{\overline{Y}}$

Let us suppose, we have selected a sample y_1, y_2, y_3,. . .,y_n of size n from a population of size N. Now a *statistic* is defined as a real-valued function of the sample values only. For example:

$$\text{sample mean} = \overline{y} = \frac{1}{n}\sum_{i=1}^{n} y_i,$$

$$\text{sample variance} = s_y'^2 = \frac{1}{n}\sum_{i=1}^{n}(y_i - \overline{y})^2;$$

$$\text{sample coefficient of variation} = c_y = \frac{s_y'}{\overline{y}}.$$

5.4 Estimator

An *estimator* is a statistic when it is used to estimate the population parameter. From each and every sample, estimator(s) can be worked out, as such estimators for a particular population parameter behave like a random variable. The particular value, which the estimator takes for a given sample, is known as an *estimate*. Let the probability of getting the ith sample be p_i, and let t_i (i =1, 2, 3 . . ...N_0) be the estimate, i.e., the value of estimator t based on this sample for the parameter θ, N_0 being the total number of possible samples for the specified probability scheme. The expected value or the average value of the estimator t is given by $E(t) = \sum_{i=1}^{N_0} t_i p_i$. The estimator t is said to be an *unbiased estimator* of the parameter θ if $E(t) = \theta$. In case $E(t)$ is not equal to θ, the estimator is said to be *biased* estimator of parameter θ, and the bias of t is given as $B(t) = E(t) - \theta$. The difference between the estimate t_i based on the ith sample and the parameter θ, i.e., $(t_i - \theta)$, may be called the error of the estimate. A commonly used loss function is the squared error $(t_i - \theta)^2$, and the expected loss function is known as mean square error (MSE). The MSE of an estimator t of θ is $M(t) = E(t-\theta)^2 = \sum_{i=1}^{M_o} p_i(t_i - \theta)^2$. The variance of t is defined by $V(t) = E[t - E(t)]^2 = \sum_{i=1}^{M_o} p_i[t_i - E(t)]^2$

We have $M(t) = E(t-\theta)^2$
$= E[t - E(t) + E(t) - \theta]^2$
$= E[t - E(t)]^2 + [E(t) - \theta]^2$
$+ 2E[t - E(t)][E(t) - \theta]$
$= V(t) + [B(t)]^2$, (since $E\{t - E(t)\} = 0$).

Efficient Estimator Given two estimators t_1 and t_2 for the population parameter θ, the estimator t_1 is said to be more efficient than t_2 if MSE $(t_1) <$ MSE(t_2).

5.5 Subject Matter of Sampling

Whole subject matter of sampling is directed toward (a) *selection of proper method to obtain a representative sample*, (b) *to determine the size of the sample*, (c) *to ensure good quality of*

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information, and (d) *to estimate parameters, minimizing errors toward valid inferences about the population*.

Once the purpose and objective of the study is fixed, one has to prepare a suitable sampling plan to fulfill the objective of the study. An ideal sampling plan should be concerned about:

(a) Definition of population and sampling units
(b) Scope of study area or domain (i.e., crop, animals, forest plants, human beings, economic parameters, etc.) to be covered
(c) Preparation of sampling frame
(d) Time period allowed
(e) Amount of cost permissible
(f) Coverage, i.e., type of information (qualitative or quantitative) to be collected
(g) Type of parameters to be estimated and type of inference to be made about the population
(h) Sampling design
(i) Selection of sample and collection of data through trained investigators
(j) Analysis of sampled data to arrive at the population figures to fulfill the objective of the study

All the above steps aim at reducing the sampling error at a given cost within limited resources toward drawing efficient inference about the population under consideration.

A good sampling plan is "essential" for drawing an efficient sample. Along with a good sampling plan, its execution is also the most important. It is necessary to have a "good" sampling plan followed by its "efficient execution" to get good estimates of the population parameters. A "good" sampling plan, if not executed properly, may give "bad" (unreliable, inaccurate) results leading to wastage of time, energy, and money used. For efficient execution of the sampling plan, the investigators responsible for the data collection must possess necessary qualifications. The investigators must be properly trained before the data collection. They must be taught how to handle the equipments and make correct observations and measurements and note them down carefully. A proper supervision of the fieldwork must be followed by scrutiny and editing of the collected data. Sincere attempts are needed to identify the sample units, in specifying the units (s) of measurements at every stage and to minimize the error in recording of the data. Initially, a pilot survey may be undertaken to select the suitable sampling plan among the alternative plans. An efficient execution of sampling plan cannot only reduce both the sampling and non-sampling errors but also helps in reducing the cost of study.

5.6 Errors in Sample Survey

In every sphere of scientific endeavor, there are possibilities of error. In sampling, also mainly there are two types of errors associated with estimates worked out from the sample: (i) sampling error and (ii) non-sampling error.

Sampling Error The error due to differences in samples is generally termed as sampling error. It is our common experience that even if we use different samples, drawn exactly the same way from the same population, the estimates from each sample may differ from the other in spite of using the same questionnaires, instructions, and facilities that are provided for selection of all the samples. This difference is termed as sampling error.

Non-sampling Error Non-sampling errors on the other hand are mainly due to differential behavior of respondents as well as interviewers/supervisors. Thus, difference in response, difficulties in defining, difference in interpretations and inability in recalling information, and so on are the major sources of non-sampling errors.

5.7 Sample Size

The number of units to be taken into consideration while recording information from the population, i.e., sample size, plays an important role.

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A number of factors govern the size of the sample to be drawn for a specific purpose. (i) Objective and scope of the study, (ii) nature of population and sampling unit, (iii) the sampling technique and estimation procedure to be used, (iv) structure of variability in the population, (v) structure of time and cost component, (vi) size of the population, etc. are the major decisive factors in fixing the size of the sample for a particular study. An efficient and optimum sample either minimizes the mean squared error of the estimator for a fixed cost or minimizes the cost for a fixed value of mean squared error. Fixing of optimum sample size becomes complicated when more than one parameter is to be estimated or more than one variable is under study. In fact, it is very difficult to have a fixed rule for getting sample size. However, based on past information or information gathered through pilot study conducted before the main study and giving due consideration to the above decisive factors, sample sizes are fixed for specific studies. Krejcie and Morgan (1970) have provided the following formula guiding the determination of sample size from a finite population:

$$S = \frac{\chi^2 NP\,(1-P)}{d^2(N-1)\ +\ \chi^2 P(1-P)}$$

where

S = required sample size
χ^2 = the table value of χ^2 for one degree of freedom at the desired confidence level
N = the population size
P = the population proportion (assumed to be 0.50 since this would provide the maximum sample size)
d = the degree of accuracy expressed as a proportion (0.05)

Example 5.1 Let us find out the sample size for drawing sample from a population of 100 units (N). If we select 5 % level of significance ($d = 0.05$) and $P = 0.5$, then the sample size would be

$$\begin{aligned} S &= \frac{\chi^2 NP\,(1-P)}{d^2\,(N-1)\ +\ \chi^2 P(1-P)} \\ &= \frac{3.841\ \times\ 100 \times 0.5(1-0.5)}{0.05^2(100-1)\ +\ 3.841 \times 0.5(1-0.5)} \\ &= \frac{96.025}{1.20775} = 79.5073 \sim 80 \end{aligned}$$

The following table gives an idea about the sample size in accordance with the above formula for different population size:

Population size (N)	10	25	50	100	150	200	300	400	500	600	700	800	900	1000	1100	1200	1300	1400	1500	1600	1700	1800
Sample size (n)	10	24	44	80	108	132	169	196	217	234	248	260	269	278	285	291	297	302	306	310	313	317
% of elements	100	96	89	80	72	66	56	49	43	39	35	32	30	28	26	24	23	22	20	19	18	18

Population size (N)	1900	2000	2100	2200	2300	2400	2500	2600	2700	2800	2900	3000	3100	3200	3300	3400	3500	3600	3700	3800	3900	4000
Sample size (n)	320	322	325	327	329	331	333	335	336	338	339	341	342	343	344	345	346	347	348	349	350	351
% of elements	17	16	15	15	14	14	13	13	12	12	12	11	11	11	10	10	10	10	9	9	9	9

Determination of Sample Size When Population Size Is Unknown

Some information are essential about the population on hand; also the nature of the sample one wants to draw is essential before drawing the sample from a population of unknown size. It is very difficult to draw a perfect sample which can mimic the population, so one needs to fix the allowable error limit and also the confidence interval with respect to the parameter. Commonly used confidence levels are 90 %, 95 %, 99 %, etc. Also, one should have an idea about

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the quantum of variance one expects in responses. Mostly, 0.5 is used to have a large sample with the expectation of minimization of error. Incorporating the above information in the following formula, required sample size is determined for unknown population size.

$S = \frac{\text{Z-score}^2 \times \text{Sd}(1-\text{Sd})}{\text{Margin of error}^2}$ Z score for different confidence interval is 1.645, 1.96, and 2.326 for 90 %, 95 %, and 99 %, respectively.

Let us suppose that we have 95 % confidence interval with 0.5 Sd and 5 % being the margin of error, then the sample size would be

$$S = \frac{\text{Z-score}^2 \times \text{Sd}(1-\text{Sd})}{\text{Margin of error}^2}$$
$$= \frac{(1.96)^2 \times 0.5(0.5)}{(0.05)^2} = \frac{(3.8416 \times 0.25)}{0.0025}$$
$$= \frac{0.9604}{0.0025} = 384.16 = 384$$

Instead of 95 %, if we take 90 % confidence interval with the same Sd and level of error, then the required sample size would be

$$S = \frac{\text{Z-score}^2 \times \text{Sd}(1-\text{Sd})}{\text{Margin of error}^2}$$
$$= \frac{(1.645)^2 \times 0.5(0.5)}{(0.05)^2} = \frac{(2.706 \times 0.25)}{0.0025}$$
$$= \frac{0.67651}{0.0025} = 270.603 \sim 271$$

Again instead of 0.5 Sd, if we take 0.4 Sd with same confidence level and level of error, then the required sample size would be

$$S = \frac{\text{Z-score}^2 \times \text{Sd}(1-\text{Sd})}{\text{Margin of error}^2}$$
$$= \frac{(1.645)^2 \times 0.4(0.6)}{(0.05)^2} = \frac{(2.706 \times 0.24)}{0.0025}$$
$$= \frac{0.64945}{0.0025} = 259.776 \sim 260$$

Thus, depending upon the desired level of accuracy and confidence level, the sample size is fixed. Moreover, unknown population size does not create acute problem because of the fact that the population size is irreverent unless the size of the sample exceeds a few percent of the total population. Thus, a sample of 500 elements is equivalently useful in examining a population of either 1,500,000 or 100,000. As such, the survey system ignores population size when the population is either large or unknown.

5.8 Selection of Sample (Sampling Technique)

Depending upon the nature and scope of the investigation and situations under which the study is being carried out, appropriate sampling technique is being chosen. Available sampling techniques can broadly be categorized in to two categories (a) *probability sampling* and (b) *non-probability sampling*. When the units in the *sample* are selected using some probability mechanism, such a procedure is called *probability sampling*. The procedure of selecting a *sample* without using any probability mechanism is termed as *non-probability sampling*:

Probability sampling	Non-probability sampling
(1) Simple random sampling	(1) Quota sampling
(2) Varying probability sampling	(2) Judgment sampling
(3) Stratified sampling	(3) Purposive sampling
(4) Systematic sampling	
(5) Cluster sampling	
(6) Multistage sampling	
(7) Multiphase and double sampling	
(8) Sampling on two occasions	
(9) Inverse sampling	

Besides the above, some complex and mixed sampling techniques like (a) two-stage or three-stage sampling with stratification, (b) double sampling for stratification, (c) sampling on successive occasions are useful in studies related with socioeconomic, agronomic, and animal husbandry aspects.

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5.9 Different Sampling Techniques

5.9.1 Probability Sampling

In this type of sampling scheme, sampling units are selected with definite probability rule; sampling units cannot be selected as per the whims of the investigator or user. Depending upon the nature of the population and objective of the study, different sampling techniques have been developed to fit the respective situation following definite probability rule. In the following sections, let us discuss in brief some of the useful and widely used sampling techniques.

5.9.1.1 Simple Random Sampling

The basic assumption in simple random sampling is that the population is assumed to be homogenous in nature. Units are drawn into the sample from the population with the condition that each and every element in the population has got equal probability to be included in the sample. There are two methods of selecting sampling units using simple random sampling technique from a population, viz., *simple random sampling with replacement (SRSWR)* and *simple random sample without replacement (SRSWOR)*.

In *simple random sampling with replacement* (SRSWR), if there are "N" units in the population, then every unit has got $1/N$ probability to be included in the sample. After selecting a unit, it is noted and returned to the population, before the second unit is selected from the population and the process is continued till n (the sample size) number of units is selected from the population. Thus, from a population of N units, we select each and every unit by giving equal probability $1/N$ to all units with the help of random numbers.

On the other hand, in *simple random sampling without replacement* (SRSWOR) after selection of the first unit from N number of unit in the population with $1/N$ probability, the selected unit is not returned in to the population before drawing of the second unit. Thus, the second unit is selected with $1/(N-1)$ probability from $(N-1)$ units. Subsequent units are selected accordingly from the rest $(N-2)$, $(N-3)$, $(N-4)$..... respectively units at each stage. The beauty of this method is that in spite of reduced number of elements in the population after each draw, it can be shown that the probability of drawing selecting a unit in the sample remains same. We shall demonstrate the same as follows.

Let us suppose we are to draw a sample of n units from a population of N units using SRSWOR. Under the given conditions, the probability of drawing any unit in the first drawing out of N units is $1/N$ and that of second unit from the remaining $(N-1)$ units is $1/(N-1)$, third unit from $(N-2)$ remaining units is $1/(N-2)$, and so on. If M_r be an event such that a specific unit is selected at the rth draw, then the probability of M_r is given as

$P(M_r)$ = the probability of the specific unit being not selected in $r-1$ previous draws and has been selected only during the rth draw is

$$\begin{aligned}
&\prod_{i=1}^{r-1} P(\text{that the element is not selected at } i\text{th draw}) \\
&\quad \times P(\text{that the element is selected at } i\text{th draw}) \\
&= \prod_{i=1}^{r-1}\left[1-\frac{1}{N-(i-1)}\right]\times\frac{1}{N-(r-1)} \\
&= \prod_{i=1}^{r-1}\frac{N-i}{N-i+1}\times\frac{1}{N-(r-1)} \\
&= \frac{N-1}{N}\times\frac{N-2}{N-1}\times\frac{N-3}{N-2} \\
&\quad \times\frac{N-4}{N-3}\cdots\cdots\cdots\cdots\frac{N-r+1}{N-r+2}\times\frac{1}{N-r+1} \\
&= \frac{1}{N} \\
&\therefore P(M_r) = P(M_1) = \frac{1}{N}
\end{aligned}$$

Let us illustrate how to use random number from a random number table for drawing a random sample from a finite population.

Example 5.2 The number of calves in lifetime per adult for 50 different goats is given below. The problem is to find out the average no. of calves per goat from a sample of 10 breeds (i) with replacement and (ii) without replacement from the population:

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Goat no.	Calves	Goat no.	Calves	Goat no.	Calves	Goat no.	Calves	Goat no.	Calves
1	8	11	4	21	14	31	10	41	6
2	12	12	5	22	15	32	8	42	7
3	10	13	7	23	2	33	9	43	8
4	8	14	12	24	5	34	11	44	12
5	9	15	14	25	15	35	3	45	11
6	11	16	8	26	17	36	8	46	9
7	3	17	10	27	8	37	10	47	12
8	8	18	10	28	9	38	12	48	15
9	10	19	5	29	12	39	7	49	18
10	12	20	6	30	13	40	9	50	16

The sampling units are the goat number, which varies from 1 to 50. Thus *N*, the population size is 50, a two-digit number:

(a) *Method-1 (direct approach)*

Consider only two-digit random numbers from 01 to 50 and reject the numbers greater than 50 and 00. One can start at any point of the random number table arranged in row and column; one can move in any random way; and it can be vertically downward or upward, to the right or to the left. Let us start at random from a number vertically downward. The numbers selected from the random number table are given in the following table:

Random numbers found from the table	Selected random numbers	
	SRSWR	SRSWOR
12	12	12
4	04	4
36	36	36
80	-	-
36	36	-
32	32	32
95	—	—
63	-	-
78	—	—
18	18	18
94	—	—
11	11	11
87	—	—
45	45	45
15	15	15
32	32	-
71	—	—
77	-	-
55	-	-
95	-	–
27	-	27
33	-	33

The random samples of size 10 with replacement and without replacement consist of the unit numbers 12, 4, 36, 36, 32, 18, 11, 45, 15, and 32 and 12, 4, 36, 32, 18, 11, 45, 15, 27, and 33, respectively. It can be seen from the above table that we have discarded the random numbers above 50, viz., 80, 95, 63, 78, 94, and 87. While selecting the random numbers according the SRSWR, we have kept some random numbers, viz., 36 and 32, more than once because these units after selection are returned to the population before selecting the next unit. But no repetition of random number is found in SRSWOR method. Demerit of the direct approach is that a large number of random numbers are rejected simply because these are more than the population size.

Now, from the selected samples (using SRSWR and SRSWOR), respectively, one can find out the average number of calves per goat:

SRSWR method		SRSWOR method	
Goat	Calves	Goat	Calves
12	5	12	5
4	8	4	8
36	8	36	8
36	8	32	8
32	8	18	10
18	10	11	4
11	4	45	11
45	11	15	14
15	14	27	8
32	8	33	9

Using the above calve data, one find that the average number of calves per goat for two methods is coming out to be:

SRSWR: $(5 + 8 + 8 + \ldots\ldots\ldots + 11 + 14 + 8)/10 = 8.4$

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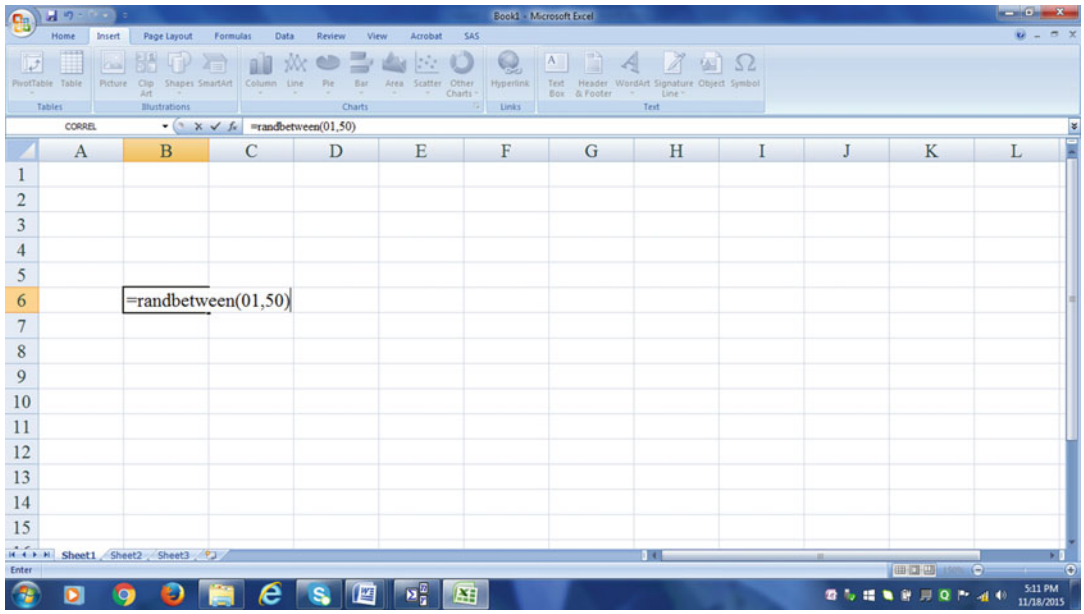
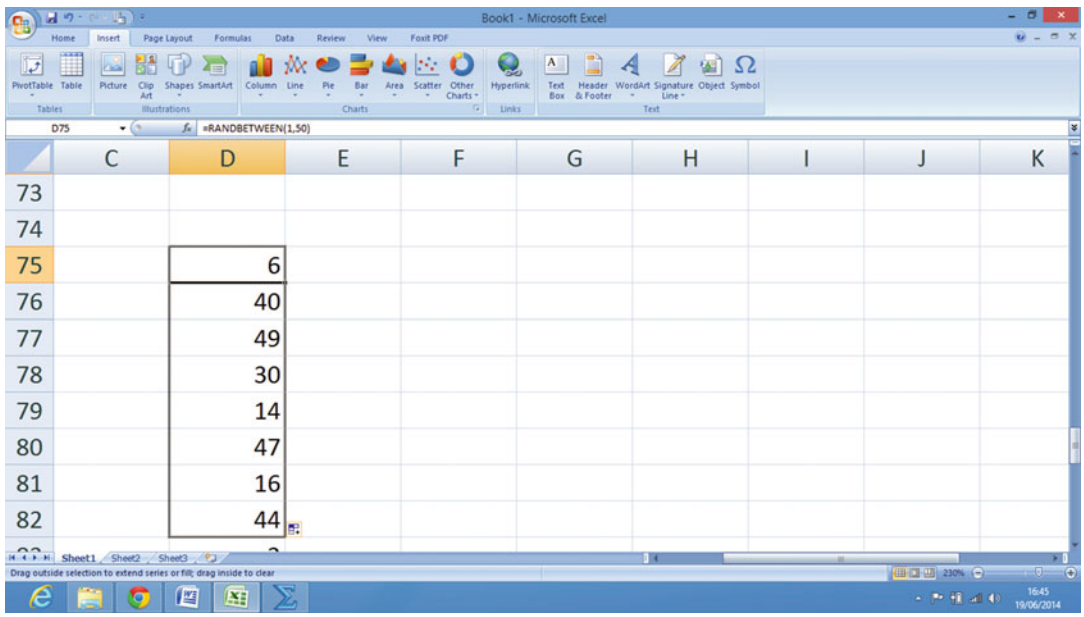
SRSWOR: (5 + 8 + 8 + ... + 8 + 9)/ 10 = 8.5

(b) *Method-II (using random number generated through MS Excel)*

In MS Excel, one can generate random numbers within a given range. For the above example, random numbers are to be generated between 01 and 50. Ten random numbers are to be generated using SRSWR and SRSWOR. This can be accomplished using following steps:

Step1: Select any cell and write=rand between 01 and 50 to get the first random number between 01 and 50. Then, copy the formula to subsequent cells in column or row to get as many random numbers as one wants.





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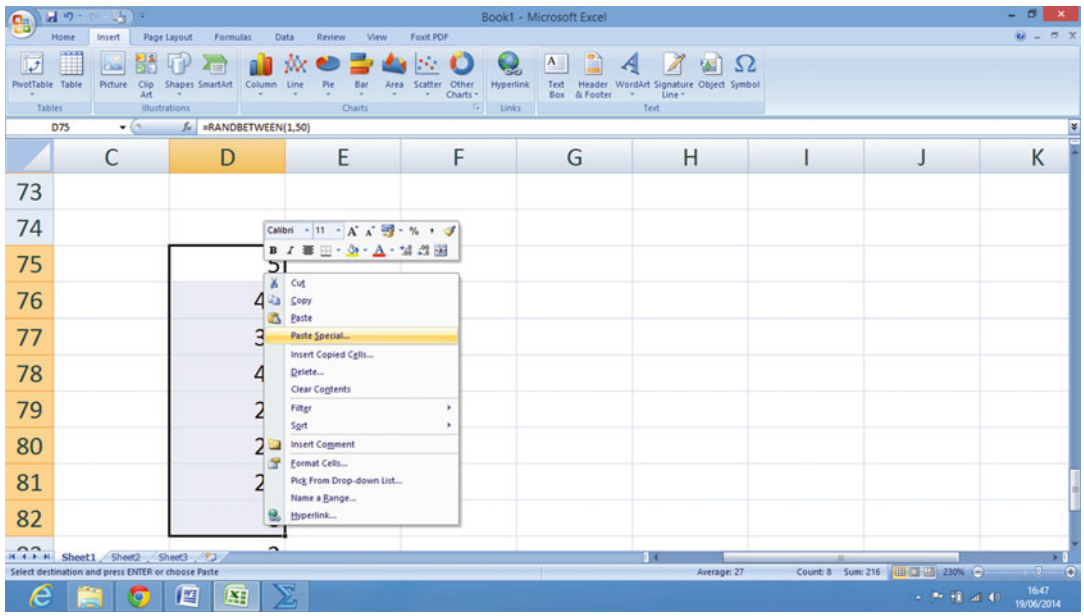
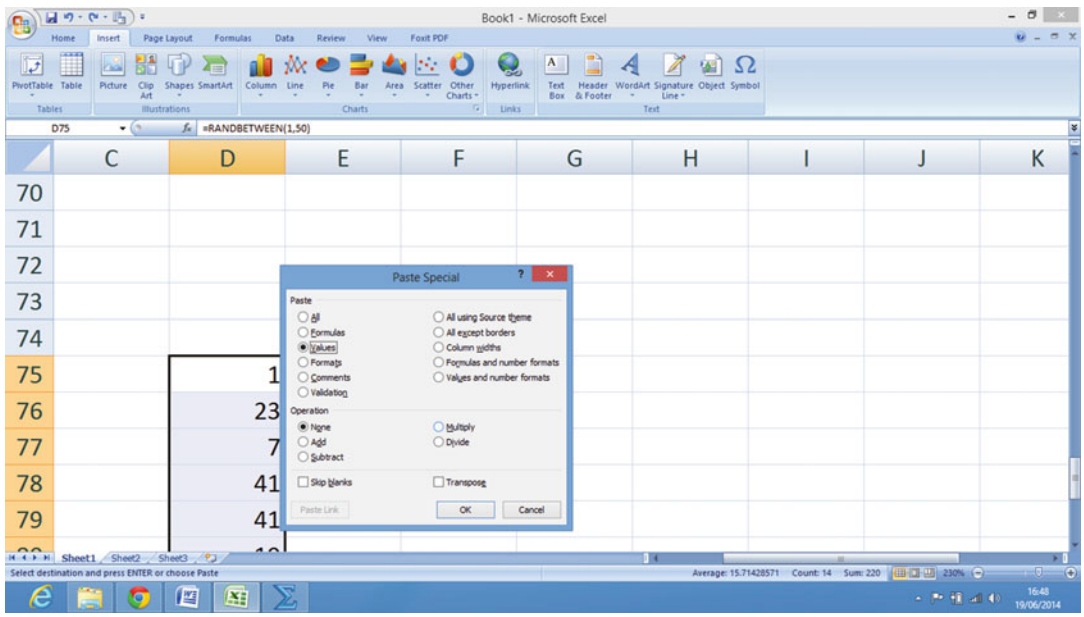
The random numbers, thus, generated changes with every operation, so by using copy and paste special option, these are required to be fixed, as given below:



Step 2: Copy the cells containing random numbers, and then using paste special value command, fix the random numbers; otherwise, these will change every time the cell is activated.



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Step 3: From the random number generated, select the random numbers with repetition and without repetition for SRSWR and SRSWOR, respectively.

Simple random sampling is the most simple and easy method of drawing sample. It is also very easy to estimate the parameters through this technique. But the only problem with this technique is that if the population is not homogeneous, then it will fail to produce a representative part of the population, and subsequently the estimates of the population parameters will not be accurate.

If a sample(y_1, y_2, y_3. . . . .y_n) of n units are drawn from a population of N units adopting SRSWR, then the sample mean $\overline{y} = \frac{1}{n}\sum_{i=1}^{n} y_i$ is an unbiased estimator of the population mean $\overline{Y}$ $\left(E(\overline{y}) = \overline{Y}\right)$, and the sampling variance of the sample mean, i.e.,

$V(\overline{y})$ is given as $\frac{\sigma^2}{n}$ where σ^2 is the population variance. But unlike sample mean sample variance is not an unbiased estimator of population variance. On the other hand mean square (s^2) is an unbiased estimator of the population variance i.e. $E(s^2) = \sigma^2$ where, $s^2 = \frac{1}{n-1}\sum_{i=1}^{n}(y_i - \overline{y})^2$.

As such the standard error of the sample mean is given by $\mathrm{SE}(\overline{y}) = \frac{\sigma}{\sqrt{n}}$ and the estimated S.E.$(\overline{y}) = \frac{s}{\sqrt{n}}$. For SRSWOR $E(\overline{y}) = \overline{Y}$, $V(\overline{y}) = \frac{N-n}{N-1}\frac{\sigma^2}{n} = \frac{N-n}{N}\frac{S^2}{n} = (1-f)\frac{S^2}{n}$, $E(s^2) = S^2$ where $S^2 = \frac{1}{N-1}\sum_{i=1}^{n}\left(Y_i - \overline{Y}\right)^2$ is the population mean square, an unbised estimator of population variance and $f = \frac{n}{N}$ = sampling fraction.

The factor $\frac{N-n}{N} = (1-f)$ is correction factor for the finite population.

Readers may please note that $V_{\mathrm{WOR}}(\overline{y}) = \frac{N-n}{N-1}\frac{\sigma^2}{n} = \left(1 - \frac{n-1}{N-1}\right)\frac{\sigma^2}{n}$ approaches to $\frac{\sigma^2}{n}$ as $N \to \infty$.

Thus $V(\overline{y}) = V_{\mathrm{WOR}}(\overline{y})$ when $N \to \infty$.

5.9.1.2 Varying Probability Sampling (Probability Proportional to Size Sampling)

While selecting farmers for any study, we frequently come across with the situation that the farm size varies among the farmers and it will not be wise to select farmers for drawing a sample assigning equal probability to each farmer having differences in their farm sizes. Let us suppose there are N number of units in a population with X_1, X_2, X_3 ---------X_i----------,X_N as their respective farm sizes. Using SRS, we would have selected units with probability of being selected as $1/N$, providing equal weightage to all the farms varying in sizes. But in this probability proportional to size sampling, the probability of selecting ith unit is $\frac{X_i}{X}$, with $X = \sum_{i=1}^{N} X_i$.

Probability proportional to size sampling method considers both heterogeneity in the population and the varying size of the population units/elements. Thus, this method uses auxiliary information (unit size), which helps in getting more efficient estimator of the population parameter.

If a sample of n units is drawn from a population of N units with PPSWR, then an unbiased estimator of the population total Y is given by

$\hat{Y}_{PPS} = \frac{1}{n}\sum_{i=1}^{n}\frac{y_i}{p_i}$ with its estimated sampling variance

$\hat{V}\left(\hat{Y}_{PPS}\right) = \frac{1}{n(n-1)}\sum_{i=1}^{n}\left(\frac{y_i}{p_i} - \hat{Y}_{PPS}\right)^2$, where $p_i = \frac{y_i}{Y}$

Selection of Sample

There are two methods, (i) *cumulative total method* and (ii) *Lahiri's method*, to select a sample according to this PPS method. Let us discuss the methods in brief:

(a) *Cumulative total method*. Let X_i (i = 1,2,3, ..., N) be the size of the ith unit in the

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population, and suppose that these are integers. Then in the first step, we assign 1 to X_1 number to the first unit having X_1 size, $(X_1 + 1)$ to $(X_1 + X_2)$ to the second unit having size X_2, $(X_1 + X_2 + 1)$ to $(X_1 + X_2 + X_3)$ to the third unit having size X_3, and so on. In the second step, we are to select a random number from 1 to $X = \left(\sum_{i=1}^{N} X_i\right)$ using any of the method described above, and the unit in whose range the random number falls is taken in the sample. The above steps are repeated n times to get a sample of size n with probability proportional to size with replacement.

Example 5.3 To estimate the average milking capacity of a particular breed of cow, information from 25 herds were collected. The following table gives the herd number and herd size. The procedure to select five herds using PPS sampling cumulative total method is delimited below:

Herd	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
Herd size (no.)	10	15	20	30	25	30	12	18	28	42	55	50	60	20	34	38	45	55	70	80	55	65	85	42	16

We are to select five farms with probability proportional to size with replacement.

Solution

Here in this example, the herd size is taken as the criteria. With the above data, let us frame the following:

Herd	Herd size (no.)	Cumulative herd size total	Numbers associated	PPSWR
1	10	10	01–10	
2	15	25	11–25	
3	20	45	26–45	
4	30	75	46–75	
5	25	100	76–100	√
6	30	130	101–130	
7	12	142	131–142	
8	18	160	143–160	
9	28	188	161–188	
10	42	230	189–230	
11	55	285	231–285	
12	50	335	286–335	
13	60	395	336–395	
14	20	415	396–415	
15	34	449	416–449	√
16	38	487	450–487	
17	45	532	488–532	√
18	55	587	533–587	
19	70	657	588–657	√
20	80	737	658–737	
21	55	792	738–792	
22	65	857	793–857	
23	85	942	858–942	√
24	42	984	943–984	
25	16	1000	985–1000	

We shall select five random numbers from 1 to 1000 from the random number table, and suppose the random numbers selected from the random number are 502, 648, 902, 91, and 440. The herds associated with these numbers are 17th, 19th, 23rd, 5th, and 15th, respectively. Thus, according to PPS with replacement, the sample should contain 5th, 15th, 17th, 19th, and 23rd herd from the 25 herds at random.

(ii) *Lahiri's method*

Lahiri's (1951) method of PPS sampling uses only two values, i.e., the population size (N) and the highest size of the population elements; it does not accumulate the sizes of the elements of the population. A random number from 1 to N is selected and noted to the corresponding unit of the population. Another random number from 1 to M (the maximum or any convenient number greater than the maximum size among the elements of the population) is drawn. If the

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second random number is smaller or equal to the size of the unit provisionally marked corresponding to the first random number, the unit is selected into the sample. If not, the entire procedure is repeated until a unit is finally selected, and the whole process is repeated until sample of desired size is achieved.

Example 5.4 To demonstrate the process let us take the same example in 5.3. To estimate the average milking capacity of a particular breed of cow, information from 25 herds were collected. The following table gives the herd number and herd size. The procedure to select five herds using PPS sampling cumulative total method is delimited below:

Herd	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
Herd size (no.)	10	15	20	30	25	30	12	18	28	42	55	50	60	20	34	38	45	55	70	80	55	65	85	42	16

We are to select five farms with probability proportional to size with replacement using Lahiri's method.

In this example, we have $N = 25$ and $M = 85$. First, we are to select a random number from 1 to 25 and a second random number from 1 to 85. Referring to the random number table, the pair is (10, 40). Here $40 < X_{10} = 42$. Hence, the tenth unit is selected in the sample. Suppose we choose another pair (19, 80). Here $80 > X_{19} = 70$. So the 19th unit is rejected. We choose another pair (7, 55). Here $55 > X_7 = 12$. Thus, the seventh unit is also rejected. Let the fourth pair of random numbers be (3,12); $12 < X_3 = 20$. So the third unit is selected in the sample. The process is continued till we have sample of desired size (5) here.

5.9.1.3 Stratified Sampling

Both the simple random sampling and the probability proportional to size methods of sampling are mostly used in homogenous population situation. Under the heterogeneous population situation, these methods result in lesser efficient samples. Moreover, these two methods are comparatively costly. Stratified random sampling is one of the methods of tackling the heterogeneous population. The essence of stratified random sampling method lies on dividing the whole heterogeneous population of size N in to small groups (known as strata) of comparative homogeneous elements/units. Thus, the strata are homogeneous within and heterogeneous among themselves as much as possible; random samples are drawn from each of the homogeneous stratum. A suitable stratifying factor like age, sex, educational or income level, geographical area, economic status, soil fertility pattern, stress level, tiller size, sex of fish, different species of fish, and so on is used for the purpose of stratification. Efficiency in stratification leads to the efficient stratified random sampling.

In stratified sampling method, we come across two types of problems, (i) how many strata should one form with a given population and (ii) how many units from each stratum should be selected for the sample? The basic principle followed during stratification is that stratification can be done to the extent which produces lesser variance and such that only one unit is selected from each stratum. Moreover, it is not always true that too many numbers of strata always lead to lesser variance. The second problem of allocation of number of units to be selected from different strata is being dealt with different method like (a) *equal allocation*, (b) *proportional allocation*, (c) *optimum allocation,* (d) *Neyman's allocation.* Before discussing all these methods, let us first discuss the unbiased estimator of population mean and total from stratified population.

Suppose we have a population with population mean $\overline{Y}$ and variance σ^2. The population is stratified into L strata with N_h be the sizes of hth stratum having mean $\overline{Y_h}$ and variance σ_h^2 ($h = 1,2,3,\ldots L$).

Therefore, $N = N_1, +N_2 + \ldots\ldots + N_L$.

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We may write, $\overline{Y} = \sum_{h=1}^{L} W_h \overline{Y_h}, \sigma^2 = \sum_{h=1}^{L} W_h \sigma_h^2 + \sum_{h=1}^{L} W_h \left(\overline{Y_h} - \overline{Y}\right)^2$,
where, $W_h = \frac{N_h}{N}$

Let us take a random sample of size n by selecting n_h units from hth stratum such that $\sum_{h=1}^{L} n_h = n$. Let $\overline{y}_h$ and ${s_h}^2$ be the sample mean and sample mean square for the nth stratum where, $\overline{y}_h = \frac{1}{n_h} \sum_{j=1}^{n_h} y_{hj}$ and ${s_h}^2 = \frac{1}{n_h - 1} \sum_{j=1}^{n_h} \left(y_{hj} - \overline{y}_h\right)^2$.

Unbiased estimator for the population mean $\overline{Y}$ and the population total Y are given by $\hat{\overline{Y}} = \overline{y}_{st} = \sum_{h=1}^{L} W_h \overline{y}_h$ and $\hat{Y} = N\overline{y}_{st}$ and their estimated variances are given by

$$\hat{V}(\overline{y}_{st}) = \sum_{h=1}^{L} {W_h}^2 (1 - f_h) \frac{{s_h}^2}{n_h}$$
$$\hat{V}(N\overline{y}_{st}) = N^2 \hat{V}(\overline{y}_{st}), \text{ where, } f_h = \frac{n_h}{N_h}$$

With this idea, let us now discuss the methods of allocation of number of units to be selected from different strata.

(a) *Equal allocation:* Total sample size is divided equally among the strata, i.e., sample n_h to be selected from hth stratum such that $n_h = n/\mathrm{L}$.

(b) *Proportional allocation:* In proportional allocation, $n_h \propto$ (proportional to) N_h, i.e., $N_h = nW_h$; $h = 1, 2, 3, \ldots, \mathrm{L}$.

(c) *Optimum allocation:* The simplest cost function is of the form $C = C_0 + \sum_{n=1}^{L} C_h n_h$, where C_0 is an overhead cost, C_h is the cost of sampling a unit from the hth stratum, and C is the total cost. We have to find n_h such that $V(\overline{y}_{st})$ is minimum for specified cost $C = C'$. To solve this problem, we have $n_h = (C' - C_0) \frac{W_h S_h / \sqrt{C_h}}{\sum_{h=1}^{L} W_h S_h \sqrt{C_h}}$, $h = 1, 2, 3, \ldots, \mathrm{L}$, where ${S_h}^2$ is the population mean square for the hth stratum.

This is known as optimum allocation.

(d) *Neyman allocation:* A special case arises when the $C_h = C''$, i.e., if the cost per unit is the same in all the strata. In this case, $n_h = n \frac{W_h S_h}{\sum_{h=1}^{L} W_h S_h} = n \frac{N_h S_h}{\sum_{h=1}^{L} N_h S_h}$. This allocation is known as *Neyman allocation*, after the name of Neyman (1934). In particular, if $S_1 = S_2 = \ldots = S_L$, one can see that Neyman allocation reduces to proportional allocation.

5.9.1.4 Cluster Sampling

While dealing with huge population, simple random sampling becomes not so easy because of the nature of the population and the cost and time involvement in the process. As such, subsection or grouping of the population is needed for efficient sampling. In stratified sampling, discussed in previous section, the strata are the subsection of the population and which are formed in such a way that there are homogeneity among the units of the stratum and heterogeneity among the strata. *As such, these strata fail to picturize the nature of the population individually*; individually, each of these is subsection of the population. On the other hand in cluster sampling, clusters are thought of as a typical part of population rather than subsection. We need to select larger units/clusters instead of units directly from the population. For example, in a large country wide survey, one can have list of blocks or villages, which can be used as cluster having all the properties of the population not the subsection of the population for probability sampling.

In cluster sampling, the whole population is divided into a number of clusters each consisting of several units and continues to hold the nature of the population from which these are formed. Cluster size may vary from cluster to cluster. The

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best size of cluster depends on the cost of collecting information from the clusters and the resulting variance. Our aim is to reduce both the cost and variance, and for that we can have a pilot survey also, if felt necessary. Then some clusters are selected at random out of all the clusters. The advantages of cluster sampling from the point of view of cost arise mainly due to the fact that collection of data for nearby units is easier, faster, cheaper, and more convenient than observing units scattered over a region, as in the case of simple random sampling.

Suppose we have a population divided into N clusters having M units each, i.e., the size of the population is NM. Let X_{ij} be the value of the character X under study for jth observation corresponding to ith cluster (i =1, 2, 3,. . . . .N and j = 1, 2, 3, ...M). The population mean $\overline{X}$ is defined as $\overline{X} = \frac{1}{NM}\sum_{i}^{N}\sum_{j}^{M} X_{ij} = \frac{1}{N}\sum_{i=1}^{N}\overline{X_i}$, where, $\overline{X_i}$ is the ith cluster mean. A sample of n clusters is drawn with SRSWOR, and all the units in the selected clusters should be surveyed. An unbiased estimator of the population mean $\overline{X}$ is given by

$\hat{\overline{X}}_c = \frac{1}{n}\sum_{i=1}^{n}\overline{x_i}$ and its estimated variance is

$\hat{\mathrm{V}}\left(\hat{\overline{X}_c}\right) = \frac{N-n}{N}\frac{s_b^2}{n}$, where, $\overline{x_i} = \frac{1}{M}\sum_{j=1}^{M} x_{ij} =$ mean for the ith selected cluster and

$s_b{}^2 = \frac{1}{n-1}\sum_{i=1}^{n}\left(\overline{x}_i - \hat{\overline{X}_c}\right)^2$

The cluster sampling is useful when the study area is very big, and listing of population units is not available or possible under the given conditions of resources and time, but the same may be available for small segments of the population. The problem with cluster sampling arises when the clusters fail to represent the true nature of the population.

5.9.1.5 Multistage Sampling

For study in larger area, we have suggested for cluster sampling method. This cluster sampling method can be made more efficient by forming clusters at different stages. Suppose in a household survey of farmers, as per cluster sampling method, the whole country can be visualized as composed of number blocks, and from blocks, the farmers could be selected. The process can be made more efficient, instead of taking blocks as the clusters, if we select some districts at random, followed by sum blocks from each of the selected districts at random, followed by some villages from each of the selected blocks at random and ultimately some households at random from the selected villages. Thus, there are different stages of clustering, and in each stage, units are selected at random. In this case, selected districts, blocks, and villages form the first-stage, second-stage, and third-stage units, respectively, with farmers as the ultimate sampling units. The whole process of such sampling is known as multistage sampling method.

Multistage sampling is a very flexible sampling technique. It is useful especially for an underdeveloped condition where sampling frame is not available. But it is less accurate than single-stage sampling and is tedious when the number of stages is more. The whole process depends on the expertise of the supervisor.

Suppose we have a population, which is divided into N first-stage units (fsu) having M second-stage units (ssu) each. The population mean $\overline{X} = \frac{1}{NM}\sum_{i}^{N}\sum_{j}^{M} X_{ij} = \frac{1}{N}\sum_{i=1}^{N}\overline{X}_i$.

If a sample of N first-stage units (fsu) is selected from N first-stage units (fsu) with SRSWOR and a sample of M second-stage units (ssu) is selected from each selected fsu with SRSWOR, then an unbiased estimator for $\overline{Y}$ is given by

$\hat{\overline{X}}_t = \frac{1}{n}\sum_{i=1}^{n}\overline{x}_i$ with its estimated variance

$\hat{V}\left(\hat{\overline{X}}_t\right) = (1-f_1)\frac{s_b{}^2}{n} + \frac{f_1(1-f_2)}{nm}s_2{}^2$, where

$\overline{x_i} = \frac{1}{m}\sum_{j=1}^{m} y_{ij}$, $\mathrm{s}_b^2 = \frac{1}{n-1}\sum_{i=1}^{n}\left(\overline{x}_i - \hat{\overline{X}}_t\right)^2$ and

$s_2^2 = \frac{1}{n(m-1)}\sum_{i=1}^{n}\sum_{j=1}^{m}\left(x_{ij} - \overline{x}_i\right)^2, f_1 = \frac{n}{N}, f_2 = \frac{m}{M}$

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Multistage sampling is a very useful and flexible sampling technique especially under the situation of nonavailability of sampling frame. The efficiency of the sampling process depends on the expertise of the supervisor. Moreover, it is comparatively less accurate than single-stage sampling, and as the number of stages increases, the process becomes very tedious, and the estimation procedure becomes complicated.

5.9.1.6 Multiphase and Double (Two-Phase) Sampling

A variant form of tackling large population is multiphase sampling, i.e., to carry out sampling in two or more phases. With the help of auxiliary information collected and used in subsequent subsampling stages, sampling procedure is accomplished. Two-phase or double sampling is the simplest procedure in multiphase sampling. The usual procedure is to take a large sample of size m from the population of N units to observe the x-values of the auxiliary character and to estimate the population parameter (say mean), while a subsample of size n is drawn from m to study the character under consideration.

Suppose we want to select a sample of farmers with probability proportional to size of farm for a country. It is very difficult to have information on farm size from each of the farmers for a huge country. The multiphase sampling, here two-phase sampling (say), starts with an initial random sample of families having varied farm sizes, and information on their farm sizes are collected; then a subsample is taken from the initial sample with probability proportional to size of the farms. This will serve as the test sample for the character under study from a selected sample on the basis of farm size. Thus, in multiphase sampling, every sample is obtained from previous sample.

The difference in between multiphase sampling and the multistage sampling is that in multistage sampling, the sampling units at each stage are the clusters of units of the next stage and the ultimate observable units are selected in stages, sampling at each stage being done from each of the sampling units or clusters selected in the previous stage. On the other hand, in multiphase sampling, information are collected initially from a wider sample of the population, and subsequent information are collected from subsequent samples.

5.9.1.7 Systematic Sampling

Systematic sampling is simple and convenient to apply. The basic idea of systematic sampling is to select units for sample in a systematic way, as such not fully in random manner. In systematic random sampling, only the first unit is selected at random, and the rest units of the sample get selected automatically according to some predesigned pattern. Suppose we have a population of N units and the N units of the population are numbered from 1 to N in some order. Let $N = nk$, where n is the sample size and k is an integer, and a random number less than or equal to k is selected first, and every kth unit thereafter is selected in systematic manner. There are two methods of systematic selection of sample according to this method, (a) as *linear systematic sampling* and (b) *circular systematic sampling*. Let us now discuss the methods in brief:

(a) *Linear systematic sampling (LSS):* As has already been stated, a population of size N is numbered, and to select a sample of size n, we select number k such that $N = nk$ where k is an integer. At first, a random number r in between 1 to k is selected. We start with rth unit, and thereafter every unit at every kth interval is selected for the desired sample. Thus, in this procedure, the sample comprises the units r, $r + k$, $r + 2k$,. . .., and $r + (n-1)k$. The selected random number r is known as the random start, and k is called the sampling interval.

(b) *Circular systematic sampling*: The problem with linear systematic sampling is if $N \neq nk$. To counter the problem, the circular systematic sampling will be useful. In this method, the sampling interval k is taken as an integer nearest to N/n; a random number is chosen from 1 to k, and every kth unit is drawn in the sample. Under this condition, the sample size will be n or one less than n. Some workers suggest that one should

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continue to draw units until one gets a sample of size n.

It is also economical and requires less time than simple random sampling. But it does not give a right representation of the population and also may not give efficient result if the population is not in a systematic manner. It can also be shown that in case of circular systematic sampling, though the sample mean is an unbiased estimator of the population mean, an unbiased estimate of the variance is not available for a systematic sample with one random start because a systematic sample is regarded as a random sample of one unit. Some biased estimators are possible on the basis of a systematic sample. If two or more systematic samples are available, an unbiased estimate of the variance of the estimated mean can be made.

Systematic sampling is simple, and it is widely used in various types of surveys, i.e., in census work, forest surveys, in milk yield surveys, in fisheries, etc., because in many situations, it provides estimates more efficient than simple random sampling.

5.9.1.8 Inverse Sampling

So far the methods of sampling discussed are to draw sample of desired size, but we may come across a situation where we do not know the exact size of the sample to be drawn. Suppose we want to draw a sample of plants in which there must be at least k mutant plants (in which rare mutation has taken place). Thus, in this process of sampling, drawing of sample units should continue at random until k number mutant plants have been selected in the sample. The drawing will continue and the sample size will go on increasing. Such a sampling procedure is known as inverse sampling. Thus, though costly, time-consuming, and labor consuming, this sampling gives due weightage to rare elements in the population. Inverse sampling is generally used for the estimation of a rare population parameter. For example, inverse sampling designs have been used to populations in which the variable of interest tends to be at or near zero for many of population units and distinctly different from zero for a few population units.

Suppose p denotes the proportion of units in the population possessing the rare attribute under study. Evidently, Np number of units in the population will possess the rare attributes. To estimate p, units are drawn one by one with SRSWOR. Sampling is discontinued as soon as the number of units in the sample possessing the rare attribute (a predetermined number, m) is reached. Let us denote by n the number of units required to be drawn in the sample to obtain m units possessing the rare attribute. An unbiased estimator of p is given by $\hat{p} = \frac{m-1}{n-1}$, and an unbiased estimator of the variance of $\hat{p}$ is $\hat{V}(\hat{p}) = \frac{\hat{p}(1-\hat{p})}{(n-2)}\left[1 - \frac{n-1}{N}\right]$

5.9.1.9 Bootstrap Sampling

The main idea of sampling from population is to handle lesser number of elements instead of a population that consists of huge number of elements and to use the sample statistic to estimate the population parameter in a befitting manner. Thus, the sampling distribution of sample statistic is important in this aspect. One way to achieve the same is to draw number of samples from the population, but the procedure does not make any sense as it would be too costly and against the principle of sampling theory as such. Here lies the importance of bootstrap sampling. In order to get idea about the sampling distribution of the sample statistic, we use repeated samples of same size from the original sample drawn from the population. If the number of resample (with replacement) be very large, then one would get good idea about the sampling distribution of a particular statistic from the collection of its values arising out of these repeated samples. In literature, one can find the terminologies, *surrogate population* and *phantom samples*, corresponding to original random sample drawn from the population and resamples of the same size with replacement from the surrogate sample, respectively. The sample summary/statistic is then computed from each of the bootstrap samples (generally a few thousands). At the elementary application stage of bootstrap,

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one produces a large number of "copies" of a sample statistic, computed from these phantom bootstrap samples. A histogram of the set of these computed values is referred to as the bootstrap distribution of the statistic. Then, a confidence interval $100(1-\alpha)\%$ is set corresponding to unknown population parameter of interest; the value of α is decided by the experimenter according to the situation.

5.9.2 Non-probability Sampling

5.9.2.1 Quota Sampling

In this method of non-probability sampling, definite number of sampling units is selected from different subsections of the population. Selection of units for sampling is left to the expertise/convenience of the sampler, and an interviewer selects the respondents in nonrandom manner. The greatest weakness of the procedure is nonrandom selection of the units for sampling purpose. In most of the cases, each interviewer/sampler is assigned to record information from a fixed number of respondents (quota) that are taken as representation of whole sample.

As such, this procedure of sampling is less costly and convenient, does not require any sampling frame, and provides quick response. The success of the entire exercise depends on the skill and the efficiency of the interviewer/sampler.

5.9.2.2 Judgment Sampling

In this method of sampling, most emphasis is provided to the purpose or objective of the sampling. As such, those units are only selected which can serve the purpose of sampling. Thus, in judgment sampling, the basic idea is to select a sample of desired size giving full judgment to the purpose of the study, and the elements of the sample is selected in such a way so as to fulfill the objective of the study. Though the method is very simple, it may lead to biased and inefficient sample depending upon the efficiency of the supervisor.

5.9.2.3 Purposive Sampling

The choice of the supervisor is the most important parameter in selecting a unit into the sample. As such, purposive sampling does not follow the basic theories of sampling. Selection of element to be included in the sample is entirely made on the basis of the choice of the supervisor. Likewise to that of judgment sampling, the purposive sampling is very easy to handle, but it provides rarely a representative part of the population. Thus, the results from purposive sampling are mostly biased and inefficient.

Besides the above, there are various sampling schemes depending up on the nature of the population in hand and the situations. In many cases, combinations of more than one method are used, e.g., in estimation of marine fish landing in India, a multistage stratified in combination of systematic sampling is adopted. For getting an immediate idea about any phenomenon under consideration (like crop loss due to sudden outbreak of pest/disease, damage of life due to tsunami, etc.), sampling technique for rapid assessment (STRA) is also used.

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Random number table

	00–04	05–09	10–14	15–19	20–24	25–29	30–34	35–39	40–44	45–49
00	54,463	22,662	65,905	70,639	79,365	67,382	29,085	69,831	47,058	08,186
01	15,389	85,205	18,850	39,226	42,249	90,669	96,325	23,248	60,933	26,927
02	85,941	40,756	82,414	02,015	13,858	78,030	16,269	65,978	01,385	15,345
03	61,149	69,440	11,286	88,218	58,925	03,638	52,862	62,733	33,451	77,455
04	05,219	81,619	10,651	67,079	92,511	59,888	84,502	72,095	83,463	75,577
05	41,417	98,326	87,719	92,294	46,614	50,948	64,886	20,002	97,365	30,976
06	28,357	94,070	20,652	35,774	16,249	75,019	21,145	05,217	47,286	76,305
07	17,783	00,015	10,806	83,091	91,530	36,466	39,981	62,481	49,177	75,779
08	40,950	84,820	29,881	85,966	62,800	70,326	84,740	62,660	77,379	90,279
09	82,995	64,157	66,164	41,180	10,089	41,757	78,258	96,488	88,629	37,231
10	96,754	17,676	55,659	44,105	47,361	34,833	86,679	23,930	53,249	27,083
11	34,357	88,040	53,364	71,726	45,690	66,334	60,332	22,554	90,600	71,113
12	06,318	37,403	49,927	57,715	50,423	67,372	63,116	48,888	21,505	80,182
13	62,111	52,820	07,243	79,931	89,292	84,767	85,693	73,947	22,278	11,551
14	47,534	09,243	67,879	00,544	23,410	12,740	02,540	54,440	32,949	13,491
15	98,614	75,993	84,460	62,846	59,844	14,922	48,730	73,443	48,167	34,770
16	24,856	03,648	44,898	09,351	98,795	18,644	39,765	71,058	90,368	44,104
17	96,887	12,479	80,621	66,223	86,085	78,285	02,432	53,342	42,846	94,771
18	90,801	21,472	42,815	77,408	37,390	76,766	52,615	32,141	30,268	18,106
19	55,165	77,312	83,666	36,028	28,420	70,219	81,369	41,943	47,366	41,067
20	75,884	12,952	84,318	95,108	72,305	64,620	91,318	89,872	45,375	85,436
21	16,777	37,116	58,550	42,958	21,460	43,910	01,175	87,894	81,378	10,620
22	46,230	43,877	80,207	88,877	89,380	32,992	91,380	03,164	98,656	59,337
23	42,902	66,892	46,134	01,432	94,710	23,474	20,423	60,137	60,609	13,119
24	81,007	00,333	39,693	28,039	10,154	95,425	39,220	19,774	31,782	49,037
25	68,089	01,122	51,111	72,373	06,902	74,373	96,199	97,017	41,273	21,546
26	20,411	67,081	89,950	16,944	93,054	87,687	96,693	87,236	77,054	33,848
27	58,212	13,160	06,468	15,718	82,627	76,999	05,999	58,680	96,739	63,700
28	70,577	42,866	24,969	61,210	76,046	67,699	42,054	12,696	93,758	03,283
29	94,522	74,358	71,659	62,038	79,643	79,169	44,741	05,437	39,038	13,163
30	42,626	86,819	85,651	88,678	17,401	03,252	99,547	32,404	17,918	62,880
31	16,051	33,763	57,194	16,752	54,450	19,031	58,580	47,629	54,132	60,631
32	08,244	27,647	33,851	44,705	94,211	46,716	11,738	55,784	95,374	72,655
33	59,497	04,392	09,419	89,964	51,211	04,894	72,882	17,805	21,896	83,864
34	97,155	13,428	40,293	09,985	58,434	01,412	69,124	82,171	59,058	82,859
35	98,409	66,162	95,763	47,420	20,792	61,527	20,441	39,435	11,859	41,567
36	45,476	84,882	65,109	96,597	25,930	66,790	65,706	61,203	53,634	22,557
37	89,300	69,700	50,741	30,329	11,658	23,166	05,400	66,669	48,708	03,887
38	50,051	95,137	91,631	66,315	91,428	12,275	24,816	68,091	71,710	33,258
39	31,753	85,178	31,310	89,642	98,364	02,306	24,617	09,609	83,942	22,716
40	79,152	53,829	77,250	20,190	56,535	18,760	69,942	77,448	33,278	48,805

(continued)

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	00–04	05–09	10–14	15–19	20–24	25–29	30–34	35–39	40–44	45–49
41	44,560	38,750	83,635	56,540	64,900	42,912	13,953	79,149	18,710	68,318
42	68,328	83,378	63,369	71,381	39,564	05,615	42,451	64,559	97,501	65,747
43	46,939	38,689	58,625	08,342	30,459	85,863	20,781	09,284	26,333	91,777
44	83,544	86,141	15,707	96,256	23,068	13,782	08,467	89,469	93,842	55,349
45	91,621	00,881	04,900	54,224	46,177	55,309	17,852	27,491	89,415	23,466
46	91,896	67,126	04,151	03,795	59,077	11,848	12,630	98,375	52,068	60,142
47	55,751	62,515	21,108	80,830	02,263	29,303	37,204	96,926	30,506	09,808
48	85,156	87,689	95,493	88,842	00,664	55,017	55,539	17,771	69,448	87,530
49	07,521	56,898	12,236	60,277	39,102	62,315	12,239	07,105	11,844	01,117

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Statistical Inference

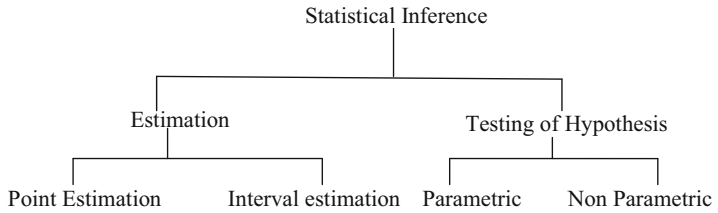
6

6.1 Introduction

As has already been discussed, the objective of statistics is to study the population behavior. And in the process generally we are provided with the samples parts of the population. The experimenter or the researchers are to infer about the population behavior based on the sample observations. Here lies the importance of accuracy and efficiency. The whole process of studying the population behavior from the sample characteristics is dealt in *statistical inference*. Statistical inference mainly has two components, viz., *estimation and testing of hypothesis*. In estimation part, we are generally concerned with estimating/identifying measures or to have an idea about the measures which can be used for measuring population characters efficiently. On the other hand, in testing of hypothesis, we are concerned about testing/deciding how far the information based on sample observations could be used for population. In this context, one must have idea about the *parameter* and the *statistic*. *A parameter is the real-valued function of the population observations, whereas a statistics is the valued function of the sample observations*. For example, the population mean

$\mu = \frac{1}{N}\sum_{i=1}^{N} X_i$ is a population parameter, where as sample mean $\overline{x} = \frac{1}{n}\sum_{i=1}^{n} x_i$ is sample statistic.

There may be more than one statistic to estimate a particular parameter; now the question is which statistic can effectively estimate the population parameter? All these are answered in estimation part. On the other hand, after selecting a best estimator corresponding to a particular population parameter and working out its value from the sample observations, how far the value is acceptable or, otherwise, for the population is being dealt in testing of hypothesis. Sometimes, hypothetical value about the population parameter, based on preconception or previous knowledge, is also being tested through testing of hypothesis to ascertain the acceptability of such value for the population.



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6.1.1 Estimation

Estimation is the process of knowing the unknown population parameter with the help of population observations. Suppose $x_1, x_2, x_3,\ldots\ldots\ldots, x_n$ be a random sample from a population, in which θ be a parameter. Now estimation problem lies in estimating the θ with the help of the above sample values $x_1, x_2, x_3,\ldots\ldots\ldots, x_n$.

Any statistic which is used to estimate (or to guess) $\psi(\theta)$, a function of parameter θ, is said to be an estimator of $\psi(\theta)$. The experimentally determined value (i.e., from sample) of an estimator is called its estimate. In order to estimate the population parameter θ, one can draw a number of samples from the population and can propose number of statistic to estimate the parameter θ. Suppose, $x_1, x_2, x_3,\ldots\ldots\ldots, x_n$ be a sample drawn from $N(\mu, \sigma^2)$, then one can have statistic like $\sum x_i$ and $\sum x_i^2$ for the population parameter. Now the question is among the statistic(s), which one is the best one to estimate the population parameter under question. So there must be certain criteria to judge a good estimator. According to R. A. Fisher, an estimator which is *unbiased*, *consistent*, *efficient*, *and sufficient* is known as a good estimator. In the next sections, we would discuss about the unbiasedness, consistency, efficiency, and sufficiency properties of the estimators.

Unbiased Estimator: An estimator t of parameter θ is said to be *unbiased estimator* of θ if $E(t)-\theta = 0$. On the other hand, $E(t) - \theta \neq 0$ indicates that t is a biased estimator.

Consistent Estimator: An estimator t is said to be a *consistent estimator* of the parameter θ if the probabilistic value of the estimator t approaches toward θ as the sample size increases, i.e., $P\left\{\begin{matrix} Lt|t-\theta| = 0 \\ n \to \infty \end{matrix}\right\} = 0$ where n is the sample size. Thus, consistency is a large sample property.

Efficient Estimator: Already we have come to know that there might be more than one estimators to estimate a particular population parameter. Now among the estimators, the estimator having minimum variance is known as the *efficient estimator* for the corresponding population parameter. Suppose we have t, t_1, t_2, t_3..... estimators to estimate the population parameter θ, now among these estimator t would be called as efficient estimator if $V(t) < V(t_i)$, $i = 1,2,3,\ldots\ldots$. In comparison to any other estimator t_i, t is said to be efficient if $\frac{V(t)}{V(t_i)} < 1$ and the value of this ratio of two variances is termed as efficiency.

Sufficient Estimator: If $f(X/\theta)$ be the density function of a random variable X, θ is the unknown fixed parameter, and θ belongs to parametric space, then the necessary and sufficient condition for an estimator t to be *sufficient* for θ is that the joint probability density function of $x_1, x_2, x_3 \ldots. x_n$ should be of the form $f(x_1, x_2, x_3\ldots. x_n|\theta) = g(t/\theta)\ h\ (x_1, x_2, x_3 \ldots\ldots x_n)$, where $g(t/\theta)$ is the marginal density of t for fixed θ and $h\ (x_1, x_2, x_3..x_n)$ does not depend on θ.

It has been noticed that not all the good estimators posses all the above good properties. For example, if we have a sample from normal population $N(\mu, \sigma^2)$, then sample mean $(\overline{x} = \frac{1}{n}\sum_{i=1}^{n} x_i)$ as well as the sample median (m_d); both are the consistent estimator for population mean. Similarly, the sample variance $S_x{}^2$ and the sample mean square $(s_x{}^2)$ are both consistent estimators for population variance σ^2, but $s_x{}^2$ is an unbiased estimator for σ^2, and $S_x{}^2$ is a biased estimator for σ^2. Thus, one should prefer sample mean square as an estimator of population variance instead of sample variance. *Any estimator which is characterized by unbiasedness and having minimum variance is known as "minimum variance unbiased estimator" (MVUE)*. There are different methods of estimation of parameters viz. (a) *method of maximum likelihood*, (b) *method of moments*, (c) *method of minimum variance*, (d) *method of least squares*, (e) *method of minimum* χ^2, (f) *method of inverse probability*; which are generally used depending upon the situation. We shall skip the details of these procedures at this level of study.

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Sampling Distribution: By this time, we have come to know that a number of samples can be drawn from a population and there are different sample statistic(s) to estimate and test a particular parameter of the population. A statistic is a function of sample observations; as such, there is every possibility that it will vary from sample to sample and it will behave like a random variable. So the knowledge of probability distribution of such statistic, i.e., sampling distribution, plays a great role in inferring about the population parameter based on such statistic. In this context, the idea of *central limit theorem* is most important in statistical inference. In its simplest form, according to the central limit theorem, when samples of size n are drawn from some population with mean$\mu$and varianceσ^2, the distribution of mean can be represented with a normal probability distribution with mean μ and standard deviation $\sigma/\sqrt{n}$, if n is sufficiently large. Thus, for large samples, the mean is supposed to be distributed normally.

Degrees of Freedom: In statistical inference, *degrees of freedom* is a very important concept. Let us suppose that to promote rearing of hybrid cattle, the government has taken a plan to distribute n number of such cattles among selected farmers; cattles are kept in a place, and the farmers in queue are going there and selecting one cattle each. In the process, each farmer can enjoy the freedom of selecting cattle from the group of cattle excepting the last farmer, because he/she has no other option but to take the last cattle. In the process, out of n farmers $(n-1)$, farmers can exercise their freedom of selecting cattle. Thus, by degrees of freedom, we simply mean the number of free observations. Suppose we are calculating the arithmetic mean from n number of observations. Now arithmetic mean being fixed for a given sample, $n-1$ number of observations can vary, but rest one cannot vary because it has to take only that value which keeps the arithmetic mean for the given observations constant. As such, the degree of freedom in this case is also $n-1$. Instead of taking one variable at a time, if we consider two variables at a time for n observations, then the degrees of freedom would be $n-2$. Thus, degree of freedom is actually *the number of observations less the number of restrictions*. Degree of freedom is actually the number of independent observations associated with the estimation of variance. Depending upon the number of restrictions, the degree of freedom is worked out, e.g., in regression analysis the degrees of freedom associated with mean sum of squares due to regression is $n-k$, where k is the number of variables/parameters involved in the regression analysis.

Statistical Hypothesis: We all know about Avogadro's hypothesis, and likewise in statistics, *a statistical hypothesis is an assertion/statement about the probability distribution of population characteristic(s) which is (are) to be verified on the basis of sample information*. For example, the statement about the students of particular university is that the IQ of the students is 0.9 in 1.0 point scale or the average milk yield of a particular breed of cow is 3500 / for liter per lactation. Now on the basis of sample observations, we are to verify the statements that the IQ of the students 0.9 in 1.0 point scale or not, and average milk yield of a particular breed of cow is 3500 / for liter per lactation or not.

Null Hypothesis and Alternative Hypothesis: Statistical hypothesis can broadly be categorized into (a) null hypothesis and (b) alternative hypothesis. *Initial, unbiased/unmotivated statistical hypothesis whose validity is to be verified for possible acceptance or rejection on the basis of sample observations is called null hypothesis. And the statistical hypothesis which differs from the null hypothesis is called the alternative hypothesis.* In the above two examples, the statements that (a) the students of a particular university has the IQ 0.9 in 1.0 point scale and (b) the average milk yield of the particular breed of cow is 3500 / of liter per lactation are null hypotheses, whereas any hypothesis like (c) IQ of the students is not 0.9 in 1.0 point scale or (d) the average milk yield of the particular breed of cow is not 3500 / of liter per lactation or the average milk yield of the particular breed of cow is less than 3500 / of liter per lactation or the average milk yield of the particular breed of cow is more 3500 / of liter per lactation etc. are the examples of alternative hypothesis. In fact to every null hypothesis, there exists at least one alternative hypothesis.

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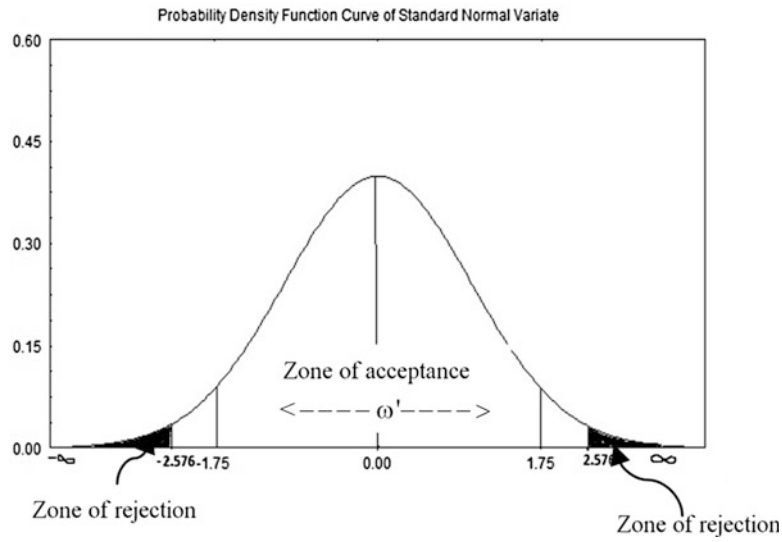
Simple and Composite Hypothesis: Depending upon the amount of information provided in a hypothesis, a statistical hypothesis can be categorized into (a) *simple hypothesis* and (b) *composite hypothesis*. Let us consider the following two hypotheses, (i) the average milk yield of the particular breed of cow is 3500 / of liter per lactation with standard deviation 25 / of liter and given that the milk yield follows a normal distribution and (ii) the average milk yield of the particular breed of cow is 3500 / of liter per lactation, and it follows a normal distribution. *Simple hypothesis* specifies all the parameters of the probability distribution of the random variable; on the other hand, in a *composite hypothesis*, information about one or more parameters of the population remains missing. Thus, the first hypothesis is a simple hypothesis, because it provides complete information about the population. On the other hand, the second hypothesis is composite hypothesis because it does not completely specify the population.

***Parametric* or *Nonparametric Hypothesis*:** It is not necessary that every statistical hypothesis will be related to the parameter of the population. Suppose we want to verify the hypothesis that the freshwater fish production in India has changed randomly since independence. This hypothesis does not involve any parameter, as such is known as nonparametric hypothesis. On the other hand, if we want to verify that the average freshwater fish production in India since independence has remained μ_0 million tons per year with s.d. σ tons following a normal distribution; in this example, parameters of the population distribution are involved; hence, this is a parametric hypothesis. Thus, depending upon the involvement or noninvolvement of the population parameter in a statistical hypothesis, it is either *parametric* or *nonparametric* hypothesis.

Critical Region: *The critical region for a particular hypothesis test is a subset of sample space defined in such a way that it leads to rejection or acceptance of a null hypothesis depending upon whether the value of the statistic falls within the zone or otherwise*. Suppose a random sample x_1, x_2, x_3, $\ldots\ldots x_n$ be represented by a point $\underset{\sim}{x}$ in n-dimensional sample space Ω and ω being a subset of the sample space, defined such that it leads to the rejection of the null hypothesis on the basis of given sample if the corresponding sample point $\underset{\sim}{x}$ falls in the subset ω. This subset ω is known as the *critical region* of the test, and as it rejects the null hypothesis, it is also known as the *zone of rejection*. The complementary region to the critical region of the sample space, i.e., ω' or $\overline{\omega}$, is known as the *zone of acceptance*. Two boundary values of the critical region are also included in the region of acceptance:



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The area beyond the $\pm$ 2.576 values (critical values) (shaded area) is known as the zone of rejection, and the rest of the area is known as zone of acceptance. If the calculated value of the test statistic falls beyond the critical values of the corresponding critical region of the tests, then null hypothesis is rejected; otherwise, the null hypothesis cannot be rejected.

Errors in Decision: While drawing inference about the population based on sample observation, there are different steps like drawing of appropriate sample, collection of appropriate information about the population as well as recording of sample characteristics, tabulation, processing of raw information from sample, application of appropriate statistical tool, and ultimately drawing inference about the population using inferential methods on sample values. In any or all these steps, there are possibilities of committing error. In fact, the following table presents the situation which could arise during the inferential procedure:

Null hypothesis (Ho)	Decision taken	
	Reject Ho	Not to reject Ho
True	Incorrect decision	Correct decision
False	Correct decision	Incorrect decision

Thus, from the above table, it is clear that the conclusion drawn about the population parameter based on sample observation may not be always true; we may reject true null hypothesis, or we may accept a false null hypothesis. Thus, out of four possibilities, there are two possibilities in which we can commit error.

Rejection of null hypothesis when it is really true is known as the *type I error*, and acceptance of a false null hypothesis is known as *type II error*. The probability of type 1 error is known as the level of significance and denoted by α , and that of type II error is generally denoted by β. We always try to keep α and β as small as possible. But there exists an inverse relationship between the α and β, i.e., a test that minimizes α, in fact maximises β. That is why we fix α, at desired level, and minimize β. The probability of decision of rejecting a false null hypothesis (correct decision) is known as the *power of the test* and is denoted by $1-\beta$. In practice, α is taken to a number very close to zero.

Level of Significance: The probability of committing type I error, i.e., α, is called the level of significance. The level of significance is also known as the *size of the critical region*. If the calculated value of a test statistic lies in the critical region, the null hypothesis is said to be rejected at α level of significance. Generally, the level of significance depends on the objective of the study. Sometimes we may have to opt for 0.01 % or 0.001 % level of significance, particularly in relation to medical studies. A researcher has the freedom to select his or her level of significance depending upon the objective of the study.

6.1.1.1 Point Estimation

As the name suggest, in point estimation, we are in search of a value of the estimator from the sample values which is used to estimate the population parameter. Let $x_1, x_2, x_3 \ldots ...x_n$ be a random sample from a density $f(X/\theta)$, where θ is an unknown parameter, and "t" be a function of $x_1, x_2, x_3 \ldots ...x_n$ so that t is a statistic and hence a random variable; and if t is used to estimate θ, then t is called a *point estimator* of θ. Again if the realized value of t from the sample is used for θ, then t is called a *point estimate* of θ.

6.1.1.2 Interval Estimation

As the name suggests, in contrast to the procedure of point estimation, in interval estimation method, we are in search of an interval, from the sample observations, within which the unknown population parameter is supposed to lie with greatest probability. That is, we are in search of a probability statement, from the sample values, about the parameter θ of the population from which the sample has been drawn. Let $x_1, x_2, x_3 \ldots ...x_n$ be a random sample drawn from a population, we are in search of two functions

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"u_1" and "u_2," so that the probability of θ lying in the interval (u_1, u_2) is given by a value say $1-\alpha$, that means $P(u_1 \le \theta \le u_2) = 1-\alpha$. Thus, the interval (u_1, u_2), for which $P(u_1 \le \theta \le u_2) = 1-\alpha$, if exists, is known as *confidence interval* for the parameter θ; *"u_1" and "u_2" are known as lower and upper confidence limits*, respectively, and $1-\alpha$ *is called the confidence coefficient*.

Steps in Construction of Confidence Interval

(i) The first step in the construction of confidence interval is to decide the most appropriate estimator of the population parameter (say θ).

(ii) In the second step, ascertain the sampling distribution of the estimate $\hat{\theta}$ of θ.

(iii) In the next step, one has to find out the estimate (i.e., the value of the estimator) from the given sample.

(iv) Next we are to work out a function $\Phi(\hat{\theta}, \theta)$, (say) for which sampling distribution is not dependent on θ.

iv) Next we are to fix the confidence coefficient and select $\Phi_{\alpha/2}$ and $\Phi_{\left(1-\frac{\alpha}{2}\right)}$ such that $P(\Phi \ge \Phi_{\alpha/2}) = \alpha/2$ and $P\left(\Phi \le \Phi_{\left(1-\frac{\alpha}{2}\right)}\right) = \alpha/2$ where, $\Phi_{\alpha/2}$ and $\Phi_{\left(1-\frac{\alpha}{2}\right)}$ are the upper and lower $100(\alpha/2)$ % point of the distribution of Φ respectively.

Thus, $P\left(\Phi_{\left(1-\frac{\alpha}{2}\right)} \le \Phi(\theta, \theta) \le \Phi_{\frac{\alpha}{2}}\right) = 1-\alpha$

Example 6.1

Average milk yield per lactation for a sample of 100 cows is found to be 3750 kg with standard deviation 700 kg. Find out the 95 % confidence interval for population average milk yield μ.

Solution Let X denotes the milk yield of cows. Since the sample size is large and under the assumption of random and independent observations, 95 % confidence interval of the population mean μ is given by $\bar{x} \pm \tau_{0.025} \frac{\hat{\sigma}}{\sqrt{n}}$.

Given that $\bar{x} = 3750$ kg and $\hat{\sigma} = 700$ kg, so the 95 % confidence interval is given as $\bar{x} \pm \tau_{0.025} \frac{\hat{\sigma}}{\sqrt{n}}$, where τ is a standard normal variate and as per the standard normal distribution $P(\tau_{0.025}) = 1.96$. Hence, the 95 % confidence interval for this problem is given as

$$\bar{x} - \tau_{0.025} \frac{\hat{\sigma}}{\sqrt{n}} \le \mu \le \bar{x} + \tau_{0.025} \frac{\hat{\sigma}}{\sqrt{n}}$$

$$\Rightarrow 3750 - 1.96 \times 700/\sqrt{100} \le \mu \le 3750 + 1.96 \times 700/\sqrt{100}$$

$$\Rightarrow 3750 - 137.2 \le \mu \le 3750 + 137.2$$

$$\Rightarrow 3612.8 \le \mu \le 3887.2$$

Readers may note that as per central limit theorem, we have taken the sample of size 100 as large sample, and hence its mean is supposed to behave like a normal probability distribution.

So the average milk yield will vary in between 3612.8 kg and 887.2 kg at 5 % level of significance.

Example 6.2

The following figures are pertaining to the daily milk yield (kg) provided by ten randomly selected cows of a particular breed. Find out the 95 % confidence interval of average daily milk yield of the particular breed of cows assuming that the milk per day follows normal distribution with unknown mean and variance. Milk yield (kg/day) is 5,6,8,10,5,9,8,7,8,9.

Solution Let X denotes the milk yield (kg) per day per cow. Given that the population is normally distributed with unknown mean μ and σ as standard deviation, our problem is to find confidence limits for the population mean μ of X. Under the assumption, the 95 % confidence limits of μ should be as follows:

$$\bar{x} - t_{0.025, n-1} \frac{s}{\sqrt{n}} \le \mu \le \bar{x} + t_{0.025, n-1} \frac{s}{\sqrt{n}},$$

where $\bar{x}$ and s are, respectively, the sample mean and square root of the sample mean square. To get the values of these two quantities, let us make the following table:

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x_i	5	6	8	10	5	9	8	7	8	9
$(x_i-\bar{x})^2$	6.25	2.25	0.25	6.25	6.25	2.25	0.25	0.25	0.25	2.25
Mean	7.5									
Mean square	2.944									

Now using the values of mean, mean square, and $t_{0.025,9}$ from table *t*-distribution, we have

$$\bar{x} - t_{0.025,n-1}\frac{s}{\sqrt{n}} \leq \mu \leq \bar{x} + t_{0.025,n-1}\frac{s}{\sqrt{n}},$$

$$\Rightarrow 7.5\text{-}2.262 \times 1.716/\sqrt{10} \leq \mu \leq 7.5 + 2.262\text{x}1.716/\sqrt{10}$$

$$\Rightarrow 6.273 \leq \mu \leq 8.727$$

6.1.2 Testing of Hypothesis

As mentioned already, in testing of hypothesis part, we generally discuss the acceptability or otherwise of the statistical hypothesis related to population based on the sample observation. Generally, a set of rules is specified in taking decision with respect to the acceptance or rejection of the statistical hypothesis under consideration. In the process, a test statistic is framed based on the sampling distribution of the best estimator of the population parameter, i.e., to decide the probability distribution; the statistic should follow under the given circumstances, as there are number of probability distribution specifically suited for different situations. More specifically, a *test statistic* is a function of sample observations whose computed value when compared with the probability distribution it follow leads us to take final decision with regard to acceptance or rejection of null hypothesis.

Types of Test: We have already mentioned that for each and every null hypothesis, there exists one or more alternative hypotheses. *Depending upon the nature of alternative hypothesis, a test is one sided (one tailed) or both sided (two tailed).* Let us suppose we are to test Ho: $\mu = \mu_0$, a specific value of μ in the population. To this null hypothesis, we can have the following three alternative hypotheses H_1: $(i)\ \mu \neq \mu_0, (ii)\ \mu > \mu_0, (iii)\ \mu < \mu_0$

When the test is framed to test the null hypothesis against the alternative hypothesis $\mu \neq \mu_0$, then we are interested to test only $\mu = \mu_0$; the test is *both-sided (or two-tailed) test*, and we are to consult the both-sided tables of the probability distribution; the test statistic follows. If the test is significant, the calculated value of the test statistic based on sample observation will be greater than the corresponding table value; Ho is rejected and infer that $\mu \neq \mu_0$; it may be more than or less than μ_0. But if we consider the alternative hypothesis either (ii) or (iii), then we are to consult the critical value corresponding to upper α probability or lower α probability value, respectively. On rejection of the Ho, i.e., if the calculated value of the test statistic be greater than the critical value corresponding to upper α probability or less than the critical value corresponding to lower α probability value, respectively, we infer that $\mu > \mu_0$ or $\mu < \mu_0$ accordingly. In both the cases, the test is *one-sided or one-tailed* test.

Steps in Testing of Statistical Hypothesis
Likewise to that of steps in interval estimation, in this section, we shall discuss about the steps to be followed during the testing of hypothesis. As testing of hypothesis is an important part of statistical inference, sincere approach is required in each and every step so that inference about the population could be drawn with accuracy as much as possible. Testing of hypothesis is mainly accomplished through the following steps: (1) defining the objective of the study; (2) knowing/gathering information about the population; (3) framing the appropriate statistical hypothesis to be tested; (4) selection of appropriate test statistic and its sampling distribution; (5) fixing the level of significance; (6) deciding upon the critical value of the test statistic depending upon its sampling distribution, degrees of freedom, and type of test (both sided or one sided); (7) calculation of test statistic from sample information; (8) comparing the calculated value of the test statistic with that of the critical value(s) decided previously step (6); (9) decision with respect to rejection or acceptance of the null

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hypothesis; and ultimately (10) drawing the inference about the population in the line of the objectives.

One should not have any confusion in fixing the objective of the study, i.e., whether to test the equality of two population means from two different samples drawn from same parent population or from two different populations or to test whether population mean can be taken as μ_o (a specified value) or not and so on. Information or knowledge about the population and its distribution from which the parameters understudy have been taken help the process. Depending upon the objective of the study and available knowledge about the population from which the parameter understudy, we should frame the appropriate null hypothesis and corresponding alternative hypothesis(es). This step is very important because selection of null hypothesis and corresponding alternative hypothesis will lead us to the type of test (i.e., one sided or two sided) to be performed. One should be very careful to select such a statistic whose sampling distribution will best reflect the distribution of population from which the samples have been drawn and parameter to be tested. It has been mentioned earlier that selection of appropriate level of significance depends on so many factors like objective of the study, type of parameter, type of study object and precision required, etc. Though in modern computer, oriented statistical softwares provide exact probability at which the test is significant, it is important that the experimenter should have a prefixed level of significance guided by the objective of the study, type of parameter, and type of study object and precision required, and he or she should stick onto this level of significance. The type of test (one sided or both sided), test statistic and its distribution, etc. decide the critical value(s) for a particular test under the given setup. A test is significant (i.e., rejection of null hypothesis) or nonsignificant (acceptance of null hypothesis) depending upon the values of the calculated value of the test statistic and the table value of the statistic at prefixed level of significance. The fault in selection of the critical values may lead to wrong conclusion about the population understudy.

6.2 Testing of Hypothesis

It has already been mentioned that the testing of hypotheses can broadly be classified into two categories, (i) *parametric* and (ii) *nonparametric*. In parametric hypothesis testing, we are concerned about the population parameters, its value, and so on. But in nonparametric testing of hypotheses, we are in the mood of judging the nature of the population like how the observation changes in a population randomly or following a definite pattern etc. Nonparametric tests are very useful for qualitative characters of the population.

Parametric tests are mostly based on certain assumptions about the parent population and its parameters, e.g., the assumptions of normality, independence, and homoscedasticity (mean constant variance). In statistics, a method is said to be "robust" if the inferences made by using the method is valid even if one or more of these assumptions are violated. In practical situations, sometimes it is hard to have typical normal population. We come across with population in which one or more characteristics of normal distribution are violated, and as a remedial measure, we take help of the transformation technique to make the variables normally distributed. As a result, in almost all the exact tests, the parent population is assumed to be normal, and we estimate and/or test the parameters under different situations. Another way of assuming normality behavior of the variable is by taking large samples and using the central limit theorem. On the other hand, in nonparametric tests, instead of the normality assumption or taking a large sample, continuity of the distribution function is assumed.

Nonparametric methods should not be confused with "distribution-free" methods. A statistical method is nonparametric if the parent distribution is dependent on some general assumption like continuity. On the other hand, a distribution-free method depends neither on the form nor on the parameters of the parent distribution, as is the case of parametric method, which depends on number of parameters. Thus, a nonparametric test is a statistical test where the information on parameters of the parent population from which sample (s) have been drawn random need be known.

In the following section, let us discuss merits and demerits of the nonparametric methods.

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Merits of the Nonparametric Methods

(i) Nonparametric methods are useful for those data which are classificatory in nature, i.e., measured in nominal scales. That's why nonparametric tests found their wide range of use in socioeconomic studies along with other studies.
(ii) Nonparametric tests are also useful for qualitative characters which can be ranked only as well as for the data which can be ranked from numerical figures.
(iii) Irrespective of the nature of the population distribution, nonparametric statistical tests are exact.
(iv) Nonparametric tests are useful even under unknown population distribution, for very small sample size, and are comparatively easy.
(v) Sample made up of observations from different populations can also be put under nonparametric tests

Demerits of the Nonparametric Methods

(i) Probability of committing type II error is more in nonparametric method than in parametric method. As a result, when assumptions are valid, parametric test is superior over the comparable nonparametric method, because we know that the power of a test is given by one probability of type II error.
(ii) For estimation of population parameters, nonparametric method cannot be used.
(iii) Mostly, the nonparametric methods do not take into consideration the actual scale of measurement and substitute either ranks or grade.
(iv) Suitable nonparametric method is lacking for testing interaction effects in analysis of variance.

6.2.1 Parametric Tests

Parametric tests can be categorized into (i) tests based normal population, (ii) tests based on large samples and utilizing the properties of central limit theorem, and (iii) other tests. In the first place, we shall discuss the parametric statistical tests.

6.2.1.1 Statistical Test of Population Parameters Based on Normal Population

For a variable distributed normally, the $P\{\tau \le -\tau_{\alpha/2}\} = P\{\tau \ge \tau_{\alpha/2}\} = \alpha/2$ and $P\{\tau \le -\tau_{\alpha/2}\} + P\{\tau \ge \tau_{\alpha/2}\} = \alpha$ the zone of rejection and the rest zone under standard normal probability curve is $1-\alpha$ the zone of acceptance. Here, τ is the standard normal variate and defined as $\tau = \frac{X-\mu}{\sigma}$, where X, μ, σ are the random variable, its mean, and standard deviation, respectively. Depending upon the type of test (i.e., one sided or both sided) and the level of significance, the upper and lower value of the critical zone (i.e., the zone of acceptance and the zone of rejection) under standard normal probability curve is determined. The table below presents the critical values' 5 % and 1 % level of significance:

Type of test	Level of significance $\alpha = 0.05$	Level of significance $\alpha = 0.01$
Both-sided test (two-tailed test)	1.96	2.576
One-sided (left tailed)	−1.645	−2.33
One-sided (right tailed)	1.645	2.33

In the following section, we shall discuss some of the mostly used tests based on normal population:

(i) *Test for specified values of population mean*
In this type of testing of hypotheses, we come across two situations, (a) population variance is known or (b) population variance is unknown. The test procedures are different for two different situations; in the first situation, the test statistic follows like a standard normal variate, whereas in the second situation, i.e., under unknown population variance situation, the test statistic follows t-distribution. Let us discuss both the tests along with examples (Tables 6.1 and 6.2).

(a) *Test for specified values of population mean with known population variance*

Let $x_1, x_2, x_3, \ldots\ldots\ldots x_n$ be a random sample drawn from a normal population $N(\mu, \sigma^2)$. Variance σ^2 is known. Now we have to test H_0:

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Table 6.1 Table of ordinate and area of the standard normal deviate

τ	$\phi(\tau)$	$\Phi(\tau)$	τ	$\phi(\tau)$	$\Phi(\tau)$	τ	$\phi(\tau)$	$\Phi(\tau)$
0.00	0.3989423	0.5000000	0.50	0.3520653	0.6914625	1.00	0.2419707	0.8413447
0.01	0.3989223	0.5039894	0.51	0.3502919	0.6949743	1.01	0.2395511	0.8437524
0.02	0.3988625	0.5079783	0.52	0.3484925	0.6984682	1.02	0.2371320	0.8461358
0.03	0.3987628	0.5119665	0.53	0.3466677	0.7019440	1.03	0.2347138	0.8484950
0.04	0.3986233	0.5159534	0.54	0.3448180	0.7054015	1.04	0.2322970	0.8508300
0.05	0.3984439	0.5199388	0.55	0.3429439	0.7088403	1.05	0.2298821	0.8531409
0.06	0.3982248	0.5239222	0.56	0.3410458	0.7122603	1.06	0.2274696	0.8554277
0.07	0.3979661	0.5279032	0.57	0.3391243	0.7156612	1.07	0.2250599	0.8576903
0.08	0.3976677	0.5318814	0.58	0.3371799	0.7190427	1.08	0.2226535	0.8599289
0.09	0.3973298	0.5358564	0.59	0.3352132	0.7224047	1.09	0.2202508	0.8621434
0.10	0.3969525	0.5398278	0.60	0.3332246	0.7257469	1.10	0.2178522	0.8643339
0.11	0.3965360	0.5437953	0.61	0.3312147	0.7290691	1.11	0.2154582	0.8665005
0.12	0.3960802	0.5477584	0.62	0.3291840	0.7323711	1.12	0.2130691	0.8686431
0.13	0.3955854	0.5517168	0.63	0.3271330	0.7356527	1.13	0.2106856	0.8707619
0.14	0.3950517	0.5556700	0.64	0.3250623	0.7389137	1.14	0.2083078	0.8728568
0.15	0.3944793	0.5596177	0.65	0.3229724	0.7421539	1.15	0.2059363	0.8749281
0.16	0.3938684	0.5635595	0.66	0.3208638	0.7453731	1.16	0.2035714	0.8769756
0.17	0.3932190	0.5674949	0.67	0.3187371	0.7485711	1.17	0.2012135	0.8789995
0.18	0.3925315	0.5714237	0.68	0.3165929	0.7517478	1.18	0.1988631	0.8809999
0.19	0.3918060	0.5753454	0.69	0.3144317	0.7549029	1.19	0.1965205	0.8829768
0.20	0.3910427	0.5792597	0.70	0.3122539	0.7580363	1.20	0.1941861	0.8849303
0.21	0.3902419	0.5831662	0.71	0.3100603	0.7611479	1.21	0.1918602	0.8868606
0.22	0.3894038	0.5870644	0.72	0.3078513	0.7642375	1.22	0.1895432	0.8887676
0.23	0.3885286	0.5909541	0.73	0.3056274	0.7673049	1.23	0.1872354	0.8906514
0.24	0.3876166	0.5948349	0.74	0.3033893	0.7703500	1.24	0.1849373	0.8925123
0.25	0.3866681	0.5987063	0.75	0.3011374	0.7733726	1.25	0.1826491	0.8943502
0.26	0.3856834	0.6025681	0.76	0.2988724	0.7763727	1.26	0.1803712	0.8961653
0.27	0.3846627	0.6064199	0.77	0.2965948	0.7793501	1.27	0.1781038	0.8979577
0.28	0.3836063	0.6102612	0.78	0.2943050	0.7823046	1.28	0.1758474	0.8997274
0.29	0.3825146	0.6140919	0.79	0.2920038	0.7852361	1.29	0.1736022	0.9014747
0.30	0.3813878	0.6179114	0.80	0.2896916	0.7881446	1.30	0.1713686	0.9031995
0.31	0.3802264	0.6217195	0.81	0.2873689	0.7910299	1.31	0.1691468	0.9049021
0.32	0.3790305	0.6255158	0.82	0.2850364	0.7938919	1.32	0.1669370	0.9065825
0.33	0.3778007	0.6293000	0.83	0.2826945	0.7967306	1.33	0.1647397	0.9082409
0.34	0.3765372	0.6330717	0.84	0.2803438	0.7995458	1.34	0.1625551	0.9098773
0.35	0.3752403	0.6368307	0.85	0.2779849	0.8023375	1.35	0.1603833	0.9114920
0.36	0.3739106	0.6405764	0.86	0.2756182	0.8051055	1.36	0.1582248	0.9130850
0.37	0.3725483	0.6443088	0.87	0.2732444	0.8078498	1.37	0.1560797	0.9146565
0.38	0.3711539	0.6480273	0.88	0.2708640	0.8105703	1.38	0.1539483	0.9162067
0.39	0.3697277	0.6517317	0.89	0.2684774	0.8132671	1.39	0.1518308	0.9177356
0.40	0.3682701	0.6554217	0.90	0.2660852	0.8159399	1.40	0.1497275	0.9192433
0.41	0.3667817	0.6590970	0.91	0.2636880	0.8185887	1.41	0.1476385	0.9207302
0.42	0.3652627	0.6627573	0.92	0.2612863	0.8212136	1.42	0.1455641	0.9221962
0.43	0.3637136	0.6664022	0.93	0.2588805	0.8238145	1.43	0.1435046	0.9236415
0.44	0.3621349	0.6700314	0.94	0.2564713	0.8263912	1.44	0.1414600	0.9250663
0.45	0.3605270	0.6736448	0.95	0.2540591	0.8289439	1.45	0.1394306	0.9264707
0.46	0.3588903	0.6772419	0.96	0.2516443	0.8314724	1.46	0.1374165	0.9278550
0.47	0.3572253	0.6808225	0.97	0.2492277	0.8339768	1.47	0.1354181	0.9292191
0.48	0.3555325	0.6843863	0.98	0.2468095	0.8364569	1.48	0.1334353	0.9305634
0.49	0.3538124	0.6879331	0.99	0.2443904	0.8389129	1.49	0.1314684	0.9318879

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Table 6.1 (continued)

τ	$\phi(\tau)$	$\Phi(\tau)$	τ	$\phi(\tau)$	$\Phi(\tau)$	τ	$\phi(\tau)$	$\Phi(\tau)$
1.50	0.1295176	0.9331928	2.00	0.0539910	0.9772499	2.50	0.0175283	0.9937903
1.51	0.1275830	0.9344783	2.01	0.0529192	0.9777844	2.51	0.0170947	0.9939634
1.52	0.1256646	0.9357445	2.02	0.0518636	0.9783083	2.52	0.0166701	0.9941323
1.53	0.1237628	0.9369916	2.03	0.0508239	0.9788217	2.53	0.0162545	0.9942969
1.54	0.1218775	0.9382198	2.04	0.0498001	0.9793248	2.54	0.0158476	0.9944574
1.55	0.1200090	0.9394292	2.05	0.0487920	0.9798178	2.55	0.0154493	0.9946139
1.56	0.1181573	0.9406201	2.06	0.0477996	0.9803007	2.56	0.0150596	0.9947664
1.57	0.1163225	0.9417924	2.07	0.0468226	0.9807738	2.57	0.0146782	0.9949151
1.58	0.1145048	0.9429466	2.08	0.0458611	0.9812372	2.58	0.0143051	0.9950600
1.59	0.1127042	0.9440826	2.09	0.0449148	0.9816911	2.59	0.0139401	0.9952012
1.60	0.1109208	0.9452007	2.10	0.0439836	0.9821356	2.60	0.0135830	0.9953388
1.61	0.1091548	0.9463011	2.11	0.0430674	0.9825708	2.61	0.0132337	0.9954729
1.62	0.1074061	0.9473839	2.12	0.0421661	0.9829970	2.62	0.0128921	0.9956035
1.63	0.1056748	0.9484493	2.13	0.0412795	0.9834142	2.63	0.0125581	0.9957308
1.64	0.1039611	0.9494974	2.14	0.0404076	0.9838226	2.64	0.0122315	0.9958547
1.65	0.1022649	0.9505285	2.15	0.0395500	0.9842224	2.65	0.0119122	0.9959754
1.66	0.1005864	0.9515428	2.16	0.0387069	0.9846137	2.66	0.0116001	0.9960930
1.67	0.0989255	0.9525403	2.17	0.0378779	0.9849966	2.67	0.0112951	0.9962074
1.68	0.0972823	0.9535213	2.18	0.0370629	0.9853713	2.68	0.0109969	0.9963189
1.69	0.0956568	0.9544860	2.19	0.0362619	0.9857379	2.69	0.0107056	0.9964274
1.70	0.0940491	0.9554345	2.20	0.0354746	0.9860966	2.70	0.0104209	0.9965330
1.71	0.0924591	0.9563671	2.21	0.0347009	0.9864474	2.71	0.0101428	0.9966358
1.72	0.0908870	0.9572838	2.22	0.0339408	0.9867906	2.72	0.0098712	0.9967359
1.73	0.0893326	0.9581849	2.23	0.0331939	0.9871263	2.73	0.0096058	0.9968333
1.74	0.0877961	0.9590705	2.24	0.0324603	0.9874545	2.74	0.0093466	0.9969280
1.75	0.0862773	0.9599408	2.25	0.0317397	0.9877755	2.75	0.0090936	0.9970202
1.76	0.0847764	0.9607961	2.26	0.0310319	0.9880894	2.76	0.0088465	0.9971099
1.77	0.0832932	0.9616364	2.27	0.0303370	0.9883962	2.77	0.0086052	0.9971972
1.78	0.0818278	0.9624620	2.28	0.0296546	0.9886962	2.78	0.0083697	0.9972821
1.79	0.0803801	0.9632730	2.29	0.0289847	0.9889893	2.79	0.0081398	0.9973646
1.80	0.0789502	0.9640697	2.30	0.0283270	0.9892759	2.80	0.0079155	0.9974449
1.81	0.0775379	0.9648521	2.31	0.0276816	0.9895559	2.81	0.0076965	0.9975229
1.82	0.0761433	0.9656205	2.32	0.0270481	0.9898296	2.82	0.0074829	0.9975988
1.83	0.0747663	0.9663750	2.33	0.0264265	0.9900969	2.83	0.0072744	0.9976726
1.84	0.0734068	0.9671159	2.34	0.0258166	0.9903581	2.84	0.0070711	0.9977443
1.85	0.0720649	0.9678432	2.35	0.0252182	0.9906133	2.85	0.0068728	0.9978140
1.86	0.0707404	0.9685572	2.36	0.0246313	0.9908625	2.86	0.0066793	0.9978818
1.87	0.0694333	0.9692581	2.37	0.0240556	0.9911060	2.87	0.0064907	0.9979476
1.88	0.0681436	0.9699460	2.38	0.0234910	0.9913437	2.88	0.0063067	0.9980116
1.89	0.0668711	0.9706210	2.39	0.0229374	0.9915758	2.89	0.0061274	0.9980738
1.90	0.0656158	0.9712834	2.40	0.0223945	0.9918025	2.90	0.0059525	0.9981342
1.91	0.0643777	0.9719334	2.41	0.0218624	0.9920237	2.91	0.0057821	0.9981929
1.92	0.0631566	0.9725711	2.42	0.0213407	0.9922397	2.92	0.0056160	0.9982498
1.93	0.0619524	0.9731966	2.43	0.0208294	0.9924506	2.93	0.0054541	0.9983052
1.94	0.0607652	0.9738102	2.44	0.0203284	0.9926564	2.94	0.0052963	0.9983589
1.95	0.0595947	0.9744119	2.45	0.0198374	0.9928572	2.95	0.0051426	0.9984111
1.96	0.0584409	0.9750021	2.46	0.0193563	0.9930531	2.96	0.0049929	0.9984618
1.97	0.0573038	0.9755808	2.47	0.0188850	0.9932443	2.97	0.0048470	0.9985110
1.98	0.0561831	0.9761482	2.48	0.0184233	0.9934309	2.98	0.0047050	0.9985588
1.99	0.0550789	0.9767045	2.49	0.0179711	0.9936128	2.99	0.0045666	0.9986051

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Table 6.1 (continued)

τ	$\phi(\tau)$	$\Phi(\tau)$	τ	$\phi(\tau)$	$\Phi(\tau)$	τ	$\phi(\tau)$	$\Phi(\tau)$
3.00	0.0044318	0.9986501	3.34	0.0015084	0.9995811	3.68	0.0004573	0.9998834
3.01	0.0043007	0.9986938	3.35	0.0014587	0.9995959	3.69	0.0004408	0.9998879
3.02	0.0041729	0.9987361	3.36	0.0014106	0.9996103	3.70	0.0004248	0.9998922
3.03	0.0040486	0.9987772	3.37	0.0013639	0.9996242	3.71	0.0004093	0.9998964
3.04	0.0039276	0.9988171	3.38	0.0013187	0.9996376	3.72	0.0003944	0.9999004
3.05	0.0038098	0.9988558	3.39	0.0012748	0.9996505	3.73	0.0003800	0.9999043
3.06	0.0036951	0.9988933	3.40	0.0012322	0.9996631	3.74	0.0003661	0.9999080
3.07	0.0035836	0.9989297	3.41	0.0011910	0.9996752	3.75	0.0003526	0.9999116
3.08	0.0034751	0.9989650	3.42	0.0011510	0.9996869	3.76	0.0003396	0.9999150
3.09	0.0033695	0.9989992	3.43	0.0011122	0.9996982	3.77	0.0003271	0.9999184
3.10	0.0032668	0.9990324	3.44	0.0010747	0.9997091	3.78	0.0003149	0.9999216
3.11	0.0031669	0.9990646	3.45	0.0010383	0.9997197	3.79	0.0003032	0.9999247
3.12	0.0030698	0.9990957	3.46	0.0010030	0.9997299	3.80	0.0002919	0.9999277
3.13	0.0029754	0.9991260	3.47	0.0009689	0.9997398	3.81	0.0002810	0.9999305
3.14	0.0028835	0.9991553	3.48	0.0009358	0.9997493	3.82	0.0002705	0.9999333
3.15	0.0027943	0.9991836	3.49	0.0009037	0.9997585	3.83	0.0002604	0.9999359
3.16	0.0027075	0.9992112	3.50	0.0008727	0.9997674	3.84	0.0002506	0.9999385
3.17	0.0026231	0.9992378	3.51	0.0008426	0.9997759	3.85	0.0002411	0.9999409
3.18	0.0025412	0.9992636	3.52	0.0008135	0.9997842	3.86	0.0002320	0.9999433
3.19	0.0024615	0.9992886	3.53	0.0007853	0.9997922	3.87	0.0002232	0.9999456
3.20	0.0023841	0.9993129	3.54	0.0007581	0.9997999	3.88	0.0002147	0.9999478
3.21	0.0023089	0.9993363	3.55	0.0007317	0.9998074	3.89	0.0002065	0.9999499
3.22	0.0022358	0.9993590	3.56	0.0007061	0.9998146	3.90	0.0001987	0.9999519
3.23	0.0021649	0.9993810	3.57	0.0006814	0.9998215	3.91	0.0001910	0.9999539
3.24	0.0020960	0.9994024	3.58	0.0006575	0.9998282	3.92	0.0001837	0.9999557
3.25	0.0020290	0.9994230	3.59	0.0006343	0.9998347	3.93	0.0001766	0.9999575
3.26	0.0019641	0.9994429	3.60	0.0006119	0.9998409	3.94	0.0001698	0.9999593
3.27	0.0019010	0.9994623	3.61	0.0005902	0.9998469	3.95	0.0001633	0.9999609
3.28	0.0018397	0.9994810	3.62	0.0005693	0.9998527	3.96	0.0001569	0.9999625
3.29	0.0017803	0.9994991	3.63	0.0005490	0.9998583	3.97	0.0001508	0.9999641
3.30	0.0017226	0.9995166	3.64	0.0005294	0.9998637	3.98	0.0001449	0.9999655
3.31	0.0016666	0.9995335	3.65	0.0005105	0.9998689	3.99	0.0001393	0.9999670
3.32	0.0016122	0.9995499	3.66	0.0004921	0.9998739			
3.33	0.0015595	0.9995658	3.67	0.0004744	0.9998787			

Table 6.2 Value of the standard normal deviate (τ) at α level

α	0.05	0.025	0.01	0.05
τ	1.645	1.960	2.326	2.576

$\mu = \mu_0$. The alternative hypotheses may be H_1: $i)\ \mu \neq \mu_0$, $ii)\ \mu > \mu_0$, $iii)\ \mu < \mu_0$.

The test statistic under the given null hypothesis is $\tau = \frac{\overline{x}-\mu_0}{\sigma/\sqrt{n}}$, where $\overline{x}$ is the sample mean, n is the number of observations in the sample, and this τ follows a standard normal distribution.

Inference:

(a) For H_1: $\mu \neq \mu_0$, i.e., for both-sided test, reject H_0 if calculated value of $|\tau| < \tau_{\alpha/2}$, where $\tau_{\alpha/2}$ is the table value of τ at upper $\alpha/2$ level of significance, i.e., 1.96 and 2.576, respectively, for 5 % and1 % level of significance; otherwise, do not reject the null hypothesis (Table 6.3).

(b) If we have the alternative hypothesis H_1: $\mu > \mu_0$, i.e., for right-sided test, reject H_0 if calculated value of $\tau > \tau_\alpha$, where τ_α is the table value of τ at upper α level of

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Table 6.3 Values of t statistic at different degrees of freedom and level of significance

	Probability of a larger value, sign ignored								
Degree of freedom	0.500	0.400	0.200	0.100	0.05	0.025	0.01	0.005	0.001
1	1.000	1.376	3.078	6.314	12.706	25.452	63.657	127.321	636.619
2	0.816	1.061	1.886	2.920	4.303	6.205	9.925	14.089	31.599
3	0.765	0.978	1.638	2.353	3.182	4.177	5.841	7.453	12.924
4	0.741	0.941	1.533	2.132	2.776	3.495	4.604	5.598	8.610
5	0.727	0.920	1.476	2.015	2.571	3.163	4.032	4.773	6.869
6	0.718	0.906	1.440	1.943	2.447	2.969	3.707	4.317	5.959
7	0.711	0.896	1.415	1.895	2.365	2.841	3.499	4.029	5.408
8	0.706	0.889	1.397	1.860	2.306	2.752	3.355	3.833	5.041
9	0.703	0.883	1.383	1.833	2.262	2.685	3.250	3.690	4.781
10	0.700	0.879	1.372	1.812	2.228	2.634	3.169	3.581	4.587
11	0.697	0.876	1.363	1.796	2.201	2.593	3.106	3.497	4.437
12	0.695	0.873	1.356	1.782	2.179	2.560	3.055	3.428	4.318
13	0.694	0.870	1.350	1.771	2.160	2.533	3.012	3.372	4.221
14	0.692	0.868	1.345	1.761	2.145	2.510	2.977	3.326	4.140
15	0.691	0.866	1.341	1.753	2.131	2.490	2.947	3.286	4.073
16	0.690	0.865	1.337	1.746	2.120	2.473	2.921	3.252	4.015
17	0.689	0.863	1.333	1.740	2.110	2.458	2.898	3.222	3.965
18	0.688	0.862	1.330	1.734	2.101	2.445	2.878	3.197	3.922
19	0.688	0.861	1.328	1.729	2.093	2.433	2.861	3.174	3.883
20	0.687	0.860	1.325	1.725	2.086	2.423	2.845	3.153	3.850
21	0.686	0.859	1.323	1.721	2.080	2.414	2.831	3.135	3.819
22	0.686	0.858	1.321	1.717	2.074	2.405	2.819	3.119	3.792
23	0.685	0.858	1.319	1.714	2.069	2.398	2.807	3.104	3.768
24	0.685	0.857	1.318	1.711	2.064	2.391	2.797	3.091	3.745
25	0.684	0.856	1.316	1.708	2.060	2.385	2.787	3.078	3.725
26	0.684	0.856	1.315	1.706	2.056	2.379	2.779	3.067	3.707
27	0.684	0.855	1.314	1.703	2.052	2.373	2.771	3.057	3.690
28	0.683	0.855	1.313	1.701	2.048	2.368	2.763	3.047	3.674
29	0.683	0.854	1.311	1.699	2.045	2.364	2.756	3.038	3.659
30	0.683	0.854	1.310	1.697	2.042	2.360	2.750	3.030	3.646
35	0.682	0.852	1.306	1.690	2.030	2.342	2.724	2.996	3.591
40	0.681	0.851	1.303	1.684	2.021	2.329	2.704	2.971	3.551
45	0.680	0.850	1.301	1.679	2.014	2.319	2.690	2.952	3.520
50	0.679	0.849	1.299	1.676	2.009	2.311	2.678	2.937	3.496
55	0.679	0.848	1.297	1.673	2.004	2.304	2.668	2.925	3.476
60	0.679	0.848	1.296	1.671	2.000	2.299	2.660	2.915	3.460
70	0.678	0.847	1.294	1.667	1.994	2.291	2.648	2.899	3.435
80	0.678	0.846	1.292	1.664	1.990	2.284	2.639	2.887	3.416
90	0.677	0.846	1.291	1.662	1.987	2.280	2.632	2.878	3.402
100	0.677	0.845	1.290	1.660	1.984	2.276	2.626	2.871	3.390
120	0.677	0.845	1.289	1.658	1.980	2.270	2.617	2.860	3.373
Infinity	0.675	0.842	1.282	1.645	1.960	2.241	2.576	2.807	3.291

Note: Values for both-sided test

significance, i.e., 1.645 and 2.33, respectively, for 5 % and1 % level of significance; otherwise, do not reject the null hypothesis.

(c) If we have the alternative hypothesis H_1: $\mu < \mu_0$, i.e., for left-sided test, reject H_0 if calculated value of $\tau > \tau_{1-\alpha}$, where $\tau_{1-\alpha}$ is the table value of τ at lower α level of

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significance; otherwise, do not reject the null hypothesis.

Example 6.3
A random sample of ten eggs is drawn from a huge lot of eggs of a particular breed of chick and found that the average weight of egg is 65 g. Test whether the average weight of egg is taken as 70 g at 5 % level of significance. The weight per egg is assumed to follow normal distribution with variance 7.

Solution To test H_0: population mean $\mu = 65$ against $H_1 : \mu \neq 65$.

This is both-sided test. As the sample has been drawn from normal population with known variance, the appropriate test statistic will be $\tau = \frac{\bar{x}-\mu_0}{\sigma/\sqrt{n}}$. For this problem, $\tau = \frac{65-70}{7/\sqrt{10}} = \frac{-5}{2.21} = 2.25$.

From the table of the standard normal variate, we have $\tau_{0.01}$ (=2.576) > $|\tau|_{\text{cal}}$ (=2.25). So the test is nonsignificant at 1 % level of significance. Hence, we accept the null hypothesis, i.e., $H_0 : \mu = \mu_0$. So the average egg weight for the given sample can be taken as 70 g.

(b) *Test for specified value of population mean with unknown population variance.*

Let $x_1, x_2, x_3, \ldots\ldots\ldots x_n$ be a random sample drawn from a normal population $N(\mu, \sigma^2)$. Variance σ^2 is unknown. Now we have to test H_0: $\mu = \mu_0$. The alternative hypotheses may be H_1: $(i)\ \mu \neq \mu_0, (ii)\ \mu > \mu_0, (iii)\ \mu < \mu_0$.

The test statistic under the given null hypothesis is $t = \frac{\bar{x}-\mu_0}{s/\sqrt{n}}$, with $(n-1)$ degrees of freedom; $\bar{x}$ and s^2 are the sample mean and sample mean square, respectively. Sample mean square $s^2 = \frac{1}{n-1}\sum_{i=1}^{n}(x_i - \bar{x})^2$

Inference

(a) If we consider the first alternative hypothesis $H_1: \mu \neq \mu_0$, i.e., for both-sided test, reject H_0 if calculated value of $t > t_{\alpha/2,n-1}$, or cal $t < t_{1-\alpha/2,n-1} = -t_{\alpha/2,n-1}\ i.e.\ \text{cal}\,|t| > t_{\frac{\alpha}{2},n-1}$ where $t_{\alpha/2,n-1}$ is the table value of t at upper $\alpha/2$ level of significance with $(n-1)$ d.f.; otherwise, do not reject the null hypothesis.

(b) If we have the alternative hypothesis H_1: $\mu > \mu_0$, i.e., for right-sided test, reject H_0 if calculated value of $t > t_{\alpha,n-1}$, where $\tau_{\alpha,n-1}$ is the table value of t at upper α level of significance with $(n-1)$ d.f.; otherwise, do not reject the null hypothesis.

(c) If we have the alternative hypothesis H_1: $\mu < \mu_0$, i.e., for left-sided test, reject H_0 if calculated value of $t < t_{1-\alpha,n-1}$, where $t_{1-\alpha,n-1}$ is the table value of t at lower α level of significance with $(n-1)$ d.f.; otherwise, do not reject the null hypothesis.

Example 6.4
Given bellow are the milk yield per cow per day of ten randomly selected Jersey cows. Milk yield is assumed to follow normal distribution with unknown variance. Can we assume that the average milk per cow per day for the Jersey cow be 20/day.

Milk yield per day: 14, 16, 19, 21, 22, 17, 18, 22, 25, 19.

Solution Given that (i) milk yield per day follows a normal distribution with unknown variance and (ii) population hypothetical mean is 20 /day.

To test H_0, population mean $\mu = 20$ against $H_1 : \mu \neq 20$. The test statistic under the null hypothesis is $t = \frac{\bar{x}-\mu_0}{s/\sqrt{n}}$ with $(n-1)$ d.f., and the test is a both-sided test. We have sample mean

$$\bar{x} = \frac{1}{n}\sum_{i=1}^{n} x_i = \frac{1}{n}[14+16+19.\ldots.+19] = 19.30$$

$$\text{and } s^2 = \frac{1}{n-1}\sum_{i=1}^{n}(x_i-\bar{x})^2$$

$$= \frac{1}{9}\left[\sum_{1}^{10} x_i^2 - 10.(19.30)^2\right] = 10.67$$

So, $t = \frac{19.30-20}{10.67/\sqrt{10}} = \frac{-0.70}{3.37} = -0.20.$

The table value of "t" at 9 d.f. at 2.5 % level of significance is 2.262 which is greater than the absolute value of the calculated value of "t," i.e., $|t| < t_{0.025,9}$. So the test is nonsignificant and the null hypothesis cannot be rejected. That means the milk yield per cow per day for the Jersey cow breed may be taken as 20/day.

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(ii) *Test for significance for specified population variance*

In this type of testing of hypotheses also, we come across with two situations, (a) population mean is known or (b) population mean is unknown. The test procedures are different for two different situations; in both situations, the test statistic follows like χ^2 variate but in the first situation with n degrees of freedom, whereas in the second situation, i.e., under unknown population mean situation with $n-1$degrees of freedom, one degree of freedom is less due to estimation of population mean from the sample observation. Let us discuss both the tests along with examples.

(a) *Test for significance for specified population variance with known population mean*: Suppose we have $x_1, x_2, x_3, \ldots\ldots\ldots x_n$ be a random sample drawn from a normal population with mean μ and variance σ^2, i.e., $N(\mu, \sigma^2)$. We want to test $H_0 : \sigma^2 = \sigma_0^2$ where ${\sigma_0}^2$ is any specified value for the population variance and the population mean is known. Under the given condition, we can have the following alternative hypotheses:

$$(i) H_1 : \sigma^2 \neq \sigma_0^2, (ii) H_1 : \sigma^2 > \sigma_0^2,$$
$$(iii) H_1 : \sigma^2 < \sigma_0^2$$

Under the given null hypothesis H_0: $\sigma^2 = {\sigma^2}_0$, the test statistic is $\chi_n^2 = \dfrac{\sum_{i=1}^{n}(x_i - \mu)^2}{\sigma_0^2}$ with n d.f.

(i) When we consider $H_1 : \sigma^2 \neq \sigma_0^2$, i.e., a both-sided test, the null hypothesis is rejected if the calculated value of ${\chi_n}^2$ is greater than the table value of χ^2 at upper $\alpha/2$ level of significance and at "n" degrees of freedom, i.e., Cal $\chi_n^2 >$ tab $\chi_{\alpha/2,n}^2$ or calculated ${\chi_n}^2 <$ tabulated ${\chi_{\alpha/2,n}}^2$; otherwise, do not reject the null hypothesis.

(ii) If we consider $H_1 : \sigma^2 > \sigma_0^2$, i.e., a right-sided test, the null hypothesis is rejected if calculated value of χ^2 is greater than the table value of χ^2 at upper α level of significance and at "n" degrees of freedom, i.e., cal ${\chi_n}^2 >$ tab ${\chi_n}^2$; otherwise, do not reject the null hypothesis.

(iii) If we consider $H_1 : \sigma^2 < \sigma_0^2$, i.e., left-sided test, the null hypothesis is rejected if calculated value of ${\chi_n}^2$ is less than the table value of χ^2 at lower α level of significance and at "n" degrees of freedom, i.e., cal ${\chi_n}^2 <$ tab $\chi_{1-\alpha,n}^2$; otherwise, do not reject the null hypothesis (Table 6.4).

Example 6.5

The following data are from random sample of ten layer of particular breed of chicks for counting the number of eggs laid per months. Do these data support that the variance of number of eggs laid per month be 7. Given that the mean number of eggs laid per layer chicken is 26.

No. of eggs per month: 24, 26, 27, 30, 25, 29, 22, 19, 28, 27.

Solution Given that (i) the population mean is 29, (ii) the same has been drawn from a normal population, and (iii) sample size is 10.

To test H_0: $\sigma^2 = 7$ against $\sigma^2 \neq 7$.

Under the H_0, the test statistic is

$$\chi_{10}^2 = \frac{\sum_{i=1}^{n}(x_i - \mu)^2}{\sigma_0^2}$$
$$= \frac{[4+0+1+16+1+9+16+49+4+1]}{7}$$
$$= \frac{101}{7} = 14.42$$

From the table, we have the value of $\chi_{0.025}^2, 10 = 20.483$ and $\chi_{0.975}^2, 10 = 3.25$. The calculated value of χ^2, i.e., 14.42, lies between these two values. So the null hypothesis cannot be rejected. That means we can conclude that the population variance can be taken as 7.

(b) *Test of significance for hypothetical population variance when population mean (μ) is unknown*

Suppose we have $x_1, x_2, x_3, \ldots\ldots\ldots x_n$ be a random sample drawn from a normal population with mean μ and variance σ^2, i.e., $N(\mu, \sigma^2)$. We want to test $H_0 : \sigma^2 = \sigma_0^2$ where ${\sigma_0}^2$ is any specified value for the population variance and the population mean

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Table 6.4 Cumulative distribution of χ^2

Degree of freedom	Probability of greater value												
	0.995	0.990	0.975	0.950	0.900	0.750	0.500	0.250	0.100	0.05	0.025	0.010	0.005
1	0.00	0.00	0.00	0.00	0.02	0.10	0.45	1.32	2.71	3.84	5.02	6.63	7.88
2	0.01	0.02	0.05	0.10	0.21	0.58	1.39	2.77	4.61	5.99	7.38	9.21	10.60
3	0.07	0.11	0.22	0.35	0.58	1.21	2.37	4.11	6.25	7.81	9.35	11.34	12.84
4	0.21	0.30	0.48	0.71	1.06	1.92	3.36	5.39	7.78	9.49	11.14	13.28	14.86
5	0.41	0.55	0.83	1.15	1.61	2.67	4.35	6.63	9.24	11.07	12.83	15.09	16.75
6	0.68	0.87	1.24	1.64	2.20	3.45	5.35	7.84	10.64	12.59	14.45	16.81	18.55
7	0.99	1.24	1.69	2.17	2.83	4.25	6.35	9.04	12.02	14.07	16.01	18.48	20.28
8	1.34	1.65	2.18	2.73	3.49	5.07	7.34	10.22	13.36	15.51	17.53	20.09	21.95
9	1.73	2.09	2.70	3.33	4.17	5.90	8.34	11.39	14.68	16.92	19.02	21.67	23.59
10	2.16	2.56	3.25	3.94	4.87	6.74	9.34	12.55	15.99	18.31	20.48	23.21	25.19
11	2.60	3.05	3.82	4.57	5.58	7.58	10.34	13.70	17.28	19.68	21.92	24.72	26.76
12	3.07	3.57	4.40	5.23	6.30	8.44	11.34	14.85	18.55	21.03	23.34	26.22	28.30
13	3.57	4.11	5.01	5.89	7.04	9.30	12.34	15.98	19.81	22.36	24.74	27.69	29.82
14	4.07	4.66	5.63	6.57	7.79	10.17	13.34	17.12	21.06	23.68	26.12	29.14	31.32
15	4.60	5.23	6.26	7.26	8.55	11.04	14.34	18.25	22.31	25.00	27.49	30.58	32.80
16	5.14	5.81	6.91	7.96	9.31	11.91	15.34	19.37	23.54	26.30	28.85	32.00	34.27
17	5.70	6.41	7.56	8.67	10.09	12.79	16.34	20.49	24.77	27.59	30.19	33.41	35.72
18	6.26	7.01	8.23	9.39	10.86	13.68	17.34	21.60	25.99	28.87	31.53	34.81	37.16

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19	6.84	7.63	8.91	10.12	11.65	14.56	18.34	22.72	27.20	30.14	32.85	36.19	38.58
20	7.43	8.26	9.59	10.85	12.44	15.45	19.34	23.83	28.41	31.41	34.17	37.57	40.00
21	8.03	8.90	10.28	11.59	13.24	16.34	20.34	24.93	29.62	32.67	35.48	38.93	41.40
22	8.64	9.54	10.98	12.34	14.04	17.24	21.34	26.04	30.81	33.92	36.78	40.29	42.80
23	9.26	10.20	11.69	13.09	14.85	18.14	22.34	27.14	32.01	35.17	38.08	41.64	44.18
24	9.89	10.86	12.40	13.85	15.66	19.04	23.34	28.24	33.20	36.42	39.36	42.98	45.56
25	10.52	11.52	13.12	14.61	16.47	19.94	24.34	29.34	34.38	37.65	40.65	44.31	46.93
26	11.16	12.20	13.84	15.38	17.29	20.84	25.34	30.43	35.56	38.89	41.92	45.64	48.29
27	11.81	12.88	14.57	16.15	18.11	21.75	26.34	31.53	36.74	40.11	43.19	46.96	49.64
28	12.46	13.56	15.31	16.93	18.94	22.66	27.34	32.62	37.92	41.34	44.46	48.28	50.99
29	13.12	14.26	16.05	17.71	19.77	23.57	28.34	33.71	39.09	42.56	45.72	49.59	52.34
30	13.79	14.95	16.79	18.49	20.60	24.48	29.34	34.80	40.26	43.77	46.98	50.89	53.67
40	20.71	22.16	24.43	26.51	29.05	33.66	39.34	45.62	51.81	55.76	59.34	63.69	66.77
50	27.99	29.71	32.36	34.76	37.69	42.94	49.33	56.33	63.17	67.50	71.42	76.15	79.49
60	35.53	37.48	40.48	43.19	46.46	52.29	59.33	66.98	74.40	79.08	83.30	88.38	91.95
70	43.28	45.44	48.76	51.74	55.33	61.70	69.33	77.58	85.53	90.53	95.02	100.43	104.21
80	51.17	53.54	57.15	60.39	64.28	71.14	79.33	88.13	96.58	101.88	106.63	112.33	116.32
90	59.20	61.75	65.65	69.13	73.29	80.62	89.33	98.65	107.57	113.15	118.14	124.12	128.30
100	67.33	70.06	74.22	77.93	82.36	90.13	99.33	109.14	118.50	124.34	129.56	135.81	140.17

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is known. Under the given condition, we can have the following alternative hypotheses:

$$(i)\, H_1 : \sigma^2 \neq \sigma_0^2, (ii)\, H_1 : \sigma^2 > \sigma_0^2, (iii)\, H_1 : \sigma^2 < \sigma_0^2$$

Under the null hypothesis H_0: $\sigma^2 = {\sigma^2}_0$ with unknown population mean, the test statistic is $\chi^2_{(n-1)} = \frac{\sum_{i=1}^{n}(x_i - \bar{x})^2}{\sigma_0^2}$ with $(n-1)$ degrees of freedom where $\bar{x}$ is the sample mean $= \frac{1}{n}\sum_{i=1}^{n} x_i$

(i) When we consider $H_1 : \sigma^2 \neq \sigma_0^2$, i.e., a both-sided test, the null hypothesis is rejected if the calculated value of χ^2_{n-1} is greater than the table value of χ^2 at upper $\alpha/2$ level of significance and at "$n-1$" degrees of freedom, i.e., cal χ^2_{n-1} > tab $\chi^2_{\alpha/2,n-1}$ or calculated χ^2_{n-1} < tabulated $\chi^2_{\alpha/2,n-1}$; otherwise, do not reject the null hypothesis.

(ii) If we consider $H_1 : \sigma^2 > \sigma_0^2$, i.e., a right-sided test, the null hypothesis is rejected if calculated value of χ^2 is greater than the table value of χ^2 at upper α level of significance and at "$n-1$" degrees of freedom, i.e., cal χ^2_{n-1} > tab $\chi^2_{1-\alpha,n-1}$; otherwise, do not reject the null hypothesis.

(iii) If we consider $H_1 : \sigma^2 < \sigma_0^2$, i.e., left-sided test, the null hypothesis is rejected if calculated value of χ^2_{n-1} is less than the table value of χ^2 at lower α level of significance and at "$n-1$" degrees of freedom, i.e., cal χ^2_{n-1} < tab $\chi^2_{1-\alpha,n-1}$; otherwise, do not reject the null hypothesis.

Example 6.6

A random sample of 30 broiler chicks at the age of 40 days gives an average weight per chicks as 1.80 kg with variance 0.08 from a normal population. Test at 5 % level of significance whether the variance of the chicks can be taken as 0.10. The population mean is unknown.

Solution Given that:

(i) Sample size "n" = 30
(ii) Sample mean $(\bar{x})$ =1.80
(iii) Sample variance = 0.08
(iv) The sample has been drawn from normal population with unknown mean.

To test $H_0 : \sigma^2 = 0.10$ against $H_1 : \sigma^2 \neq 0.10$, the test is both-sided test, and under the null hypothesis, the test statistic is $\chi^2_{29} = \frac{\sum_{i=1}^{n}(x_i - \bar{x})^2}{\sigma_0^2} = \frac{30 \times 0.08}{0.10} = 24$,

From the table, we have $\chi^2_{0.95,29} = 17.708$ and $\chi^2_{0.05,29} = 42.557$. Since $17.708 < \text{Cal } \chi^2 < 42.557$, H_0 cannot be rejected. That means we can accept that the variance of weight of broiler chicken may be 0.10.

(iii) *Test of equality of two population variances*
Sometimes, it is required to test whether the two populations are the same or not with respect to their variabilities. Suppose we have two independent random samples $x_{11}, x_{12}, x_{13}, \ldots\ldots x_{1m}$ and $x_{21}, x_{22}, x_{23}, \ldots\ldots x_{2n}$ drawn from two normal populations $N(\mu_1, {\sigma_1}^2)$ and $N(\mu_2, {\sigma_2}^2)$, respectively. Now we want to test whether these two populations differ in variability or not, i.e., to test H_0: $\sigma_1^2 = \sigma_2^2$. In testing this hypothesis, we may come across with two different situations, (a) population means μ_1 and μ_2 are known and (b) population means μ_1 and μ_2 are unknown but equal.

(a) *Test of equality of two population variances when population means are known*: Under the given null hypothesis with known means of the population means μ_1 and μ_2 are known against the alternative hypotheses (i) H_1: $\sigma_1^2 \neq \sigma_2^2$, (ii) $H_1 : \sigma_1^2 > \sigma_2^2$, (iii) $H_1 : \sigma_1^2 < \sigma_2^2$; the test statistic is $F_{\alpha;m,n} = \frac{\sum_{i=1}^{m}(x_{1i} - \mu_1)^2/m}{\sum_{i=1}^{n}(x_{2i} - \mu_2)^2/n}$ with m and n d.f.; and α is the level of significance.

(i) If we are going to test the H_0: ${\sigma_1}^2 = \sigma_2^2$ against the alternative hypothesis $H_1 : \sigma_1^2 \neq \sigma_2^2$, we reject H_0 if Cal $F >$ tab $F_{\alpha/2,\,(m,n)}$ or Cal $F < F_{(1-\alpha/2),\,(m,n)}$.

(ii) If we are going to test the H_0: ${\sigma_1}^2 = \sigma_2^2$ against the alternative hypothesis $H_1 : \sigma_1^2 > \sigma_2^2$, we reject H_0 if Cal $F >$ tab $F_{\alpha,\,(m,n)}$.

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(iii) If we are going to test the H_0: ${\sigma_1}^2 = \sigma_2^2$ against the alternative hypothesis $H_1 : \sigma_1^2 < \sigma_2^2$, we reject the H_0 if Cal $F < F_{(1-\alpha),\ (m,n)}$

(b) *Test of equality of two population variances when population means are unknown*: Under the given null hypothesis with unknown means of the two populations, the test statistic will be $F_{m-1,n-1} = \frac{s_1^2}{s_2^2}$ with $(m-1, n-1)$ d.f., where ${s_1}^2$ and ${s_2}^2$ are the sample mean squares of the samples of sizes m and n, respectively.

(i) If we are going to test the H_0: ${\sigma_1}^2 = \sigma_2^2$ against the alternative hypothesis $H_1 : \sigma_1^2 \neq \sigma_2^2$, we reject H_0 if Cal $F >$ tab $F_{\alpha/2,\ (m-1,n-1)}$ or Cal $F < F_{(1-\alpha/2),\ (m-1,n-1\ )}$.

(ii) If we are going to test the H_0: ${\sigma_1}^2 = \sigma_2^2$ against the alternative hypothesis $H_1 : \sigma_1^2 > \sigma_2^2$, we reject H_0 if Cal $F >$ tab $F_{\alpha,\ (m-1,n-1)}$.

(iii) If we are going to test the H_0: ${\sigma_1}^2 = \sigma_2^2$ against the alternative hypothesis $H_1 : \sigma_1^2 < \sigma_2^2$, we reject the H_0 if Cal $F < F_{(1-\alpha),\ (m-1,n-1)}$ (Tables 6.5 and 6.6).

Example 6.7

Two random samples of male Sirohi goat breed are drawn as follows. It is assumed that the parent populations are normal with $N(\mu_1, {\sigma_1}^2)$ and $N(\mu_2, {\sigma_2}^2)$ and the respective mean weights are 45.34 and 47.74 kg. Can we assume from the data that both populations have the same variability, measured in terms of variance at 5 % level of significance?

Solution Null hypothesis $H_0 : \sigma_1^2 = \sigma_2^2$ against the alternative hypothesis $H_1 : \sigma_1^2 \neq \sigma_2^2$. Given that the populations are normal with mean 45.34 and 47.47 kg, respectively; under the given circumstance, the test statistic will be

$$F = \frac{\sum_{i=1}^{n_1} (x_i - \mu_1)^2 \Big/ n_1}{\sum_{i=1}^{n_2} (x_i - \mu_2)^2 \Big/ n_2} \quad \text{with } n_1 \text{ and } n_2$$

d.f. Under the given alternative hypothesis, the test is two-sided test. Given that $n_1 = 7$, $n_2 = 8$, $\mu_1 = 45.34\,\text{kg}$, and $\mu_2 = 47.74\,\text{kg}$; from the given information, we have

$$\sum_{i=1}^{7} (x_i - \mu_1)^2 \Big/ n_1 = 7.01;$$

$$\sum_{i=1}^{8} (x_i - \mu_2)^2 \Big/ n_2 = 4.80$$

The test is both sided; we are to compare the calculated value of F with table value of $F_{0.025;7,8}$

Cal $F = 1.45$; from the table we have, $F_{0.025;7,8} = 4.52$ and $F_{0.975;7,8} = 0.20$.

Since $0.20 <$ Cal $F < 4.52$, so the test is nonsignificant, and the null hypothesis cannot be rejected, that means we can conclude that both populations have the same variance.

Example 6.8

Two random samples of large white Yorkshire swine breed are drawn from two normal populations which were fed with same feed. Body weights at maturity are recorded. Test whether the variability in body weight of both

Sample	Body weight in kg							
Sirohi 1	43.56	48.34	43.43	46.56	48.43	42.45	41.42	
Sirohi 2	47.32	49.43	47.43	51.23	50.77	52.43	47.72	53.34

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Table 6.5 Values of F statistic at $P = 0.05$ for different degrees of freedom; (Values of $F0.05;v_1,v_2$)

v_1/v_2	1	2	3	4	5	6	7	8	9	10	12	15	20	24	30	40	60	120	∞
1	161.45	199.50	215.71	224.58	230.16	233.99	236.77	238.88	240.54	241.88	243.91	245.95	248.01	249.05	250.10	251.14	252.20	253.25	254.30
2	18.51	19.00	19.16	19.25	19.30	19.33	19.35	19.37	19.38	19.40	19.41	19.43	19.45	19.45	19.46	19.47	19.48	19.49	19.50
3	10.13	9.55	9.28	9.12	9.01	8.94	8.89	8.85	8.81	8.79	8.74	8.70	8.66	8.64	8.62	8.59	8.57	8.55	8.53
4	7.71	6.94	6.59	6.39	6.26	6.16	6.09	6.04	6.00	5.96	5.91	5.86	5.80	5.77	5.75	5.72	5.69	5.66	5.63
5	6.61	5.79	5.41	5.19	5.05	4.95	4.88	4.82	4.77	4.74	4.68	4.62	4.56	4.53	4.50	4.46	4.43	4.40	4.36
6	5.99	5.14	4.76	4.53	4.39	4.28	4.21	4.15	4.10	4.06	4.00	3.94	3.87	3.84	3.81	3.77	3.74	3.70	3.67
7	5.59	4.74	4.35	4.12	3.97	3.87	3.79	3.73	3.68	3.64	3.57	3.51	3.44	3.41	3.38	3.34	3.30	3.27	3.23
8	5.32	4.46	4.07	3.84	3.69	3.58	3.50	3.44	3.39	3.35	3.28	3.22	3.15	3.12	3.08	3.04	3.01	2.97	2.93
9	5.12	4.26	3.86	3.63	3.48	3.37	3.29	3.23	3.18	3.14	3.07	3.01	2.94	2.90	2.86	2.83	2.79	2.75	2.71
10	4.96	4.10	3.71	3.48	3.33	3.22	3.14	3.07	3.02	2.98	2.91	2.85	2.77	2.74	2.70	2.66	2.62	2.58	2.54
11	4.84	3.98	3.59	3.36	3.20	3.09	3.01	2.95	2.90	2.85	2.79	2.72	2.65	2.61	2.57	2.53	2.49	2.45	2.40
12	4.75	3.89	3.49	3.26	3.11	3.00	2.91	2.85	2.80	2.75	2.69	2.62	2.54	2.51	2.47	2.43	2.38	2.34	2.30
13	4.67	3.81	3.41	3.18	3.03	2.92	2.83	2.77	2.71	2.67	2.60	2.53	2.46	2.42	2.38	2.34	2.30	2.25	2.21
14	4.60	3.74	3.34	3.11	2.96	2.85	2.76	2.70	2.65	2.60	2.53	2.46	2.39	2.35	2.31	2.27	2.22	2.18	2.13
15	4.54	3.68	3.29	3.06	2.90	2.79	2.71	2.64	2.59	2.54	2.48	2.40	2.33	2.29	2.25	2.20	2.16	2.11	2.07
16	4.49	3.63	3.24	3.01	2.85	2.74	2.66	2.59	2.54	2.49	2.42	2.35	2.28	2.24	2.19	2.15	2.11	2.06	2.01
17	4.45	3.59	3.20	2.96	2.81	2.70	2.61	2.55	2.49	2.45	2.38	2.31	2.23	2.19	2.15	2.10	2.06	2.01	1.96
18	4.41	3.55	3.16	2.93	2.77	2.66	2.58	2.51	2.46	2.41	2.34	2.27	2.19	2.15	2.11	2.06	2.02	1.97	1.92
19	4.38	3.52	3.13	2.90	2.74	2.63	2.54	2.48	2.42	2.38	2.31	2.23	2.16	2.11	2.07	2.03	1.98	1.93	1.88
20	4.35	3.49	3.10	2.87	2.71	2.60	2.51	2.45	2.39	2.35	2.28	2.20	2.12	2.08	2.04	1.99	1.95	1.90	1.84
22	4.30	3.44	3.05	2.82	2.66	2.55	2.46	2.40	2.34	2.30	2.23	2.15	2.07	2.03	1.98	1.94	1.89	1.84	1.78
24	4.26	3.40	3.01	2.78	2.62	2.51	2.42	2.36	2.30	2.25	2.18	2.11	2.03	1.98	1.94	1.89	1.84	1.79	1.73
26	4.23	3.37	2.98	2.74	2.59	2.47	2.39	2.32	2.27	2.22	2.15	2.07	1.99	1.95	1.90	1.85	1.80	1.75	1.69
28	4.20	3.34	2.95	2.71	2.56	2.45	2.36	2.29	2.24	2.19	2.12	2.04	1.96	1.91	1.87	1.82	1.77	1.71	1.65
30	4.17	3.32	2.92	2.69	2.53	2.42	2.33	2.27	2.21	2.16	2.09	2.01	1.93	1.89	1.84	1.79	1.74	1.68	1.62
40	4.08	3.23	2.84	2.61	2.45	2.34	2.25	2.18	2.12	2.08	2.00	1.92	1.84	1.79	1.74	1.69	1.64	1.58	1.51
60	4.00	3.15	2.76	2.53	2.37	2.25	2.17	2.10	2.04	1.99	1.92	1.84	1.75	1.70	1.65	1.59	1.53	1.47	1.39
120	3.92	3.07	2.68	2.45	2.29	2.18	2.09	2.02	1.96	1.91	1.83	1.75	1.66	1.61	1.55	1.50	1.43	1.35	1.25
∞	3.84	3.00	2.60	2.37	2.21	2.10	2.01	1.94	1.88	1.83	1.75	1.67	1.57	1.52	1.46	1.39	1.32	1.22	1.00

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Table 6.6 Values of F statistic at $P = 0.01$ for different degrees of freedom; (Values of $F0.01;v_1,v_2$)

v_1/v_2	1	2	3	4	5	6	7	8	9	10	12	15	20	24	30	40	60	120	∞
1	4052	4999	5403	5625	5764	5859	5928	5981	6022	6056	6106	6157	6209	6235	6261	6287	6313	6339	6366
2	98.50	99.00	99.17	99.25	99.30	99.33	99.36	99.37	99.39	99.40	99.42	99.43	99.45	99.46	99.47	99.47	99.48	99.49	99.50
3	34.12	30.82	29.46	28.71	28.24	27.91	27.67	27.49	27.35	27.23	27.05	26.87	26.69	26.60	26.50	26.41	26.32	26.22	26.13
4	21.20	18.00	16.69	15.98	15.52	15.21	14.98	14.80	14.66	14.55	14.37	14.20	14.02	13.93	13.84	13.75	13.65	13.56	13.46
5	16.26	13.27	12.06	11.39	10.97	10.67	10.46	10.29	10.16	10.05	9.89	9.72	9.55	9.47	9.38	9.29	9.20	9.11	9.02
6	13.75	10.92	9.78	9.15	8.75	8.47	8.26	8.10	7.98	7.87	7.72	7.56	7.40	7.31	7.23	7.14	7.06	6.97	6.88
7	12.25	9.55	8.45	7.85	7.46	7.19	6.99	6.84	6.72	6.62	6.47	6.31	6.16	6.07	5.99	5.91	5.82	5.74	5.65
8	11.26	8.65	7.59	7.01	6.63	6.37	6.18	6.03	5.91	5.81	5.67	5.52	5.36	5.28	5.20	5.12	5.03	4.95	4.86
9	10.56	8.02	6.99	6.42	6.06	5.80	5.61	5.47	5.35	5.26	5.11	4.96	4.81	4.73	4.65	4.57	4.48	4.40	4.31
10	10.04	7.56	6.55	5.99	5.64	5.39	5.20	5.06	4.94	4.85	4.71	4.56	4.41	4.33	4.25	4.17	4.08	4.00	3.91
11	9.65	7.21	6.22	5.67	5.32	5.07	4.89	4.74	4.63	4.54	4.40	4.25	4.10	4.02	3.94	3.86	3.78	3.69	3.60
12	9.33	6.93	5.95	5.41	5.06	4.82	4.64	4.50	4.39	4.30	4.16	4.01	3.86	3.78	3.70	3.62	3.54	3.45	3.36
13	9.07	6.70	5.74	5.21	4.86	4.62	4.44	4.30	4.19	4.10	3.96	3.82	3.66	3.59	3.51	3.43	3.34	3.25	3.17
14	8.86	6.51	5.56	5.04	4.69	4.46	4.28	4.14	4.03	3.94	3.80	3.66	3.51	3.43	3.35	3.27	3.18	3.09	3.00
15	8.68	6.36	5.42	4.89	4.56	4.32	4.14	4.00	3.89	3.80	3.67	3.52	3.37	3.29	3.21	3.13	3.05	2.96	2.87
16	8.53	6.23	5.29	4.77	4.44	4.20	4.03	3.89	3.78	3.69	3.55	3.41	3.26	3.18	3.10	3.02	2.93	2.84	2.75
17	8.40	6.11	5.18	4.67	4.34	4.10	3.93	3.79	3.68	3.59	3.46	3.31	3.16	3.08	3.00	2.92	2.83	2.75	2.65
18	8.29	6.01	5.09	4.58	4.25	4.01	3.84	3.71	3.60	3.51	3.37	3.23	3.08	3.00	2.92	2.84	2.75	2.66	2.57
19	8.18	5.93	5.01	4.50	4.17	3.94	3.77	3.63	3.52	3.43	3.30	3.15	3.00	2.92	2.84	2.76	2.67	2.58	2.49
20	8.10	5.85	4.94	4.43	4.10	3.87	3.70	3.56	3.46	3.37	3.23	3.09	2.94	2.86	2.78	2.69	2.61	2.52	2.42
22	7.95	5.72	4.82	4.31	3.99	3.76	3.59	3.45	3.35	3.26	3.12	2.98	2.83	2.75	2.67	2.58	2.50	2.40	2.31
24	7.82	5.61	4.72	4.22	3.90	3.67	3.50	3.36	3.26	3.17	3.03	2.89	2.74	2.66	2.58	2.49	2.40	2.31	2.21
26	7.72	5.53	4.64	4.14	3.82	3.59	3.42	3.29	3.18	3.09	2.96	2.81	2.66	2.58	2.50	2.42	2.33	2.23	2.13
28	7.64	5.45	4.57	4.07	3.75	3.53	3.36	3.23	3.12	3.03	2.90	2.75	2.60	2.52	2.44	2.35	2.26	2.17	2.06
30	7.56	5.39	4.51	4.02	3.70	3.47	3.30	3.17	3.07	2.98	2.84	2.70	2.55	2.47	2.39	2.30	2.21	2.11	2.01
40	7.31	5.18	4.31	3.83	3.51	3.29	3.12	2.99	2.89	2.80	2.66	2.52	2.37	2.29	2.20	2.11	2.02	1.92	1.80
60	7.08	4.98	4.13	3.65	3.34	3.12	2.95	2.82	2.72	2.63	2.50	2.35	2.20	2.12	2.03	1.94	1.84	1.73	1.60
120	6.85	4.79	3.95	3.48	3.17	2.96	2.79	2.66	2.56	2.47	2.34	2.19	2.03	1.95	1.86	1.76	1.66	1.53	1.38
∞	6.63	4.61	3.78	3.32	3.02	2.80	2.64	2.51	2.41	2.32	2.18	2.04	1.88	1.79	1.70	1.59	1.47	1.32	1.00

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populations can be taken equal or not at 5 % level of significance:

Sample	Body weight in kg									
1.	318.32	454.32	370.54	399.43	391.43	317.32	365.34	354.53	375.32	383.43
2.	312.44	343.77	398.32	377.32	327.34	345.98	347.42	367.43	345.78	389.59

Solution Given that (i) the populations are normal and the means of the populations are unknown, (ii) sample sizes in each sample is 10, i.e., $n_1 = n_2 = 10$.

To test, $H_0 : \sigma_1^2 = \sigma_2^2$ against $H_1 : \sigma_1^2 \neq \sigma_2^2$.

Under the given conditions, the test statistic is $F = \frac{s_1^2}{s_2^2}$ with (n_1-1) and (n_2-1) d.f, where ${s_1}^2$ and ${s_2}^2$ are the sample mean squares.

We have $s_1^2 = \frac{1}{n_1-1}\sum_{i=1}^{10}(x_{1i} - \overline{x}_1)^2$; $s_2^2 = \frac{1}{n_2-1}\sum_{i=1}^{10}(x_{2i} - \overline{x}_2)^2$; $\overline{x}_1 = \frac{1}{n_1}\sum_{i=1}^{10} x_{1i}$; and $\overline{x}_2 = \frac{1}{n_2}\sum_{i=1}^{10} x_{2i}$.

From the given data, we have $\overline{x}_1 = 372.99$ kg., $\overline{x}_2 = 355.53$ kg., $s_1^2 = 1584.59$, $s_2^2 = 738.80$, and $F = \frac{s_1^2}{s_2^2} = 2.14$. As the test is both sided, we are compare the calculated value of F with $F_{\alpha/2,9,9}$ *i. e.* $F_{0.025,9,9}$ and $F_{1-\alpha/2;9,9}$ *i.e.* $F_{0.975;9,9}$. From the table we have, $F_{0.025;9,9} = 4.03$ and $F_{0.975;9,9} = 0.2481$.

Since $0.2481 < \text{Cal}\, F < 4.03$, the test is non-significant, and the null hypothesis cannot be rejected, that means we can conclude that both the populations have the same variance.

(iv) *Test for equality of two population means*

Sometimes, it is required to test whether the two populations are the same or not with respect to their arithmetic means. Suppose we have two independent random samples $x_{11}, x_{12}, x_{13}, \ldots\ldots x_{1m}$ and $x_{21}, x_{22}, x_{23}, \ldots\ldots x_{2n}$ drawn from two normal populations $N(\mu_1, {\sigma_1}^2)$ and $N(\mu_2, {\sigma_2}^2)$, respectively. Now we want to test whether these two populations differ in their central tendencies measured in terms of arithmetic mean or not, i.e., to test H_0: $\mu_1 = \mu_2$. In testing this hypothesis, we may come across two different situations, (a) population variances ${\sigma^2}_1$ and ${\sigma^2}_2$ are known and (b) population variances ${\sigma^2}_1$ and ${\sigma^2}_2$ are unknown but equal ${\sigma^2}_1 = {\sigma^2}_2 = \sigma^2$.

(a) *Test of equality of two population means when population variances are known*: Under the given null hypothesis H_0: $\mu_1 = \mu_2$ with known population variances ${\sigma^2}_1$ and ${\sigma^2}_2$ against the alternative hypothesis $H_1 : \mu_1 \neq \mu_2$, the test statistic would be $\tau = \frac{\overline{x}_1 - \overline{x}_2}{\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}}$, which follows a standard normal distribution, and $\overline{x}_1$ and $\overline{x}_2$ are the arithmetic means of the first and second samples, respectively. As the test is both sided, we are to compare the calculated value of τ with that of the table value under standard normal value at $\alpha/2$ level of significance for taking decision.

(b) *Test of equality of two population means when population variances are unknown but equal (two sample t test or Fisher t test)* Before performing this test, one should ascertain that first $H_0 : \sigma_1^2 = \sigma_2^2$ by F-test statistic discussed in test iii (b). If it is accepted, then we perform t test statistic; otherwise, we are to opt for Cochran's approximation to Fisher-Behrens problem as discussed latter on. For the first time, let us suppose that the test concerning $\sigma_1^2 = \sigma_2^2$ has been accepted.

So to test H_0: $\mu_1 = \mu_2$ against H_1: $\mu_1 \neq \mu_2$ under the given condition that ${\sigma^2}_1 = {\sigma^2}_2 = \sigma^2$

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(unknown), the test statistic is no longer τ rather it would be $t = \frac{\bar{x}-\bar{y}}{s\sqrt{\frac{1}{n_1}+\frac{1}{n_2}}}$ with $(n_1 + n_2-2)$ degrees of freedom, where $s^2 = \frac{(n_1-1)s_1^2+(n_2-1)s_2^2}{n_1+n_2-2}$ and ${s_1}^2$ and ${s_2}^2$ are the sample mean squares for two samples, respectively.

The sample mean square for any variable X is defined as $s^2 = \frac{1}{n-1}\sum_{i=1}^{n}(x_i - \bar{x})^2$. According to the alternative hypothesis, the test would be a both-sided test, and we are to compare the table value of t at $\frac{\alpha}{2}$ level of significance at $(n_1 + n_2-2)$ d.f.

If the calculated absolute value of "t" is greater than the table value of "t" at upper $\frac{\alpha}{2}$ level of significance and at $(n_1 + n_2 - 2)$ d.f., then the test is significant, and the null hypothesis is rejected, that means the two population means are unequal; otherwise, these are equal.

Cochran's Approximation to the Fisher-Behrens Problem The problem of testing the significance of equality of two population means under unknown and unequal population variances (i.e., $\sigma_1^2 \neq \sigma_2^2$) is known as *Fisher-Behrens problem*. In case testing, the significance of equality of two population means under unknown and unequal population variances (i.e., $\sigma_1^2 \neq \sigma_2^2$), i.e., in case of existence of *Fisher-Behrens problem*, we are to opt for Cochran's approximation. Cochran's approximation is applicable for the null hypothesis H_0: $\mu_1 = \mu_2$ against $H_1: \mu_1 > \mu_2$. According this approximation, the test statistic $t = \frac{\bar{x}-\bar{y}}{s\sqrt{\frac{1}{n_1}+\frac{1}{n_2}}}$ as used in previous case does not follow t-distribution, and as such ordinary t-table value will not be sufficient for comparing. According to Cochran's approximation, the calculated value of above t statistic is to be compared with $t^* = \frac{t_1 s_1^2/n_1 + t_2 s_2^2/n_2}{s_1^2/n + s_2^2/n_2}$, where t_1 and t_2 are the table values of t-distribution at (n_1-1) and (n_2-1) degrees of freedom, respectively, with upper α level of significance. Other decisions will be as usual, but one should note that this is not a both-sided test rather one-sided (right) test.

Example 6.9

The following data give the body weight at 7 weeks of two *sample* breeds, Caribro Vishal and Caribro Dhanraja chicken, under same feeding condition. It is also known that the variability measures in terms of variance of two breeds are 0.02 and 0.05, respectively. Test whether these two breeds differ significantly with respect to body weight (kg). Given that the weight of chicks follows normal distribution:

Breed	Body weight at 7 weeks in kg									
Caribro Vishal	2.02	2.15	1.93	2.03	2.11	1.95	2.13	1.89	2.20	2.16
Caribro Dhanarja	2.13	1.89	2.02	1.88	2.10	2.14	1.98	2.03	1.96	

Solution Let the level of significance be 0.05.

So the null hypothesis $H_0 : \mu_V = \mu_D$ (under known population variance) is to be tested against the alternative hypothesis $H_1 : \mu_V \neq \mu_D$, a both-sided test.

Under the given condition, the test statistic is $\tau = \frac{|\overline{V}-\overline{D}|}{\sqrt{\frac{\sigma_V^2}{n_1}+\frac{\sigma_D^2}{n_2}}}$ which follows a standard normal variate.

From the sample observation, we have

$$n_V = 10;\ n_D = 9 \text{ and } \overline{V} = 2.06;\ \overline{D} = 2.02$$

$$\tau = \frac{|2.06 - 2.02|}{\sqrt{\frac{0.02}{10} + \frac{0.05}{9}} = \frac{0.04}{\sqrt{0.002+0.005}} = \frac{0.04}{\sqrt{0.007}} = 0.49}$$

We know that at α =0.05, the value of $\tau_{\alpha/2}$ =1.96, as the calculated $|\tau| < 1.96$, so the test is nonsignificant, and we cannot reject the null hypothesis. We conclude the breeds do not differ significantly with respect to body weight.

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Example 6.10 Given below are the two samples of body weights of two broiler breeds. Is it possible to draw inference that the body weight of breed Cornish Crosses is more than that of Delaware broilers, assuming that the body weight follows normal population:

Broiler breed	Sample size	Mean weight (kg)	Sample mean square
Cornish crosses(X)	13	4.80	1.20
Delaware broilers(Y)	12	3.78	0.83

Solution H_0: Both the breeds of broiler have the same body weight, i.e., $H_0 : \mu_1 = \mu_2$, against the alternative hypothesis, H_1: Cornish Crosses has more body weight than Delaware broiler, i.e., $H_1 : \mu_1 > \mu_2$. Let us select the level of significance, α =0.05. According to H_1, the test is a one-sided test. We assume that $\sigma_X^2 = \sigma_Y^2 = \sigma^2$. The test statistic, under the given null hypothesis and unknown variance but equal, is $t = \frac{\bar{x}-\bar{y}}{s\sqrt{\frac{1}{n_1}+\frac{1}{n_2}}}$, with $(n_1 + n_2 - 2)$ d.f. where $\bar{x}$ and $\bar{y}$ are the sample mean body weight of two breeds Cornish Crosses and Delaware broilers, respectively, and s^2 is the composite sample mean square and given by $s^2 = \frac{(n_1-1)s_x^2+(n_2-1)s_y^2}{n_1+n_2-2}$, ${s_x}^2$, and ${s_y}^2$ by the sample mean squares as usual.

First, we test $H_0 : \sigma_X^2 = \sigma_Y^2$ by $F = \frac{s_x^2}{s_y^2}$ with $(n_1 - 1, n_2 - 1)$ d.f. against $H_0 : \sigma_X^2 \neq \sigma_Y^2$.

Thus, $F = \frac{1.20}{0.83} = 1.44$ with (12, 11) d.f. From the table we have, $F_{0.025,12,11} = 3.32$ and $F_{0.975,11,12} = 0.30$. Since $0.30 < \text{cal}\, F < 3.22$, $H_0 : \sigma_X^2 = \sigma_Y^2$ cannot be rejected. So we can perform t test to test $H_0 : \mu_1 = \mu_2$.We have $s^2 = \frac{(n_1-1)s_x^2+(n_2-1)s_y^2}{n_1+n_2-2} = s^2 = \frac{(13-1)1.20^2+(12-1)0.84^2}{13+12-2} = \frac{17.82+7.63}{23} = 1.08$

$$\therefore t = \frac{\bar{x}-\bar{y}}{s\sqrt{\frac{1}{n_1}+\frac{1}{n_2}}} = \frac{4.80\text{-}3.78}{1.04\sqrt{\frac{1}{13}+\frac{1}{12}}} = \frac{1.02}{1.04\sqrt{0.16}} = 2.45.$$

As per the alternative hypothesis, the test is one sided (right sided), so we are to compare table value of t at upper 5 % level of significance.

From the table, we have $t_{0.05,23} = 1.71$. Since Cal $t > 1.71$, the test is significant, and we reject the null hypothesis, i.e., we accept $\mu_1 > \mu_2$. That means the body weight of Cornish Crosses is more than that of the body weight of Delaware broilers.

Example 6.11 Given bellow are the samples about egg weight of two duck breeds. Is it possible to draw inference that the egg weight of breed Khaki is more than that of Khaki Campbell, assuming that the egg weight follows normal population?

Duck breed	No. of egg	Mean weight (g)	Sample mean square
Khaki (K)	15	67.5	3.94
Khaki Campbell(C)	17	64	7.4

Solution We are to test the null hypothesis H_0: $\mu_K = \mu_C$ (under unknown and unequal population variances) against alternative hypothesis $H_1 : \mu_K > \mu_C$. This is a typical Fisher-Behrens problem.

Let the level of significance α =0.05. Under the given conditions, we apply Cochran's approximation to Fisher-Behrens problem. Thus, the test statistic is given by

$t = \frac{\overline{K}-\overline{C}}{\sqrt{\frac{s_K^2}{n_K}+\frac{s_C^2}{n_C}}}$, which is then compared with the value of $t^* = \frac{t_K s_K^2/n_K + t_C s_C^2/n_C}{s_K^2/n_K + s_C^2/n_C}$, and appropriate decision is taken.

We have $t = \frac{67.5-64}{\sqrt{\frac{3.94}{15}+\frac{7.4}{17}}} = \frac{3.5}{0.83} = 4.18$.

The table value of t at upper 5 % level of significance with $(n_K-1) = 14$ d.f. and $(n_C-1) = 16$ d.f. is 1.76 and 1.74, respectively. Hence,

$$t^* = \frac{1.76 \times 3.94/15 + 1.74 \times 7.40/17}{3.94/15 + 7.40/17}$$

$$= \frac{1.21}{0.69} = 1.74.$$

Now the Cal $t > t^*$; hence, we can reject the null hypothesis, i.e., H_1 is accepted. That means we can conclude that the egg weight of the Khaki duck is greater than that of Khaki Campbell breed of duck.

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(v) *Test for parameters of bivariate normal population*

So far we have discussed about the tests taking one variable at a time, but as we know in population, variables tend to move together; bivariate normal distribution comes into play when we consider two variables at a time. Here, in this section, we shall discuss some of the tests based on bivariate normal distribution.

(a) *To test equality of two population means with unknown population parameters*

The test, we are going to discuss now is known as *paired t* test.

Suppose (x_1,y_1), (x_2,y_2), (x_3,y_3) ..... (x_n,y_n) be n pairs of observations in a random sample drawn from a bivariate normal distribution with parameters μ_X, μ_y, ${\sigma_X}^2$, ${\sigma_y}^2$ and ρ where $\mu_X$and μ_y are the means and ${\sigma_X}^2$, ${\sigma_y}^2$ are the variances and ρ is the population correlation coefficient between X and Y. We want to test the null hypothesis $H_0 : \mu_X = \mu_y$ *i.e.* H_0: $\mu_X - \mu_y = \mu_d = 0$ i.e., the difference between the two population means is equal to zeroThe test statistic under H_0 will be $t = \frac{\overline{d}}{\frac{s_d}{\sqrt{n}}}$ with $(n-1)$ d.f., where $\overline{d} = \frac{1}{n}\sum_{i=1}^{n} d_i = \frac{1}{n}\sum_{i=1}^{n}(x_i - y_i)$ and ${s_d}^2 = \frac{1}{n-1}\sum_{i=1}^{n}(d_i - \overline{d})^2$.

The table value of "t" at $(n-1)$ d.f. for α level of significance will be compared with the calculated value of "t" to test the significance of the test according to the nature of alternative hypothesis.

Example 6.12
An experiment was conducted to know the effect of feeding of cotton cake on milk yield of Borgou cattle breed. A sample of ten cattle was taken. Initial milking capacity and yield after feeding for 15 days were recorded. Test whether feeding cotton cake has an effect on milking capacity or not:

Initial yield (liters)	1.38	1.35	1.36	1.40	1.42	1.37	1.39	1.41	1.34	1.37
Final yield (liters)	2.11	1.87	2.15	2.34	2.95	1.67	1.76	2.45	1.56	2.11

Solution Let x represent the initial yielding capacity, and y is the final yielding capacity. So $x - y = d$. Assuming that X and Y follow a bivariate normal distribution with parameters μ_x, μ_y, σ_x, σ_y and ρ_{xy}, we want to test $H_0 : \mu_x = \mu_y$ against $H_1 : \mu_x < \mu_y$.

The test statistic under H_0 is $t = \frac{\overline{d}}{sd/\sqrt{n}}$ with $(n-1)$ d.f.:

Initial yield (liters)	1.38	1.35	1.36	1.40	1.42	1.37	1.39	1.41	1.34	1.37
Final yield (liters)	2.11	1.87	2.15	2.34	2.95	1.67	1.76	2.45	1.56	2.11
X−Y (d)	−0.73	−0.52	−0.79	−0.94	−1.53	−0.30	−0.37	−1.04	−0.22	−0.74

So $\overline{d} = -0.72$ and $sd = \sqrt{\frac{1}{(10-1)}\left[\sum d_i^2 - 10\overline{d}^2\right]} = \sqrt{\frac{1}{(10-1)}\left[\sum d_i^2 - 10\overline{d}^2\right]}$
$= \sqrt{\frac{1}{9}[6.55 - 10 \times 0.51]} = 0.39$

$$t = \frac{-0.72}{0.39/\sqrt{10}} = \frac{-0.72}{0.12} = -5.83.$$

Conclusion From the table values, we have $t_{0.05,9} = 2.26$ and $t_{0.01,9} = 3.24$. The calculated value of t is less than the table value at both the levels of significance. Hence, the test is significant at 1 % level of significance. So we reject the null hypothesis $H_0 : \mu_x = \mu_y$ and accept the $H_1 : \mu_x < \mu_y$, i.e., there was significant effect of cotton cake on cattle milk yield.

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(b) *To test for significance of population correlation coefficient*

As usual, suppose (x_1,y_1), (x_2,y_2), (x_3,y_3) $\ldots\ldots\ldots(x_n,y_n)$ be n pairs of observations in a random sample drawn from a bivariate normal distribution with parameters μ_X, μ_y, ${\sigma_X}^2$, ${\sigma_y}^2$and ρ where μ_X and μ_y are the means and ${\sigma_X}^2$, σ_y^2 are the variances and ρ is the population correlation coefficient between X and Y.

Here, we want to test, i.e., H_0: $\rho = 0$ against $H_1 : \rho \neq 0$. This test is also used to test the significance of the sample correlation coefficient "r" to the population correlation coefficient. The test statistic under H_0 will be $t = \frac{r\sqrt{n-2}}{\sqrt{1-r^2}}$ at $(n-2)$ d.f. where "r" is the sample correlation coefficient between X and Y.

If the calculated value of $|t|$ is less than the tabulated value of "t" at $(n-2)$ d.f. for upper $\frac{\alpha}{2}$ level of significance, we cannot reject the null hypothesis, i.e., sample correlation coefficient cannot be taken as zero, or the variables are uncorrelated. Otherwise, we reject the null hypothesis, and sample correlation coefficient is significant to the population correlation coefficient, and the variables have significant correlation between them.

Example 6.13
The correlation coefficient between the age and weight of 25 Caribro Tropicana broiler is found to be 0.92. Test for the existence of correlation between these two characters using 1 % level of significance.

Solution Under the given information, we want to test $H_0 : \rho = 0$ against $H_1 : \rho \neq 0$. The test statistic is given by $t = \frac{r\sqrt{(n-2)}}{\sqrt{1-r^2}}$ with $(n-2)$ d.f.

Given that $r = 0.92$, $n = 25$, so

$$t = \frac{0.92\sqrt{(25-2)}}{\sqrt{1-0.92^2}} = \frac{0.92 \times \sqrt{23}}{\sqrt{0.1536}} = 11.257$$

The table value of $t_{0.01,23} = 2.807$. Since calculated t value is more than table t value at 23 d.f., the null hypothesis $H_0 : \rho = 0$ is rejected. So we can conclude that the age and weight of Caribro Tropicana broiler chicken are correlated.

(c) *Test for equality of two population variances from a bivariate normal distribution*

Let (x_1,y_1), (x_2,y_2), (x_3,y_3) $\ldots\ldots\ldots(x_n,y_n)$ be n pairs of observations in a random sample drawn from a bivariate normal distribution with parameters μ_X, μ_y, ${\sigma_X}^2$, ${\sigma_y}^2$and ρ where μ_X and μ_y are the means and ${\sigma_X}^2$, ${\sigma_y}^2$ are the variances and ρ is the population correlation coefficient between X and Y.

The null hypothesis for testing the equality of two variances is $H_0 : \sigma_X^2 = \sigma_y^2$.

Let us derive two new variables U and V such that $U = X + Y$ and $V = X-Y$. So the Cov(U, V) = Cov(X + Y, $X-Y$) = $\sigma_X^2 - \sigma_y^2$. Under the null hypothesis $H_0 : \sigma_X^2 = \sigma_y^2$, Cov($U$,$V$) = 0 and thus U and V are two normal variates with correlation coefficient $\rho_{UV} = 0$ when H_0 is true.

Hence, H_0: $\sigma_X^2 = \sigma_y^2$ is equivalent to test H_0: $\rho_{UV} = 0$.

So the test statistic is given by $t = \frac{r_{uv}\sqrt{(n-2)}}{\sqrt{1-{r_{uv}}^2}}$ with$(n-2)$d.f, where r_{uv} is the sample correlation coefficient between "u" and "v" and is a both-sided test, and the inference will be accordingly.

Example 6.14
To know the effect of light regime on the weight of egg, an experiment is conducted; 15 layers are selected randomly and egg weight is recorded before applying light regime and after 1 month of applying light regime. Work out the significant difference in variability of egg weight before and after light regime:

Particulars	Egg weight (g)														
Before (x)	38.35	36.81	39.39	43.40	36.40	39.63	40.58	37.21	41.98	38.08	37.58	38.10	41.39	39.90	38.02
After (y)	39.23	39.81	41.10	44.70	38.40	40.12	41.12	37.98	42.12	39.56	39.52	39.12	42.90	42.20	39.10

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Solution The null hypothesis to test is $H_0 : \sigma_x = \sigma_y$ against $H_1 : \sigma_x \neq \sigma_y$. This is equivalent to test $\rho_{uv} = 0$, where u and v are $x + y$ and $x-y$, respectively. The test statistic for the same will be

$$t = \frac{r_{uv}}{\sqrt{1-r_{uv}^2}}\sqrt{n-2} \text{ with } (n-2) \text{ d.f.}$$

We have

Before (x)	38.35	36.81	39.39	43.40	36.40	39.63	40.58	37.21	41.98	38.08	37.58	38.10	41.39	39.90	38.02
After (y)	39.23	39.81	41.10	44.70	38.40	40.12	41.12	37.98	42.12	39.56	39.52	39.12	42.90	42.20	39.10
$u = (x + y)$	77.58	76.63	80.49	88.10	74.80	79.75	81.70	75.19	84.10	77.64	77.11	77.22	84.29	81.10	77.12
$v = (x-y)$	−0.88	−3.00	−1.71	−1.30	−2.00	−0.49	−0.54	−0.77	−0.14	−1.48	−1.94	−1.02	−1.51	−1.30	−1.08

$$r_{uv} = \frac{\sum uv - n\,\overline{uv}}{\sqrt{\left(\sum u^2 - n\overline{u}^2\right)\left(\sum v^2 - n\overline{v}^2\right)}} = 0.30$$

Thus, $t = \frac{0.30}{\sqrt{1-0.30^2}}\sqrt{15-2} = 1.13$.

From the table, we get $t_{0.025,13} = 2.16$. Thus, the calculated value of $|t|$ is less than the table value. So we cannot reject the null hypothesis of equality of variances. So there exists no difference in egg weight due to application of light regime.

(d) *Test for specified values of intercept and regression coefficient in a simple linear regression*

Let us suppose we have a regression equation $Y = \alpha + \beta X$. In regression analysis, we may be interested to know whether both the coefficients or either of the coefficients α and β have the specified values α_0 and β_0 in the population or not. Now we can have the following three types of null hypotheses to test:

(*i*) $H_0 : \alpha = \alpha_0$; only α is specified but unspecified value for β

(ii) $H_0 : \beta = \beta_0$; only β is specified but unspecified value for α

(iii) $H_0 : \alpha = \alpha_0,\ \beta = \beta_0$ both α and β are specified

Under the given conditions the standard errors of $\hat{\alpha} = a$ and $\hat{\beta} = b$ are given by

$$s_\alpha = \sqrt{\left(\frac{1}{n} + \frac{\bar{x}^2}{SSxx}\right)\frac{\text{Res}SS}{n-2}} \quad \text{and} \quad s_b = \sqrt{\left(\frac{\frac{\text{Res}SS}{n-2}}{SSxx}\right)}$$

respectively and

$$\begin{aligned}\text{Res}SS &= \sum_{i=1}^{n}(y_i - \bar{y})^2 - b\sum_{i=1}^{n}(x_i - \bar{x})(y_i - \bar{y}) \\ &= SS(y) - b^2 SS(xx)\end{aligned}$$

Let us now discuss the testing procedure of the above mentioned three null hypotheses:

(i) To test H_0: $\alpha = \alpha_0$ against $H_1 : \alpha \neq \alpha_0$

$$t = \frac{a-\alpha_0}{\text{estSE}(\hat{\alpha})} = \frac{a-\alpha_0}{\sqrt{\left(\frac{1}{n}+\frac{\bar{x}^2}{SSxx}\right)\frac{\text{Res}SS}{n-2}}} \text{ with } (n-2)\text{d.f.}$$

If the calculated value of $|t| \geq t_{\alpha/2,(n-2)}$, the null hypothesis is rejected; otherwise, we cannot reject the null hypothesis.

(ii) To test $H_0 : \beta = \beta_0$

$$t = \frac{b-\beta_0}{\text{estSE}(\hat{\beta})} = \frac{b-\beta_0}{\sqrt{\left(\frac{\frac{\text{Res}SS}{n-2}}{SSxx}\right)}} \text{with } (n-2) \text{ d.f.}$$

If the calculated value of $|t| \geq t_{\alpha/2,(n-2)}$, the null hypothesis is rejected, otherwise we can not reject the null hypothesis.

(iii) To test $H_0 : \alpha = \alpha_0, \beta = \beta_0$; this is equivalent to testing the overall significance of the regression equation.

$$F = \frac{\left\{\sum_{i=1}^{n}(y_i - \alpha_0 - \beta_0 x_i)^2 - \text{Res}SS\right\}/2}{\text{Res}SS/(n-2)} \text{ with } (2, n-2) \text{ d.f.}$$

If the calculated value of $F \geq F_{\alpha;2,n-2}$, the null hypothesis is rejected, otherwise we can not reject the null hypothesis.

Example 6.15 The following table gives the information on energy supplied by 100 g of poultry feed and its protein content in gram. Find out the regression equation of energy on protein

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content of the feed. Test for (i) the significance of specified intercept value of 95, (ii) the significance of specified slope coefficient of 25, and (iii) overall significance of the regression equation:

Observation	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
Energy (K cal)	163	191	185	170	170	161	170	173	178	167	182	184	174	168	162	182	191	161	164	185
Protein (g)	12.9	13.3	13.9	13.5	13.8	13.1	13.1	13.2	13.6	12.97	13.76	13.77	13.34	12.98	12.77	13.77	13.98	12.87	12.99	13.87

Solution Let the level of significance be 0.05. From the given information, let us frame the following table:

Observation	Energy (K cal) X_1	Protein X_2	${X_1}^2$	${X_2}^2$	$X_1 X_2$	*Est* X_1	e	e^2	$\{X_1 - (95 + 25X_2)\}^2$
1.	163	12.9	26569	166.41	2102.70	164.561	−1.561	2.435	152490.3
2.	191	13.3	36481	176.89	2540.30	172.577	18.423	339.408	183612.3
3.	185	13.9	34225	193.21	2571.50	184.602	0.398	0.159	191406.3
4.	170	13.5	28900	182.25	2295.00	176.585	−6.585	43.365	170156.3
5.	170	13.8	28900	190.44	2346.00	182.598	−12.598	158.698	176400
6.	161	13.1	25921	171.61	2109.10	168.569	−7.569	57.286	154842.3
7.	170	13.1	28900	171.61	2227.00	168.569	1.431	2.048	162006.3
8.	173	13.2	29929	174.24	2283.60	170.573	2.427	5.891	166464
9.	178	13.6	31684	184.96	2420.80	178.589	−0.589	0.347	178929
10.	167	12.97	27889	168.22	2165.99	165.963	1.037	1.075	157014.1
11.	182	13.76	33124	189.34	2504.32	181.796	0.204	0.042	185761
12.	184	13.77	33856	189.61	2533.68	181.996	2.004	4.015	187705.6
13.	174	13.34	30276	177.96	2321.16	173.379	0.621	0.386	170156.3
14.	168	12.98	28224	168.48	2180.64	166.164	1.836	3.372	158006.3
15.	162	12.77	26244	163.07	2068.74	161.955	0.045	0.002	149189.1
16.	182	13.77	33124	189.61	2506.14	181.996	0.004	0.000	185976.6
17.	191	13.98	36481	195.44	2670.18	186.205	4.795	22.993	198470.3
18.	161	12.87	25921	165.64	2072.07	163.959	−2.959	8.757	150350.1
19.	164	12.99	26896	168.74	2130.36	166.364	−2.364	5.590	155039.1
20.	185	13.87	34225	192.38	2565.95	184.000	1.000	0.999	190750.6
Sum	3481	267.47	607769	3580.11	46615.23	3481	0.000	656.867	3424725
Mean	174.05	13.37	30388.45	179.00	2330.76				
$\text{Var}(X_1) = 95.048$		$\text{Var}(X_2) = 0.155$		$\text{Cov}(X_1,X_2) = 3.103$		$r_{x1x2} = 0.809$			

$b_{x_1x_2} = r_{x_1x_2}\frac{S_{x_2}}{S_{x_1}} = 0.809\sqrt{\frac{95.048}{0.155}} = 20.043$ and the intercept $a = \bar{x}_1 - 20.043\bar{x}_2 = 174.05 - 20.043 \times 13.37 = -93.97$

So the regression equation of X_1 on X_2 is given as $X_1 = -93.97 + 20.043X_2$.

(i) According to the given condition t_0 test H_0 : $\alpha = \alpha_0(= 95)$ against $H_1 : \alpha \neq \alpha_0(95)$

$$t = \frac{a - \alpha_0}{\text{estSE}(\hat{\alpha})} = \frac{a - \alpha_0}{\sqrt{\left(\frac{1}{n} + \frac{\bar{x}^2}{SSxx}\right)\frac{\text{Res}SS}{n-2}}} \text{ with } (n-2) \text{ d.f.}$$

$$t = \frac{a - \alpha_0}{\sqrt{\left(\frac{1}{n} + \frac{\overline{x_2}^2}{SSxx}\right)\frac{\text{Res}SS}{n-2}}}$$

$$= \frac{-93.97 - 95}{\sqrt{\left(\frac{1}{20} + \frac{13.37^2}{20 \times 0.155}\right)\frac{656.867}{18}}} = \frac{-188.97}{45.892}$$

$$= 4.118$$

Now the calculated value of $|t| \geq t_{\alpha/2,(n-2)}$ i.e. $t_{0.025,18} = 2.101$,

$\therefore$ The null hypothesis is rejected i.e. in population $\alpha \neq 95$.

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(ii) According to the given condition to test $H_0 : \beta = \beta_0 (= 25)$, against $H_1 : \beta \neq \beta_0 (= 25)$

$$t = \frac{b-\beta_0}{\text{estSE}(\hat{\beta})} = \frac{b-\beta_0}{\sqrt{\left(\frac{\text{Res}SS}{n-2}\right)}} \text{ with } (n-2) \text{ d.f.}$$

$$t = \frac{b-\beta_0}{\sqrt{\left(\frac{\text{Res}SS}{n-2}\right)}} = \frac{20.043-25}{\sqrt{\left(\frac{656.867}{18}\right)}} = \frac{-4.957}{3.431}$$

$$= -1.445$$

The calculated value of $|t| < t_{\alpha/2,(n-2)}$ i.e. $t_{0.025,18} = 2.018$, the null hypothesis can not be rejected,

So one can conclude that at 5 % level of significance the slope coefficient may be taken as 25.

(iii) According to the given condition to test $H_0 : \alpha = \alpha_0,\ \beta = \beta_0$

we have the test statistic $F = \frac{\left[\sum_{i=1}^{n}(y_i-\alpha_0-\beta_0 x_i)^2 - \text{Res}SS\right]/2}{\text{Res}SS/(n-2)}$ with $(2, n-2)$d.f.

$$F = \frac{\left[\sum_{i=1}^{n}(y_i-\alpha_0-\beta_0 x_i)^2 - \text{Res}SS\right]/2}{\text{Res}SS/(n-2)}$$

$$= \frac{[3424725 - 656.867]/2}{656.867/(18)} = 46914.543$$

The calculated value of $F > F_{0.05;2,18}(=3.55)$, so the null hypotheses are rejected, i.e., in population *we cannot expect the regression of energy on protein content as energy = 95 + 25 protein.*

Example 6.16

The following data are pertaining to weight of eggs and number of eggs laid per cycle by certain poultry bird, and the regression equation worked for weight of eggs (Y) on number of eggs hatched (X) is $Y = 52.29 + 0.0182X$. Test for the regression coefficients:

Solution In order to test the significance of regression coefficient, we have the following null and alternative hypotheses, respectively:

$$H_0 : \beta_1 = 0$$
$$H_1 : \beta_1 \neq 0$$

Assuming that the dependent variable follows normal distribution, we have the following test statistic under the given hypotheses:

$$t = \frac{b_1-0}{SE(b_1)} = \frac{b_1}{\sqrt{\frac{s^2}{SS_{xx}}}} = \frac{b_1}{s}\sqrt{SS_{xx}} \quad \text{with} \quad n-2$$

degrees of freedom, where s is the standard deviation of the model and an estimate of the population variance and is worked out as the square root of the residual mean sum of square.

Let the level of significance be α =0.05.

Using the above information, let us frame the following table:

Observation	Y	X	$\hat{Y}$	Residual (e)	e^2
1.	45	80	53.74	−8.74	76.422
2.	48	80	53.74	−5.74	32.970
3.	49	85	53.83	−4.83	23.356
4.	50	88	53.89	−3.89	15.111
5.	51	92	53.96	−2.96	8.761
6.	52	92	53.96	−1.96	3.841
7.	53	90	53.92	−0.92	0.853
8.	54	91	53.94	0.06	0.003
9.	55	92	53.96	1.04	1.082
10.	56	92	53.96	2.04	4.162
11.	57	89	53.91	3.09	9.577
12.	58	86	53.85	4.15	17.215
13.	59	84	53.81	5.19	26.888
14.	60	82	53.78	6.22	38.710
15.	61	80	53.74	7.26	52.679
Sum	808.00	1303.00	808.00	0.00	311.63
Res SS=311.63					
S^2 = ResMS = ResSS/$(n-2)$ = 311.63/13 = 23.95					

Also from the above, we have the $SS_{xx} = \sum_{i=1}^{n}(x_i - \bar{x})^2 = 315.73$

Weight of egg(s) (g)	45	48	49	50	51	52	53	54	55	56	57	58	59	60	61
Hatching	80	80	85	88	92	92	90	91	92	92	89	86	84	82	80

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Thus, we have $t = \frac{b_1 - 0}{SE(b_1)} = \frac{b_1}{\sqrt{\frac{S^2}{SS_{xx}}}} = \frac{b_1}{S}\sqrt{SS_{xx}} = \frac{0.018}{\sqrt{23.95}}\sqrt{315.73} = 0.065.$

Now the calculated value of $|t| < t_{\alpha/2,(n-2)} = t_{0.025,13} = 2.16$, so the test is nonsignificant, and the null hypothesis cannot be rejected. Thus, one should conclude that at 5 % level of significance on the population regression coefficient of egg weight on number of eggs laid per hatching cycle cannot be taken different from zero.

(vii) *Test for significance of the population multiple correlation coefficient*

As has been discussed in Chap. 8 of this book, multiple correlation coefficient is the correlation coefficient between the dependent variable and the estimated values of the dependent variable from the line of regression of the dependent variable on other variables. Suppose we have p variables X_1, X_2,..... X_p and following a p-variate normal distribution, then the multiple correlation of X_1 on X_2, X_3,..... X_p is given by $\rho_{1.2,3,\ldots\ldots p}$, and the corresponding sample multiple correlation coefficient can be written as $R_{1.2,3,\ldots\ldots p}$ from a random sample of size n. In this section of inference, we are interested to test whether the population multiple correlation is zero or not, i.e., to test $H_0 : \rho_{1.2,3,\ldots\ldots,p} = 0$ against the alternative hypothesis $H_1 : \rho_{1.\ 2,\ 3,\ldots\ldots,p} > 0$. Under H_0, the appropriate test statistic will be $F = \frac{R^2{}_{1.23\ldots\ldots p}/(p-1)}{\left(1-R^2{}_{1.23\ldots\ldots p}\right)/(n-p)}$ with $(p-1,\ n-p)$ d.f. According to the given alternative hypothesis, the test is right-sided test; this is because of the fact that the multiple correlation coefficient is the ratio of two variances and cannot be negative. If the calculated value of F be greater than the table value of F at specified level of significance and appropriate degrees of freedom, then the null hypothesis is rejected; otherwise, one cannot reject the null hypothesis.

Example 6.17

Thirty Jersey cows were tested for dependence of their milking capacity (X_1) on weight of the cows (X_2), number of lactation (X_3), and age (X_4). The multiple correlation coefficient of milking capacity (X_1) on all other three variables was found to be 0.898. Test for significance of multiple correlation coefficient at 5 % level of significance.

Solution Assuming that all the variables under consideration behave like normal variables, under the given condition, i.e., $H_0 : \rho_{1.234} = 0$ against $H_1 : \rho_{1.234} > 0$, the test statistic under is given by

$$F = \frac{R^2_{1.234}/(p-1)}{\left(1-R^2_{1.234}\right)/(n-p)} = \frac{R^2_{1.234}/(4-1)}{\left(1-R^2_{1.234}\right)/(30-4)}$$

$$\therefore F = \frac{R^2_{1.234}/(p-1)}{\left(1-R^2_{1.234}\right)/(n-p)} = \frac{(0.898)^2/3}{\left(1-0.898^2\right)/26}$$

$$= \frac{0.268}{0.028} = 9.571$$

The calculated value of F is greater than the table value of $F_{0.05,3,26} = 2.98$, so the test is significant, and null hypothesis is rejected. That means population multiple correlation coefficient differs significantly from zero.

(viii) *Test for significance of population partial correlation coefficient*

As has been discussed in Chap. 8 of this book, partial correlation coefficient is the correlation coefficient between the dependent variable and one of the independent variables after eliminating the effects of other variables on both the variables. Suppose we have p variables X_1, X_2,..... X_p and following a p-variate normal distribution, then the partial correlation coefficient of X_1 and X_2 after eliminating the effects of X_3,. . . . . X_p from both X_1 and X_2 is given by $\rho_{12.3,4\ldots\ldots p}$, and the corresponding sample partial correlation coefficient from a random sample of size "n" is given by $r_{12.34\ldots\ldots\ldots p}$. Under the given conditions, the test statistic for $H_0 : \rho_{12.34\ldots\ldots\ldots p} = 0$ against $H_0 : \rho_{12.34\ldots\ldots\ldots p} \neq 0$ is

$$t = \frac{r_{12.34\ldots\ldots\ldots p}\sqrt{n-p}}{\sqrt{1-r^2{}_{12.34\ldots\ldots\ldots p}}} \text{ with } (n-p) \text{ d.f.}$$

If the calculated value of $|t|$ be greater than the table value of t at specified level of significance

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and $n-2$ degrees of freedom, then the null hypothesis is rejected; otherwise, there is no reason to reject the null hypothesis.

Example 6.18
Thirty Jersey cows were tested for dependence of their milking capacity (X_1) on weight of the cows (X_2), number of lactation (X_3), and age (X_4). The partial correlation coefficient of milking capacity (X_1) of Jersey cow with the no. of lactation (X_3) by eliminating the effect of weight (X_2) and age of cow (X_4) is found to be 0.777. Test for significance of partial correlation coefficient at 5 % level of significance.

Solution Assuming that the variables behave like normal variables, we have the test statistic $t = \frac{r_{13.24}\sqrt{n-p}}{\sqrt{1-r_{13.24}^2}}$ at $\alpha = 0.05$ and $n-p$ d.f. for $H_0 : \rho_{13.24} = 0$ against $H_1 : \rho_{13.24} \neq 0$.

From the given information, we have $t = \frac{r_{13.24}\sqrt{n-p}}{\sqrt{1-r_{13.24}^2}} = \frac{0.777\sqrt{30-4}}{\sqrt{1-0.777^2}} = \frac{3.961}{0.629} = 6.297$ with $(30-4) = 26$ d.f.

From the table, we have $t_{0.05,26} = 2.055$. Since the calculated $|t| > 2.055$, the null hypothesis of zero partial correlation coefficient between milking capacity and no. of lactation is rejected.

6.2.1.2 Statistical Test of Population Parameters for Large Samples

As has already been discussed, if a *large* random sample of size n is drawn from an arbitrary population with mean μ and variance σ^2 and any statistic be "t" with mean $E(t)$ and variance $V(t)$, then t is asymptotically normally distributed with mean $E(t)$ and variance $V(t)$, i.e., $t \sim N(E(t),V(t))$ as $n \to \infty$. Any sample having sample size 30 or more is treated as a large sample. A test procedure where the null hypotheses are tested against the alternative hypothesis based on large sample is known as the large sample test. Corresponding estimator is supposed to follow like a standard normal variate $\tau = \frac{t-E(t)}{\sqrt{V(t)}} \sim N(0,1)$.

In the following section, we shall discuss some of the important and mostly used large sample tests.

(i) *Test for specified value of population mean*

Let $x_1, x_2, x_3, \ldots\ldots\ldots x_n$ be a random sample drawn from a population with mean μ and variance σ^2 and given that the size of the sample is $n \geq 30$. Now we have to test H_0: $\mu = \mu_0$. From the given sample, one can calculate the sample mean $\bar{x}$. According to large sample theory $\bar{x} \sim N\left(\mu, \frac{\sigma^2}{n}\right)$ as $n \to \infty$., under the given situation, our null hypothesis would be $\mu = \mu_0$, a specified value. Here we come across with two situations, (i) the population variance σ^2 is known (ii) the population variance σ^2 is not known. Like parametric setup, here also we have two approximate test statistics under two situations to test the H_0: $\mu = \mu_0$ and are given by

$$\tau = \frac{\bar{x}-\mu_0}{\sigma/\sqrt{n}}, \text{when } \sigma^2 \text{is known and}$$

$$\tau = \frac{\bar{x}-\mu_0}{s_n/\sqrt{n}}, \text{ when } \sigma^2 \text{ is unknown,}$$

where $s_n^2 = \frac{1}{n}\sum_{i=1}^{n}(x_i - \bar{x})^2$ is the sample variance.

Depending upon the nature of the alternative hypothesis and level of significance, the table value of the standard normal variate τ is to be decided. If the calculated value of τ falls in the zone of rejection, the null hypothesis is to be rejected; otherwise, one cannot reject the null hypothesis at the specified level of significance.

Example 6.19
A fishing community in Uganda claims that the average amount of fish catch per day is 33.12 kg using motorized boat with a variance of 4.72. Information from 30 boats were collected and found that the average fish catch per day is 37.62 kg per boat with s.d. of 2.45. Conclude whether the claims are justified or not.

Solution Let us suppose that we are to test the null hypothesis at 5 % level of significance.

Given that (i) population mean (μ) =33.12 kg and variance (σ^2) = 4.72.

(ii) Sample size (n) = 30, $\bar{x}$ = 37.62, and s_n = 2.45.

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Thus, under the given condition, the null hypothesis $H_0 : \mu = 33.12$ kg against the alternative hypothesis $H_1 : \mu \neq 33.12$ kg, the test statistic would be $\tau = \frac{\overline{x}-\mu_0}{\sigma/\sqrt{n}}$ which follows a standard normal distribution. As per the alternative hypothesis, the test is a both-sided test:

$$\therefore \tau = \frac{37.62 - 33.12}{2.17/\sqrt{30}} = \frac{4.5}{0.40} = 11.25$$

The calculated value of $|\tau| = 11.25$ is greater than $\tau_{0.025} = 1.96$. So the test is significant and the null hypothesis is rejected. Thus, we reject the claim that a fishing community in Uganda catches 33.12 kg fish using motorized boat.

In fact, instead of taking alternative hypothesis as $H_1 : \mu \neq 33.12$ kg, if we take alternative hypothesis as $H_1 : \mu > 33.12$ kg to test the null hypothesis $H_0 : \mu = 33.12$ kg, we would have rejected the null hypothesis in favor of the alternative hypothesis. Let us examine.

We want to test the null hypothesis $H_0 : \mu = 33.12$ kg against the alternative hypothesis $H_1 : \mu > 33.12$ kg, a right-sided test.

Under the given condition, the test statistic will remain the same, but we are to compare the calculated value of the test statistic with upper table value of the test statistic at 5 % level of significance.

Thus, $\tau = \frac{\overline{x}-\mu_0}{\sigma/\sqrt{n}} = \frac{37.62-33.12}{2.17/\sqrt{30}} = \frac{4.5}{0.40} = 11.25$

The calculated value of $\tau = 11.25$ is greater than $\tau_{0.05} = 1.645$. So the test is significant and the null hypothesis is rejected. Thus, we reject the claim and conclude that the average fish weight caught by the fishers of Uganda is more than the claimed 33.12 kg/day.

Example 6.20

A particular hatchery of broiler chicks claims that the average weight of chicks of his hatchery would be 2.24 kg at 42 days of age. A sample of 77 chicks were tested and found that the average weight was 2.16 kg with variance 0.014. Using 5 % level of significance, test whether the claim is justified or not.

Solution Given that (i) the sample is large n (=77 > 30),

(ii) Sample mean ($\overline{x}$) = 2.16, sample variance = 0.014

(iii) Population variance is unknown

We want to test $H_0 : \mu = 2.24$ kg against

$$H_1 : \mu \neq 2.24$$

The approximate test statistic under the given condition is

$$\tau = \frac{\overline{x} - \mu_0}{s_n/\sqrt{n}} = \frac{2.16 - 2.24}{0.014/\sqrt{77}} = \frac{-0.08}{0.0015} = -53.33$$

Thus, the calculated value of |τ|, i.e., 53.33, is greater than the table value of $\tau_{0.025} = 1.96$. Hence, the test is significant and the null hypothesis is rejected. So we conclude that the claim of the company is not justified.

(ii) *Test for significance of specified population standard deviation*

Suppose $x_1, x_2, x_3, \ldots\ldots\ldots x_n$ be a large random sample of size n drawn from a population with mean μ and variance σ^2. We want to test H_0: $\sigma = \sigma_0$ where $\sigma^2{}_0$ is any specified value for the population variance.

When the sample size n is large, then the sampling distribution of the sample standard deviation s_n follows approximately normal distribution with mean $E(s_n) = \sigma$ and variance $V(s_n) = \sigma^2/2n$, i.e., as $n \to \infty$, $s_n \sim N\left(\sigma, \frac{\sigma^2}{2n}\right)$

To test the above null hypothesis, we have the following approximate test statistic: $\tau = \frac{s_n - \sigma_0}{\sqrt{\frac{\sigma_0^2}{2n}}} \sim N(0,1)$

For acceptance or rejection of H_0, we have to compare the calculated value of τ with the appropriate tabulated value keeping in view the alternative hypothesis.

Example 6.21

To test the variability in size of eggs, a sample of 50 eggs was examined and found that the variance of the size of egg was 64. But the concerned poultry farm claims that the variability in size of egg was 25 only. Based on the information provided, can we conclude that the claim of the poultry farm is justified or not?

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Solution The sample size is large with $n = 50$. The population variance of egg size is assumed to be 25. Under the given condition, we are to test the null hypothesis

$H_0 : \sigma = 5$, against the alternative hypothesis $H_1 : \sigma \neq 5$.

The test statistic is a both-sided test with a given sample variance being 64. For the above null hypothesis, the appropriate test statistic would be $\tau = \frac{s_n - \sigma_0}{\sqrt{\frac{\sigma_0^2}{2n}}}$; S_n and σ_0 are the sample and population standard deviation respectively. Let the level of significance be 0.05:

$$\tau = \frac{s_n - \sigma_0}{\sqrt{\frac{\sigma_0^2}{2n}}} = \frac{8.0 - 5.0}{\sqrt{25/(2 \times 50)}} = \frac{3.0}{0.50} = 6.00$$

The calculated value of $|\tau| >$ tabulated value of $\tau_{0.05}$ (1.96). The test is significant and the null hypothesis is rejected. So the population variance of the size of eggs cannot be taken as 25. Hence, the claim of the poultry farm is not justified.

(iv) *Test for significant difference between two standard deviations*

Suppose we have drawn two independent samples, $(x_{11}, x_{12}, \ldots\ldots\ldots, x_{1m})$ and $(x_{21}, x_{22}, \ldots\ldots\ldots, x_{2n})$, of sizes m and n with means $\bar{x}_1$, $\bar{x}_2$ and variance ${S_m}^2$, ${S_n}^2$ from two populations with variances ${\sigma_1}^2$ and ${\sigma_2}^2$, respectively. We want to test for the equality of two standard deviations σ_1 and σ_2. Thus, the null hypothesis is $H_0 : \sigma_1 = \sigma_2$.

According to large sample criteria, both ${S_m}^2$, ${S_n}^2$ are distributed as $S_m \sim N\left(\sigma_1, \frac{\sigma_1^2}{2m}\right)$ and $S_n \sim N\left(\sigma_2, \frac{\sigma_2^2}{2n}\right)$.

Now $E(S_m - S_n) = E(S_m) - E(S_n) = \sigma_1 - \sigma_2$ and

$$SE(S_m - S_n) = \sqrt{V(S_m - S_n)} = \sqrt{\frac{{\sigma_1}^2}{2m} + \frac{{\sigma_2}^2}{2n}}$$

As the samples are large, so $(S_m - S_n) \sim N\left(\sigma_1 - \sigma_2, \frac{{\sigma_1}^2}{2m} + \frac{{\sigma_2}^2}{2n}\right)$.

The test statistic under H_0 would be $\tau = \frac{(s_m - s_n)}{\sqrt{\frac{{\sigma_1}^2}{2m} + \frac{{\sigma_2}^2}{2n}}}$.

In most of the cases, population variances ${\sigma_1}^2$ and ${\sigma_2}^2$ remain unknown, and for large samples, ${\sigma_1}^2$ and ${\sigma_2}^2$ are replaced by the corresponding sample variances, and the test statistic reduces to $\tau = \frac{(S_m - S_n)}{\sqrt{\left(\frac{S_m^2}{2m} + \frac{S_n^2}{2n}\right)}} \sim N(0, 1)$.

Example 6.22 The following table gives the egg production features of two independent random samples from a poultry farm in Bihar state of India. Test whether the variability of two samples are the same or not:

Sample	Sample size	Wt of egg(cg)	S.D
Sample 1	48	6548.26	1027.34
Sample 2	37	6786.73	2343.23

Solution: Let the variability be measured in terms of standard deviation. So under the given condition, we are to test:

H_0: the standard deviations of both the samples are equal against

H_1: the standard deviations of the samples are not equal.

That is, $H_0 : \sigma_1 = \sigma_2$ against $H_1 : \sigma_1 \neq \sigma_2$

Let the level of significance be $\alpha = 0.05$.

Under the above null hypothesis, the test statistic is

$$\tau = \frac{(S_m - S_n)}{\sqrt{\left(\frac{S_m^2}{2m} + \frac{S_n^2}{2n}\right)}} \sim N(0, 1),$$

$$\therefore \tau = \frac{(S_m - S_n)}{\sqrt{\left(\frac{S_m^2}{2m} + \frac{S_n^2}{2n}\right)}} = \frac{(1027.34 - 2343.23)}{\sqrt{\left(\frac{1027.34^2}{2\times 48} + \frac{2343.23^2}{2\times 37}\right)}}$$

$$= \frac{-1315.89}{\sqrt{(10994.0362 + 74199.01)}} = \frac{-1315.89}{291.878}$$

$$= -4.508$$

The calculated value of $|\tau| >$ tabulated value of $\tau_{0.05}$ (1.96). The test is significant and the null hypothesis is rejected. So the population variance of weight of eggs is not same. Hence, the poultry

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farm has got different variabilities in weights of eggs.

(iii) *Test of significance between two means*

Analogous to that of testing of equality of two sample means from two normal populations, in large sample case also, sometimes, it is required to test whether the two populations are same or not with respect to their arithmetic means. Suppose we have two independent random large samples $x_{11}, x_{12}, x_{13}, \ldots\ldots x_{1m}$ and $x_{21}, x_{22}, x_{23}, \ldots\ldots x_{2n}$ drawn from two populations $(\mu_1, {\sigma_1}^2)$ and $(\mu_2, {\sigma_2}^2)$, respectively. Now we want to test whether these two populations differ in their central tendencies measured in terms of arithmetic mean or not, i.e., to test H_0: $\mu_1 = \mu_2$. As two large samples are drawn independently from two population, so $\bar{x}_1 \sim N\left(\mu_1, \sigma_1^2/n_1\right)$ and $\bar{x}_2 \sim N(\mu_2, {\sigma_2}^2/n_2)$.

Therefore,
$E(\bar{x}_1 - \bar{x}_2) = E(\bar{x}_1) - E(\bar{x}_2) = \mu_1 - \mu_2$ and

$$V(\bar{x}_1 - \bar{x}_2) = V(\bar{x}_1) + V(\bar{x}_2) = \frac{{\sigma_1}^2}{n_1} + \frac{{\sigma_2}^2}{n_2}$$

$$\therefore \bar{x}_1 - \bar{x}_2 \sim N\left(\mu_1 - \mu_2, \frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}\right)$$

The standard normal variate corresponding to the difference between the two means, $\overline{d} = \bar{x}_1 - \bar{x}_2$ would be

$$\tau = \frac{\overline{d} - E\left(\overline{d}\right)}{SE\left(\overline{d}\right)} = \frac{(\bar{x}_1 - \bar{x}_2) - E(\bar{x}_1 - \bar{x}_2)}{\sqrt{V(\bar{x}_1 - \bar{x}_2)}}$$
$$= \frac{(\bar{x}_1 - \bar{x}_2) - (\mu_1 - \mu_2)}{\sqrt{\frac{{\sigma_1}^2}{n_1} + \frac{{\sigma_2}^2}{n_2}}}$$

Thus, to test $H_0 : \mu_1 = \mu_2$ and the test statistic is $\tau = \frac{(\bar{x}_1 - \bar{x}_2)}{\sqrt{\frac{{\sigma_1}^2}{n_1} + \frac{{\sigma_2}^2}{n_2}}}$, In testing this hypothesis, we may come across two different situations, (a) population variances σ_1^2 and σ_2^2 are known and (b) population variances σ_1^2 and $\sigma_2^2 = \sigma_1^2$ are unknown but equal $\sigma_1^2 = \sigma_2^2 = \sigma^2$.

(a) *Test of equality of two population means when population variances are known*: Under the given null hypothesis H_0: $\mu_1 = \mu_2$ with known population variances ${\sigma^2}_1$ and ${\sigma^2}_2$ against the alternative hypotheses $H_1 : \mu_1 \neq \mu_2$, the test statistic would be $\tau = \frac{\bar{x}_1 - \bar{x}_2}{\sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}}$, which follows a standard normal distribution, and $\bar{x}_1$ and $\bar{x}_2$ are the arithmetic means of the first and second samples, respectively. As the test is both sided, we are to compare the calculated value of τ with that of the table value under standard normal value at $\alpha/2$ level of significance for taking decision.

(b) *Test of equality of two population means when population variances are unknown but equal*: Before performing this test, one should ascertain that first $H_0 : \sigma_1^2 = \sigma_2^2$ by F-test statistic discussed in test iii(b). If it is accepted then, we perform the test using $\tau = \frac{\bar{x}_1 - \bar{x}_2}{\sqrt{\hat{\sigma}^2\left(\frac{1}{n_1} + \frac{1}{n_2}\right)}}$ where $\hat{\sigma}^2 = \frac{n_1 {s_{n_1}}^2 + n_2 {s_{n_2}}^2}{n_1 + n_2}$ is the estimate of common population variance.

Thus, the test statistic under ${\sigma_1}^2 = {\sigma_2}^2 = \sigma^2$ (unknown) comes out to be

$\tau = \frac{\bar{x}_1 - \bar{x}_2}{\sqrt{\hat{\sigma}^2\left(\frac{1}{n_1} + \frac{1}{n_2}\right)}}$ which follows N (0, 1).

When population variance is unknown, then these are replaced by respective sample variances $s^2_{n_1}$ and $s^2_{n_2}$.

For acceptance or rejection of H_0, we have to compare the calculated value of τ with the appropriate tabulated value keeping in view the alternative hypotheses.

Example 6.23

To compare the shelf life of milk from two large samples, sample of 50 each was selected and found that the average shelf life of first sample milk was 36 h and that of second sample was 42 h

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with a standard deviation of 6 and 5 h, respectively. Assuming that both the milk samples have same variability, test whether the shelf life second sample is more than the first sample or not.

Solution Given that:

	Mean	SD	Sample size
First sample	36	6	50
Second sample	42	5	50

Under the given condition of $\sigma_1^2 \neq \sigma_2^2$ and both being unknown, the null hypothesis and the alternative hypothesis remain same. That is, H_0: average shelf life of milk of first sample and second sample are equal against H_1: average shelf life of milk of second sample > first sample.

Let the level of significance be $\alpha = 0.05$, being a one-sided test the critical value is 1.645 for standard normal variate τ. The test statistic is

$$\tau = \frac{\bar{x}_1 - \bar{x}_2}{\sqrt{\left(\frac{s_{n_1}^2}{n_1} + \frac{s_{n_2}^2}{n_2}\right)}} \sim N(0,1)$$

Thus, $\tau = \frac{42-36}{\sqrt{\left(\frac{36}{50}+\frac{25}{50}\right)}} = \frac{6}{\sqrt{\frac{61}{50}}} = \frac{6}{\sqrt{1.22}} = 5.43$

Since Cal $\tau > \tau_{0.05} = 1.645$, the test is significant; we reject the null hypothesis and accept the alternative hypothesis, i.e., average shelf life of milk of second sample > first sample.

Example 6.24

To compare the vase life of flower from two large samples, samples of 50 each were selected and found that the average vase life of first sample of flower was 36 h and that of second sample was 42 h with a standard deviation of 6 and 5 h, respectively. Assuming that the samples have different variability, test whether the vase life of flower of second sample > first sample.

Solution Given that:

	Mean	SD	Sample size
First sample	36	6	50
Second sample	42	5	50

Under the given condition $\sigma_1^2 = \sigma_2^2 = \sigma^2$ (unknown), and the null hypothesis is H_0: average vase life of flower of both the samples are equal against H_1: average vase life of second sample > first sample. Also suppose that the equality of variances hold good. So the test statistic under H_0 is

$$\tau = \frac{\bar{x}_1 - \bar{x}_2}{\sqrt{\widehat{\sigma}^2\left(\frac{1}{n_1} + \frac{1}{n_2}\right)}} \sim N(0,1)$$

Where

$\widehat{\sigma}^2 = \frac{n_1 s_{n_1}^2 + n_2 s_{n_2}^2}{n_1+n_2} = \frac{50 \times 6^2 + 50 \times 5^2}{50+50} = \frac{50(36+25)}{100} = \frac{61}{2}$

So $\tau = \frac{42-36}{\sqrt{\frac{61}{2}\left(\frac{1}{50}+\frac{1}{50}\right)}} = \frac{6}{\sqrt{1.22}} = 5.43$

Let the level of significance be $\alpha = 0.05$. This is a one-tailed test. Since the Cal $\tau > \tau_{0.05} = 1.645$, the test is significant; we reject the null hypothesis and accept the alternative hypothesis, i.e., average vase life of flower of second sample > first sample.

(v) *Test for significance of specified population proportion*

In our daily life, often we want to test the proportion of a particular characteristic of the population with the help of the sample drawn from the population. Likewise to that of testing the specific mean or standard deviation value for the population as discussed in Sect. 6.2.1.2 (iii) and (iv) here in this section, we are interested in testing the specific value of the proportion for a particular characteristic of the population based on sample observations.

Suppose a random large sample of size n is drawn from a population. If we denote P (unknown) as the population proportion of individual units having a particular characteristic, our objective is to test the null hypothesis H_0: $P = P_0$ where P_0 is the specified value. Let n_1 be the number of units in the sample on size n having the particular characteristic under consideration, so ($p = n_1/n$) is the sample proportion possessing the characteristic. This n_1 is supposed to be distributed as binomial with

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parameters n and P. Under large sample assumption, the binomial distribution tends to normal with mean nP and variance $nP\ (1-P)$, i.e., as $n \to \infty$, $n_1 \sim N(nP,\ nP(1-P))$. The standard normal variate corresponding to n_1 is $\tau = \frac{n_1 - nP}{\sqrt{nP(1-P)}} \sim N(0,1)$. Now $E(p) = E(n_1/n) = \frac{nP}{n} = P$ and $V(p) = V(n_1/n) = \frac{1}{n^2} nP(1-P) = \frac{P(1-P)}{n}$. For large n, $p \sim N(P, \frac{P(1-P)}{n})$. The standard normal variate corresponding to p is $\tau = \frac{p-P}{\sqrt{\frac{P(1-P)}{n}}}$. So the test statistic under H_0 is $\tau = \frac{p-P_0}{\sqrt{\frac{P_0(1-P_0)}{n}}} \sim N(0,1)$.

Example 6.25
A retailer purchase a huge quantity of fish from a wholesaler knowing that 7 % of the fish are rotten. To test the claim of the wholesaler, he randomly selects a sample of 70 fish and found that 60 of these are good. Test whether the claim by the wholesaler is justified or not at 5 % level of significance.

Solution The null hypothesis will be that the proportion of good fish in the lot is 0.93., i.e., H_0: $P = 0.93$ against the alternative hypothesis $H_1 : P \neq 0.93$. The test statistic under the given null hypothesis would be

$\tau = \frac{p-P_0}{\sqrt{\frac{P_0(1-P_0)}{n}}}$, which is a both sided test.

$$\therefore \tau = \frac{p - P_0}{\sqrt{\frac{P_0(1-P_0)}{n}}} = \frac{0.85 - 0.93}{\sqrt{\frac{0.93(0.07)}{70}}} = -2.62$$

The calculated value of $|\tau|$ is greater than the tabulated value of τ at 5 % level of significance, i.e., 1.96. So the test is significant and we reject the null hypothesis. That means we conclude that the claim of wholesaler is not justified.

Example 6.26
A sample of 120 chicks from poultry was selected at random. It is found that 37 % of the chicks are suffering from gout problem. Can we conclude that in population, there are 45 % of the chicks that are suffering from gout problem?

Solution Given that 37 % chicks in the sample are suffering from gout, i.e., $p = 0.37$. Under the given conditions, the null hypothesis is the equality of proportion of gout and non-gout, i.e., $H_0 : P = 0.45$ against $H_1 : P \neq 0.45$

Let the level of significance be $\alpha = 0.05$. The test statistic for the above null hypothesis will be

$$\tau = \frac{p - P_0}{\sqrt{\frac{P_0(1-P_0)}{n}}}$$

$$\text{So } \tau = \frac{0.37 - 0.45}{\sqrt{\frac{045(0.55)}{120}}} = -1.76$$

This is a two-sided test. Since Cal $|\tau| < \tau_{0.025} = 1.96$, so the test is nonsignificant; we cannot reject the null hypothesis. Hence, we conclude that the proportion of gout and non-gout chicks in the population is 45:55.

(vi) *Test for equality of two population proportions*

Likewise to that two sample mean tests, one can also be interested to test equality of two proportions. Let us have two independent random large samples of sizes n_1 and n_2 from two populations, where P_1 and P_2 are the proportions of possessing a particular characteristic in two populations, respectively, and p_1 and p_2 be the proportions possessing that characteristic in the samples, respectively. For large sample sizes, p_1 and p_2 tend to distribute normally: $p_1 \sim N\left(P_1, \frac{P_1(1-P_1)}{n_1}\right)$ and $p_2 \sim N\left(P_2, \frac{P_2(1-P_2)}{n_2}\right)$ $E(p_1) = P_1$, $\mathrm{E}(p_2) = P_2; E(p_1 - p_2) = P_1 - P_2$ [as the samples are in dependent] $V(p_1 - p_2) = V(p_1) + V(p_2) - 2\mathrm{cov}(p_1, p_2) = V(p_1) + V(p_2)$ [as the samples are independent] $\therefore p_1 - p_2 \sim N\left(P_1 - P_2, \frac{P_1(1-P_1)}{n_1} + \frac{P_2(1-P_2)}{n_2}\right)$. The standard normal variate corresponding to $(p_1 - p_2)$ is $\tau = \frac{(p_1-p_2)-(P_1-P_2)}{\sqrt{\frac{P_1(1-P_1)}{n_1} + \frac{P_2(1-P_2)}{n_2}}}$

We are interested to test the equality of two population proportions, i.e., $H_0 : P_1 = P_2 = P$ (say).

Under the null hypothesis, the appropriate test statistic under H_0 is $\tau = \frac{(p_1-p_2)-(\mathrm{P_1\text{-}P_2})}{\sqrt{\frac{P(1-P)}{n_1} + \frac{P(1-P)}{n_2}}}$

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If the population proportion value of P is unknown, one can use its unbiased estimator $\hat{P} = \frac{n_1 p_1 + n_2 p_2}{n_1 + n_2}$ based on both the samples. Under the unknown equal variance condition, the test statistic becomes

$$\tau = \frac{(p_1 - p_2)}{\sqrt{\hat{P}\left(1 - \hat{P}\right)\left(\frac{1}{n_1} + \frac{1}{n_2}\right)}}$$

Example 6.27
From two large samples of 700 and 900 chicks, 10 % and 14 % are found to be suffering from a particular disease. Can we conclude that the proportions of diseased chicks are equal in both the lots?

Solution Under the given condition, the null hypothesis is $H_0 : P_1 = P_2$ against the alternative hypothesis $H_1 : P_1 \neq P_2$. That means there exists no significant difference between the two proportions against the existence of significant difference.

Let the level of significance be $\alpha = 0.05$.

The appropriate test statistic for the above null hypothesis is

$$\tau = \frac{(p_1 - p_2)}{\sqrt{\widehat{P}\left(1 - \widehat{P}\right)\left(\frac{1}{n_1} + \frac{1}{n_2}\right)}}, \text{ where } \widehat{P} = \frac{n_1 p_1 + n_1 p_1}{n_1 + n_2}$$

$$\widehat{P} = \frac{700 \times 0.1 + 900 \times 0.14}{700 + 900} = 0.122$$

$$\therefore \tau = \frac{(p_1 - p_2)}{\sqrt{\widehat{P}\left(1 - \widehat{P}\right)\left(\frac{1}{n_1} + \frac{1}{n_2}\right)}}$$

$$= \frac{(0.1 - 0.14)}{\sqrt{0.122(1 - 0.122)\left(\frac{1}{700} + \frac{1}{900}\right)}} =$$

$$\frac{-0.04}{0.016} = -2.5$$

Since the calculated value of $|\tau|$ is greater than the tabulated value of τ (1.96) at 5 % level of significance, so the null hypothesis is rejected and concludes that a proportion of diseased chicks are not equal in both the lots.

6.2.1.3 Other Tests

(vii) χ^2 – *Test for goodness of fit*

In testing of hypothesis, often we are interested in testing whether the observed values in the samples are in tune with the expected values in the population or not. Based on the frequency distribution, we try to match the probability distribution which a particular characteristic follows. Suppose with a given frequency distribution, we have tried to fit a normal distribution. Now according to normal probability law, there should be some expected frequencies corresponding to each and every class of the frequency distribution. How far the observed frequencies are matching with the expected frequencies is required to be ascertained or tested. In breeding experiments, we know that the progenies at different generations should follow particular ratios among the different types; now the question is whether the observed ratios are in tune with the expected ratios or not. The answer to all these is possible with the help of the χ^2 test for goodness of fit. This is essentially a test of frequencies as such also known as frequency χ^2. There are other examples where χ^2 test for goodness of fit has been used.

If a population is grouped into n mutually exclusive groups based on nominal or interval categories such that the probability of individual units belonging to the ith class is P_i, $i = 1,2,3,4\ldots n$ and $\sum_{i=1}^{n} P_i$, a random sample of m individuals drawn from the population and the respective observed class frequencies are O_1, O_2, $O_3 \ldots O_n$ where $\sum_{i=1}^{n} O_i = m$. Then the random variable $U_n = \sum_{i=1}^{n} \frac{(O_i - mP_i)^2}{mP_i}$ is asymptotically distributed as a χ^2 with $(n-1)$ d.f. This χ^2 is known as frequency χ^2 or Pearsonian chi-square. Karl Pearson proved that the limiting distribution of this χ^2 is the ordinary χ^2 distribution.

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In doing so, we come across with two situations, (*a*) *the population completely specified or (b) the population is not completely specified*. In the first case, our problem is to test $H_0 : P_1 = P_1^0, P_2 = P_2^0, P_3 = P_3^0 \ldots\ldots\ldots, P_n = P_n^0$ where $P_i^0 (i = 1, 2, 3, \ldots.n)$ are specified values. The test under H_0 is $\chi^2 = \sum_{i=1}^{n} \frac{\left(O_i - mP_i^0\right)^2}{mP_i^0} = \sum_{i=1}^{n} \frac{(O_i - e_i)^2}{e_i} = \sum_{i=1}^{n} \frac{(O_i)^2}{mP_i^0} - m$ which is distributed as χ^2 with $(n-1)$ d.f. as $m \to \infty$ and e_i= expected frequency of the ith class $= mP_i^0 (i = 1, 2, 3, \ldots., n)$. It should be noted that $\sum_{i=1}^{n} O_i = \sum_{i=1}^{n} e_i = m$. It is assumed that the quantities P_i^0 are given by Ho and are not estimated from the sample.

Usually, the parameters of this distribution may not be known but will have to be estimated from the sample, i.e., when the population is not completely specified. The test statistic under H_0 is $\chi^2 = \sum_{i=1}^{n} \frac{(O_i - e_i)^2}{e_i} = \sum_{i=1}^{n} \frac{\left(O_i - m\hat{P}_i\right)^2}{m\hat{P}_0}$ which is χ^2 distribution with $(n-s-1)$ d.f. where s $(<n-1)$ is the number of parameters of this distribution to be estimated from the sample and $\hat{P}_i$ is the estimated probability that a single item in the sample falls in the *i*th class which is a function of the estimated parameters.

The value of calculated χ^2 will be greater if the differences between the observed frequencies (O_i) and the expected frequencies (e_i) are greater. Hence, it would appear that a very high value of calculated χ^2 should indicate falsity of the given hypothesis. If α be the level of significance, then we reject H_0 if Cal $\chi^2 > \chi_{\alpha, d.f}^2$; otherwise, we cannot reject it.

Example 6.28

In a breeding trial of two different types of peas (colored and white) breeds were crossed. In F_1 generation, the following three types of peas were produced. Do the data agree with the theoretical expectation of 1:2:1 ratio? Colored, 24; white, 30; and mixed, 56.

Solution Total frequency = 24 + 30 + 56 = 110. The expected frequencies are as follows:

Colored $= \frac{110}{4} \times 1 = 27.5$
White $= \frac{110}{4} \times 1 = 27.5$
Intermediate $= \frac{110}{4} \times 2 = 55$

H_0: The observed frequencies support the theoretical proportions, i.e.,

$P_1 = \frac{1}{4}$, $P_2 = \frac{2}{4}$, and $P_3 = \frac{1}{4}$

Against

H_1: The observed frequencies do not follow the theoretical frequencies, i.e.,

$P_1 \neq \frac{1}{4}$, $P_2 \neq \frac{2}{4}$, and $P_3 \neq \frac{1}{4}$

Under H_0, the test statistic is

$$\chi^2 = \sum_{i=1}^{k} \frac{(o_i - e_i)^2}{e_i} \text{ with } k - 1 \text{ d.f.}$$

Let the level of significance be 0.05.

$$\therefore \chi^2 = \sum_{i=1}^{k} \frac{(o_i - e_i)^2}{e_i}$$
$$= \frac{(24 - 27.5)^2}{28} + \frac{(56 - 55)^2}{55} + \frac{(30 - 27.5)^2}{28}$$
$$= \frac{12.25}{28} + \frac{1}{55} + \frac{6.25}{28}$$
$$= 0.4374 + 0.0181 + 0.2232 = 0.6788$$

From the table we have $\chi_{0.05,2}^2 = 5.991$. So the calculated value of χ^2 is less than the table value of χ^2. Hence, we cannot reject the null hypothesis. That means the data agree with the theoretical ratio.

Example 6.29

In a trial with specific fish feed, the following frequency distribution of fish weight was formed. Examine whether the fish weight data fit well with normal distribution with 3000 g mean weight and s.d. of 560 g.

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Fish weight (g) class	750–1250	1250–1750	1750–2250	2250–2750	2750–3250	3250–3750	3750–4250	4250–4750
Observed frequency	2	3	26	60	62	29	4	4

Solution The problem is to test whether the data fit well with the normal distribution or not.

H_0 : The data fits well against
H_1 : The data do not fit well

In normal population, there are two parameters, i.e., μ and σ^2. These are estimated from the given sample frequency distribution. Then $\hat{P}_i$ probabilities for each class interval are calculated, and expected frequency for each class interval is calculated by $E_i = n\,\hat{P}_i$

Let the level of significance be $\alpha = 0.05$.

The test statistic is given by $\chi^2 = \sum_{i=1}^{n} \frac{(O_i - E_i)^2}{E_i}$ at $(k - 2 - 1)$ d.f. = at 5 d.f.

Fish weight (g) class	Observed frequency	Expected frequency	(Obs.−Exp.)^2	$\frac{(\text{Obs.}-\text{Exp.})^2}{\text{Exp.}}$
750–1250	2	2	0.00	0.0000
1250–1750	3	3	0.00	0.0000
1750–2250	26	28	4.00	0.1428
2250–2750	60	63	9.00	0.1428
2750–3250	62	58	16.00	0.2758
3250–3750	29	28	1.00	0.0357
3750–4250	4	5	1.00	0.2000
4250–4750	4	3	1.00	0.3333
Total	**190**			1.13

From the table, we have $\chi^2_{0.05,5} = 11.07$, i.e., the calculated value of χ^2 is less than the table value of χ^2. So the test is nonsignificant, and there is no reason to reject the null hypothesis. So we conclude that the data do not fit well with the normal distribution.

(viii) χ^2 *Test for independence of attributes*

The degree of linear associationship has been discussed for numerical data. The associationship or independence of qualitative characters could be assessed through χ^2 test for independence. If two qualitative characters "A" and "B" are categorized in to m and n groups, respectively, and their frequency distribution is as provided in the table below, then independence of two characters can be judged through this test.

B / A	B_1	B_2	…	B_j	…	B_n	Total
A_1	f_{11}	f_{12}		f_{1j}		f_{1n}	$f_{1.}$
A_2	f_{21}	f_{22}		f_{2j}		f_{2n}	$f_{2.}$
⋮							
A_i	f_{i1}	f_{i2}		f_{ij}		f_{in}	$f_{i.}$
⋮							
A_m	f_{m1}	f_{m2}		f_{mj}		f_{mn}	$f_{m.}$
Total	$f_{.1}$	$f_{.2}$		$f_{.j}$		$f_{.n}$	N

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From the above table, the expected cell frequencies are obtained by multiplying the respective row and column frequency and dividing the same by the total frequency. For example, the expected frequency corresponding to A_iB_j cell is $\frac{f_{i.} \times f_{.j}}{N}$. It may be noted that the total of row frequencies and the total of column frequencies for both the observed and expected frequencies must be equal to the total frequency. Thus, $\sum_{i=1}^{m} f_{i.} = \sum_{j=1}^{n} f_{.j} = N$ and $\sum_{i=1}^{m} \hat{f}_{i.} = \sum_{j=1}^{n} \hat{f}_{.j} = N$. Under the null hypothesis of independence of attributes, the approximate test statistic for the test of independence of attributes is derived from the χ^2 test for goodness of fit as given below

$$\chi^2_{m-1,n-1} = \sum_{i=1}^{m} \sum_{j=1}^{n} \frac{\left(f_{ij} - e_{ij}\right)^2}{e_{ij}}$$

where

f_{ij} = observed frequency for contingency table category in i row and column j ,

e_{ij} = expected frequency for contingency table category in i row and column j,

which is distributed as a χ^2 variate with $(m-1)(n-1)$ d.f.

Note None of the expected cell frequency should less than five.

The special case m×n contingency table is the "2 × 2" contingency table in which both the attributes are categorized in two groups each as given below:

Attribute A	Attribute B		Total
	B_1	B_2	
A_1	a	b	a + b
A_2	c	d	c + d
Total	a + c	b + d	a + b + c + d = N

The formula for calculating χ^2 value is $\chi^2 = \frac{N(ad-bc)^2}{(a+c)(b+d)(a+b)(c+d)}$. Obviously, as there are only two rows and two columns, then the degrees of freedom for the above χ^2 will be (2–1)(2–1) = 1.

The calculated value of χ^2 is to be compared with the table value of χ^2 at specified level of significance and at $(m-1)$, $(n-1)$, or (2–1)(2–1) degrees of freedom, respectively, for $m \times n$ and 2×2 contingency χ^2 table.

Yates Correction The above χ^2 test is valid only when the expected frequency in each cell should be sufficiently large, at least five. This condition gives rise to a problem when the expected frequency of cell(s) is less than five. By merging two adjacent rows or column having cell frequency less than five, this problem could be overcome in case of $m \times n$ tables, but this creates a real problem in case of 2×2 contingency table. In 2×2 table, the possibility of merging cell frequencies is ruled out. Yates has given a rule to overcome this problem of 2×2 tables, which is popularly known as Yates' correction for the formula of χ^2. The formula for adjusted χ^2 is given as $\chi^2_c = \frac{N\left(|ad-bc|-\frac{N}{2}\right)^2}{(a+b)(c+d)(a+c)(b+d)}$ with 1 d.f.

Example 6.30

In a study to facilitate augmentation of education across the race/cast, information were collected to know whether education is independent of cast/race or not. The following table gives the frequency distribution of education standard among different community in a village of 300 families. Test whether the education is independent of cast/race.

	General	SC/ ST	OBC	Others
Preschool	25	5	5	6
Primary	35	25	7	5
Secondary	25	35	8	5
Graduation	45	15	10	6
Postgraduation and above	25	6	5	2

Solution We are to test for independence of two attributes, i.e., category family and the education standard. Under the given condition, we have the null hypothesis:

H_0: educational standard and category of family are independent against

H_1: educational standard and category of family are not independent.

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Let the level of significance be 0.05.

Under the given H_0, the test statistic is $\chi^2 = = \sum_{i=1}^{m}\sum_{j=1}^{n}\frac{\left(f_{ij}-e_{ij}\right)^2}{e_{ij}}$

For the calculation purpose, let us frame the following table.

Table of observed frequencies:

	General	SC/ ST	OBC	Others	Total
Preschool	25	5	5	6	41
Primary	35	25	7	5	72
Secondary	25	35	8	5	73
Graduation	45	15	10	6	76
Postgraduation and above	25	6	5	2	38
Total	155	86	35	24	300

Using the row totals and column totals corresponding to each cell, expected frequencies are calculated as $\frac{f_{i.}\times f_{.j}}{N} = \frac{R_i C_j}{N}$, where R_i and C_j are the ith row and jth column total respectively. With the help of the calculated expected frequencies, let us construct the following table.

Table of expected frequencies:

	General	SC/ ST	OBC	Others	Total
Preschool	21.18	11.75	4.78	3.28	41
Primary	37.20	20.64	8.40	5.76	72
Secondary	37.72	20.93	8.52	5.84	73
Graduation	39.27	21.79	8.87	6.08	76
Postgraduation and above	19.63	10.89	4.43	3.04	38
Total	155	86	35	24	300

Using the observed and expected frequencies from the above tables, we find out the $\frac{\left(f_{ij}-e_{ij}\right)^2}{e_{ij}}$ for each cell χ^2 value for each cell and frame the following table:

	General	SC/ ST	OBC	Others
Preschool	0.69	3.88	0.01	2.26
Primary	0.13	0.92	0.23	0.10
Secondary	4.29	9.46	0.03	0.12
Graduation	0.84	2.11	0.14	0.00
Postgraduation and above	1.47	2.20	0.07	0.36

From the above table, we calculate $\chi^2 = \sum_{i=1}^{5}\sum_{j=1}^{4}\frac{\left(f_{ij}-e_{ij}\right)^2}{e_{ij}} = 29.3128$ at (5–1)(4–1) = 12 d.f.

The table value of $\chi^2_{0.05,12} = 21.026$ is less than the calculated value of χ^2. Hence, the test is significant and the null hypothesis is rejected. We can conclude that the two attributes educational standard and the categories of family are not independent to each other.

Example 6.31

The following table gives the frequency distribution of scent and color of 200 roses in a garden. Test whether scent is independent of color of flower or not.

Color / Scent	Pink	Red
Intense	35	75
Light	55	35

Solution Under the given condition, we are to test whether the color of flower and intensity of fragrance are independent of each other or not. Thus, we are to test H_0: color of flower and intensity of fragrance are independent of each other against the alternative hypothesis

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H_1: color of flower and intensity of fragrance are not independent of each other. Let us set the level of significance at 0.05.

The test statistic follows a χ^2 distribution with 1 d.f. Let the level of significance be 0.05.

$\chi^2 = \frac{(ad-bc)^2N}{(a+b)(c+d)(a+c)(b+d)}$ where a, b, c, and d are the cell frequencies for first, second, third, and fourth cells in the given frequency distribution table, respectively. As none of the frequencies has value lesser than five, we don't have to go for Yates' correction.

So $\chi^2 = \frac{(ad-bc)^2N}{(a+b)(c+d)(a+c)(b+d)} = \frac{(35\times35-75\times55)^2\times200}{110\times90\times90\times110}$ $= 17.1615$.

The table value of $\chi^2_{0.05,1} = 3.841$ is less than the calculated value of χ^2. Hence, the test is significant and the null hypothesis is rejected. We can conclude that the two attributes color of flower and intensity of fragrance are not independent of each other.

Example 6.32 The following 2 × 2 table gives the frequency distribution of body shape and test of 100 Hilsa fishes. Test whether the two attributes shape and test are independent or not.

Fish type		Test	
		Beautiful	Moderate
	Flattened	45	15
	Elongated	3	37

Solution Under the given condition, we are to test whether the two attributes, viz., body shape and test of fishes, are independent of each other or not. That means the null and alternative hypotheses are, respectively,

H_0: body shape and test are independent of each other, against

H_1: body shape and test are not independent of each other.

Let the level of significance be 0.05.

The test statistic for the problem will be χ^2 with 1 d.f. It is expected that a cell frequency will be less than five, so we are to adopt the formula for χ^2 with Yates correction. Thus, $\chi_c{}^2 = \frac{\left(|ad-bc|-\frac{N}{2}\right)^2N}{(a+b)(c+d)(a+c)(b+d)} = \frac{\left(|45\times37-15\times3|-\frac{100}{2}\right)^2100}{(45+15)(37+3)(3+45)(15+37)}$ $= 41.1475$

At 0.05 level of significance and the corresponding table value at 1d.f. are 3.84. So the calculated value of $\chi_c{}^2$ is more than the table value of χ^2 at 1d.f. at 5 % level of significance. Hence, the test is significant and the null hypothesis is rejected. We can conclude that the two attributes are not independent to each other.

(ix) *Bartlett's test for homogeneity of variances*

In breeding trials, the parents are selected based on their performance to particular character or characters. So characterization and evaluation is a process needed before taking up the breeding program. In characterization and evaluation trial, a huge number of progenies/varieties/breeds are put under evaluation over different climatic situations, i.e., over different seasons/locations/management practices etc. So pooling of data becomes necessary to have an overall idea about the materials put under evaluation. For pooling of data, test for homogeneity of variance is necessary of such experiments. If homogeneity of variances is accepted, then one can go for pooling data. Otherwise, there are different methods for analysis of combining such data. Readers may consult *Applied and Agricultural Statistics – II* by Sahu and Das for the purpose. The F-test can serve the purpose of testing homogeneity of two variances. When more than two experimental data are required to be pooled, then homogeneity of variance test through F statistic does not serve the purpose. Bartlett's test for homogeneity gives a way out to solve the problem. Bartlett's test for homogeneity of variances is essentially based on χ^2 test. Let us suppose we have k independent samples drawn from k normal populations, with means μ_1, μ_1, μ_1,....., μ_k; and variances $\sigma_1{}^2$, $\sigma_2{}^2$, $\sigma_3{}^2$, ..., $\sigma_k{}^2$; each of size n_i (n_1,n_2,n_3...n_i....n_k), the observed values are x_{ij} (x_{11},x_{12},x_{13}....x_{1n1}; x_{21},x_{22},x_{23},.....,x_{2n2}; .....; x_{k1},x_{k2},x_{k3},....., x_{knk}). The problem that is related in testing the null hypothesis is $H_0 : \sigma_1^2 = \sigma_2^2 = \ldots\ldots\ldots = \sigma_k^2$ $(= \sigma^2, \text{say})$ against the alternative hypothesis H_1

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that these variances are not all equal. The approximate test statistic under H_0 is

$$\chi^2_{k-1} = \frac{\left[\sum_{i=1}^{k}(n_i-1)\log_e \frac{s^2}{s_i^2}\right]}{1+\frac{1}{3(k-1)}\left\{\sum_{i=1}^{k}\frac{1}{(n_i-1)} - \frac{1}{\sum_{i=1}^{k}(n_i-1)}\right\}}$$

where,

$s_i^2 = \frac{1}{n_i-1}\sum_{j=1}^{n_i}\left(x_{ij}-\bar{x}_i\right)^2$ = sample mean square for the ith sample, ($i = 1, 2, 3, \ldots k$).

and $s^2 = \dfrac{\sum_{i=1}^{k}(n_i-1)(s_i)^2}{\sum_{i=1}^{k}(n_i-1)}$

If the calculated value of $\chi^2 > \chi^2_{\alpha,k-1}, H_0$ is rejected.

Example 6.34

An experiment with different feeding for a particular breed of swine is conducted in three season, viz., *summer*, *rainy*, *and spring* seasons; the same experimental protocol was followed in all the seasons. Three seasons data were analyzed separately, and the respective error mean square along with the degrees of freedom is given below. Test whether pooling of data from the three experiments can be done or not:

Season	d.f.	Error mean square
Summer	17	477
Rainy	15	387
Spring	15	377

Solution For the purpose of pooling data of three seasons, testing of homogeneity of variances of the experiments is required. We know that the error mean squares are the estimates of the variances. So the null hypothesis for the present problem is

H_0: Variances of the three experiments conducted in three seasons are homogenous in nature, against the alternative hypothesis

H_1: Variances of the three experiments conducted in three seasons are not homogenous in nature.

The test statistic is

$$\chi^2_{k-1} = \frac{\left[\sum_{i=1}^{k}(n_i-1)\log\frac{s^2}{s_i^2}\right]}{\left[1+\frac{1}{3(k-1)}\left\{\sum_{i=1}^{k}\frac{1}{(n_i-1)} - \frac{1}{\sum_{i=1}^{k}(n_i-1)}\right\}\right]}$$

For the present problem,

$$\chi^2_2 = \frac{\left[\sum_{i=1}^{3}(n_i-1)\log\frac{s^2}{s_i^2}\right]}{\left[1+\frac{1}{3(3-1)}\left\{\sum_{i=1}^{3}\frac{1}{(n_i-1)} - \frac{1}{\sum_{i=1}^{3}(n_i-1)}\right\}\right]}$$

at 2 d.f

Let the level of significance $\alpha = 0.05$.

$$s^2 = \frac{1}{\sum_{i=1}^{3}(n_i-1)}\sum_{i=1}^{3}(n_i-1)(s_i)^2$$

$$= \frac{18,328}{44} = 416.545$$

For this example, we have following table:

(n_i-1)	s_i^2	$(n_i-1)s_i^2$	$(n_i-1)\log\frac{s^2}{s_i^2}$	$\frac{1}{(n_i-1)}$
16	477	7632	−2.168	0.063
14	387	5418	1.030	0.071
14	377	5278	1.396	0.071
Total		18328	0.258	0.205

$$\therefore \chi^2_2 = \frac{0.258}{\left[1+\frac{1}{6}\left\{0.205-\frac{1}{44}\right\}\right]} = \frac{0.258}{1.030} = 0.250 \text{ with 2 d.f.}$$

From the table, we have $\chi^2_{0.05,2} = 5.99$.

The calculated value of χ^2 (0.250) is less than the table value of $\chi^2_{0.05,2}$; hence, we cannot reject the null hypothesis. That means the variances are homogeneous in nature. So we can pool the information of three experiments.

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(x) *Test for significance of specified population correlation coefficient*

Under large sample setup, let (x_1,y_1), (x_2,y_2) .....(x_n,y_n) be a random sample drawn from a bivariate normal population with population correlation coefficient ρ. Under $\rho \neq 0$, the distribution of sample correlation coefficient r is complex. But R. A. Fisher has proved that the statistic Z defined as $Z = \frac{1}{2}\log_e \frac{1+r}{1-r}$ is distributed approximately as normal variate with mean $\xi = \frac{1}{2}\log_e \frac{1+\rho}{1-\rho}$ and $V(Z) = \frac{1}{n-3}$. Our objective is to test $H_0 : \rho = \rho_0 (\neq 0)$ The approximate test statistic under H_0 is given by The approximate test statistic under is given by $\tau = \frac{Z-\xi_0}{\sqrt{\frac{1}{n-3}}\sim N(0,1)}$ and $\xi_0 = \frac{1}{2}\log_e \frac{1+\rho_0}{1-\rho_0}$

If the calculated absolute value of the τ be greater than the table value at specified level of significance, the test is significant, and the null hypothesis is rejected; otherwise, there is no reason to reject the null hypothesis at the specific level of significance.

Example 6.35
The correlation coefficient between the age and the milking capacity of a randomly selected 50 cattle of a particular breed is found to be 0.76. Test whether the sample has come from a bivariate normal population with correlation coefficient between age and milking capacity of cattle as 0.67 or not.

Solution Under the given condition, the null hypothesis is $H_0 : \rho = 0.67$ against the alternative $H_1 : \rho \neq 0.67$.

Given that $r = 0.76$. and $n = 50$.

Under H_0 the test statistic is

$$\tau = (Z - \xi_0)\sqrt{n-3} \text{ where}$$

$$Z = \frac{1}{2}\log_e \frac{1+r}{1-r} = \frac{1}{2}\log_e \frac{1+0.76}{1-0.76} = 0.996$$

$$\xi_0 = \frac{1}{2}\log_e \frac{1+\rho_0}{1-\rho_0} = \frac{1}{2}\log_e \frac{1+0.67}{1-0.67} = 0.810$$

$$\tau = (0.996 - 0.810)\sqrt{50-3} = 1.275$$

Thus, the calculated value of $|\tau|$ is less than 1.96 the critical value of the standard normal variate. So we cannot reject the null hypothesis.

6.3 Nonparametric Method

In biostatistics, nonparametric tests are of much importance. In the following section, we discuss some of the nonparametric tests useful in agriculture, veterinary, fishery, and allied fields.

6.3.1 One Sample Test

(i) *Sign test for specified value of median*

Likewise to that mean test in parametric method, here we want to test the specified value for median. Suppose, we have a random sample x_1, x_2, x_3,.....x_n of size "n" drawn from a population for which median θ is unknown. We want to test H_0: $\theta = \theta_0$, a specified value of θ against the alternative hypotheses (i) $\theta \neq \theta_0$, (ii) $\theta > \theta_0$, (iii) $\theta < \theta_0$.

We know that median divides the whole distribution in two equal halves and there will be equal number of observations below and above the value θ_0, if θ_0 be the median of the distribution. Let us denote the observations greater than θ_0 with plus (+) signs and the observations smaller than θ_0 with minus (−) signs, ignoring the values equals to the median. Suppose we have r plus (+) signs and s minus (−) signs.

Thus, $r + s = m \leq n$. The distribution of r given $r + s = m$ is binomial with probability ½. This "r" can be taken to test H_0. The null hypothesis H_0: $\theta = \theta_0$ is equivalent to testing H_0: $P = 1/2$, where P is the probability of $\times > \theta_0$. Here we come across with three types of situations:

(a) For testing the null hypothesis H_0: $P = 1/2$ against the alternative hypothesis, H_1: $\theta \neq \theta_0$, the critical region for α level of significance is given by $r \leq r'_{\alpha/2}$ and $r \geq r_{\alpha/2}$ where $r_{\alpha/2}{}'$ and $r_{\alpha/2}$ are the largest and smallest integer such that $\sum_{r=0}^{r'_{\alpha/2}} \binom{m}{r}\left(\frac{1}{2}\right)^m \leq \frac{\alpha}{2}$ and $\sum_{r=\alpha/2}^{m} \binom{m}{r}\left(\frac{1}{2}\right)^m \leq \frac{\alpha}{2}$.

(b) For testing the null hypothesis H_0: $P=1/2$ against the alternative hypothesis H_1: $\theta > \theta_0$, the critical region for αlevel of significance is given by $r \geq r_\alpha$, where r_α is the smallest integer. such that $\sum_{r\,=\,r_\alpha}^{m} \binom{m}{r}\left(\frac{1}{2}\right)^m \leq \alpha$.

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(c) For testing the null hypothesis H_0: $P = 1/2$ against the alternative hypothesis H_1: $\theta < \theta_0$, the critical region for α level of significance is given by $r \leq r'_{\alpha}$ where $r_{\alpha}{}'$ is the larger integer such that $\sum_{r=0}^{m} \binom{m}{r} \left(\frac{1}{2}\right) \leq \alpha$.

Example 6.36
The following data are pertaining to the length of tiger prawn in a particular pond. Justify whether the median length of prawn can be taken as 25 cm or not.

22.2, 26.5, 30.0, 18.0, 15.6, 20.0, 22.0, 19.5, 26.7, 28.5, 20.0, 24.6, 22.0, 32.5, 32.0

Solution In the first step, we have to assign the signs to each of the given observation as follows:

Length of tiger prawn	22.20	26.50	30.00	18.00	15.60	20.00	22.00	
Sign	–	+	+	–	–	–	–	
Length of tiger prawn	19.50	26.70	28.50	20.00	24.60	22.00	32.50	32.00
Sign	–	+	+	–	–	–	+	+

There are 5 (=r) plus (+) signs and 9 (=s) minus (−) signs, and one observation is equal to the median value and discarded. This r follows binomial distribution with parameter ($m = r + s = 5 + 9 = 14$) and p (=1/2). Thus, testing of H_0: $\theta = 25$ cm against $H_1 : \theta \neq 25$ cm is equivalent to testing of $H_0 : p = 1/2$ against $H_1 : p \neq 1/2$.

The critical region for $\alpha = 0.05$ (two-sided test) is $r \geq r_{\alpha/2}$ and $r \leq r'_{\alpha/2}$ where r is the number of plus signs and $r_{\alpha/2}$ and $r'_{\alpha/2}$ are the smallest and largest integer, respectively, such that $\sum_{r_{\alpha/2}}^{14} \binom{14}{x} \left(\frac{1}{2}\right)^{14} \leq \alpha/2$ and $\sum_{0}^{r'_{\alpha/2}} \binom{14}{x} \left(\frac{1}{2}\right)^{14} \leq \alpha/2$.

From the table, we get $r_{0.025} = 3$ and $r'_{0.025} = 11$ for 14 distinct observation at $p = 1/2$. For this example, we have $3 < r = 5 < 11$, so we cannot reject the null hypothesis at 5 % level of significance, i.e., we conclude that the median of the length of prawn length can be taken as 25 cm.

(ii) *Test of randomness*

(a) *One sample run test*: To judge the behavior of a series of observation, one sample run test is used. This test helps us to decide whether a given sequence/arrangements are random or not.

Here we define a run as a sequence of letters (signs) of the same kind delimited by letters (signs) of other kind at both ends. Let m be the number of elements of one kind and n be the number of element of other kind. That is, m might be the number of heads and n might be the number of tails, or m might be the number of pluses and n might be the number of minuses; also, suppose that N be the total number of two different kinds mentioned above. So $N \geq m + n$. The occurrence of sequence of two different kinds is noted first and determines the number of runs in total taking runs in both kinds. Let x_1, x_2, x_3, $\ldots x_n$ be a sample drawn from a single population. At the first instance, we find out the median of the sample and denote observations below the median by a minus sign and observations above the median by plus signs. The value equal to the median need not be considered. Then we count the number of runs (r) of plus and minus signs. If both the m and n are equal to or less than 20, then the following Tables 6.7a and 6.7b gives the critical value corresponding to m and n. If the observed value of r falls within the critical value, we accept H_0.

If m or n or both are large, the number of runs below and above the sample median value is a random variable with mean $E(r) = \frac{N+2}{2}$ and variance $\mathrm{Var}(r) = \frac{N(N-2)}{4(N-1)}$. This formula is exact when the "N" is even. Under large sample setup, "r" is normally distributed with above expectation and variance. Thus, the appropriate test statistic is a standard normal variate: $\tau = \frac{r - E(r)}{\sqrt{\mathrm{Var}(r)}} \sim N(0, 1)$.

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Table 6.7a Lower critical values of "r" in the run test

n_1/n_2	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
2											2	2	2	2	2	2	2	2	2
3					2	2	2	2	2	2	2	2	2	3	3	3	3	3	3
4				2	2	2	3	3	3	3	3	3	3	3	4	4	4	4	4
5				2	2	3	3	3	3	4	4	4	4	4	4	4	5	5	5
6		2	2	3	3	3	3	4	4	4	4	5	5	5	5	5	5	6	6
7		2	2	3	3	3	4	4	5	5	5	5	5	6	6	6	6	6	6
8		2	3	3	3	4	4	5	5	5	6	6	6	6	6	7	7	7	7
9		2	3	3	4	4	5	5	5	6	6	6	7	7	7	7	8	8	8
10		2	3	3	4	5	5	5	6	6	7	7	7	7	8	8	8	8	9
11		2	3	4	4	6	5	6	6	7	7	7	8	8	8	9	9	9	9
12	2	2	3	4	4	5	6	6	7	7	7	8	8	8	9	9	9	10	10
13	2	2	3	4	5	5	6	6	7	7	8	8	9	9	9	10	10	10	10
14	2	2	3	4	5	5	6	7	7	8	8	9	9	9	10	10	10	11	11
15	2	3	3	4	5	6	6	7	7	8	8	9	9	10	10	11	11	11	12
16	2	3	4	4	5	6	6	7	8	8	9	9	10	10	11	11	11	12	12
17	2	3	4	4	5	6	7	7	8	9	9	10	10	11	11	11	12	12	13
18	2	3	4	6	5	6	7	8	8	9	9	10	10	11	11	12	12	13	13
19	2	3	4	5	6	6	7	8	8	9	10	10	11	11	12	12	13	13	13
20	2	3	4	5	6	6	7	8	9	9	10	10	11	12	12	13	13	13	14

Table 6.7b Upper critical values of "r" in the run test

n_1/n_2	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
2																			
3																			
4				9	9														
5			9	10	10	11	11												
6		9	10	11	12	12	13	13	13	13									
7			11	12	13	13	14	14	14	14	15	15	15						
8			11	12	13	14	14	15	15	16	16	16	16	17	17	17	17	17	17
9				13	14	14	15	16	16	16	17	17	18	18	18	18	18	18	18
10				13	14	15	16	16	17	17	18	18	18	19	19	19	20	20	20
11				13	14	15	16	17	17	18	19	19	19	20	20	20	21	21	21
12				13	14	16	16	17	18	19	19	20	20	21	21	21	22	22	22
13					15	16	17	18	19	19	20	20	21	21	22	22	23	23	23
14					15	16	17	18	19	20	20	21	22	22	23	23	23	24	24
15					15	16	18	18	19	20	21	22	22	23	23	24	24	25	25
16						17	18	19	20	21	21	22	23	23	24	25	25	25	25
17						17	18	19	20	21	22	23	23	24	25	25	26	26	26
18						17	18	19	20	21	22	23	24	25	25	26	26	27	27
19						17	18	20	21	22	23	23	24	25	26	26	27	27	27
20						17	18	20	21	22	23	24	25	25	26	27	27	28	28

Any value of r equal to or smaller than the value shown in lower critical value of r and greater than or equals to the upper critical value shown in table is significant at 0.05 level of significance.

Example 6.37

A batch of 20 agriculture students are randomly inquired about their family background, i.e., whether they are coming from Below Poverty Level (BPL-B) or Above Poverty Level (APL-A) group. The following is the statement

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in terms of A and B for APL and BPL groups, respectively. Test whether the students inquired appeared for inquiry in random manner or not.

A,B,A,B,A,A,A,B,B,A,B,A,A,B,A,A,A,B,B,A

Solution

H_0: The order of APL and BPL student enquired was random against

H_1: The order of APL and BPL student enquired was not random.

Let the level of significance be 0.05.

Now from the given information, we have $A = 12(m)$ and $B = 8(n)$.

The number of runs formed by the students of their turn in facing the enquiry is as follows:

A, B, A, B, A,A,A, B,B, A, B, A,A, B, A,A,A, B, B, A

Thus, we have 13 runs. For 12 and 8, the critical values from above Tables 6.7a and 6.7b are 6 and 16, respectively. That is, a random sample should have number of runs in between 6 and 16. In this problem, we have 13, which is well within the desired range. So we conclude that the null hypothesis of APL and BPL student inquired at random cannot be ruled out.

Example 6.38

The following figures give the production (million tons) of cat fish production of India for the year 1951 through 2010. Test whether the cat fish production has changed randomly or followed a definite trend:

Year	1951	1952	1953	1954	1955	1956	1957	1958	1959	1960
Production	17.35	18.75	23.32	21.70	18.68	23.31	27.38	29.87	20.27	25.04
Year	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970
Production	10.93	19.31	17.57	22.73	18.91	22.56	24.30	23.78	26.89	50.62
Year	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980
Production	48.84	42.43	52.63	76.18	68.67	43.52	53.48	39.20	48.76	43.71
Year	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990
Production	59.37	67.63	60.64	57.26	44.50	52.93	44.77	64.41	49.79	38.23
Year	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000
Production	39.34	36.53	43.26	45.45	38.49	35.50	44.09	52.12	46.53	57.06
Year	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010
Production	49.14	57.61	53.47	52.14	45.42	56.54	65.34	92.36	107.57	85.67

Solution We are to test the null hypothesis.

H_0: The series is random against the alternative hypothesis.

H_1: The series is not random.

Let the level of significance be $\alpha = 0.05$.

Let us first calculate the median and assign positive signs to those values which are greater than the median value and minus signs to those values which are less than the median value; the information are provided in the table given below.

Median = 44.30 (thousand tones)

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Year	1951	1952	1953	1954	1955	1956	1957	1958	1959	1960
Production	17.35	18.75	23.32	21.70	18.68	23.31	27.38	29.87	20.27	25.04
Signs	−	−	−	−	−	−	−	−	−	−
Year	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970
Production	10.93	19.31	17.57	22.73	18.91	22.56	24.30	23.78	26.89	50.62
Signs	−	−	−	−	−	−	−	−	−	+
Year	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980
Production	48.84	42.43	52.63	76.18	68.67	43.52	53.48	39.20	48.76	43.71
Signs	+	−	+	+	+	−	+	−	+	−
Year	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990
Production	59.37	67.63	60.64	57.26	44.50	52.93	44.77	64.41	49.79	38.23
Signs	+	+	+	+	+	+	+	+	+	−
Year	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000
Production	39.34	36.53	43.26	45.45	38.49	35.50	44.09	52.12	46.53	57.06
Signs	−	−	−	+	−	−	−	+	+	+
Year	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010
Production	49.14	57.61	53.47	52.14	45.42	56.54	65.34	92.36	107.57	85.67
Sign	+	+	+	+	+	+	+	+	+	+

As the sample size is large, one should apply randomness test through normality test of the number of runs, r. Here, the number of runs is found to be 14, i.e., $r = 14$.

$$\mathrm{E}(r) = \frac{N+2}{2} = \frac{60+2}{2} = 31 \text{ and}$$

$$\mathrm{Var}(r) = \frac{N(N-2)}{4(N-1)} = \frac{60(60-2)}{4(60-1)} = \frac{2480}{236} = 14.74$$

$$\tau = \frac{r - E(r)}{\sqrt{\mathrm{Var}(r)}} = \frac{14-31}{\sqrt{14.74}} = \frac{-17}{3.84} = -4.42$$

Thus, $|\tau| = 4.42 > 1.96$ (the critical value at $\alpha = 0.05$; hence, the null hypothesis of randomness is rejected. We can conclude that the cat fish production of India has not changed in random manner but followed a definite pattern.

(b) *Test of turning points*

Another large sample nonparametric test for randomness is the test of turning points. The process is to record the departure from trends in a given data set. Precisely, the technique involved in counting peaks and troughs in the series. A "peak" is defined as a value greater than its two neighboring values, and a "trough" is defined as a value which is lower than of its two neighbors. Both the peaks and troughs are treated as turning points of the series. At least three consecutive observations are required to define a turning point. Suppose we have three consecutive points U_1, U_2, U_3, of which either $U_1 > U_2 < U_3$ or $U_1 < U_2 > U_3$; then U_2 is termed as a turning point in both the cases. In general form, if the series is random, then these three values could have occurred in any order, viz., in six ways. But in only four of these ways would there be a turning point. Hence, the probability of turning points in a set of three values is 4/6 = 2/3.

Let us generalize the three point case into n point case; let $U_1, U_2, U_3 \ldots\ldots\ldots\ldots\ldots\ldots\ldots U_n$ be a set of observations, and let us define a marker variable X_i by

$$X_i = 1 \text{ when } U_i < U_{i+1} > U_{i+2} \text{ and } U_i > U_{i+1} < U_{i+2}$$

$$= 0; \text{otherwise}, \forall, i = 1,2,3 \ldots\ldots\ldots (n-2).$$

Hence, the number of turning points "p" is then $p = \sum_{i=1}^{n-2} x_i$, and we have $E(p) = \sum_{i=1}^{n-2} E(x_i) =$

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$\frac{2}{3}(n-2)$ and $E(p^2) = E\sum_{i=1}^{n-2}(x_i)^2 = \frac{40n^2-144n+131}{90}$

$\mathrm{Var}(p) = E(p^2) - (E(p))^2 = \frac{16n-29}{90}$. It can easily be verified that as "n," the number of observations, increases, the distribution of "p" tends to normality. Thus, for testing the null hypothesis, H_0: series is random, we have the test statistic $\tau = \frac{p-E(p)}{\sqrt{\mathrm{Var}(p)}} \sim N(0,1)$.

Example 6.39

The fresh milk production (million tons) of a country since 1961 is given bellow. Test whether the milk production of the country has changed randomly or not:

Year	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970
Production (*m. t*)	5.23	5.46	5.55	6.34	6.77	6.89	6.90	7.24	7.25	7.35
Year	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980
Production (*m. t*)	7.35	***7.32***	7.76	9.02	9.97	***10.67***	*9.86*	10.09	10.50	*11.96*
Year	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990
Production (*m. t*)	*11.68*	11.82	11.82	12.30	12.45	12.88	13.40	13.94	14.53	14.93
Year	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000
Production (*m. t*)	15.55	*16.27*	*16.07*	16.27	16.99	19.09	19.24	19.27	19.66	20.38
Year	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010
Production (*m. t*)	21.15	22.31	22.94	24.20	25.38	*26.19*	*26.14*	28.44	29.09	30.72

Solution From the given information, one can have (1) number of observation = 50 and (2) number of turning point $p = 9$ (bold and underlined values).

Year	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970
Production (*mt*)	5.23	5.46	5.55	6.34	6.77	6.89	6.90	7.24	7.25	7.35
Year	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980
Production (*mt*)	7.35	*7.32*	7.76	9.02	9.97	*10.67*	*9.86*	10.09	10.50	*11.96*
Year	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990
Production (*mt*)	*11.68*	11.82	11.82	12.30	12.45	12.88	13.40	13.94	14.53	14.93
Year	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000
Production (*mt*)	15.55	*16.27*	*16.07*	16.27	16.99	19.09	19.24	19.27	19.66	20.38
Year	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010
Production (*mt*)	21.15	22.31	22.94	24.20	25.38	*26.19*	*26.14*	28.44	29.09	30.72

The null hypothesis is to test H_0: The series is random.

We have the expectation of turning point (p) $E(p) = \frac{2}{3}(n-2) = \frac{2}{3}(50-2) = \frac{92}{3} = 30.67$ and the variance $\mathrm{Var}(p) = \frac{16n-29}{90} = \frac{16*50-29}{90} = \frac{711}{90} = 8.56$

Thus, the test statistic

$$\tau = \frac{p - \mathrm{E}(p)}{\sqrt{\mathrm{Var}(p)}} = \frac{9 - 30.67}{\sqrt{8.56}} = \frac{-21.67}{2.92} = -7.42$$

We know that the τ is the standard normal variate, and the value of standard normal variate at $P = 0.05$ is 1.96. as the calculated value of $|\tau| = 7.42 > 1.96$, so the test is significant; we reject the null hypothesis. We can conclude that

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at 5 % level of significance, there is no reason to take that the milk production of the country has changed randomly since 1961.

(iii) *Kolmogorov-Smirnov one sample test*

χ^2 test for goodness of fit is valid under certain assumptions like large sample size etc. The parallel test to the abovementioned χ^2 tests which can also be used under small sample conditions is Kolmogorov-Smirnov one sample test. In this one sample test for goodness of fit, we test the null hypothesis that the sample of observations x_1, x_2, x_3, ...x_n has come from a specified population distribution against the alternative hypothesis that the sample has come from other distribution. Suppose x_0, x_2, x_3, ...x_n be a random sample from a population of distribution function $F(x)$ and the sample cumulative distribution function is given as $F_n(x)$ where $F_n(x)$ is defined as $F_n(x) = \frac{k}{n}$ where k is the number of observations equal to or less than x. Now for fixed value of x, $F_n(x)$ is a statistic following binomial distribution with parameter $(n, F(x))$. To test bothsided goodness of fit for H_0: $F(x) = F_0(x)$ for all x against the alternative hypothesis H_1: $F(x) \neq F_0(x)$, the test statistic is $D_n = \underset{x}{Sup}\,[|F_n(x) - F_0(x)|]$. The distribution D_n does not depend on F_0 as long as F_0 is continuous. Now if F_0 represents the actual distribution function of x, then the value of D_n is expected to be small; on the other hand, a large value of D_n is an indication of the deviation of distribution function from F_0.

Example 6.40 A die is thrown 90 times, and the frequency distribution of appearance of different faces of die is given as follows. Examine whether the dies were unbiased or not.

Faces of die	1	2	3	4	5	6
Frequency	10	15	20	10	15	20

Solution If the die is unbiased, then the appearance of different faces of die should follow a rectangular distribution. Let $F_0(x)$ be the distribution function of a rectangular distribution over the range [0,1], then $H_0 : F(x) = F_0(x)$. We know that

$F_0(x) = 0$ if $x < 0$
$= x$ if $0 \leq x \leq 1$ for a rectangular distributions.
$= 1$ if $x > 1$

We make following table:

x	f	$F_0(x)$	$F_n(x)$	$\lvert F_n(x) - F_0(x)\rvert$
1.	10	1/6 = 0.166	10/90 = 0.111	0.055
2.	15	2/6 = 0.333	25/90 = 0.277	0.055
3.	20	3/6 = 0.500	45/90 = 0.500	0.000
4.	10	4/6 = 0.667	55/90 = 0.611	0.055
5.	15	5/6 = 0.833	70/90 = 0.777	0.055
6.	20	6/6 = 1.000	90/90 = 1.000	0.055

Let the level of significance be $\alpha = 0.05$. From tables, we get for $n = 6$ the critical value of K-S statistic D_n at 5 % level of significance is 0.519.

Thus, the calculated value of $D_n = \underset{x}{Sup}\,[|F_n(x) - F_0(x)|] = 0.055 < $ the table value (0.519). That means we conclude that the given sample is from the rectangular parent distribution; hence, the die is unbiased (Table 6.8).

6.3.2 Two Sample Test

(i) *Paired sample sign test*: For bivariate population, the idea of one sample sign test can very well be extended by introducing a transformed variable equals to the difference between the values of the pair of observation. Suppose we have a random paired sample of n observations (x_1,y_1), (x_2,y_2), (x_3,y_3),.....(x_n,y_n) be drawn from a bivariate population. Thus, we are not measuring two variables for n observations, but n observations are measured twice; that's why these are related and paired. Let us define $d_i = x_i - y_i$ $(i = 1,2,3, ..n)$. It is assumed that the distribution function of difference d_i, is also continuous.

Our problem is to test the median of the differences Med(d) equals to zero, i.e., H_0: Med$(d) = 0$, i.e., Prob.$(d > 0)$ = Prob. $(d < 0) = \frac{1}{2}$. Readers may please note that Med(d) is not necessarily equal to Med

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Table 6.8 Critical values of K-S one sample test statistic at different level of significance (α) for both one-sided and two-sided test

One-sided test											
$\alpha =$	.10	.05	.025	.01	.005	$\alpha =$	.10	.05	.025	.01	.005
Two-sided test											
$\alpha =$	.20	.10	.50	.02	.01	$\alpha =$	.20	.10	.50	.02	.01
$n = 1$	0.900	0.950	0.975	0.990	0.995	$n = 21$	0.226	0.259	0.287	0.321	0.344
2	0.684	0.776	0.842	0.900	0.929	22	0.221	0.253	0.281	0.314	0.337
3	0.565	0.636	0.708	0.785	0.829	23	0.216	0.247	0.275	0.307	0.330
4	0.493	0.565	0.624	0.689	0.734	24	0.212	0.242	0.269	0.301	0.323
5	0.447	0.510	0.563	0.627	0.669	25	0.208	0.238	0.264	0.295	0.317
6	0.410	0.468	0.519	0.577	0.617	26	0.204	0.233	0.259	0.291	0.311
7	0.381	0.436	0.483	0.538	0.576	27	0.200	0.229	0.254	0.284	0.305
8	0.358	0.410	0.454	0.507	0.542	28	0.197	0.225	0.250	0.277	0.300
9	0.339	0.387	0.430	0.480	0.513	29	0.193	0.221	0.246	0.275	0.295
10	0.323	0.369	0.409	0.457	0.489	30	0.190	0.218	0.242	0.700	0.290
11	0.308	0.352	0.391	0.437	0.468	31	0.187	0.214	0.238	0.266	0.285
12	0.296	0.338	0.375	0.419	0.450	32	0.184	0.211	0.234	0.262	0.281
13	0.285	0.325	0.361	0.404	0.432	33	0.182	0.208	0.231	0.258	0.277
14	0.275	0.314	0.349	0.390	0.418	34	0.179	0.205	0.227	0.254	0.273
15	0.266	0.304	0.338	0.377	0.404	35	0.177	0.202	0.224	0.251	0.269
16	0.258	0.295	0.327	0.366	0.392	36	0.740	0.199	0.221	0.247	0.265
17	0.250	0.286	0.318	0.355	0.381	37	0.172	0.196	0.218	0.244	0.262
18	0.244	0.279	0.309	0.346	0.371	38	0.170	0.194	0.215	0.241	0.258
19	0.237	0.271	0.301	0.337	0.361	39	0.168	0.191	2.130	0.238	0.255
20	0.232	0.265	0.294	0.329	0.352	40	0.165	0.189	0.210	0.235	0.252

(x)–Med(y), so that H_0 is not that Med(x) = Med(y) but the Med(d) = 0. Like the one sample sign test, we assign plus (+) and minus (−) signs to the difference values (d_i) which are greater and lesser than zero, respectively. We perform the one sample sign test as given in the previous section and conclude accordingly.

Example 6.41
Ten cows of particular breed were subjected to hormonal treatment. Weight of milk per day before and 3 weeks after the treatment was recorded and are given below. Test whether there is any significant effect of hormonal treatment on milk yield of the cows or not.

		1	2	3	4	5	6	7	8	9	10
Milk weight (kg)	Before	5.5	4.8	4.5	6.2	4.8	5.9	3.7	4.0	4.8	5.2
	After	5.6	5.1	4.8	6.0	5.2	5.7	4.5	4.6	4.9	5.5

Solution Let d_i (i = 1,2,3…10) be the change in weight of milk yield by ten cows due to hormonal treatment. The null hypothesis under the given condition is $H_0 : \theta = 0$ against the alternative hypothesis $H_1 : \theta > 0$ where θ is the median of the distribution of the differences:
We have eight minus signs and two plus signs, and we know that under the null hypothesis, the

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		1	2	3	4	5	6	7	8	9	10
Milk weight (kg)	Before (X)	5.5	4.8	4.5	6.2	4.8	5.9	3.7	4.0	4.8	5.2
	After (Y)	5.6	5.1	4.8	6.0	5.2	5.7	4.5	4.6	4.9	5.5
Difference in weight	($x-y$)	−0.1	−0.3	−0.3	0.2	−0.4	0.2	−0.8	−0.6	−0.1	−0.3

number of plus signs follows a binomial distribution with parameter n and p. In this case, the parameters are $n = 10$ and $p = ½$. The critical region ω is given by

$r \geq r_\alpha$, where r_α is the smallest integer value such that

$$P(r \geq r_\alpha / Ho) = \sum_{x=0}^{10} \binom{10}{x} \left(\frac{1}{2}\right)^{10} \leq \alpha$$

$$= 0.05 i.e. 1 - \sum_{x=r0}^{r_\alpha - 1} \binom{10}{x} \left(\frac{1}{2}\right)^{10} \leq 0.05$$

$$\Rightarrow \sum_{x=0}^{r_\alpha - 1} \binom{10}{x} \left(\frac{1}{2}\right)^{10} \geq 1 - 0.05 = 0.95$$

From the table, we have $r_\alpha = 9$, corresponding to $n = 10$ at 5 % level of significance, but for this example, we got $r = 8$ which is less than the table value. So we cannot reject the null hypothesis.

(ii) *Two sample run test*: Similar to that of the one sample run test, sometimes we want to test the null hypothesis that whether two independent samples drawn at random have come from the same population distribution or not. In testing the above hypothesis, we assume that the population distributions are continuous. The procedure is as follows.

Suppose we have two random and independent samples $x_1, x_2, x_3, \ldots \ldots x_{n_1}$ and $y_1, y_2, y_3, \ldots \ldots y_{n_2}$ of sizes n_1 and n_2, respectively. This $n_1 + n_2 = N$ number of values are then arranged either in ascending or descending order which (may) give rise to the following sequence: $x\,x\,y\,x\,x\,x\,y\,y\,x\,x\,y\,y\,y \ldots \ldots$. Now we count the "runs." A run is a sequence of values coming from one sample surrounded by the values from the other sample. Let the number of runs in total $n_1 + n_2 = N$ arranged observations be "r." The number of runs "r" is expected to be very high if the two samples are thoroughly mixed that means the two samples are coming from the identical distributions; otherwise, the number of runs will be very small. Table for critical values of r for given values of n_1 and n_2 is provided for both n_1 and n_2 less than 20. If the calculated "r" value is greater than the critical value of run for a given set of n_1 and n_2, then we cannot reject the null hypothesis; otherwise, any value of calculated "r" is less than or equal to the critical value of "r" for a given set n_1 and n_2; the test is significant and the null hypothesis are rejected.

For large n_1 and n_2 (say >10) or any one of them is greater than 20, the distribution of r is asymptotically normal with $E(r) = \frac{2n_1n_2}{N} + 1$ and $\mathrm{Var}(r) = \frac{2n_1n_2(2n_1n_2 - N)}{N^2(N-1)}$, and we can perform an approximate test statistic as $\tau = \frac{r - E(r)}{\sqrt{\mathrm{Var}(r)}} \sim N(0,1)$.

Example 6.42

Two independent batches of Black Bengal goat of sample size 9, each were selected randomly, and the number of calves per bearing was recorded. On the basis of number of calves per bearing, can we say whether the two batches came from the same population or not?

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Sample	Goat 1	Goat 2	Goat 3	Goat 4	Goat 5	Goat 6	Goat 7	Goat 8	Goat 9
Sample 1	2	2	3	3	3	2	2	3	3
Sample2	2	3	2	3	3	3	2	2	2

Solution Null hypothesis is H_0: Samples have come from identical distribution against the alternative hypothesis that they have come from different populations.

We arrange the observations as follows:

No. of calves	2	2	2	2	2	2	2	2	2
Sample	1	1	1	1	2	2	2	2	2
No. of calves	3	3	3	3	3	3	3	3	3
Sample	1	1	1	1	1	2	2	2	2

The value of "r" counted from the above table is 4, and the table value of "r" (Tables 6.7a and 6.7b) corresponding to 9 and 9 is 5 and 16. Thus, we are to reject the null hypothesis of equality of distributions. Hence, we conclude that the two samples have not been drawn from the same population.

(iii) *Two sample median test*: In parametric setup, we have test procedure for testing equality of two means, i.e., whether the means arising out of two samples drawn at random have come from the same population or not. In nonparametric setup, we have a parallel test in the form of two sample median test. The objective of this test is to test that the two independent random samples drawn are from identical distributions or not; thus, to test whether the two samples drawn are differing in population with different location parameters (median) or not.

Let us draw two random independent samples of sizes m and n from two populations. Make an ordered combined sample of size $m + n = N$, and get the median ($\hat{\theta}$) of the combined sample. Next, we count the number of observations below and above the estimated median value $\hat{\theta}$ for all the two samples, which can be presented as follows:

	Number of observations		
	$< \hat{\theta}$	$\geq \hat{\theta}$	Total
Sample 1	m_1	m_2	m
Sample 2	n_1	n_2	n
Total	m	n	N

If m and n are small, the exact probability of the above table with fixed marginal frequencies is given as $P = \dfrac{m!n!m!n!}{m_1!n_1!m_2!n_2!N!}$. On the other hand, if the fixed marginal frequencies are moderately large, we can use the χ^2 statistic for 2×2 contingency table using the formula ${\chi_1}^2 = \dfrac{(m_1n_2 - m_2n_1)^2N}{m.n.m.n}$.

Example 6.43
The following table gives the nuts per bunch of areca nut in two different samples. Test whether the two samples have been drawn from the same variety or not:

Sample	Bunch 1	Bunch 2	Bunch 3	Bunch 4	Bunch 5	Bunch 6	Bunch 7	Bunch 8	Bunch 9	Bunch 10	Bunch 11	Bunch 12	Bunch 13
Sample 1	489	506	170	168	278	289	294	289	310	394	361	256	252
Sample 2	478	346	171	218	249	285	281	291	282	283	249	180	300

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Solution Under the given condition, we can go for median test to test the equality of medians of two samples with respect to number of nuts per bunch.

Taking both the groups as one can have the following arrangement:

168	170	171	180	218	249	249	252	256	278	281	282	**283**	**285**	289	289	291	300	294	310	346	361	394	478	489	506

From the above arrangements, we have the median score as the average of 12th and 13th ordered observation, that is, $(283 + 285)/2 = 284$.

Now a 2 × 2 contingency table is prepared as follows:

	Below median	Above median	Total
Sample 1	5(m_1)	8(m_2)	13(m)
Sample 2	8(n_1)	5(n_2)	13(n)
Total	13	13	26(N)

$$\chi_1^2 = \frac{(m_1n_2 - m_2n_1)^2N}{m.n.m.n} = \frac{(5.5 - 8.8)^2.26}{13.13.13.13}$$
$$= \frac{(39)^2.26}{28561} = \frac{39546}{28561} = 1.384$$

For this 2 × 2 contingency table using the formula, the calculated value of $\chi^2 = 1.384 <$ the table value of $\chi^2 = 3.841$ at 5 % level of significance. So we cannot reject the null hypothesis that the two samples have come from the different population, that is, the two samples are drawn from two different varieties.

(iv) *Kolmogorov-Smirnov two samples test*: Parallel to the χ^2 test for the homogeneity of two distributions is the Kolmogorov-Smirnov two sample test that is the test for homogeneity of two populations. χ^2 test is valid under certain assumptions and also a large sample test. Kolmogorov-Smirnov two sample test can also be used under small sample conditions. Suppose we have two random independent samples (x_1, x_2, x_3, ……x_m) and (x_{21}, x_{22}, x_{23}, ……x_{2n}) from two continuous cumulative distribution functions "F" and "G," respectively. The empirical distribution functions of the variable are given by

$$\begin{aligned} F_m(x_1) &= 0 \text{ if } x_1 < x_{(i)} \\ &= i/m \text{ if } x_{(1i)} \le x_1 < x_{1(i+1)} \\ &= 1 \text{ if } x_1 \ge x_{1(m)} \text{ and} \\ G_n(x_2) &= 0 \text{ if } x < x_{2(i)} \\ &= i/n \text{ if } x_{2(i)} \le x_2 < x_{2(i+1)} \\ &= 1 \text{ if } x_2 \ge x_{2(n)} \end{aligned}$$

where $x_{1(i)}$ and $x_{2(i)}$ are the ordered values of the two samples, respectively. Combined values of x_1 and x_2 are ordered. In combined ordered arrangements of m number of x_1 values and n number of x_2 values, F_m and G_n represent the respective proportions of x_1 and x_2 values that do not exceed x_1. Thus, we are interested to test whether the two distribution functions are identical or not, i.e., to test H_0: $F(x_1) = G(x_2)$ against the alternative hypothesis H_1: $F(x_1) \neq G(x_2)$, the test statistic is $D_{m,n} = \underset{x_1}{Sup}\,[|F_m(x_1) - G_n(x_2)|]$.

Under the null hypothesis, one would expect very small value of $D_{m,n}$; on the other hand, a large value of $D_{m,n}$ is an indication of the parent distributions that are not identical. From Table 6.9, given below are the critical values of D for different sample sizes (n_1,n_2) at different level of significance. If the calculated value of $D <$ critical value $D_{m,n}$, α we accept H_0, i.e., the parent distributions are identical, otherwise not.

Example 6.44 Two samples of four each are taken independently at random for the number of panicle per plant in paddy. Test whether the two samples belong to identical parent population distribution or not:

Sample	1	2	3	4	5
S1	20	24	22	20	
S2	18	10	15	24	26

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Table 6.9 Critical values of K-S two sample test statistic at different level of significance (α) for both one-tailed and two-tailed test

One-sided test	$\alpha =$	0.10	0.05	0.025	0.01	0.05	$\alpha =$		0.10	0.05	0.025	0.01	0.05
Two-sided test	$\alpha =$	0.20	0.10	0.05	0.02	0.01	$\alpha =$		0.20	0.10	0.05	0.02	0.01
$N_1 = 1$	$N_2 = 9$	17/18					$N_1 = 6$	$N_2 = 7$	23/42	4/7	29/42	5/7	5/6
	10	9/10						8	1/2	7/12	2/3	3/4	3/4
$N_1 = 2$	$N_2 = 3$	5/6						9	1/2	5/9	2/3	13/18	7/9
	4	3/4						10	1/2	17/30	19/30	7/10	11/15
	5	4/5	4/5					12	1/2	7/12	7/12	2/3	3/4
	6	5/6	5/6					18	4/9	5/9	11/18	2/3	2/3
	7	5/7	6/7					24	11/24	1/2	7/12	5/8	2/3
	8	3/4	7/4	7/8			$N_1 = 7$	$N_2 = 8$	27/56	33/56	5/8	41/56	3/4
	9	7/9	8/9	8/9				9	31/63	5/9	40/63	5/7	47/63
	10	7/10	4/5	9/10				10	33/70	39/70	43/70	7/10	5/7
$N_1 = 3$	$N_2 = 4$	3/4	3/4					14	3/7	1/2	4/7	9/14	5/7
	5	2/3	4/5	4/5				28	3/7	13/28	15/28	17/28	9/14
	6	2/3	2/3	5/6			$N_1 = 8$	$N_2 = 9$	4/9	13/24	5/8	2/3	3/4
	7	2/3	5/7	6/7	6/7			10	19/40	21/40	13/40	17/40	7/10
	8	5/8	3/4	3/4	7/8			12	11/24	1/2	7/12	5/8	2/3
	9	2/3	2/3	7/9	8/9	8/9		16	7/16	1/2	9/16	5/8	5/8
	10	3/5	7/10	4/5	9/10	9/10		32	13/32	7/16	1/2	9/16	19/32
	12	7/12	2/3	3/4	5/6	11/12	$N_1 = 9$	$N_2 = 10$	7/15	1/2	26/45	2/3	31/45
$N_1 = 4$	$N_2 = 5$	3/5	3/4	4/5	4/5			12	4/9	1/2	5/9	11/18	2/3
	6	7/12	2/3	3/4	5/6	5/6		15	19/45	22/45	8/15	3/5	29/45
	7	17/28	5/7	3/4	6/7	6/7		18	7/18	4/9	1/2	5/9	11/18
	8	5/8	5/8	3/4	7/8	7/8		36	13/36	5/12	17/36	19/36	5/9
	9	5/9	2/3	3/4	7/9	8/9	$N_1 = 10$	$N_2 = 15$	2/5	7/15	1/2	17/30	19/30
	10	11/20	13/20	7/10	4/5	4/5		20	2/5	9/20	1/2	11/20	3/5
	12	7/12	2/3	2/3	3/4	5/6		40	7/20	2/5	9/20	1/2	
	16	9/1	5/8	11/16	3/4	13/16	$N_1 = 12$	$N_2 = 15$	23/60	9/20	1/2	11/20	7/12
$N_1 = 5$	$N_2 = 6$	3/5	2/3	2/3	5/6	5/6		16	3/8	7/16	23/48	13/24	7/12
	7	4/7	23/35	5/7	29/35	6/7		18	13/36	5/12	17/36	19/36	5/9
	8	11/20	5/8	27/40	4/5	4/5		20	11/30	5/12	7/15	31/60	17/30
	9	5/9	3/5	31/45	7/9	4/5	$N_1 = 15$	$N_2 = 20$	7/20	2/5	13/30	29/60	31/60
	10	1/2	3/5	7/10	7/10	4/5	$N_1 = 16$	$N_2 = 20$	27/80	31/80	17/40	19/40	41/40
	15	8/15	3/5	2/3	11/15	11/15							
	20	1/2	11/20	3/5	7/10	3/4							
Larger sample approximation		0.10		0.05		0.025		0.01		0.05			
		$1.07\sqrt{\frac{m+n}{mn}}$		$1.22\sqrt{\frac{m+n}{mn}}$		$1.36\sqrt{\frac{m+n}{mn}}$		$1.52\sqrt{\frac{m+n}{mn}}$		$1.63\sqrt{\frac{m+n}{mn}}$			

This table gives the values of $D^{+}_{m,n,\alpha}$ and $D^{-}_{m,n,\alpha}$ for which $\alpha \geq P\{D^{+}_{m,n} > D^{+}_{m,n,\alpha}\}$ selected values of N_1 = smaller sample size, N_2 = larger sample size, and α.

Solution Here the problem is to test whether the two samples have come from the same parent population or not, that is, $H_0 : Fm = Gn$ against the alternative hypothesis $H_1 : Fm \neq Gn$ where F and G are the two distribution from which the above samples have been drawn independently at random; also m and n are the sample sizes, respectively. For this example, $m = 4$ and $n = 5$. Under the given null hypothesis, we apply K-S two sample test having the statistic $D_{m,n} = Sup_x[|F_m(x) - G_n(x)|]$.

We make a cumulative frequency distribution for each sample of observations using the same intervals for both distributions. For the calculation of $D_{m,n}$, we construct the following table:

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x	Sample	$F_m(x)$	$G_n(x)$	$\lvert F_m(x) - G_n(x)\rvert$
10	2	0 = 0.00	1/5 = 0.20	0.20
15	2	0 = 0.00	2/5 = 0.40	0.40
18	2	0 = 0.00	3/5 = 0.60	*0.60*
20	1	1/4 = 0.25	3/4 = 0.60	0.35
20	1	2/4 = 0.50	3/4 = 0.60	0.10
22	1	3/4 = 0.75	3/4 = 0.60	0.15
24	1	4/4 = 1.00	4/4 = 0.60	0.40
25	2	4/5 = 0.80	4/5 = 0.80	0.20
26	2	5/5 = 1.00	5/5 = 1.00	0.00

Let the level of significance be $\alpha = 0.05$. From the Table 6.9, we get for $m = 4$ and $n = 5$ the critical value of K-S statistic; $D_{m,n}$ at 5 % level of significance is 0.80.

Thus, the calculated value of $D_n = \underset{x}{Sup}\,[|F_n(x) - F_0(x)|] = 0.60 <$ the table value of 0.80. That means we conclude that the parent distribution is identical.

The Kruskal-Wallis test (one-way ANOVA): Parallel to one-way analysis of variance is the Kruskal-Wallis test. In this test, we compare the means of number of treatments at a time, likewise to that of parametric one-way analysis of variance, but in this case, we need not to follow the assumptions of the parametric analysis of variance. The main objective of such test is to whether the sample means have come from the same population or from different population.

Group-1	G_{11}	G_{12}	.....		G_{1n1}
Group-2	G_{21}	G_{22}	.....	G_{2n2}	
Group-3	G_{31}	G_{32}	..... G_{3n3}		
:	.....				
:	.....				
Group-K	G_{k1}	G_{k2}	.....		G_{knk}

Let there are K groups (samples) with $n_1, n_2, \ldots\ldots n_k$ with the same or different sizes, and G_{ij} is the ith observation of jth group or sample. The method starts with arrangements of combined values in order (increasing or decreasing); then these values are ranked; if tied values are there, the mean of the possible ranks for the tied values are provided. Rank sum (R) of each of the groups is worked out. The test statistic is $H = \frac{12}{n(n+1)} \sum_{j=1}^{k} \frac{R_j^2}{n_j} - 3(n+1)$ where R_j and n_j are the rank sum and size of the jth group/sample. This H follows a χ^2 distribution with $K - 1$ degrees of freedom when the size of each group is more than five; otherwise, we are to consult the table for critical values for H. The decision rule is as usual, i.e., the null hypothesis of equal means is rejected when H_{cal} exceeds the corresponding critical value (Table 6.10).

Example 6.45

The following table gives the no. of eggs per month corresponding to six groups of chicks. Using Kruskal-Wallis test, test whether six groups could be taken as one or not.

No. of eggs/month							
Group 1	29	28	31	27	26	29	30
Group 2	17	18	19	21	20		
Group 3	25	26	27	27	28	25	
Group 4	30	29	29	31	30	31	30
Group 5	23	22	24	22	24	24	23
Group 6	27	28	26	25	27	27	

Solution

$$H = \frac{12}{n(n+1)} \sum_{j=1}^{k} \frac{R_j^2}{n_j} - 3(n+1)$$

Table of ordered ranks are provided below

$$= \frac{12}{38(38+1)}[5376.571 + 45.00 + 2166.00 + 7788.893 + 567 + 2460.375] - 3(38+1)$$

$$= \frac{12}{38(39)}[18403.84] - 3(39) = 149.018 - 117.000 = 32.018$$

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Table 6.10 *The Kruskal-Wallis test* critical region: $H \geq$ tabulated value

$K = 3$			$K = 4$			$K = 5$		
Sample sizes	$\alpha = 0.05$	$\alpha = 0.01$	Sample sizes	$\alpha = 0.05$	$\alpha = 0.01$	Sample sizes	$\alpha = 0.05$	$\alpha = 0.01$
2 2 2	–	–	2 2 1 1	–	–	2 2 1 1 1	–	–
			2 2 2 1	5.679	–	2 2 2 1 1	6.750	–
3 2 1	–	–	2 2 2 2	6.167	6.667	2 2 2 2 1	7.133	7.533
3 2 2	4.714	–				2 2 2 2 2	7.418	8.291
3 3 1	5.143	–	3 1 1 1	–	–			
3 3 2	5.361	–	3 2 1 1	–	–	3 1 1 1 1	–	–
3 3 3	5.600	7.200	3 2 2 1	5.833	–	3 2 1 1 1	6.583	–
			3 2 2 2	6.333	7.133	3 2 2 1 1	6.800	7.600
4 2 1	–	–	3 3 1 1	6.333	–	3 2 2 2 1	7.309	8.127
4 2 2	5.333	–	3 3 2 1	6.244	7.200	3 2 2 2 2	7.682	8.682
4 3 1	5.208	–	3 3 2 2	6.527	7.636	3 3 1 1 1	7.111	–
4 3 2	5.444	6.444	3 3 3 1	6.600	7.400	3 3 2 1 1	7.200	8.073
4 3 3	5.791	6.745	3 3 3 2	6.727	8.015	3 3 2 2 1	7.591	8.576
4 4 1	4.967	6.667	3 3 3 3	7.000	8.538	3 3 2 2 2	7.910	9.115
4 4 2	5.455	7.036				3 3 3 1 1	7.576	8.424
4 4 3	5.598	7.144	4 1 1 1	–	–	3 3 3 2 1	7.769	9.051
4 4 4	5.692	7.654	4 2 1 1	5.833	–	3 3 3 2 2	8.044	9.505
			4 2 2 1	6.133	7.000	3 3 3 3 1	8.000	9.451
5 2 1	5.000	–	4 2 2 2	6.545	7.391	3 3 3 3 2	8.200	9.876
5 2 2	5.160	6.533	4 3 1 1	6.178	7.067	3 3 3 3 3	8.333	10.20
5 3 1	4.960	–	4 3 2 1	6.309	7.455			
5 3 2	5.251	6.909	4 3 2 2	6.621	7.871			
5 3 3	5.648	7.079	4 3 3 1	6.545	7.758			
5 4 1	4.985	6.955	4 3 3 2	6.795	8.333			
5 4 2	5.273	7.205	4 3 3 3	6.984	8.659			
5 4 3	5.656	7.445	4 4 1 1	5.945	7.909			
5 4 4	5.657	7.760	4 4 2 1	6.386	7.909			
5 5 1	5.127	7.309	4 4 2 2	6.731	8.346			
5 5 2	5.338	7.338	4 4 3 1	6.635	8.231			
5 5 3	5.705	7.578	4 4 3 2	6.874	8.621			
5 5 4	5.666	7.823	4 4 3 3	7.038	8.876			
5 5 5	5.780	8.000	4 4 4 1	6.725	8.588			
			4 4 4 2	6.957	8.871			
6 1 1	–	–	4 4 4 3	7.142	9.075			
6 2 1	4.822	–	4 4 4 4	7.235	9.287			
6 2 2	5.345	6.655						
6 3 1	4.855	6.873						
6 3 2	5.348	6.970						
6 3 3	5.615	7.410						
6 4 1	4.947	7.106						
6 4 2	5.340	7.340						
6 4 3	5.610	7.500						
6 4 4	5.681	7.795						
6 5 1	4.990	7.182						
6 5 2	5.338	7.376						
6 5 3	5.602	7.590						
6 5 4	5.661	7.936						
6 5 5	5.729	8.028						
6 6 1	4.945	7.121						
6 6 2	5.410	7.467						
6 6 3	5.625	7.725						
6 6 4	5.724	8.000						
6 6 5	5.765	8.124						
6 6 6	5.801	8.222						
7 7 7	5.819	8.378						
8 8 8	5.805	8.465						

Source: Neave, 1978

As all the groups have five or more observations, H is distributed as χ^2 with (6–1) = 5 d.f. The table value of χ^2 at 5 % level of significance and 5 d.f. is 11.0705 which is less than the calculated value, so we accept the alternative hypothesis, i.e., all the six groups are different, i.e., these have come from different populations. Different groups have different egg-laying capacity per month.

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Original scores		Ordered score			Rank					
Group	Score	Group	Score	Unified rank	Group 1	Group 2	Group 3	Group 4	Group 5	Group 6
1	29	2	17	1		1				
1	28	2	18	2		2				
1	31	2	19	3		3				
1	27	2	20	4		4				
1	26	2	21	5		5				
1	29	5	22	6.5					6.5	
1	30	5	22	6.5					6.5	
2	17	5	23	8.5					8.5	
2	18	5	23	8.5					8.5	
2	19	5	24	11					11	
2	21	5	24	11					11	
2	20	5	24	11					11	
3	25	3	25	14			14			
3	26	3	25	14			14			
3	27	6	25	14						14
3	27	1	26	17	17					
3	28	3	26	17			17			
3	25	6	26	17						17
4	30	1	27	21.5	21.5					
4	29	3	27	21.5			21.5			
4	29	3	27	21.5			21.5			
4	31	6	27	21.5						21.5
4	30	6	27	21.5						21.5
4	31	6	27	21.5						21.5
4	30	1	28	26	26					
5	23	3	28	26			26			
5	22	6	28	26						26
5	24	1	29	29.5	29.5					
5	22	1	29	29.5	29.5					
5	24	4	29	29.5				29.5		
5	24	4	29	29.5				29.5		
5	23	1	30	33.5	33.5					
6	27	4	30	33.5				33.5		
6	28	4	30	33.5				33.5		
6	26	4	30	33.5				33.5		
6	25	1	31	37	37					
6	27	4	31	37				37		
6	27	4	31	37				37		
R_j					194	15	114	233.5	63	121.5
n_j					7	5	6	7	7	6
$\frac{R_j^2}{n_j}$					5376.571	45	2166	7788.893	567	2460.375

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(iv) *Friedman's test for multiple treatments on a series of subjects (two-way ANOVA)*: In this test, we are interested to test the significance of the differences in response for k treatments applied to n subjects. It is assumed that the response of a subject to a treatment is not being influenced by its response to another treatment.

The procedure is to arrange the whole data set into a two-way table with n rows and k columns corresponding subjects and treatments. In each row, each subject is ranked of increasing order. For each of the k columns, the rank sums ($R_j^{'}s$) are calculated. The test statistic used is given as

$$\chi^2_{k-1} = \frac{12}{nk(k+1)} \sum_{j=1}^{k} R_j^2 - 3n(k+1)$$

Now, if the calculated value of χ^2 exceeds the corresponding critical value, then the null hypothesis of equality of treatments is rejected.

Example 6.46 A study was conducted to know the effect of three seasons on egg-laying capacity of particular breed of chick. The average eggs laid per season was recorded and given in the following table. Is there any significant effect of season on egg-laying capacity?

	Chick number									
Season	1	2	3	4	5	6	7	8	9	10
Summer	20	20	21	18	17	25	24	20	19	20
Rainy	20	25	25	22	22	20	22	24	19	24
Winter	25	30	22	20	19	25	28	27	22	26

Solution Here we have to test H_0: season has no effect on egg-laying capacity of particular breed of chick against H_1 season has a effect on egg-laying capacity of particular breed of chick. We are given with b=10 (Blocks); $k = 3$ (Treatments).

Rank order the egg-laying capacity for each chick with the smallest score getting a value of 1. If there are times each receives the average rank, they would have received as bellow:

		Chick number										
Season		1	2	3	4	5	6	7	8	9	10	Total
Summer	No. of egg	20	20	21	18	17	25	24	20	19	20	
	Rank	1.5	1	1	1	1	2.5	2	1	1.5	1	13.5
Rainy	No of egg	20	25	25	22	22	20	22	24	19	24	
	Rank	1.5	2	3	3	3	1	1	2	1.5	2	20
Winter	No of egg	25	30	22	20	19	25	28	27	22	26	
	Rank	3	3	2	2	2	2.5	3	3	3	3	26.5

Test statistic is given by

$$\chi^2_r = \frac{12}{3 \times 10 \times (3+1)} \times \left[(13.5)^2 + (20)^2 + (26.5)^2\right] - 3 \times 10 \times (3+1) = 8.45$$

Conclusion From the χ^2 table, we have $\chi^2_{0.05,(k-1)} = \chi^2_{0.05,2} = 5.991$. Hence, we reject H_0, and we can conclude that the egg-laying capacity will differ for different seasons (Tables 6.11, 6.12, and 6.13).

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Table 6.11 Transformed values of correlation coefficient $Z = \frac{1}{2}\log_e \frac{1+r}{1-r}$

R	0.000	0.010	0.020	0.030	0.040	0.050	0.060	0.070	0.080	0.090
0.000	0.000	0.010	0.020	0.030	0.040	0.050	0.060	0.070	0.080	0.090
0.100	0.100	0.110	0.121	0.131	0.141	0.151	0.161	0.172	0.182	0.192
0.200	0.203	0.213	0.224	0.234	0.245	0.255	0.266	0.277	0.288	0.299
0.300	0.310	0.321	0.332	0.343	0.354	0.365	0.377	0.388	0.400	0.412
0.400	0.424	0.436	0.448	0.460	0.472	0.485	0.497	0.510	0.523	0.536
0.500	0.549	0.563	0.576	0.590	0.604	0.618	0.633	0.648	0.662	0.678
0.600	0.693	0.709	0.725	0.741	0.758	0.775	0.793	0.811	0.829	0.848
0.700	0.867	0.887	0.908	0.929	0.950	0.973	0.996	1.020	1.045	1.071
0.800	1.099	1.127	1.157	1.188	1.221	1.256	1.293	1.333	1.376	1.422
R	0.000	0.001	0.002	0.003	0.004	0.005	0.006	0.007	0.008	0.009
0.900	1.472	1.478	1.483	1.488	1.494	1.499	1.505	1.510	1.516	1.522
0.910	1.528	1.533	1.539	1.545	1.551	1.557	1.564	1.570	1.576	1.583
0.920	1.589	1.596	1.602	1.609	1.616	1.623	1.630	1.637	1.644	1.651
0.930	1.658	1.666	1.673	1.681	1.689	1.697	1.705	1.713	1.721	1.730
0.940	1.738	1.747	1.756	1.764	1.774	1.783	1.792	1.802	1.812	1.822
0.950	1.832	1.842	1.853	1.863	1.874	1.886	1.897	1.909	1.921	1.933
0.960	1.946	1.959	1.972	1.986	2.000	2.014	2.029	2.044	2.060	2.076
0.970	2.092	2.110	2.127	2.146	2.165	2.185	2.205	2.227	2.249	2.273
0.980	2.298	2.323	2.351	2.380	2.410	2.443	2.477	2.515	2.555	2.599
0.990	2.647	2.700	2.759	2.826	2.903	2.994	3.106	3.250	3.453	3.800

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Table 6.12 Values of correlation coefficients in terms of Z

Z	0.000	0.010	0.020	0.030	0.040	0.050	0.060	0.070	0.080	0.090
0.00	0.000	0.010	0.020	0.030	0.040	0.050	0.060	0.070	0.080	0.090
0.10	0.100	0.110	0.119	0.129	0.139	0.149	0.159	0.168	0.178	0.187
0.20	0.197	0.207	0.216	0.226	0.236	0.245	0.254	0.264	0.273	0.282
0.30	0.291	0.300	0.310	0.319	0.327	0.336	0.345	0.354	0.363	0.371
0.40	0.380	0.389	0.397	0.405	0.414	0.422	0.430	0.438	0.446	0.454
0.50	0.462	0.470	0.478	0.485	0.493	0.500	0.508	0.515	0.523	0.530
0.60	0.537	0.544	0.551	0.558	0.565	0.572	0.578	0.585	0.592	0.598
0.70	0.604	0.611	0.617	0.623	0.629	0.635	0.641	0.647	0.653	0.658
0.80	0.664	0.670	0.675	0.680	0.686	0.691	0.696	0.701	0.706	0.711
0.90	0.716	0.721	0.726	0.731	0.735	0.740	0.744	0.749	0.758	0.757
1.00	0.762	0.766	0.770	0.774	0.778	0.782	0.786	0.790	0.793	0.797
1.10	0.800	0.804	0.808	0.811	0.814	0.818	0.821	0.824	0.828	0.831
1.20	0.834	0.837	0.840	0.843	0.846	0.848	0.851	0.854	0.856	0.859
1.30	0.862	0.864	0.867	0.869	0.872	0.874	0.876	0.874	0.881	0.883
1.40	0.885	0.888	0.890	0.892	0.894	0.896	0.898	0.900	0.902	0.903
1.50	0.905	0.907	0.909	0.910	0.912	0.914	0.915	0.917	0.919	0.920
1.60	0.922	0.923	0.925	0.926	0.928	0.929	0.930	0.932	0.933	0.934
1.70	0.935	0.937	0.938	0.939	0.940	0.941	0.942	0.944	0.945	0.946
1.80	0.947	0.948	0.949	0.950	0.951	0.952	0.953	0.954	0.954	0.955
1.90	0.956	0.957	0.958	0.959	0.960	0.960	0.961	0.962	0.963	0.963
2.00	0.964	0.965	0.965	0.966	0.967	0.967	0.968	0.969	0.969	0.970
2.10	0.970	0.971	0.972	0.972	0.973	0.973	0.974	0.974	0.975	0.975
2.20	0.976	0.976	0.977	0.977	0.978	0.978	0.978	0.979	0.979	0.980
2.30	0.980	0.980	0.981	0.981	0.982	0.982	0.982	0.983	0.983	0.983
2.40	0.984	0.984	0.984	0.985	0.985	0.985	0.986	0.986	0.986	0.986
2.50	0.987	0.987	0.987	0.987	0.988	0.988	0.988	0.988	0.989	0.989
2.60	0.989	0.989	0.989	0.990	0.990	0.990	0.990	0.990	0.991	0.991
2.70	0.991	0.991	0.991	0.992	0.992	0.992	0.992	0.992	0.992	0.992
2.80	0.993	0.993	0.993	0.993	0.993	0.993	0.993	0.994	0.994	0.994
2.90	0.994	0.994	0.994	0.994	0.994	0.994	0.995	0.995	0.995	0.995

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Table 6.13 One-tailed cumulative binomial probability under $H_0 : P = Q = 0.5$

Z																
N	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
5	0.031	0.188	0.500	0.813	0.969	1.000										
6	0.016	0.109	0.344	0.656	0.891	0.984	1.000									
7	0.008	0.063	0.227	0.500	0.773	0.938	0.992	1.000								
8	0.004	0.035	0.145	0.363	0.637	0.855	0.965	0.996	1.000							
9	0.002	0.020	0.090	0.254	0.500	0.746	0.910	0.980	0.998	1.000						
10	0.001	0.011	0.055	0.172	0.377	0.623	0.828	0.945	0.989	0.999	1.000					
11		0.006	0.033	0.113	0.274	0.500	0.726	0.887	0.967	0.994	1.000	1.000				
12		0.003	0.019	0.073	0.194	0.387	0.613	0.806	0.927	0.981	0.997	1.000	1.000			
13		0.002	0.011	0.046	0.133	0.291	0.500	0.709	0.867	0.954	0.989	0.998	1.000	1.000		
14		0.001	0.006	0.029	0.090	0.212	0.395	0.605	0.788	0.910	0.971	0.994	0.999	1.000	1.000	
15			0.004	0.018	0.059	0.151	0.304	0.500	0.696	0.849	0.941	0.982	0.996	1.000	1.000	1.000
16			0.002	0.011	0.038	0.105	0.227	0.402	0.598	0.773	0.895	0.962	0.989	0.998	1.000	1.000
17			0.001	0.006	0.025	0.072	0.166	0.315	0.500	0.685	0.834	0.928	0.975	0.994	0.999	1.000
18			0.001	0.004	0.015	0.048	0.119	0.240	0.407	0.593	0.760	0.881	0.952	0.985	0.996	0.999
19				0.002	0.010	0.032	0.084	0.180	0.324	0.500	0.676	0.820	0.916	0.968	0.990	0.998
20				0.001	0.006	0.021	0.058	0.132	0.252	0.412	0.588	0.748	0.868	0.942	0.979	0.994
21				0.001	0.004	0.013	0.039	0.095	0.192	0.332	0.500	0.668	0.808	0.905	0.961	0.987
22					0.002	0.008	0.026	0.067	0.143	0.262	0.416	0.584	0.738	0.857	0.933	0.974
23					0.001	0.005	0.017	0.047	0.105	0.202	0.339	0.500	0.661	0.798	0.895	0.953
24					0.001	0.003	0.011	0.032	0.076	0.154	0.271	0.419	0.581	0.729	0.846	0.924
25						0.002	0.007	0.022	0.054	0.115	0.212	0.345	0.500	0.655	0.788	0.885

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Correlation Analysis 7

7.1 Introduction

Every individual element in any population is composed of several quantitative as well as qualitative characters. A poultry breed is being characterized by its size, shape, color, body weight, egg-laying capacity, etc. A variety of paddy is known by its growth, yield, and other characters like plant height, number of tillers per hill, panicle length, grain size and shape, grain weight, resistance to different pest and diseases, stress tolerance, etc. Most of these characters are related with each other; for example, the body weight of poultry bird varies with that of the age and the egg-laying capacity also varies with the type breed as well as the age of the birds. Similarly, the number tillers per hill and number of effective tiller per hill, panicle length, and number of grains per panicle are associated with each other. In statistics, we study the population characters, and in population, many characters are associated with each other. While studying the population in terms of its characteristics, one may study the characters taking one at a time and can find out different measures of central tendency, dispersion, etc. for individual characters separately. But as we have just discussed, a close look in to the characters will clearly suggest that none of the characters vary in isolation; rather, these have a tendency to vary together. Hence, the importance of studying the characters together are felt. If we study many number of variables at a time, then we call it multivariate study, and when we study two variables at a time, it is known as the bivariate study. Thus, the simplest case in multivariate study is the bivariate study.

The associationship between the variables can be linear or nonlinear. In the Figs. 7.1 through 7.3, one can find three different types of associationships. In Fig. 7.1, as the values of X_1 increase, the values of X_2 also increase and vice versa (a positive associationship between the variables), but in Fig. 7.2, one can find that as the values of X_1 increase, the values of X_2 decrease and vice versa (a negative associationship between the variables). Thus, Figs. 7.1 and 7.2 present two opposite associationships. While in Fig. 7.3, one can find that there is hardly any change in the values of X_2 with the change in values of X_1. Figures 7.1 and 7.2 represent linear relationship between the variables, while Fig. 7.3 fails to present any relationship. But in Fig. 7.4, one finds different type of relationship – a nonlinear relationship between the variables X_1 and X_2.

In this chapter, we are concerned about the strength of the linear associationship between two variables, while in the next chapter, we would try to find out the exact linear relationship between the variables. As we have already mentioned that the characters tend to move together, now the question is which pair of characters has stronger tendency to move together compared to

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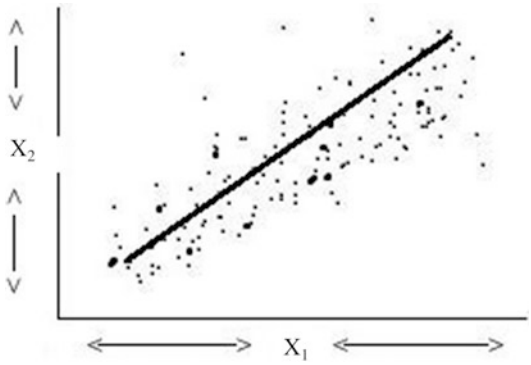

Fig. 7.1 Positive associationship

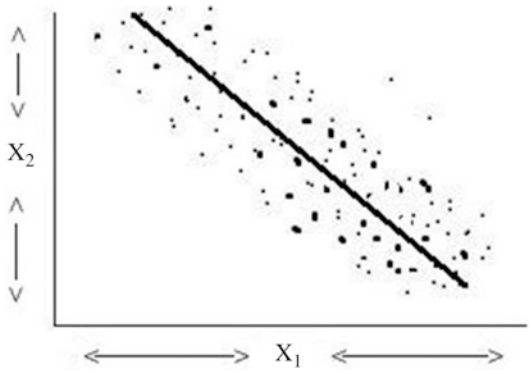

Fig. 7.2 Negative associationship

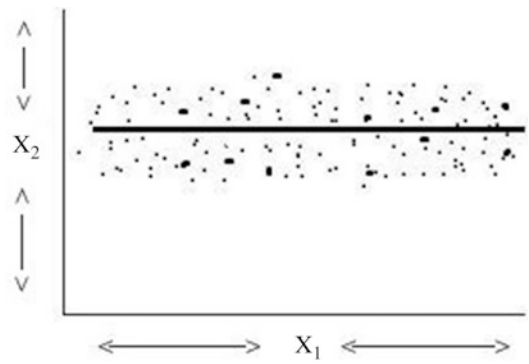

Fig. 7.3 No associationship

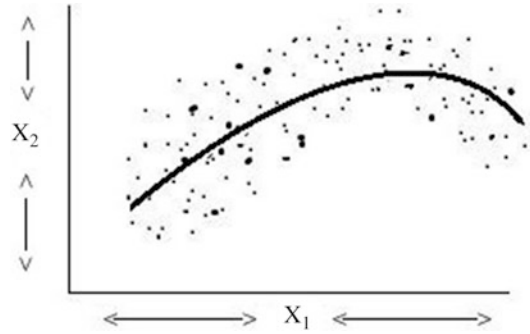

Fig. 7.4 Nonlinear associationship

other pairs in the population? Thus, we need to measure the strength of linear associationship between the variables. In fact, the degree of linear associationship is being measured with the help of the correlation coefficient.

7.2 Correlation Coefficient

It is defined as the measure of **degree** of **linear** associationship between any two given variables. Suppose we have n pairs of observations (x_{11}, x_{21}), (x_{12}, x_{22}), (x_{13}, x_{23}),. . .. . (x_{1n}, x_{2n}) for two variables X_1 and X_2, then correlation coefficient between X_1 and X_2 is given as

$$
\begin{aligned}
r_{x_1x_2} &= \frac{Cov(x_1, x_2)}{s_{x_1}.s_{x_2}} \\
&= \frac{\frac{1}{n}\sum_{i=1}^{n}(x_{1i} - \overline{x_1})(x_{2i} - \overline{x_2})}{\sqrt{\frac{1}{n}\sum_{i=1}^{n}(x_{1i} - \overline{x_1})^2}\sqrt{\frac{1}{n}\sum_{i=1}^{n}(x_{2i} - \overline{x_2})^2}} \\
&= \frac{\sum_{i=1}^{n}(x_{1i} - \overline{x_1})(x_{2i} - \overline{x_2})}{\sqrt{\sum_{i=1}^{n}(x_{1i} - \overline{x_1})^2}\sqrt{\sum_{i=1}^{n}(x_{2i} - \overline{x_2})^2}} \\
&= \frac{SP(x_1, x_2)}{\sqrt{SS(x_1).SS(x_2)}}
\end{aligned}
$$

We know

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1.

$$\begin{aligned}\mathrm{Cov}(x_1,x_2) &= \frac{1}{n}SP(x_1,x_2)\\ &= \frac{1}{n}\sum_{i=1}^{n}(x_{1i}-\overline{x_1})(x_{2i}-\overline{x_2})\\ &= \frac{1}{n}\sum_{i=1}^{n}x_{1i}x_{2i} - \frac{1}{n}\overline{x_1}\sum_{i=1}^{n}x_{2i} - \frac{1}{n}\overline{x_2}\sum_{i=1}^{n}x_{1i}\\ &\quad + \frac{1}{n}\sum_{i=1}^{n}\overline{x_1}\,\overline{x_2}\\ &= \frac{1}{n}\sum_{i=1}^{n}x_{1i}x_{2i} - 2\overline{x_1}\,\overline{x_2} + \frac{1}{n}\sum_{i=1}^{n}\overline{x_1}\,\overline{x_2}\\ &= \frac{1}{n}\sum_{i=1}^{n}x_{1i}x_{2i} - \overline{x_1}\,\overline{x_2} = S_{x_1x_2}\end{aligned}$$

2.

$$\begin{aligned}\mathrm{Var}(x_1) &= \frac{1}{n}SS(x_1) = \frac{1}{n}s_{x_1}^2 = \frac{1}{n}\sum_{i=1}^{n}(x_{1i}-\overline{x_1})^2\\ &= \frac{1}{n}\sum_{i=1}^{n}x_{1i}^2 - \overline{x_1}^2\end{aligned}$$

3.

$$\begin{aligned}\mathrm{Var}(x_2) &= \frac{1}{n}SS(x_2) = \frac{1}{n}s_{x_2}^2 = \frac{1}{n}\sum_{i=1}^{n}(x_{2i}-\overline{x_2})^2\\ &= \frac{1}{n}\sum_{i=1}^{n}x_{2i}^2 - \overline{x_2}^2\end{aligned}$$

$$\begin{aligned}r_{x_1x_2} &= \frac{\frac{1}{n}\sum_{i=1}^{n}(x_{1i}-\overline{x_1})(x_{2i}-\overline{x_2})}{\sqrt{\frac{1}{n}\sum_{i=1}^{n}(x_{1i}-\overline{x_1})^2}\sqrt{\frac{1}{n}\sum_{i=1}^{n}(x_{2i}-\overline{x_2})^2}}\\ &= \frac{\frac{1}{n}\sum_{i=1}^{n}x_{1i}x_{2i} - \overline{x}_1\overline{x}_2}{\sqrt{\left(\frac{1}{n}\sum_{i=1}^{n}x_{1i}^2 - \overline{x}_1^2\right)\left(\frac{1}{n}\sum_{i=1}^{n}x_{2i}^2 - \overline{x}_2^2\right)}}\\ &= \frac{\sum_{i=1}^{n}x_{1i}x_{2i} - n\overline{x}_1\overline{x}_2}{\sqrt{\left(\sum_{i=1}^{n}x_{1i}^2 - n\overline{x_1}^2\right)\left(\sum_{i=1}^{n}x_{2i}^2 - n\overline{x_2}^2\right)}},\end{aligned}$$

Example 7.1 The following table is related to birds per pen and area (square feet) for four different poultry farms. Calculate the correlation coefficient between area and the number of birds per pen:

Birds/pen	25	100	200	500
Area (sq. ft)	88	300	500	1000

Solution With the help of the above information, let us construct the following table:

Farms	Area (sq. ft) (Y)	Birds/ pen (X)	$(Y_i-\overline{Y})^2$	$(X_i-\overline{X})^2$	$(X_i-\overline{X})(Y_i-\overline{Y})$
1	88	25	147456.00	32851.56	69600.00
2	300	100	29584.00	11289.06	18275.00
3	500	200	784.00	39.06	−175.00
4	1000	500	278784.00	86289.06	155100.00
Sum (∑)	**1888.00**	**825.00**	**456608.00**	**130468.75**	**242800.00**
Average	**472.00**	**206.25**			

$$\mathrm{Cov}(X,Y) = \frac{1}{n}S_{xy} = \frac{\sum_{i=1}^{n}(X_i-\overline{X})(Y_i-\overline{Y})}{n} = \frac{242800}{4} = 60700$$

$$S^2{}_x = \frac{\sum_{i=1}^{n}(X_i-\overline{X})^2}{n} = \frac{130468.75}{4} = 32617.19$$

$$S^2{}_y = \frac{\sum(Y_i-\overline{Y})^2}{n} = \frac{456608}{4} = 114152$$

$$\therefore r_{xy} = \frac{\mathrm{Cov}(X,Y)}{S_XS_y} = \frac{60700}{\sqrt{(32671.19\times 114152)}} = 0.994$$

7.3 Properties

1. Correlation coefficient is worked out irrespective of the dependency, i.e., $r_{xy} = r_{yx}$.
2. Correlation coefficient is a unit free measure; as such, this can be used to compare the degree of linear associationship between any pair of variables measured in different units.

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Example 7.2 Covariance between weight of egg and number of eggs laid per hatching is 0.38 with variances of egg weight and number of eggs being 21.05 and 20.78, respectively. Find out the correlation coefficient between egg weight and egg number.

Solution Let egg weight is denoted as X and the number of eggs be denoted as Y. As per given information, we have $\text{Cov}(X, Y) = 0.38$; $S_x^2 = 21.05$ and $S_y^2 = 20.78$

$$\therefore r_{xy} = \frac{Cov(X,Y)}{S_X S_y} = \frac{0.38}{\sqrt{(21.05 \times 20.78)}} = 0.0183$$

$\therefore$ Hardly, there is any correlation between egg weight and number of eggs laid per hatching.

3. *Correlation coefficient r_{xy} lies between -1 and $+1$*, i.e., $-1 \le r_{xy} \le +1$.

Proof Let (x_{11}, x_{21}), (x_{12}, x_{22}), (x_{13}, x_{23}),..... (x_{1n}, x_{2n}) be n pairs of observations for two variables X_1 and X_2 having means $\bar{x}_1$ and $\bar{x}_2$ and variances $S_1{}^2$ and $S_2{}^2$, respectively.

One can define two variables p and q such that

$$p = \frac{x_1 - \bar{x}_1}{S_1} \text{ and } q = \frac{x_2 - \bar{x}_2}{S_2}$$
$$\therefore p_i = \frac{x_{1i} - \bar{x}_1}{S_1} \text{ and } q_i = \frac{x_{2i} - \bar{x}_2}{S_2},$$

for ith observation

$$Or, \sum_{i=1}^{n} p_i{}^2 = \sum_{i=1}^{n} \frac{(x_{1i} - \bar{x}_1)^2}{S_1^2} \text{ and } \sum_{i=1}^{n} q_i{}^2 = \sum_{i=1}^{n} \frac{(x_{2i} - \bar{x}_2)^2}{S_2^2}$$
$$Or, \sum_{i=1}^{n} p_i{}^2 = \frac{nS_1{}^2}{S_1{}^2} \text{ and } \sum_{i=1}^{n} q_i{}^2 = \frac{nS_2{}^2}{S_2{}^2}$$
$$Or, \sum_{i=1}^{n} p_i{}^2 = n \text{ and } \sum_{i=1}^{n} q_i{}^2 = n$$

Similarly,

$$\sum_{i=1}^{n} p_i q_i = \frac{\sum_{i=1}^{n} (x_{1i} - \bar{x}_1)(x_{2i} - \bar{x}_2)}{S_1.S_2}$$
$$= n \cdot \frac{S_{12}}{S_1.S_2} = n \frac{Cov(X_1, X_2)}{SD(X_1).SD(X_2)}$$
$$= n r_{x_1 x_2}$$

We know that

$$(p_i - q_i)^2 \ge 0$$
$$\therefore \sum_{i=1}^{n} (p_i - q_i)^2 \ge 0$$
$$or, \sum_{i=1}^{n} p_{i_i}^2 - 2\sum_{i=1}^{n} p_i q_i + \sum_{i=1}^{n} q_i^2 \ge 0$$
$$or, n - 2n r_{x_1 x_2} + n \ge 0$$
$$or, 2n(1 - r_{x_1 x_2}) \ge 0$$

since n is a positive number:

$$1 - r_{x_1 x_2} \ge 0$$
$$So, r_{x_1 x_2} \le 1 \quad \text{(i)}$$

Similarly,

$$\sum_{i=1}^{n} (p_i + q_i)^2 \ge 0$$
$$or, \sum_{i=1}^{n} p_i^2 + 2\sum_{i=1}^{n} p_i q_i + \sum_{i=1}^{n} q_i^2 \ge 0$$
$$or, n + 2n r_{x_1 x_2} + n \ge 0$$
$$or, 2n(1 + r_{x_1 x_2}) \ge 0$$

since n is a positive number:

$$(1 + r_{x_1 x_2}) \ge 0$$
$$or, r_{x_1 x_2} \ge -1 \quad \text{(ii)}$$

Combining (i) and (ii), we get $-1 \le r_{x_1 x_2} \le +1$.

4. *Correlation coefficient is independent of change of origin and scale.*

Let us consider (x_{11}, x_{21}), (x_{12}, x_{22}), (x_{13}, x_{23}),..... (x_{1n}, x_{2n}) as n pairs of observations for two variables X_1 and X_2 having means $\bar{x}_1$ and $\bar{x}_2$ and variances $S_1{}^2$ and $S_2{}^2$, respectively. Let us define another two variables, so that $u_i = \frac{x_{1i} - a}{b}$ and $v_i = \frac{x_{2i} - c}{d}$; $i = 1, 2, 3 \ldots ..n$

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and a, b, c, and d are constants; and a, c are changes in origins; and b, d are changes in scales for two variables X_1 and X_2, respectively. So,

$$x_{1i} = a + bu_i \text{ and } x_{2i} = c + dv_i$$

$$\therefore \frac{1}{n}\sum_{i=1}^{n} x_{1i} = \frac{1}{n}\sum_{i=1}^{n}(a + bu_i)$$

$$or,\ \bar{x}_1 = \frac{1}{n}\sum_{i=1}^{n} a + \frac{1}{n}\sum_{i=1}^{n} bu_i$$

$$or,\ \bar{x}_1 = a + b\bar{u}$$

$$\text{Similarly, } \bar{x}_2 = c + d\bar{u}$$

Again we have,

$$S_{x_1}^2 = S_1^2 = \frac{1}{n}\sum_{i=1}^{n}(x_{1i} - \bar{x}_1)^2$$

$$= \frac{1}{n}\sum_{i=1}^{n}(a + bu_i - a - b\bar{u})^2$$

$$= \frac{1}{n}\sum_{i=1}^{n}(bu_i - b\bar{u})^2 = \frac{1}{n}\sum_{i=1}^{n} b^2(u_i - \bar{u})^2$$

$$= b^2\frac{1}{n}\sum_{i=1}^{n}(u_i - \bar{u})^2 = b^2 S^2{}_u$$

Similarly, $S_{x_2}^2 = S_2^2 = d^2 S_v^2$

We know that

$$Cov(x_1, x_2) = \frac{1}{n}\sum_{i}(x_{1i} - \bar{x}_1)(x_{2i} - \bar{x}_2)$$

$$= \frac{1}{n}\sum_{i=1}^{n}\{(a + bu_i - a - b\bar{u})\}$$

$$\times \{(c + dv_i - c - d\bar{v})\}$$

$$= bd\frac{1}{n}\sum_{i=1}^{n}(u_i - \bar{u})(v_i - \bar{v})$$

$$= bdCov(u, v) = bdS_{uv}$$

Thus, using the above formulae, we can have the correlation coefficient between X_1 and X_2 as

$$r_{x_1x_2} = \frac{Cov(x_1, x_2)}{\sqrt{S_1^2.S_2^2}} = \frac{S_{12}}{S_1S_2}$$

$$= \frac{b.d.Cov(u, v)}{\sqrt{(b^2S^2{}_u)(d^2S^2{}_v)}}$$

$$= \frac{b.d.S_{uv}}{|b|.|d|.S_u.S_v}$$

$$= \frac{b.d}{|b|.|d|}.r_{uv} = \pm r_{uv}$$

Thus, the numerical value of correlation coefficient between X_1 and X_2 and between the transformed variables u and v remains the same, but the sign of r_{uv} depends on the sign of b and d, the changes in scales of the two variables X_1 and X_2. When b and d both are having same sign, then $r_{xy} = r_{uv}$, but if these two have different signs then $r_{xy} = -r_{uv}$.

Example 7.3 The number of tillers per hill and yield of wheat in kilogram per hectare for nine varieties is given below. (a) Find out the correlation coefficient between number of tillers per hill and yield of wheat, and (b) by changing origin and scale for both, the variables show that correlation coefficient remains the same:

Tillers per hill	5	15	67	30	10	20	50	40	60
Yield (kg)	1050	3250	7880	5270	2100	4280	7100	6460	7610

Solution

(a) *With the help of the above information, let us construct the following table*:

	Tillers per hill (X)	Yield (kg) (Y)	X^2	Y^2	XY
	5	1050	25	1,102,500	5250
	15	3250	225	10,562,500	48,750
	67	7880	4489	62,094,400	527,960
	30	5270	900	27,772,900	158,100
	10	2100	100	4,410,000	21,000
	20	4280	400	18,318,400	85,600
	50	7100	2500	50,410,000	355,000
	40	6460	1600	41,731,600	258,400
	60	7610	3600	57,912,100	456,600
Sum	297	45,000	13,839	274,314,400	1,916,660
Average	33	5000	1537.667	30479377.78	212962.2
Variance	448.6667	5,479,378			47962.22

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For calculation of correlation coefficient from original data, let us calculate the following quantitative:

1. Average number of tillers per hill $(5 + 10 + 15 + \ldots + 60)/9 = 33$no
2. Average yield $(1050 + 2100 + \ldots + 7610)/9 = 5000$ kg
3. Variance of number of tillers per hill $\{(5^2 + 15^2 + \ldots + 60^2)/9 - (33)^2\} = 448.667\text{no}^2$
4. Variance of body weight of lamb as $\{(1050^2 + 3250^2 + \ldots + 7610^2)/9 - (5000)^2\} = 5{,}479{,}378\ \text{kg}^2$
5. Covariance of number of tillers per hill and yield $\{5 \times 1050 + \ldots + 60 \times 7610)/9 - (33)(5000)\}$no kg $= 47962.22$no.kg

$$\therefore r_{xy} = \frac{\frac{1}{n}\sum_{i=1}^{n}(x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\frac{1}{n}\sum_{i=1}^{n}(x_i - \bar{x})^2}\sqrt{\frac{1}{n}\sum_{i=1}^{n}(y_i - \bar{y})^2}} = \frac{\frac{1}{n}\sum_{i=1}^{n}x_i y_i - \bar{x}\,\bar{y}}{\sqrt{\left(\frac{1}{n}\sum_{i=1}^{n}x_i^2 - \bar{x}^2\right)\left(\frac{1}{n}\sum_{i=1}^{n}y_i^2 - \bar{y}^2\right)}} = \frac{47962.22}{21.18175\text{x } 2340.807} = 0.967$$

(b) For calculation of correlation coefficient from changed data (change of origin and scale), let us transform both the tiller per hill and yield of wheat as:

$u_i = \frac{x_i - a}{b}$ and $v_i = \frac{y_i - c}{d}$ where, x_i, y_i, a, b, c, and d are age, body weight, "5," "4," "1000," and "1000," respectively. Thus, we have $u_i = \frac{x_i - a}{b} = \frac{x_i - 5}{4}$ and $v_i = \frac{y_i - c}{d} = \frac{y_i - 1000}{1000}$, and with the help of the transformed variables, let us construct the following table and from the transformed table calculate the following quantities:

(i) Average of transformed number of tiller per hill $(0 + 2.5 + \ldots + 13.75)/9 = 7$ no
(ii) Average of transformed yield $(0.05 + 2.25 + \ldots + 6.61)/9 = 4$tn
(iii) Variance of transformed number of tiller per hill $\{(0^2 + 2.5^2 + \ldots + 13.75^{2)}/9 - (7)^2\} = 28.0417\ \text{no}^2$
(iv) Variance of transformed yield $\{(0.05^2 + 2.25^2 + \ldots + 6.61^2)/9 - (4)^2\} = 5.4794\text{tn}^2$
(v) Covariance of transformed number of tillers per hill and yield $\{0 \times 0.050 + 2.5 \times 2.25 + \cdots + 13.75 \times 6.61)/9 - (7)(4)\}$Wk.g $= 11.9906$no tn

$$\therefore r_{xy} = \frac{\frac{1}{n}\sum_{i=1}^{n}(x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\frac{1}{n}\sum_{i=1}^{n}(x_i - \bar{x})^2}\sqrt{\frac{1}{n}\sum_{i=1}^{n}(y_i - \bar{y})^2}} = \frac{\frac{1}{n}\sum_{i=1}^{n}x_i y_i - \bar{x}\,\bar{y}}{\sqrt{\left(\frac{1}{n}\sum_{i=1}^{n}x_i^2 - \bar{x}^2\right)\left(\frac{1}{n}\sum_{i=1}^{n}y_i^2 - \bar{y}^2\right)}}, = \frac{11.9906}{5.2954 \times 2.3408} = 0.9673$$

which is exactly as that was found in previous analysis without changing the origins and scales of the variables.

5. *Correlation coefficient between X_1 and X_2 is same as the correlation coefficient between X_2 and X_1.*
We know that

$$r_{x_1x_2} = \frac{Cov(x_1, x_2)}{S_{x_1}.S_{x_2}} = \frac{\frac{1}{n}\sum_{i=1}^{n}(x_1x_2) - \overline{x_1}.\overline{x_2}}{S_{x_1}.S_{x_2}} = \frac{Cov(x_2, x_1)}{S_{x_2}S_{x_1}} = r_{x_2x_1}$$

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	Tillers per hill (X)	Yield (kg) (Y)	$u = \frac{x-5}{4}$	$v = \frac{y-1000}{1000}$	u^2	v^2	uv
	5	1050	0.0000	0.0500	0.0000	0.0025	0.0000
	15	3250	2.5000	2.2500	6.2500	5.0625	5.6250
	67	7880	15.5000	6.8800	240.2500	47.3344	106.6400
	30	5270	6.2500	4.2700	39.0625	18.2329	26.6875
	10	2100	1.2500	1.1000	1.5625	1.2100	1.3750
	20	4280	3.7500	3.2800	14.0625	10.7584	12.3000
	50	7100	11.2500	6.1000	126.5625	37.2100	68.6250
	40	6460	8.7500	5.4600	76.5625	29.8116	47.7750
	60	7610	13.7500	6.6100	189.0625	43.6921	90.8875
Sum	297	45,000	63.0000	36.0000	693.3750	193.3144	359.9150
Average	33	5000	7.0000	4.0000	77.0417	21.4794	39.9906
Variance	448.6667	5,479,378	28.0417	5.4794			11.9906

6. *Two independent variables are uncorrelated, but the converse may not be true.*

Let us consider the following two variables:

X_1	-3	-2	0	2	3	$\sum x_1 = 0$
X_2	9	4	0	4	9	$\sum x_2 = 26$
X_1X_2	-27	-8	0	8	27	$\sum x_1x_2 = 0$

Therefore,

$$\begin{aligned} r_{x_1x_2} &= \frac{Cov(x_1, x_2)}{S_{x_1}.S_{x_2}} \\ &= \frac{\frac{1}{n}\sum_{i=1}^{n}(x_1x_2) - \overline{x_1}.\overline{x_2}}{S_{x_1}.S_{x_2}} \\ &= \frac{\frac{1}{5}.0 - 0.\frac{26}{5}}{S_{x_1}.S_{x_2}} \\ &= 0 \end{aligned}$$

Thus, though two variables are uncorrelated (as $r = 0$), one can find that there exists a relationship $X_2 = {X_1}^2$ between X_1 and X_2. Thus, zero correlation coefficient between two variables does not always mean that the variables are independent.

7. *Correlation coefficient between two random variables X_1 and X_2 can be written as* $r_{x_1x_2} = \frac{\sigma^2_{x_1} + \sigma^2_{x_2} - \sigma^2_{x_1 - x_2}}{2\sigma_{x_1}\sigma_{x_2}}$

Proof Let $Y = X_1$-X_2.

Or,

$$\begin{aligned} Y - E(Y) &= X_1 - X_2 - E(X_1) + E(X_2) \\ &= [X_1 - E(X_1)] - [X_2 - E(X_2)] \end{aligned}$$

squaring both sides and taking expectations, we have

$$\begin{aligned} \sigma^2_Y &= \sigma^2_{x_1} + \sigma^2_{x_2} - 2\mathrm{cov}(X_1, X_2) \\ &= \sigma^2_{x_1} + \sigma^2_{x_2} - 2r_{x_1x_2}\sigma_{x_1}\sigma_{x_2} \end{aligned}$$

$$r_{x_1x_2} = \frac{\sigma^2_{x_1} + \sigma^2_{x_2} - \sigma^2_{x_1 - x_2}}{2\sigma_{x_1}\sigma_{x_2}}$$

Example 7.4 The difference between upper face length (Y) and nasal length (X) both measured in millimeter is given for 20 Indian adult males: 14, 15, 13, 16, 21, 19, 13, 15, 19, 20, 17, 18, 17, 18, 10, 11, 12, 10, 11, and 10. Calculate the correlation coefficient of X and Y, given $s_x = 3.57mm$ and $s_y = 4.47mm$.

Solution

We know that $r_{xy} = \frac{\sigma^2_x + \sigma^2_y - \sigma^2_D}{2\sigma_x\sigma_y}$, so first we need to calculate the ${\sigma_D}^2$ which is given by the formula:

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$$\sigma_D^2 = \frac{1}{n}\sum_{i=1}^{n}\left(D_i - \overline{D}\right)^2 = 12.89\,\text{mm}$$

$$r_{xy} = \frac{\sigma_x^2 + \sigma_y^2 - \sigma_D^2}{2\sigma_x\sigma_y} = \frac{3.57^2 + 4.47^2 - 12.89}{2 \text{ x } 3.57 \times 4.47} = 0.62.$$

Examples 7.5 Given below are the plant height (cm) and number of nodes of 10 mulberry varieties. Find out the correlation coefficient between height and number of nodes:

Height (X)	185	186	188	187	189	187	190	192	205	198
No. of nodes (Y)	69	70	74	67	74	70	71	73	76	72

Solution Let us frame the following table:

	Height (X)	No. of nodes (Y)	X^2	Y^2	XY
	185	69	34,225	4761	12,765
	186	70	34,596	4900	13,020
	188	74	35,344	5476	13,912
	187	67	34,969	4489	12,529
	189	74	35,721	5476	13,986
	187	70	34,969	4900	13,090
	190	71	36,100	5041	13,490
	192	73	36,864	5329	14,016
	205	76	42,025	5776	15,580
	198	72	39,204	5184	14,256
Total	1907	716	364,017	51,332	136,644
Average	190.70	71.60	36401.70	5133.20	13664.40
Var (X) =	$s_x^2 = \frac{1}{n}\sum_{i=1}^{n}(x_i - \overline{x})^2 = \left(\frac{1}{10}\sum_{i=1}^{n}x_i^2 - \overline{x}^2\right)$ $= 36401.7 - 190.70^2 = 35.21$				
Var (Y) =	$s_y^2 = \frac{1}{n}\sum_{i=1}^{n}(y_i - \overline{y})^2 = \frac{1}{10}\sum_{i=1}^{10}y_i^2 - \overline{y}^2$ $5133.20 - 71.60^2 = 6.64$				
Cov(X, Y) =	$s(x,y) = \frac{1}{n}\sum_{i=1}^{n}(x_i - \overline{x})(y_i - \overline{y}) = \frac{1}{n}\sum_{i=1}^{n}x_iy_i - \overline{xy}$ $= 13664.40 - 190 \times 71.60 = 10.28$				
r =	$\frac{\text{Cov(x,y)}}{\sqrt{\text{Var(x).Var(y)}}} = \frac{10.28}{\sqrt{35.21 \times 6.64}} = 0.672$				

So the correlation coefficient between height and number of nodes per plant is 0.672.

Problem 7.1

The following information is pertaining to height (cm) and body weight (kg) of eight students. Find out the correlation coefficient between height and body weight. Using the same information, solve the problem by changing the origin of height and weight to 178 cm and 66 kg, respectively, to find out whether there is any change in the correlation coefficient or not:

Height (X)	177	175	188	185	190	167	170	172
Weight (Y)	60	62	70	63	71	66	67	69

Example 7.6 The following table gives the number of panicle (X) per hill and the corresponding yield (Y) (t/ha) of paddy. Find out the correlation coefficient between the number of panicle and the yield of paddy:

Panicle/hill (X)	27	24	30	28	37	18	20	38	18	16
Yield (t/ha) (Y)	2.00	1.70	2.20	1.90	2.40	1.20	1.40	1.90	1.30	1.20

Solution

	Panicle/hill (X)	Yield (q/ha) (Y)	X^2	Y^2	XY
	27	2.00	729	4.00	54
	24	1.70	576	2.89	40.8
	30	2.20	900	4.84	66
	28	1.90	784	3.61	53.2
	37	2.40	1369	5.76	88.8
	18	1.20	324	1.44	21.6
	20	1.40	400	1.96	28
	38	1.90	1444	3.61	72.2
	18	1.30	324	1.69	23.4
	16	1.20	256	1.44	19.2
Total	256	17.2	7106	31.24	467.2
Average	25.6	1.72	710.6	3.124	46.72
Var (X) =	$s_x^2 = \frac{1}{n}\sum_{i=1}^{n}(x_i - \overline{x})^2 = \left(\frac{1}{10}\sum_{i=1}^{n}x_i^2 - \overline{x}^2\right)$ $= 710.6 - 25.6^2 = 55.24$				
Var (Y) =	$s_y^2 = \frac{1}{n}\sum_{i=1}^{n}(y_i - \overline{y})^2 = \frac{1}{10}\sum_{i=1}^{10}y_i^2 - \overline{y}^2$ $3.124 - 1.72^2 = 0.1656$				
Cov(X, Y) =	$s(x,y) = \frac{1}{n}\sum_{i=1}^{n}(x_i - \overline{x})(y_i - \overline{y}) = \frac{1}{n}\sum_{i=1}^{n}x_iy_i - \overline{xy}$ $= 46.72 - 25.6 \times 1.72 = 2.688$				
r =	$\frac{\text{Cov(x,y)}}{\sqrt{\text{Var(x).Var(y)}}} = \frac{2.688}{\sqrt{55.24 \times 0.1656}} = 0.889$				

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Example 7.7 Find out the correlation coefficient between DCP (%) and TDN (%) from the following table:

	Green roughages	
Feed	DCP (%)	TDN (%)
Berseem	2.8	12
Lucerne	3.5	12.5
Cowpea	3.2	10.8
Maize	1.2	16.5
Napier	1.5	15.8
Sorghum	1	16
Pea	2.5	12.5
Para grass	1.5	11.4
Oat	2.6	16.7

Solution Let DCP (%) and TDN (%) are denoted by X_1 and X_2, respectively:

	X_1	X_2	$X_1-\overline{X}_1$	$X_2-\overline{X}_2$	$(X_1-\overline{X}_1)^2$	$(X_2-\overline{X}_2)^2$	$(X_1-\overline{X}_1)(X_2-\overline{X}_2)$
	2.8	12	0.60	−1.80	0.36	3.24	−1.08
	3.5	12.5	1.30	−1.30	1.69	1.69	−1.69
	3.2	10.8	1.00	−3.00	1.00	9.00	−3.00
	1.2	16.5	−1.00	2.70	1.00	7.29	−2.70
	1.5	15.8	−0.70	2.00	0.49	4.00	−1.40
	1	16	−1.20	2.20	1.44	4.84	−2.64
	2.5	12.5	0.30	−1.30	0.09	1.69	−0.39
	1.5	11.4	−0.70	−2.40	0.49	5.76	1.68
	2.6	16.7	0.40	2.90	0.16	8.41	1.16
Total	**19.80**	**124.20**	**0.00**	**0.00**	**6.72**	**45.92**	**−10.06**
Average	**2.20**	**13.80**					

There are nine different types of forages, and we have to find correlation between DCP (%) and TDN (%). First, we need to calculate variances and covariance from the above table:

$$Cov(X_1,X_2)=S_{x_1x_2}=\frac{\sum_1^n (X_1-\overline{X}_1)(X_2-\overline{X}_2)}{n}$$

$$=\frac{-10.06}{9}=-1.12$$

$$S^2{}_{x_1}=\frac{\sum_1^n (X_1-\overline{X}_1)^2}{n}=\frac{6.72}{9}=5.10$$

$$S^2_{x_2}=\frac{\sum_1^n (X_2-\overline{X}_2)^2}{n}=\frac{45.92}{9}=0.75$$

$$\therefore r_{x_1x_2}=\frac{Cov(X_1,X_2)}{S_{x_1}S_{x_2}}=\frac{-1.12}{\sqrt{(5.10\times 0.75)}}$$

$$=-0.57$$

Hence, correlation between DCP (%) and TDN (%) is −0.57.

Problem 7.2 Body weight and length of ten different cows were measured. Using the following figures, find out the correlation coefficient between body weight and length of cows:

Weight (Kg)	586	672	598	625	640	705	690	595	645	685
Length (m)	1.95	2.38	2.02	2.20	2.30	2.38	2.42	2.05	2.25	2.35

7.4 Significance of Correlation Coefficients

1. *Significance of the sign of correlation coefficient:* If two variables X_1 and X_2 are positively correlated, then increase/decrease in one

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variable is associated with increase/decrease in other variables also. On the other hand, if two variables are negatively correlated, then increase/decrease in one variable is associated with decrease/increase in other variable.

2. *Significance of the value of the correlation coefficient:* We have already come to know that $-1 \leq r \leq +1$ and the significance of the sign of the coefficient. The value of the correlation coefficient actually depicts the degree/strength/intensity of linear associationship; the higher the value, the higher is the strength of the associationship.

7.5 Correlation Coefficient of Bivariate Frequency Distribution

Joint variabilities of two variables at a time are represented with the help of a bivariate frequency distribution. Likewise to that of a univariate frequency distribution, bivariate frequency distribution expresses the joint frequency distribution of two variables considered at the same time. In this section, let us discuss the procedure of working out the correlation coefficient from such bivariate frequency distribution. Bivariate frequency distribution of two variables, X_1 and X_2, may be presented in the following form:

It is to be noted that $\sum_{i=}^{m}\sum_{j=1}^{n} f_{ij} = \sum_{i=1}^{m} f_{i.} = \sum_{j=1}^{n} f_{.j} = N.$

From the above bivariate frequency distribution, table one can very well frame the univariate frequency distribution tables for the individual variables X and Y as follows:

Frequency distribution of X_1			Frequency distribution of X_2		
Class	Mid-value	Frequency	Class	Mid-value	Frequency
$x_{10} - x'_{11}$	x_{11}	$f_{1.}$	$x_{20} - x'_{21}$	x_{21}	$f_{.1}$
$x'_{11} - x'_{12}$	x_{12}	$f_{2.}$	$x_{21} - x'_{22}$	x_{22}	$f_{.2}$
$x'_{12} - x'_{13}$	x_3	$f_{3.}$	$x_{22} - x'_{23}$	x_{23}	$f_{.3}$
–	–	–	–		–
$x'_{1,i-1} - x'_{1i}$	x_{1i}	$f_{i.}$	$x'_{2j-1} - x'_{2j}$	x_{2j}	$f_{j.}$
–	–	–	–		–
$x'_{1,m-1} - x'_{1m}$	x_{1m}	$f_{m.}$	$x'_{2n-1} - x'_{2n}$	$x'_{2n-1} - x'_{2n}$	$f_{n.}$

Using the univariate frequency distribution tables, one can very well calculate the univariate measures of central tendency and dispersion for both the variables separately as follows:

$$\overline{x_1} = \frac{1}{N}\sum_{i=1}^{m}(f_{i.}.x_{1i})$$

Similarly,

$$\overline{x_2} = \frac{1}{N}\sum_{j=1}^{n}\left(f_{.j}.x_{2j}\right)$$

$$S^2{}_{x_1} = \frac{1}{N}\sum_{i=1}^{m} f_{i.}.x_{1i}^2 - \bar{x}_1{}^2$$

X1 Class ↓ \ X_2 Class →	Mid-value (x)	$x_{20} - x'_{21}$	$x_{21} - x'_{22}$	$x'_{22} - x'_{23}$	–	$x'_{2j-1} - x'_{2j}$	–	$x'_{2n-1} - x'_{2n}$	Total
		Mid-value (y)							
		x_{21}	x_{22}	x_{23}	–	x_{2j}	–	x_{2n}	
$x_{10} - x'_{11}$	x_{11}	f_{11}	f_{12}	f_{13}	–	–	–	f_{1n}	$f_{1.}$
$x'_{11} - x'_{12}$	x_{12}	f_{21}	f_{22}	f_{23}	–	–	–	f_{2n}	$f_{2.}$
$x'_{12} - x'_{13}$	x_3	f_{31}	f_{32}	f_{33}	–	–	–	f_{3n}	$f_{3.}$
–	–	–	–	–	–	–	–	–	–
$x'_{1,i-1} - x'_{1i}$	x_{1i}	–	–	–	–	f_{ij}	–	f_{in}	$f_{i.}$
–	–	–	–	–	–	–	–	–	–
$x'_{1,m-1} - x'_{1m}$	x_{1m}	f_{m1}	f_{m2}	f_{m3}	–	–	–	f_{mn}	$f_{m.}$
	Total	$f_{.1}$	$f_{.2}$	$f_{.3}$	–	$f_{.j}$	–	$f_{.n}$	$\sum_i\sum_j f_{ij} = N$

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$$S^2{}_{x_2} = \frac{1}{N}\sum_{j=1}^{n} f_{.j}.x_{2j}^2 - \bar{x}_2{}^2$$

And from the bivariate frequency distribution table, one can find out the covariance between the two variables as follows:

$$\begin{aligned} Cov(x_1, x_2) &= \frac{1}{N}\sum_{i}^{m}\sum_{j}^{n} f_{ij}\left(x_{1i} - \bar{x}_1\right)\left(x_{2j} - \bar{x}_2\right) \\ &= \frac{1}{N}\sum_{i,j} f_{ij}x_{1i}x_{2j} - \overline{x_1}.\overline{x_2} \end{aligned}$$

$$\begin{aligned} r_{x_1,x_2} &= \frac{\frac{1}{N}\sum_{i}^{m}\sum_{j}^{n} f_{ij}\left(x_{1i} - \bar{x}_1\right)\left(x_{2j} - \bar{x}_2\right)}{\sqrt{\frac{1}{N}\sum_{i=1}^{m} f_{i.}.x_{1i}^2 - \bar{x}_1{}^2}\sqrt{\frac{1}{N}\sum_{j=1}^{n} f_{.j}.x_{2j}^2 - \bar{x}_2{}^2}} \\ &= \frac{\frac{1}{N}\sum_{i,j} f_{ij}x_{1i}x_{2j} - \overline{x_1}.\overline{x_2}}{\sqrt{\frac{1}{N}\sum_{i=1}^{m} f_{i.}.x_{1i}^2 - \bar{x}_1{}^2}\sqrt{\frac{1}{N}\sum_{j=1}^{n} f_{.j}.x_{2j}^2 - \bar{x}_2{}^2}} \end{aligned}$$

Example 7.8 The following table gives frequency distribution of plant height (m) and the stick yield per hectare of jute. Using the data, find out the correlation coefficient plant height and the stick yield:

Height (m)	Stick yield (t/ha)						
	2.3–2.4	2.4–2.5	2.5–2.6	2.6–2.7	2.7–2.8	2.8–2.9	2.9–3.0
2.10–2.20	3	1	1	2	3	3	1
2.20–2.30	3	5	3	2	3	3	1
2.30–2.40	7	5	4	6	2	1	2
2.40–2.50	1	0	2	4	2	2	2
2.50–2.60	3	0	1	0	2	2	2
2.60–2.70	2	1	0	3	3	2	0
2.70–2.80	1	0	2	0	0	2	0

Solution Using the above information, let us frame the following tables:

Height (m)	Stick yield (t/ha)							
	2.3–2.4	2.4–2.5	2.5–2.6	2.6–2.7	2.7–2.8	2.8–2.9	2.9–3.0	Total
2.10–2.20	3	1	1	2	3	3	1	14
2.20–2.30	3	5	3	2	3	3	1	20
2.30–2.40	7	5	4	6	2	1	2	27
2.40–2.50	1	0	2	4	2	2	2	13
2.50–2.60	3	0	1	0	2	2	2	10
2.60–2.70	2	1	0	3	3	2	0	11
2.70–2.80	1	0	2	0	0	2	0	5
Total	20	12	13	17	15	15	8	100

Frequency distribution of height(m) (X)

Height (m)	Mid-value (x_i)	Frequency (f_i)	$f_i{x_i}^2$
2.10–2.20	2.15	14	64.72
2.20–2.30	2.25	20	101.25
2.30–2.40	2.35	27	149.11
2.40–2.50	2.45	13	78.03
2.50–2.60	2.55	10	65.03
2.60–2.70	2.65	11	77.25
2.70–2.80	2.75	5	37.81

Frequency distribution of stick yield (t/ha) (Y)

Yield class	Mid-value (y_j)	Frequency (f_j)	$f_j{y_j}^2$
2.3–2.4	2.35	20	110.45
2.4–2.5	2.45	12	72.03
2.5–2.6	2.55	13	84.53
2.6–2.7	2.65	17	119.38
2.7–2.8	2.75	15	113.44
2.8–2.9	2.85	15	121.84
2.9–3.0	2.95	8	69.62

$$\begin{aligned} \bar{x} &= \frac{1}{N}\sum_{i=1}^{m}(f_{i.}.x_i) \\ &= \frac{1}{100}[2.15 \times 14 + 2.25 \times 20 \\ &\quad + \ldots\ldots\ldots + 2.75 \times 5] \quad = 2.388\,\text{m} \end{aligned}$$

$$\begin{aligned} \bar{y} &= \frac{1}{N}\sum_{j=1}^{n}\left(f_{.j}.y_j\right) \\ &= \frac{1}{100}[2.35 \times 20 + 2.45 \times 12 + 2.55 \\ &\quad \times 13 + \ldots + 2.95 \times 8] \quad = 2.622\,\text{t} \end{aligned}$$

$$\begin{aligned} S^2{}_x &= \frac{1}{N}\sum_{i=1}^{m} f_{i.}.x_i^2 - \bar{x}^2 \\ &= \frac{1}{100}[64.72 + 101.25 + \ldots\ldots + 31.81] \\ &\quad -2.388^2 = 0.0293\,\text{m}^2 \end{aligned}$$

$$S^2{}_y = \frac{1}{N}\sum_{j=1}^{n} f_{.j}.y_j^2 - \bar{y}^2$$

$$\begin{aligned} &= [110.45 + 72.03 + \ldots\ldots + 121.84 \\ &\quad + 69.62] \quad \frac{1}{100} \quad - 2.622^2 = 0.038\,\text{t}^2 \end{aligned}$$

From this table, we shall find out the covariance between the variables as follows:

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Height (m)	Mid-value (x_i)	Stick yield (t/ha) 2.3–2.4	2.4–2.5	2.5–2.6	2.6–2.7	2.7–2.8	2.8–2.9	2.9–3.0	Frequency
		2.35	2.45	2.55	2.65	2.75	2.85	2.95	
2.10–2.20	2.15	3	1	1	2	3	3	1	14
2.20–2.30	2.25	3	5	3	2	3	3	1	20
2.30–2.40	2.35	7	5	4	6	2	1	2	27
2.40–2.50	2.45	1	0	2	4	2	2	2	13
2.50–2.60	2.55	3	0	1	0	2	2	2	10
2.60–2.70	2.65	2	1	0	3	3	2	0	11
2.70–2.80	2.75	1	0	2	0	0	2	0	5
Frequency		20	12	13	17	15	15	8	100

$$Cov(x,y) = \frac{1}{N}\sum_{i}^{m}\sum_{j}^{n} f_{ij}\left(x_i - \bar{x}\right)\left(y_j - \bar{y}\right)$$
$$= \frac{1}{N}\sum_{i,j} f_{ij}x_i y_j - \bar{x}.\bar{y}$$

$$= \frac{1}{100}\big[2.15 \times (2.35 \times 3 + 2.45 \times 1 + 2.55 \times 1 + 2.65 \times 2 + 2.75 \times 3 + 2.85 \times 3 + 2.95 \times 1) + 2.25(2.35 \times 3 + 2.45 \times 5 + 2.55 \times 3 + 2.65 \times 2 + 2.75 \times 3 + 2.85 \times 3 + 2.95 \times 1) + 2.35 \times (2.35 \times 7 + 2.45 \times 5 + 2.55 \times 4 + 2.65 \times 6 + 2.75 \times 2 + 2.85 \times 1 + 2.95 \times 2) + 2.45 \times (\ldots\ldots\ldots\ldots) + 2.55 \times (\ldots\ldots\ldots) + 2.65 \times (\ldots\ldots\ldots) + 2.75 \times (\ldots\ldots)\big] - 2.388 \times 2.622 = 0.0024$$

$$\therefore r_{xy} = \frac{Cov(X,Y)}{S_X S_y} = \frac{0.0024}{\sqrt{(0.0293 \times 0.038)}} = 0.071$$

Problem 7.3 Plant height (cm) and number of cobs per plant in 80 maize plants were studied for the associationship between plant height (X) and number of cobs per plant (Y). Using the information provided in the following table, find out the correlation coefficient between the characters:

Plant ht (X)	Number of cobs per plant (Y) 5–7	7–9	9–11	11–13	13–15	15–17
125–135	2	1	0	0	0	0
135–145	1	2	0	0	0	0
145–155	0	3	2	1	0	0
155–165	1	3	2	1	1	0
165–175	2	2	3	1	0	0
175–185	0	1	2	2	2	0
185–195	0	2	3	3	1	0
195–205	0	1	4	3	2	1
205–215	0	0	5	4	3	1
215–225	0	2	5	3	2	0

Problem 7.4 The following table gives the number of panicle-bearing tillers per hill and the number of grains per panicle in certain experiment with rice. Find out the correlation coefficient between the grains per panicle and the number of effective tiller per hill:

Number of effective tiller/hill (x)	**Class**	**No of grains/panicle (y) 30–35**	**35–40**	**40–45**	**45–50**
	10–12	10	8	7	6
	13–15	12	16	18	7
	16–18	10	25	18	15
	19–21	8	13	11	10
	22–24	10	13	16	8

7.6 Limitations

1. Correlation coefficient can only measure the degree of linear associationship; it fails to adequately measure the associationship when the associationship is nonlinear; for nonlinear

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relationship between the variables, correlation ratio is of use.

2. When more than two variables are operating in a system, then in most of the cases, a simple correlation coefficient fails to measure the actual degree of associationship between the variables. Under multivariate (more than two) situation, a high/low correlation coefficient between two variables in the system does not mean high/low direct associationship between the variables; influences of other variables on both variables are to be taken into consideration. Under such situation, partial correlation coefficient or path coefficient analysis will be more pertinent.
3. Given any two sets of values for two variables, one can work out the correlation coefficient between the variables. One can find out the correlation between year-wise fish production in India and the number of fisheries per year in United States of America. But hardly one can find any logical understanding of such correlation coefficient. This type of correlation is often called as nonsense or spurious correlation. Thus, it is essential to have clear logical understanding about the variables between which the correlation is to be worked out.
4. Sometimes it is found that two variables (say X and Y) are showing high degree of linear associationship, as measured through correlation coefficient, not because they are highly correlated but because of the influence of another variable (say Z) on both variables under consideration. Such a variable (Z) is called lurking variable. So one must ascertain the presence or absence of any lurking variable before working out the correlation coefficient between any two variables.

7.7 Rank Correlation

Correlation coefficient discussed so far deals with quantitative characters. But in real-life situation, we are to deal with both quantitative as well as qualitative variables. Unlike quantitative variables, qualitative variables are not measurable; on the contrary, they can be grouped or ranked into different groups or ranks. For example, a student is graded or ranked according to his or her performance in an examination, the aroma of tea is graded or ranked, and color can be categorized in to blue, black, white, etc. If we want to get a correlation between the color and aroma of tea, then simple correlation coefficient as mentioned in the previous section fails to answer. Similarly, the tolerance of a particular crop to stress may be ranked. Different breeds of cows can be ranked according to their resistance toward diseases and pests and at the same time according to their milk-producing capacity. In all these cases, correlation between two qualitative characters (attributes) can be worked out using *Spearman's rank correlation coefficient*.

Let us suppose n individuals are ranked based on two characters, X and Y, as given in the following table:

Element	1	2	3	4	5	...	$n-2$	$n-1$	n
Rank for X	2	4	6	n-3	7	...	$n-1$	10	12
Rank for Y	5	3	n	7	4	...	2	$n-1$	$n-2$

Assuming that no two individuals are tied in ranks for either in X or Y, the Spearman's rank correlation coefficient is given as

$$r_R = 1 - \frac{6\sum {d^2}_i}{n(n^2-1)}, \text{ where } d_i (i = 1, 2, ..., n)$$

are the difference between the ranks (x_i and y_i, respectively) obtained in two different characters by the ith individual, i.e., (x_i-y_i) = d_i.

If more than one individual have the same ranks, i.e., when the ranks are tied, then the above formula is modified as follows:

$$r_R = 1 - \frac{6\left\{\sum {d^2}_i + \frac{p(p^2-1)}{12} + \frac{q(q^2-1)}{12}\right\}}{n(n^2-1)},$$

where p and q are the number of individuals involved in tied ranks for the characters X and Y, respectively.

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Rank correlation coefficient also $-1 \leq r_R \leq +1$; the proof is left for the readers.

Rank correlation coefficient also does not have any unit.

Example 7.9 Ten varieties of tea were examined for flavor as well as for color. The ranks are shown in the table provided below; to find out the degree of linear associationship between flavor and color:

Quality	Variety									
	V_1	V_2	V_3	V_4	V_5	V_6	V_7	V_8	V_9	V_{10}
Flavor	6	1	7	3	5	4	2	8	9	10
Color	10	2	9	6	7	5	1	4	8	3

The differences between ranking in aroma and susceptibility are $-3, -1, -3, -3, 4, -1, 1, -2, 1$, and 7, and there exists no tied rank.

$$\text{So, } \sum_{i=1}^{n} d^2{}_i = 16 + 1 + 4 + 9 + 4 + 1 + 1 + 16 + 1 + 49 = 102$$

$$\Rightarrow r_R = 1 - \frac{6.\sum_{i=1}^{10} d^2{}_i}{10(10-1)} = 1 - \frac{6.102}{10.99} = 1 - 0.618 = 0.382$$

Thus, there is low associationship between the flavor and color of tea.

Example 7.10 Farmers are ranked for their educational index and knowledge index as follows. Find out the associationship between the standard of education and knowledge of the farmers:

	Farmers									
	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}
Education	9	10	3	5	6	3	2	1	7	8
Knowledge	6	9	7	4	2	1	4	3	8	10

In education, there are two-tied rank 3 and in awareness also two-tied rank 4. So the correction in education series is $\frac{2(2^2-1)}{12} = \frac{2(4-1)}{12} = \frac{1}{2}$ and that in awareness series is also $\frac{1}{2}$.

Now, the above table can be written as

	Farmers									
	F_1	F_2	F_3	F_4	F_5	F_6	F_7	F_8	F_9	F_{10}
Education	9	10	3.5	5	6	3.5	2	1	7	8
Knowledge	6	9	7	4.5	2	1	4.5	3	8	10

$$\therefore d_i = 3,\ 1,\ -3.5,\ 0.5,\ 4,\ 2.5,\ -2.5,\ -2,\ -1,\ -2$$

$$\Rightarrow \sum_{i=1}^{10} d^2{}_i = 3^2 + 1^2 + (-3.5)^2 + (0.5)^2 + 4^2 + (2.5)^2 + (-2.5)^2 + (-2)^2 + (-1)^2 + (-2)^2$$
$$= 9 + 1 + 12.25 + 0.25 + 16 + 6.25 + 6.25 + 4 + 1 + 4$$
$$= 60$$

$$r_R = 1 - \frac{6\left\{\sum d^2{}_i + \frac{p(p^2-1)}{12} + \frac{q(q^2-1)}{12}\right\}}{n(n^2-1)}$$
$$= 1 - \frac{6.\left[60 + \frac{1}{2} + \frac{1}{2}\right]}{10 \times 99}$$
$$= 1 - 0.3697$$
$$= 0.630$$

So the education and knowledge of the farmers are substantially associated.

Problem 7.5 The following figures give the fish landing of two different types of sardines for ten landing stations. Using the data, find out the correlation between two types of fish landing:

Oil sardine	115,744	221,026	205,294	183,706	188,832	120,587	77,849	100,456	130,832	278,869
Other sardines	66,810	61,717	54,525	75,990	66,472	60,556	69,808	92,542	77,188	83,167

Problem 7.6 Ten scented varieties of rice were ranked for aroma and shape of grain by two experts separately. The following data show the rank given by the experts to each variety. Find

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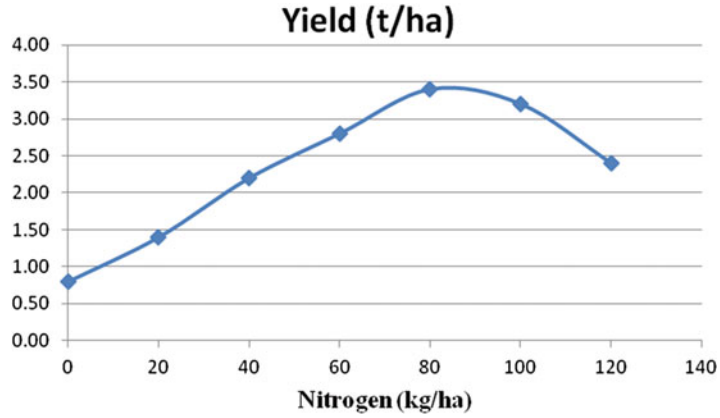
out the degree of linear associationship between the two experts:

	Varieties									
Expert	1	2	3	4	5	6	7	8	9	10
Expert A	9	10	8	5	6	3	2	1	7	4
Expert B	7	10	9	2	8	4	1	3	6	5

Problem 7.7 Find out the correlation coefficient between the marks obtained in fishery extension and fishery economics for 100 students from the following frequency distribution table:

Marks scored in fishery economics	**Marks scored in fishery extension**					
	50–60	**60–70**	**70–80**	**80–90**	**90–100**
50–60	1	5	5	4	1
60–70	3	5	9	7	5
70–80	2	8	9	7	7
80–90	2	2	5	6	4
90–100	0	1	1	1	0



7.8 Correlation Ratio

Experience of our daily life says that hardly one can find the relationship between two variables changing at a constant rate, i.e., hardly one can find the relationship between two variables as linear. In most of the cases, there exists nonlinear relationship between the variables. For example, if a farmer changes the doses of nitrogen, how the yield of the crop will change? Definitely, one cannot expect the yield to go on increasing with the increase in the dose of nitrogen. Actually, yield of the crop will increase upto certain dose of nitrogenous fertilizer, reaches to a maximum, and will start declining after there. That means there will be curvilinear path in between the dose of nitrogen and the corresponding yield. The graph may be as given below or some other form.

Correlation coefficients can only measure the degree of *linear* associationship between two variables. But under the above nonlinear situation, it fails to actually picturize the degree of associationship. Under such situation, a measure called *correlation ratio* is used to measure the degree of associationship. Correlation ratio, generally denoted as η(Eta), is the appropriate measure of degree of nonlinear relationship between two variables.

The basic idea of nonlinear relationship is that one assumes more than one values of a variable to each value of the other variable. So we assume that to each of the n values of a variable, there exists one array of values of the other variable. Suppose X is a variable taking the values $x_1, x_2, \ldots x_n$ and corresponding to each observation of the variable X, we have an array for the other variable Y. Thus, y_{ij}s are the values of the variable Y corresponding to x_i value of the variable X, and $j(1,2,\ldots m)$ is the length of the ith array, and suppose each of these values occurs with frequency f_{ij}. Thus, the frequency distribution of two variables X and Y can be arranged as given below:

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x_i / y_{ij}	x_1	x_2	–	x_i	–	x_n	Total
y_{i1}	f_{11}	f_{21}	–	f_{i1}	–	f_{n1}	$f_{.1}$
y_{i2}	f_{12}	f_{22}	–	f_{i2}	–	f_{n2}	$f_{.2}$
y_{i3}	f_{13}	f_{23}	–	f_{i3}	–	f_{n3}	$f_{.3}$
–	–	–	–	–	–	–	–
y_{ij}	f_{1j}	–	–	f_{ij}	–	f_{nj}	$f_{.j}$
–	–	–	–	–	–	–	–
y_{im}	f_{1m}	f_{2m}	–	f_{im}	–	f_{nm}	$f_{.m}$
$n_i = \sum_{j=1}^{m} f_{ij}$	n_1	n_2	–	n_i	–	n_n	$\sum_{i}^{n}\sum_{j}^{m} f_{ij} = \sum_{i=1}^{n} n_i = N$
$S_i = \sum_{j=1}^{m} f_{ij}y_{ij}$	S_1	S_2	–	S_i	–	S_n	$\sum_{i}^{n}\sum_{j}^{m} f_{ij}y_{ij} = \sum_{i=1}^{n} S_i = S$
$\overline{y}_i = \frac{S_i}{n_i}$	$\overline{y}_1 = \frac{S_1}{n_1}$	$\overline{y}_2 = \frac{S_2}{n_2}$	–	$\overline{y}_i = \frac{S_i}{n_i}$	–	$\overline{y}_n = \frac{S_n}{n_n}$	$\overline{y} = \frac{S}{N}$

From the above table, we have $\overline{y}_i = \frac{S_i}{n_i}$ and $\overline{y} = \frac{S}{N}$ that are the means of ith array and the overall mean, respectively.

Correlation ratio (η) of Y on X is defined as

$$\eta^2_{yx} = 1 - \frac{s^2{}_{ey}}{s^2{}_y} = \frac{s^2{}_{my}}{s^2{}_y}$$

where $s^2{}_{ey} = \frac{1}{N}\sum_i \sum_j f_{ij}\left(y_{ij} - \overline{y_i}\right)^2$;

$$s^2{}_{my} = \frac{1}{N}\sum_i \sum_j f_{ij}(\overline{y}_i - \overline{y})^2 \text{ and}$$

$$s^2{}_y = \frac{1}{N}\sum_i \sum_j f_{ij}\left(y_{ij} - \overline{y}\right)^2.$$

Example 7.11 An experiment was conducted to know the effect of transplanting age on fruit per plant at early harvest of tomato, and the following results were obtained. Find out the correlation ratio of yield on age of plant.

Transplanting age (age) (X)	Fruit per plant (no.) (Y)					
	15–18	19–22	23–26	27–30	31–34	35–38
1–5	**2**	**-**	**-**	**-**	**-**	**-**
6–10	**3**	**6**	**6**	**1**	**-**	**-**
11–15	**3**	**7**	**10**	**5**	**-**	**-**
16–20	**-**	**8**	**15**	**10**	**10**	**-**
21–25	**-**	**-**	**12**	**19**	**15**	**5**
26–30	**-**	**-**	**2**	**4**	**10**	**4**

Solution From the given information, we frame the following table:

	x_1	x_2	x_3	x_4	x_5	x_6	
y	3	8	13	18	23	28	Total
16.50	2	3	3	0	0	0	8
20.50	0	3	7	8	0	0	21
24.50	0	6	10	15	12	2	45
28.50	0	1	5	10	19	4	39
32.50	0	0	0	10	15	10	35
36.50	0	0	0	0	5	4	9
$n_i = \sum_{j=1}^{6} f_{ij}$	2	16	25	43	51	20	154
$S_i = \sum_{j=1}^{6} f_{ij}y_{ij}$	33.00	286.50	580.50	1141.50	1505.50	634.00	4181.00
$\frac{S_i^2}{n_i}$	544.50	6314.02	13479.21	30302.84	44441.77	20097.80	115180.14
$\sum_{j=1}^{6} f_{ij}y_{ij}^2$	544.50	6491.25	13822.25	31050.75	45140.75	20341.00	117390.50

One can get $\eta^2{}_{yx} = 1 - \frac{s^2_{ey}}{s^2_y} = \frac{s^2_{my}}{s^2_y}$.

We have

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$$Ns_y^2 = \sum_i \sum_j f_{ij}(y_{ij} - \bar{y})^2$$

$$= \sum_i \sum_j f_{ij} y_{ij}^2 - N\bar{y}^2 = \sum_i \sum_j f_{ij} y_{ij}^2 - \frac{S^2}{N}$$

$$= 117390.50 - \frac{(4181.00)^2}{154}$$

$$= 117390.50 - 113511.40 = 3879.06$$

$$Ns_{my}^2 = \sum_i \sum_j f_{ij}(\bar{y}_i - \bar{y})^2 = \sum \frac{S_i^2}{n_i} - \frac{S^2}{N}$$

$$= 115180.14 - 113511.40 = 1668.70$$

So, $\eta^2_{yx} = \frac{S^2_{my}}{S^2_y} = \frac{1668.70}{3879.06} = 0.430$.

Problem 7.8 An experiment was conducted to know the effect of age of a particular breed of cow on daily milking capacity (liters), and the following results were obtained. Find out the correlation ratio of milking capacity on age of cow.

Age of cow (X) in year	Milking capacity in liters (Y)					
	1–3	4–6	7–9	10–12	13–15	16–18
2–3	-	-	5	2	1	-
4–5	-	2	12	13	1	5
6–7	-	4	10	14	15	2
8–9	2	3	7	8	7	-
10–11	6	2	1	-	-	-
12–13	8	1	-	-	0	-

7.9 Properties of Correlation Ratio

1. $$r^2 \le \eta^2_{yx} \le 1.$$
2. η^2_{yx} is independent of change of origin and scale.
3. $r_{xy} = r_{yx}$ but $\eta_{yx}{}^2$ may or may not be equal to $\eta_{xy}{}^2$.

7.10 Coefficient of Concurrent Deviation

Another measure of degree of linear associationship between any two variables, X_1 and X_2, is given through coefficient of concurrent deviation. Unlike the original values or the grade of the two variables under consideration, it considers only the sign of the change in values of each variable from its previous values. Generally, this is used for time series data. Correlation coefficient is calculated as $r_c = \pm\sqrt{\pm\left(\frac{2c}{n} - 1\right)}$, where c is the number of positive signs of the products of the signs of deviations of the variables and n is the number of deviations. The sign of the correlation coefficient will be the sign of $\left(\frac{2c}{n} - 1\right)$.

Example 7.12 Let us have two variables, the number of boy and girl students passing out of class in each year. We are to find out the correlation coefficient between the pass out of boy and girl students. We shall use the following data:

Year	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010
Boys	120	115	117	119	125	130	110	125	122	118
Girls	85	87	89	100	95	102	97	99	105	110

Solution

Year (t)	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010
Boys ($X1$)	120	115	117	119	125	130	110	125	122	118
Girls ($X2$)	85	87	89	100	95	102	97	99	105	110
Sign of the deviation ($X1_t$-$X1_{t-1}$)= $\Delta X1_t$		−	+	+	+	+	−	+	−	−
Sign of the deviation ($X2_t$-$X2_{t-1}$) = $\Delta X2_t$		+	+	+	−	+	−	+	+	+
Product of signs of deviations= $\Delta X1_t \times \Delta X2_t$		−	+	+	−	+	+	+	−	−

Here, c = number of positive signs in products of sign =5 and

N = number of deviations = number of pairs of observations −1 = 10-1 = 9.

So the coefficient of concurrent deviation is

$$r_c = \pm\sqrt{\pm\left(\frac{2c}{n} - 1\right)} = \pm\sqrt{\pm\left(\frac{2.5}{9} - 1\right)}$$

$$= \pm\sqrt{\pm(1.11 - 1)} = +\sqrt{+(0.11)}$$

$$= +\sqrt{0.11} = 0.332$$

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7.11 Calculation of Correlation Coefficient Using MS Excel, SPSS, and SAS

Let us take the following information on energy (K cal) with different combinations of moisture, protein, lipid, and carbohydrate. With the help this example, we shall demonstrate how correlation coefficients could be calculated following (a) usual procedure of calculation, (b) using MS Excel, (c) using SPSS, and (d) using SAS software:

Observation	Energy (K cal)	Moisture	Protein	Lipid	Carbohydrate
	y	x_1	x_2	x_3	x_4
1	163	73.70	12.90	11.50	0.90
2	191	70.40	13.30	14.50	0.70
3	185	70.40	13.90	13.30	1.50
4	170	72.80	13.50	12.00	0.80
5	170	72.80	13.80	12.00	0.80
6	161	73.70	13.10	11.10	1.00
7	170	72.60	13.10	11.80	1.70
8	173	70.12	13.20	12.46	0.90
9	178	71.23	13.60	12.76	0.87
10	167	73.21	12.97	11.97	0.77
11	182	70.02	13.76	13.78	1.34
12	184	69.12	13.77	13.98	1.23
13	174	70.07	13.34	12.45	0.45
14	168	73.23	12.98	11.77	0.77
15	162	74.12	12.77	11.34	0.87
16	182	69.77	13.77	13.57	1.45
17	191	68.12	13.98	14.54	1.77
18	161	74.77	12.87	11.22	0.95
19	164	74.27	12.99	12.34	0.97
20	185	71.23	13.87	13.65	1.17

Solution

(a) From the given table, we can frame the following table in the next page, and the following quantities could be calculated:

$$\bar{y} = \frac{1}{20}\sum_{i=1}^{20} y_i = \frac{1}{20} \times 3481.000 = 174.050, \bar{x}_1 = \frac{1}{20}\sum_{i=1}^{20} x_{1i} = \frac{1}{20} \times 1435.680 = 71.784$$

$$\bar{x}_3 = \frac{1}{20}\sum_{i=1}^{20} x_{3i} = \frac{1}{20} \times 252.030 = 12.602,$$

$$\bar{x}_4 = \frac{1}{20}\sum_{i=1}^{20} x_{4i} = \frac{1}{20} \times 20.910 = 1.046$$

$$s_y^2 = \frac{1}{n}\sum_{i=1}^{n} (y_i - \bar{y})^2 = \frac{1}{n}\sum_{i=1}^{n} {y_i}^2 - \bar{y}^2 = \frac{1}{20}.607769.00 - 174.050^2 = 95.048$$

$$s_{x_1}^2 = \frac{1}{n}\sum_{i=1}^{n} (x_{1i} - \bar{x}_1)^2 = \frac{1}{n}\sum_{i=1}^{n} x_{1i}^2 - {\bar{x}_1}^2 = \frac{1}{20}.103131.44 - 71.784^2 = 3.630$$

$$s_{x_2}^2 = \frac{1}{n}\sum_{i=1}^{n} (x_{2i} - \bar{x}_2)^2 = \frac{1}{n}\sum_{i=1}^{n} x_{2i}^2 - {\bar{x}_2}^2 = \frac{1}{20}.3580.11 - 13.374^2 = 0.155$$

$$s_{x_3}^2 = \frac{1}{n}\sum_{i=1}^{n} (x_{3i} - \bar{x}_3)^2 = \frac{1}{n}\sum_{i=1}^{n} x_{3i}^2 - {\bar{x}_3}^2 = \frac{1}{20}.3198.69 - 12.602^2 = 1.137$$

$$s_{x_4}^2 = \frac{1}{n}\sum_{i=1}^{n} (x_{4i} - \bar{x}_4)^2 = \frac{1}{n}\sum_{i=1}^{n} x_{4i}^2 - {\bar{x}_4}^2 = \frac{1}{20}.24.19 - 1.046^2 = 0.116$$

$$\mathrm{Cov}(x, y) = \frac{1}{n}\sum_{i=1}^{n} (x_i - \bar{x})(y_i - \bar{y})$$

$$\mathrm{Cov}(x_1, y) = \frac{1}{n}\sum_{i=1}^{n} (x_{1i} - \bar{x})(y_i - \bar{y})$$

$$= \frac{1}{20}\sum_{i=1}^{n} x_{1i}y_i - \bar{x}_1\bar{y} = \frac{1}{20}.249547.81 - 71.784 \times 174.050 = -16.615$$

$$\mathrm{Cov}(x_2, y) = \frac{1}{n}\sum_{i=1}^{n} (x_{2i} - \bar{x})(y_i - \bar{y})$$

$$= \frac{1}{20}\sum_{i=1}^{n} x_{2i}y_i - \bar{x}_2\bar{y} = \frac{1}{20}.46615.23 - 13.374 \times 174.050 = 3.104$$

$$\mathrm{Cov}(x_3, y) = \frac{1}{n}\sum_{i=1}^{n} (x_{3i} - \bar{x})(y_i - \bar{y})$$

$$= \frac{1}{20}\sum_{i=1}^{n} x_{3i}y_i - \bar{x}_3\bar{y} = \frac{1}{20}.44066.78 - 12.602 \times 174.050 = 10.048$$

$$\mathrm{Cov}(x_4, y) = \frac{1}{n}\sum_{i=1}^{n} (x_{4i} - \bar{x})(y_i - \bar{y})$$

$$= \frac{1}{20}\sum_{i=1}^{n} x_{4i}y_i - \bar{x}_4\bar{y} = \frac{1}{20}.3668.30 - 1.046 \times 174.050 = 1.446$$

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Table for calculation of correlation coefficient

	Y	X_1	X_2	X_3	X_4	Y^2	${X_1}^2$	${X_2}^2$	${X_3}^2$	${X_4}^2$	X_1Y	X_2Y	X_3Y	X_4Y
1	163.00	73.70	12.90	11.50	0.90	26569.00	5431.69	166.41	132.25	0.81	12013.10	2102.70	1874.50	146.70
2	191.00	70.40	13.30	14.50	0.70	36481.00	4956.16	176.89	210.25	0.49	13446.40	2540.30	2769.50	133.70
3	185.00	70.40	13.90	13.30	1.50	34225.00	4956.16	193.21	176.89	2.25	13024.00	2571.50	2460.50	277.50
4	170.00	72.80	13.50	12.00	0.80	28900.00	5299.84	182.25	144.00	0.64	12376.00	2295.00	2040.00	136.00
5	170.00	72.80	13.80	12.00	0.80	28900.00	5299.84	190.44	144.00	0.64	12376.00	2346.00	2040.00	136.00
6	161.00	73.70	13.10	11.10	1.00	25921.00	5431.69	171.61	123.21	1.00	11865.70	2109.10	1787.10	161.00
7	170.00	72.60	13.10	11.80	1.70	28900.00	5270.76	171.61	139.24	2.89	12342.00	2227.00	2006.00	289.00
8	173.00	70.12	13.20	12.46	0.90	29929.00	4916.81	174.24	155.25	0.81	12130.76	2283.60	2155.58	155.70
9	178.00	71.23	13.60	12.76	0.87	31684.00	5073.71	184.96	162.82	0.76	12678.94	2420.80	2271.28	154.86
10	167.00	73.21	12.97	11.97	0.77	27889.00	5359.70	168.22	143.28	0.59	12226.07	2165.99	1998.99	128.59
11	182.00	70.02	13.76	13.78	1.34	33124.00	4902.80	189.34	189.89	1.80	12743.64	2504.32	2507.96	243.88
12	184.00	69.12	13.77	13.98	1.23	33856.00	4777.57	189.61	195.44	1.51	12718.08	2533.68	2572.32	226.32
13	174.00	70.07	13.34	12.45	0.45	30276.00	4909.80	177.96	155.00	0.20	12192.18	2321.16	2166.30	78.30
14	168.00	73.23	12.98	11.77	0.77	28224.00	5362.63	168.48	138.53	0.59	12302.64	2180.64	1977.36	129.36
15	162.00	74.12	12.77	11.34	0.87	26244.00	5493.77	163.07	128.60	0.76	12007.44	2068.74	1837.08	140.94
16	182.00	69.77	13.77	13.57	1.45	33124.00	4867.85	189.61	184.14	2.10	12698.14	2506.14	2469.74	263.90
17	191.00	68.12	13.98	14.54	1.77	36481.00	4640.33	195.44	211.41	3.13	13010.92	2670.18	2777.14	338.07
18	161.00	74.77	12.87	11.22	0.95	25921.00	5590.55	165.64	125.89	0.90	12037.97	2072.07	1806.42	152.95
19	164.00	74.27	12.99	12.34	0.97	26896.00	5516.03	168.74	152.28	0.94	12180.28	2130.36	2023.76	159.08
20	185.00	71.23	13.87	13.65	1.17	34225.00	5073.71	192.38	186.32	1.37	13177.55	2565.95	2525.25	216.45
Total	**3481.00**	**1435.68**	**267.47**	**252.03**	**20.91**	**607769.00**	**103131.44**	**3580.11**	**3198.69**	**24.19**	**249547.81**	**46615.23**	**44066.78**	**3668.30**
Mean	**174.05**	**71.78**	**13.37**	**12.60**	**1.05**									

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Now, we know that

$$r_{xy} = \frac{Cov(x,y)}{\sqrt{s_x \text{X } s_y}}$$

$$\therefore r_{x_1 y} = \frac{Cov(x_1,y)}{\sqrt{s_{x_1} \times s_y}} = \frac{-16.615}{\sqrt{3.630 \times 95.048}} = -0.895$$

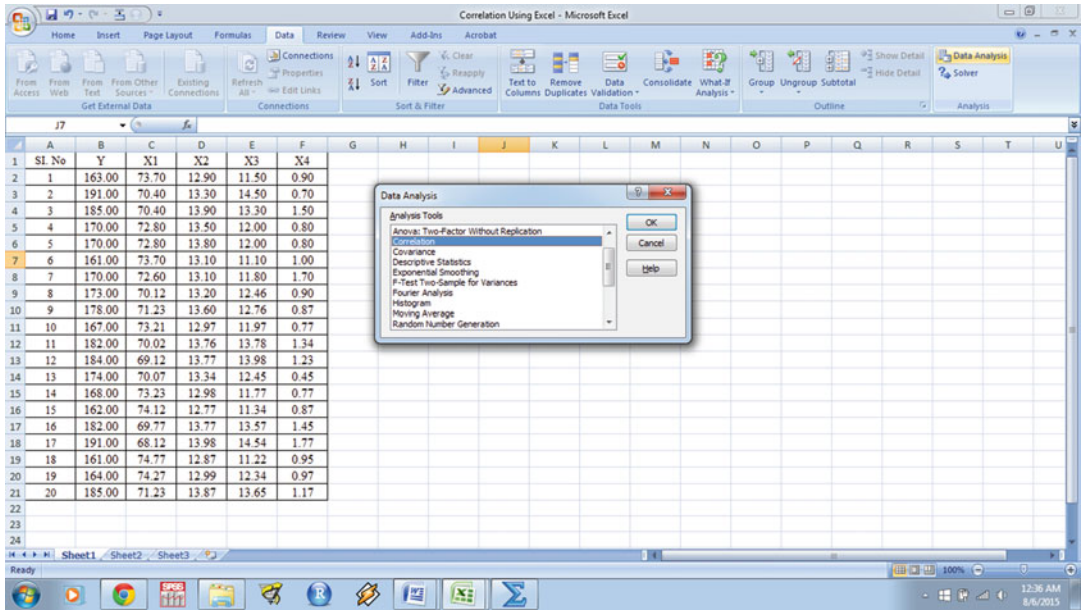
$$r_{x_2 y} = \frac{Cov(x_2,y)}{\sqrt{s_{x_2} \times s_y}} = \frac{3.104}{\sqrt{0.155 \times 95.048}} = 0.809$$

$$r_{x_3 y} = \frac{Cov(x_3,y)}{\sqrt{s_{x_3} \times s_y}} = \frac{10.048}{\sqrt{1.137 \times 95.048}} = 0.967$$

$$r_{x_4 y} = \frac{Cov(x_4,y)}{\sqrt{s_{x_4} \times s_y}} = \frac{1.446}{\sqrt{0.116 \times 95.048}} = 0.435$$

(b) *Correlation analysis using MS Excel:*

Step-1: Go to *data* followed by *data analysis.* Select *correlation* from *Analysis tool.*



Sl. No	Y	X1	X2	X3	X4
1	163.00	73.70	12.90	11.50	0.90
2	191.00	70.40	13.30	14.50	0.70
3	185.00	70.40	13.90	13.30	1.50
4	170.00	72.80	13.50	12.00	0.80
5	170.00	72.80	13.80	12.00	0.80
6	161.00	73.70	13.10	11.10	1.00
7	170.00	72.60	13.10	11.80	1.70
8	173.00	70.12	13.20	12.46	0.90
9	178.00	71.23	13.60	12.76	0.87
10	167.00	73.21	12.97	11.97	0.77
11	182.00	70.02	13.76	13.78	1.34
12	184.00	69.12	13.77	13.98	1.23
13	174.00	70.07	13.34	12.45	0.45
14	168.00	73.23	12.98	11.77	0.77
15	162.00	74.12	12.77	11.34	0.87
16	182.00	69.77	13.77	13.57	1.45
17	191.00	68.12	13.98	14.54	1.77
18	161.00	74.77	12.87	11.22	0.95
19	164.00	74.27	12.99	12.34	0.97
20	185.00	71.23	13.87	13.65	1.17

Slide 1: Showing the entered or transferred data and selection of Correlation Analysis menu from data analysis tool pack in MS Excel work book

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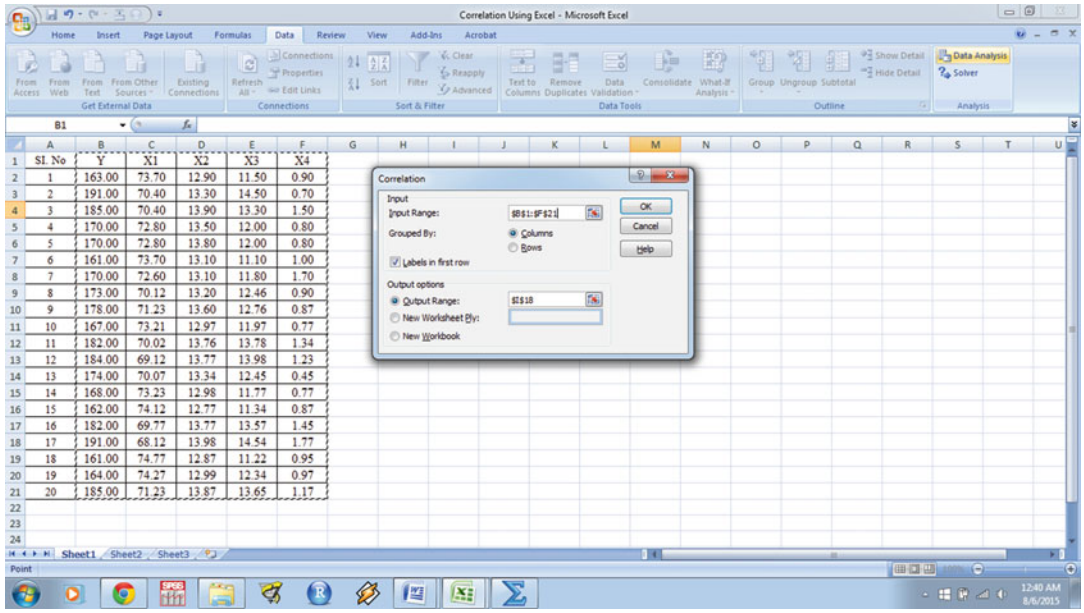
Step-2: Select input range and fill up other options as shown in slide 2.

Slide 2: Showing the entered or transferred data and selection of data range and other required entries in Correlation Analysis menu in MS Excel



Step 3: The output will be as given below:

Variable	*Y*	X_1	X_2	X_3	X_4
Y	**1.000**				
X_1	**−0.895**	1.000			
X_2	**0.809**	−0.770	1.000		
X_3	**0.967**	−0.868	0.755	1.000	
X_4	**0.435**	−0.411	0.480	0.419	1.000

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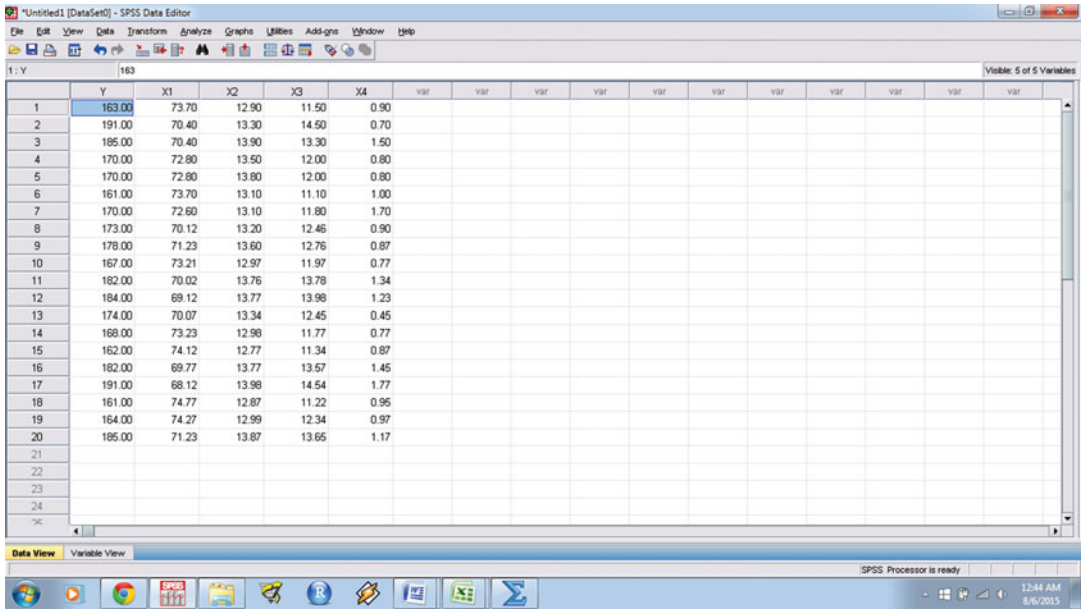
(c) *Correlation analysis using SPSS:*

Step 1: Either enter the data in SPSS data file or import from the MS EXCEL file to get the following slide.



Slide 3: SPSS data editor showing the data for correlation analysis

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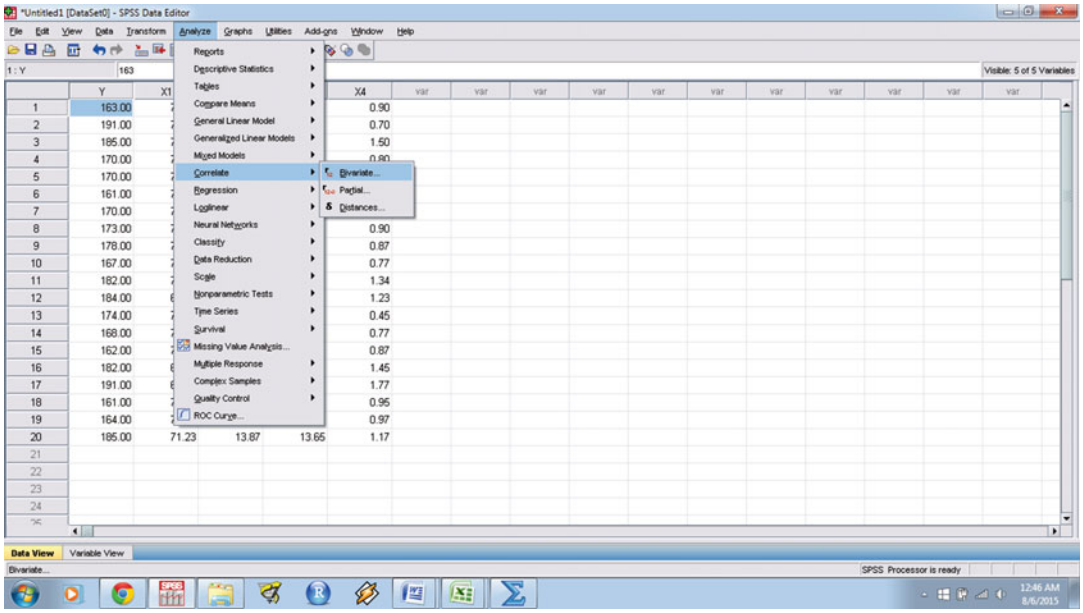
Step 2: Go to Analysis Correlate Click on bivariate as shown below.

Step 3: Pass the required variables to variable selection panel as shown below in slide 5, and click onto OK.



Slide 4: Data analysis menu in SPSS

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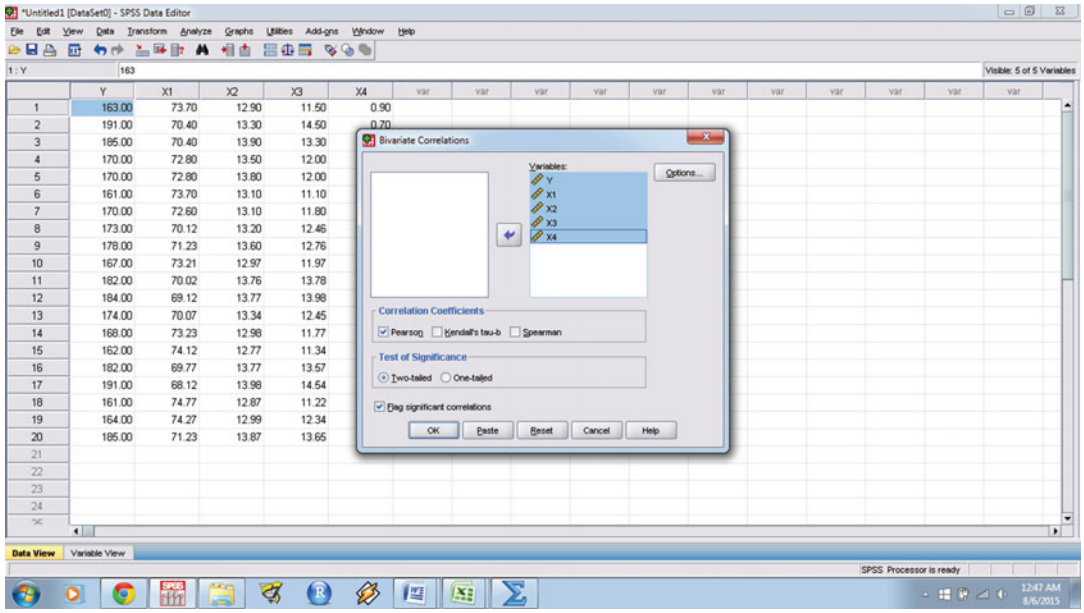
Slide 5: Selection of required options in SPSS Analysis tool.



Step 4: SPSS output will be as given below:

Slide 6: SPSS output of correlation analysis

Correlations

		Y	*X*1	*X*2	*X*3	*X*4
Y	Pearson correlation	1	-.895[a]	.809[a]	.967[a]	.435
	Sig. (two-tailed)		.000	.000	.000	.055
	N	20	20	20	20	20
X_1	Pearson correlation	-.895[a]	1	-.770[a]	-.868[a]	-.411
	Sig. (two-tailed)	.000		.000	.000	.072
	N	20	20	20	20	20
X_2	Pearson correlation	.809[a]	-.770[a]	1	.755[a]	.480[b]
	Sig. (two-tailed)	.000	.000		.000	.032
	N	20	20	20	20	20
X_3	Pearson correlation	.967[a]	-.868[a]	.755[a]	1	.419
	Sig. (two-tailed)	.000	.000	.000		.066
	N	20	20	20	20	20
X_4	Pearson correlation	.435	-.411	.480[b]	.419	1
	Sig. (two-tailed)	.055	.072	.032	.066	
	N	20	20	20	20	20

[a]Correlation is significant at the 0.01 level (two-tailed)
[b]Correlation is significant at the 0.05 level (two-tailed)

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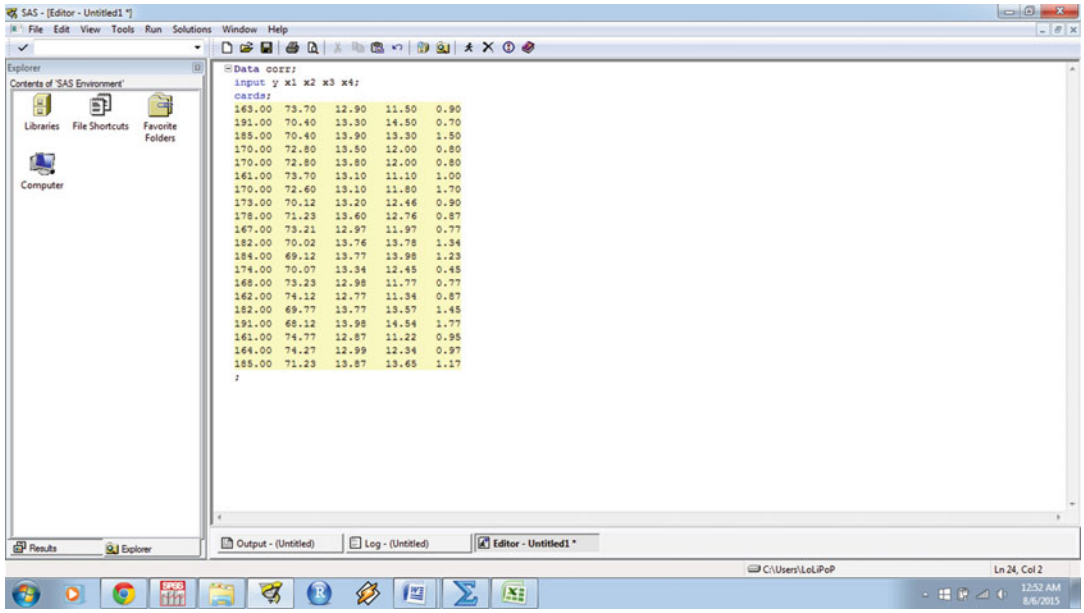
(d) *Correlation analysis using SAS*:

Using the SAS, the same analysis can be done as follows:

Step1: Enter the data or import data in SAS data editor as shown below.

Slide 7: Showing the data input for correlation analysis using the SAS.



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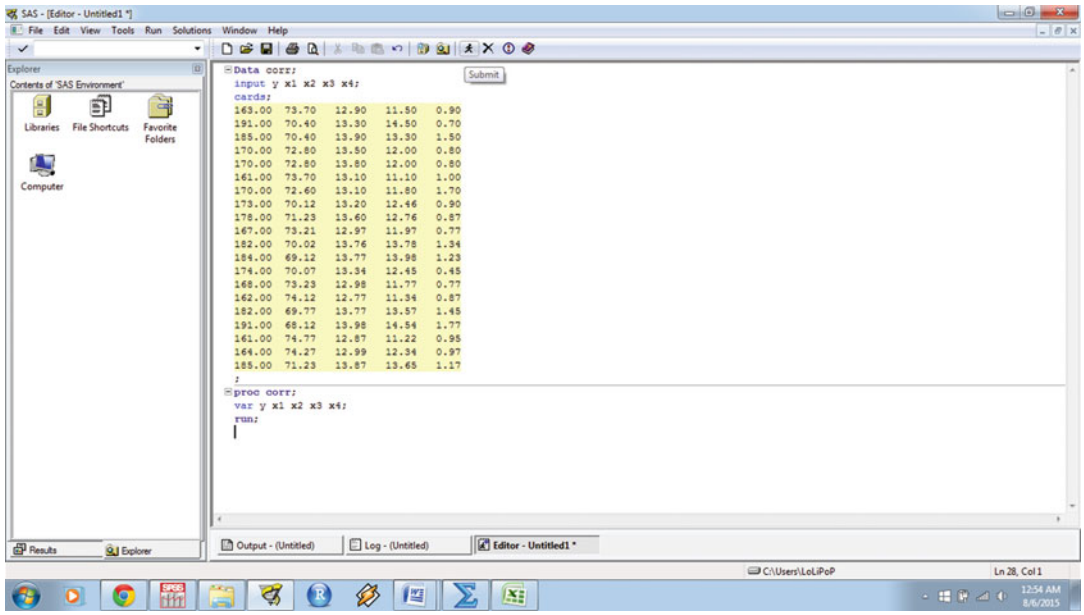
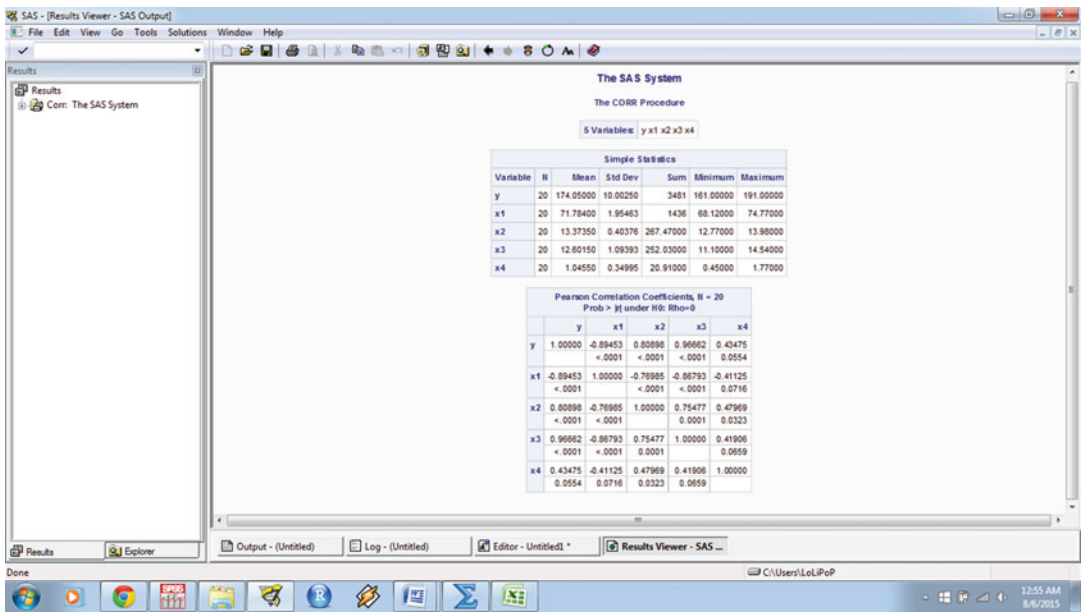
Step 2: Complete the data editor as shown in the slide 8.

Slide 8: Data ready for analysis as below



Step3: Click on the submit button to have output.

Slide 9: Correlation output using SAS



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Readers may please note that all the four processes have resulted in the same correlation coefficient between Y variable and X_1, X_2, X_3, X_4 separately. Additionally, through MS Excel, SPSS, or SAS, one can have correlation coefficients between any pair of variables. Also one can get the significant levels of the correlation coefficients through analysis either in SPSS or SAS directly, because of inbuilt nature of these two softwares, which were not possible either through manual calculation or calculation through MS Excel. Thus, the statistical softwares have these own advantages.

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Regression Analysis

8

8.1 Introduction

During correlation analysis the relationship between the variables was assumed to be linear. Correlation analysis has its focal point of interest on measuring the strength of the linear associationship; it has no intention in finding the actual linear relationship between the variables. But in all practical purposes, we need to know the exact linear relationship; we want to know how the change in one variable affects the other variable(s). In nature, population characteristics are interrelated, and thereby change in one variable is associated with change in other variables also. As such unless and otherwise we know the relationship among the variables, it is very difficult to quantify the nature of changes in variables associated with the changes in other variables. Regression analysis facilitate in knowing the linear relationship among the variables.

Regression analysis may broadly be categorized into two categories: (**a**) *simple linear regression analysis and* (**b**) *multiple linear regression analysis*. In simple linear regression analysis, we are interested in finding the linear relationship between two variables. Thus, if X_1 and X_2 are two variables, in simple regression analysis, we are interested in finding the functional form of the relationship $X_1 = f(X_2, u)$ or $X_2 = g(X_1, v)$, where "u" and "v" are the respective random components. On the other hand, in multiple regression analysis, we are in search of the linear relationship of the form $X_1 = f(X_2, X_3, ..., X_k, u)$ among the variables $X_1, X_2, X_3, ..., X_k$. Thus, in simple linear regression analysis, only two variables are involved, whereas in multiple linear regression analysis, more than two variables are involved.

Readers may please note that unlike correlation analysis, in this regression analysis, we are in search of the relationship between a variable and other variables. In fact in regression analysis, we are having two groups of variables: (a) *dependent variable and (b) independent variable*. Dependent variables are those variables whose values depend on the values of other variables, i.e., independent variables. In correlation analysis there was no such dependency; all variables are treated alike. Thus, regression analysis is the study of linear dependence of one variable (the dependent variable) on one or more independent (explanatory) variables.

Usefulness of Regression Analysis Let us take the example of academic performance of students. Academic performance of a student depends on various factors like age, weight, physique, mental strength, economic condition, social condition, and other factors. Regression analysis helps in getting the relationship between the academic performance and all other factors mentioned above; it helps in finding out the relative role of the individual factors toward

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academic performance; it also helps in predicting the academic performance for a given set of values for the factors of academic performance from the fitted regression line. One can have such innumerable examples of regression analysis from different fields of our daily life.

Does Regression Indicate Cause and Effect Relationship? Through regression analysis one can comment on the likely change in the dependent variable for the change in a particular independent variable keeping other variables at constant level, but definitely one cannot comment that the cause of such change in the dependent variable is due to the change in a particular independent variable. Precisely, we are not analyzing the cause and effect relationship through regression analysis; we are just getting the linear relationship among the variables. To have an idea about the cause and effect relationship, one must go for Granger's causality test among the variables.

8.2 Explanation of the Regression Equation

(a) *Simple linear regression equation:*

Suppose we have a linear regression equation $X_1 = 15 + 1.2X_2$. We shall now examine what are the information we can have from the above relationship:

(i) The relationship between X_1 and X_2 is linear, and it is an example of simple linear regression equation with two variables in the equation.
(ii) X_1 and X_2 are the dependent and independent variables, respectively, in the relationship.
(iii) The intercept constant is 15 and it is the mean value of X_1 under the given condition; the line of regression starts at 15 scale of the X_1 axis.
(iv) The regression coefficient is 1.2; it indicates that there would be a 1.2 unit change in the value of the dependent variable X_1 with a unit change in the independent variable X_2. It is also the slope of the regression line.

(b) *Multiple linear regression equation*:

Suppose we have a multiple linear regression equation $X_1 = 10 + 1.2X_2 - 0.8X_3 + 1.7X_4 + 0.096X_5$. From this relationship one can have the following information:

(i) The relationship between the variable X_1 and the variables X_2, X_3, X_4, and X_5 is linear.
(ii) In the relationship X_1 is the dependent and X_2, X_3, X_4, and X_5 are the independent variables.
(iii) For the given set of values for the variables, the line of regression touches the Y axis at 10.
(iv) The parameters of the regression equation are 1.2 (the coefficient of X_2), 0.8 (the coefficient of X_3), 1.7 (the coefficient of X_4), and 0.096 (the coefficient of X_5) along with the intercept 10 and excepting the intercept 10, the other parameters are also known as the partial regression coefficients of the variables X_2, X_3, X_4, and X_5, respectively.
(v) From the partial regression coefficient, one can infer that excepting X_3 all other independent variables are positively correlated with the dependent variable X_1.
(vi) One unit change in X_2 variable keeping other variables at constant level will result in a 1.2 unit change (in the same direction) in the dependent variable X_1, whereas one unit change in the variable X_3 will result in a 0.8 unit change in the dependent variable X_1 in opposite direction; i.e. one unit increase in X_3 will result in a 0.8 unit decrease in X_1. Other regression coefficients can also be interpreted in similar way.

8.3 Assumption of Linear Regression Model

The linear regression equation is based on certain assumptions, some of which are quite obvious, but some are needed for better statistical treatment during further analysis toward drawing

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meaningful interpretation about the population under investigation:

1. The regression equation is linear in a parameter, i.e., $X_1 = \beta_1 + \beta_2 X_2 + \beta_3 X_3 + \beta_4 X_4 + \beta_5 X_5 + \beta_6 X_6 + \ldots\ldots + \beta_k X_k + u$.
2. Independent variables are non-stochastic, i.e., values taken by X_2, X_3, X_4, X_5, ..., X_k are fixed in repeated samples.
3. For a given set of values of X_2, X_3, X_4, X_5, ..., X_k, the expected value of the random variable u is zero, i.e., $E(u_i) = 0$.
4. $\text{Var}(u_i) = E(u_i^2) - (E(u))^2 = E(u_i^2) = \sigma^2$ $[\because E(u) = 0$ by assumption (i)$] = \sigma^2$ $\Rightarrow$ Var (u_i/X_1) = Var (u_i/X_2) = Var (u_i/X_3) $\ldots\ldots\ldots = \sigma^2$
5. There should not be any autocorrelation between the disturbances.

$$Cov\left(u_i, u_j/X_i, X_{i'}\right) = 0 \; i \neq j$$

6. The nonexistence of the correlation between disturbances and independent variables, i.e., $r_{ui,Xi} = 0 => \text{Cov}\,(u_i, X_i)$

   $= E[u_i - E(u_i)]\,[X_i - E(X_i)]$
   $= E[ui(X_i - E(X_i)];[E[E(U_i)[X_i - E(X_i)]]$, vanishes, because $E(U_i) = 0$
   $= E(u_i.X_i) - E(u_i)\,E(X_i)$
   $= E\,(u_iX_i)$ must be equal to zero
   i.e., $E\,(u_iX_i) = 0$.

7. Multicollinearity should not exist among the independent variables, i.e., $r_{xjxj'} = 0$; otherwise there will be a problem of estimation of the regression parameters.
8. The number of observations (n) must be greater than the number of parameters (j) (number of variables in the regression equation) to be estimated, i.e., $n > j\,(= 1.\ldots.k)$.
9. In a given sample the independent variables (Xs) should be the variable in the true sense, i.e., the values of Xs must not be constant, i.e., Var $(X_j) > 0$.
10. Correct specification of the regression model is an essential condition, i.e., the model should clearly spell out (i) the functional form of the model (linear in this case), (ii) the variables and the number of variables to be included, and (iii) the probabilistic assumption about the variables.

8.4 Simple Linear Regression Analysis

The simplest form of the linear regression equation is known as the simple linear regression equation in which only two variables (one dependent and another independent) are involved. Let us suppose we are provided with n sets of observations for two variables X_1 (the dependent variable) and X_2 (the independent variable) as follows:

Observation	X_1values	X_2values
1	x_{11}	x_{21}
2	x_{12}	x_{22}
3	x_{13}	x_{23}
4	x_{14}	x_{24}
5	x_{15}	x_{25}
:	:	:
:	:	:
:	:	:
:	:	:
:	:	:
n	x_{1n}	x_{2n}

Now, the problem is to frame a regression equation of the form $X_1 = \alpha + \beta X_2 + \varepsilon$, where X_1 is the dependent variable, X_2 is the independent variable, and ε is the random error component and is normally distributed with mean zero and variance σ^2; for both the variables, we are provided with n pairs of observations. The sample regression equation of the form $x_1 = a + bx_2$ is to be framed from the given sample values for both the variables; that means we are to find out the values of a and b.

The above equation is true for every set of observations; that means

$$\begin{aligned}
x_{11} &= a + bx_{21}\\
x_{11} &= a + bx_{21}\\
x_{12} &= a + bx_{22}\\
x_{13} &= a + bx_{23}\\
x_{14} &= a + bx_{24}\\
\vdots \quad &\quad \vdots \quad \vdots\\
\vdots \quad &\quad \vdots \quad \vdots\\
\vdots \quad &\quad \vdots \quad \vdots\\
x_{1n} &= a + bx_{2n}
\end{aligned}$$

Thus, we can have

$$\begin{aligned}
&\sum_{i=1}^{n} x_{1i} = \sum_{i=1}^{n} (\,a + bx_{2i})\\
&\Rightarrow \bar{x}_1 = a + b\bar{x}_2\\
&\Rightarrow a = \bar{x}_1 - b\bar{x}_2 \qquad (8.1)
\end{aligned}$$

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Similarly,

$$\begin{aligned}\sum_{i=1}^{n} x_{1i}x_{2i} &= \sum_{i=1}^{n} x_{2i}(\,a\,+\,bx_{2i}) \\ &= a\sum_{i=1}^{n} x_{2i} + b\sum_{i=1}^{n} x_{2i}^2 \;=\; a.\,n\bar{x}_2 \;+\; b\sum_{i=1}^{n} x_{2i}^2 \\ &= (\bar{x}_1 - b\bar{x}_2)n\bar{x}_2 + b\sum_{i=1}^{n} x_{2i}^2 \;=\; n\bar{x}_1\bar{x}_2 - nb\bar{x}_2{}^2 + b\sum_{i=1}^{n} x_{2i}^2 \\ &= n\bar{x}_1\bar{x}_2 + b\left(\sum_{i=1}^{n} x_{2i}^2 - n\bar{x}_2{}^2\right) \qquad (8.2)\end{aligned}$$

$$\text{or } b\left(\sum_{i=1}^{n} x_{2i}^2 - n\bar{x}_2{}^2\right) = \sum_{i=1}^{n} x_{1i}x_{2i} - n\bar{x}_1\bar{x}_2$$

$$\text{or } b = \frac{\sum_{i=1}^{n} x_{1i}x_{2i} - n\bar{x}_1\bar{x}_2}{\left(\sum_{i=1}^{n} x_{2i}^2 - n\bar{x}_2{}^2\right)} = \frac{SP(x_1,x_2)}{SS(x_2)} = \frac{r_{x_1x_2}S_{x_1}}{S_{x_2}} \qquad (8.3)$$

where *SP is the* sum of products of the two variables and *SS* is the sum of squares of the variable, i.e., $SP(x_1,x_2) = n\ Cov(x_1,x_2)$ and *SS* (x_1 or x_2) = n Var($x_1$or x_2)

Thus,

$$\begin{aligned}x_1 &= a + bx_2 \\ &= \bar{x}_1 - b\bar{x}_2 + bx_2 \\ &= \bar{x}_1 + b(x_2 - \bar{x}_2) \\ &= \bar{x}_1 + r_{x_1x_2}\frac{S_{x_1}}{S_{x_2}}(x_2 - \bar{x}_2)\end{aligned}$$

A more convenient form is $x_1 - \bar{x}_1 = r_{x_1x_2}\frac{S_{x_1}}{S_{x_2}}(x_2 - \bar{x}_2)$.

Similarly, if one wants to form a regression line of X_2 on X_1, it would be $x_2 - \bar{x}_2 = r_{x_1x_2}\frac{S_{x_2}}{S_{x_1}}(x_1 - \bar{x}_1)$ where X_1 is the independent and X_2 is the dependent variable. In Sect. 8.9 we shall demonstrate how the parameters of the simple regression equation could be estimated using the technique of ordinary least square (OLS). In the following section, let us discuss the properties of the regression coefficients.

Example 8.1

Find out the correlation between weight of eggs and number of eggs laid per cycle in a certain poultry bird, and find the regression of the weight of eggs on hatching:

Weight of egg(s) (g)	45	48	49	50	51	52	53	54	55	56	57	58	59	60	61
Hatching	80	80	85	88	92	92	90	91	92	92	89	86	84	82	80

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Solution From the given problem, we are to calculate the correlation coefficient between the weights of eggs (Y) and the hatching (X); also we are to find out the regression equation of Y on X. Now from the above information, let us construct the following table:

Observations	Weight of eggs (Y)	Hatching (X)	$(Y-\overline{Y})$	$(X-\overline{X})$	$(Y-\overline{Y})^2$	$(X-\overline{X})^2$	$(X-\overline{X})(Y-\overline{Y})$
1.	45	80	−8.87	−6.87	78.62	47.15	60.88
2.	48	80	−5.87	−6.87	34.42	47.15	40.28
3.	49	85	−4.87	−1.87	23.68	3.48	9.08
4.	50	88	−3.87	1.13	14.95	1.28	−4.38
5.	51	92	−2.87	5.13	8.22	26.35	−14.72
6.	52	92	−1.87	5.13	3.48	26.35	−9.58
7.	53	90	−0.87	3.13	0.75	9.82	−2.72
8.	54	91	0.13	4.13	0.02	17.08	0.55
9.	55	92	1.13	5.13	1.28	26.35	5.82
10.	56	92	2.13	5.13	4.55	26.35	10.95
11.	57	89	3.13	2.13	9.82	4.55	6.68
12.	58	86	4.13	−0.87	17.08	0.75	−3.58
13.	59	84	5.13	−2.87	26.35	8.22	−14.72
14.	60	82	6.13	−4.87	37.62	23.68	−29.85
15.	61	80	7.13	−6.87	50.88	47.15	−48.98
Sum	**808.00**	**1303.00**	**0.00**	**0.00**	**311.73**	**315.73**	**5.73**
Average	**53.87**	**86.87**					

$$Cov(X,Y) = S_{xy} = \frac{\sum (X-\overline{X})(Y-\overline{Y})}{n} = \frac{5.73}{15} = 0.38$$

$$S_x^2 = \frac{\sum (X-\overline{X})^2}{n} = \frac{315.73}{15} = 21.05$$

$$S_y^2 = \frac{\sum (Y-\overline{Y})^2}{n} = \frac{311.73}{15} = 20.78$$

$$\therefore r_{xy} = \frac{Cov(X,Y)}{S_X S_y} = \frac{0.38}{\sqrt{(21.05 \times 20.78)}} = 0.0183$$

So there is a very small correlation between the two variables.

Regression Analysis Parameter estimation: $b_{yx} = \frac{S_{xy}}{S_x^2} = \frac{0.38}{21.05} = 0.0182$

$$\text{Intercept}(b_0) = \overline{Y} - b\overline{X} = 53.87 - 0.0185 \times 86.87 = 52.29$$

Hence the regression equation of the weight of eggs on hatching is $Y = 52.29 + 0.0182X$

Example 8.2

From the following data, find out the simple linear regression for X_1 on X_2 and X_1 on X_3 using the usual procedure:

X_1	1.83	1.56	1.85	1.9	1.7	1.8	1.85	1.73	1.95	1.67	1.82	1.84	1.74	1.68	1.62	1.82	1.91	1.61	1.64	1.85
X_2	13	10	12	14	12	13	12	10	14	13	16	14	11	12	11	15	15	12	13	15
X_3	12	10	11	11	12	11	11	10	11	12	14	14	9	8	9	13	13	9	10	13

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Solution We have no. of observations $n = 20$. Let us construct the following table from the above data:

Observation	X_1	X_2	X_3	${X_1}^2$	${X_2}^2$	${X_3}^2$	X_1X_2	X_1X_3
1.	1.83	13.00	12.00	3.35	169.00	144.00	23.79	21.96
2.	1.56	10.00	10.00	2.43	100.00	100.00	15.60	15.60
3.	1.85	12.00	11.00	3.42	144.00	121.00	22.20	20.35
4.	1.90	14.00	11.00	3.61	196.00	121.00	26.60	20.90
5.	1.70	12.00	12.00	2.89	144.00	144.00	20.40	20.40
6.	1.80	13.00	11.00	3.24	169.00	121.00	23.40	19.80
7.	1.85	12.00	11.00	3.42	144.00	121.00	22.20	20.35
8.	1.73	10.00	10.00	2.99	100.00	100.00	17.30	17.30
9.	1.95	14.00	11.00	3.80	196.00	121.00	27.30	21.45
10.	1.67	13.00	12.00	2.79	169.00	144.00	21.71	20.04
11.	1.82	16.00	14.00	3.31	256.00	196.00	29.12	25.48
12.	1.84	14.00	14.00	3.39	196.00	196.00	25.76	25.76
13.	1.74	11.00	9.00	3.03	121.00	81.00	19.14	15.66
14.	1.68	12.00	8.00	2.82	144.00	64.00	20.16	13.44
15.	1.62	11.00	9.00	2.62	121.00	81.00	17.82	14.58
16.	1.82	15.00	13.00	3.31	225.00	169.00	27.30	23.66
17.	1.91	15.00	13.00	3.65	225.00	169.00	28.65	24.83
18.	1.61	12.00	9.00	2.59	144.00	81.00	19.32	14.49
19.	1.64	13.00	10.00	2.69	169.00	100.00	21.32	16.40
20.	1.85	15.00	13.00	3.42	225.00	169.00	27.75	24.05
Total	35.370	257.000	223.000	62.789	3357.000	2543.000	456.840	396.500
Mean	1.769	12.850	11.150					

$$s_{X_2}^2 = \frac{1}{n}\sum_{i=1}^{n}\left(X_{2i} - \overline{X}_2\right)^2 = \frac{1}{n}\sum_{i=1}^{n}X_{2i}^2 - \overline{X}_2{}^2 = \frac{1}{20} \times 3357.000 - 12.850^2 = 2.727$$

$$s_{X_3}^2 = \frac{1}{n}\sum_{i=1}^{n}\left(X_{3i} - \overline{X}_3\right)^2 = \frac{1}{n}\sum_{i=1}^{n}X_{3i}^2 - \overline{X}_3{}^2 = \frac{1}{20} \times 2543.000 - 11.150^2 = 2.827$$

$$\begin{aligned} Cov(X_2, X_1) &= \frac{1}{n}\sum_{i=1}^{n}\left(X_{2i} - \overline{X}_2\right)\left(X_{1i} - \overline{X}_1\right) = \frac{1}{20}\sum_{i=1}^{n}X_{2i}X_{1i} - \overline{X}_2\overline{X}_1 \\ &= \frac{1}{20} \times 456.840 - 12.850 \times 1.769 = 0.116 \end{aligned}$$

$$\begin{aligned} Cov(X_3, X_1) &= \frac{1}{n}\sum_{i=1}^{n}\left(X_{3i} - \overline{X}_3\right)\left(X_{1i} - \overline{X}_1\right) = \frac{1}{20}\sum_{i=1}^{n}X_{3i}X_{1i} - \overline{X}_3\overline{X}_1 \\ &= \frac{1}{20} \times 396.500 - 11.150 \times 1.769 = 0.106 \end{aligned}$$

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(a) *Now the regression equation of X_1 on X_2 is given by*

$$(X_1 - \overline{X}_1) = b_{x_1x_2}(X_2 - \overline{X}_2)$$

$$\Rightarrow (X_1 - 1.769) = \frac{Cov(X_2, X_1)}{s_{x_2}^2}(X_2 - 12.850)$$

$$= \frac{0.116}{2.727}(X_2 - 12.850) = 0.042(X_2 - 12.850)$$

$$= 0.042X_2 - 0.539$$

$$\Rightarrow X_1 = 1.769 + 0.042X_2 - 0.539$$

$$\Rightarrow X_1 = 1.230 + 0.042X_2$$

(b) *Now the regression equation of X_1 on X_3 is given by*

$$(X_1 - \overline{X}_1) = b_{x_1x_3}(X_3 - \overline{X}_3)$$

$$\Rightarrow (X_1 - 1.769) = \frac{Cov(X_3, X_1)}{s_{x_3}^2}(X_3 - 11.150)$$

$$= \frac{0.106}{2.827}(X_3 - 11.150) = 0.037(X_3 - 11.150)$$

$$= 0.037X_3 - 0.412$$

$$\Rightarrow X_1 = 1.769 + 0.037X_3 - 0.412$$

$$\Rightarrow X_1 = 1.357 + 0.037X_3$$

Example 8.3

Find out the correlation between age (X) and brooding temperature (Y), and find out the regression of the brooding temperature on the age of chicks (Wk):

Age of chicks (Wk)	0.5	1.5	2.5	3.5	4.5	5.5
Brooding temperature	34.5	29	28.5	26	24	21

Solution From the above table, let us construct the following table:

No. of observations	Brooding temperature (Y)	Age of chicks (X)	$(Y - \overline{Y})$	$(X - \overline{X})$	$(Y - \overline{Y})^2$	$(X - \overline{X})^2$	$(X - \overline{X})(Y - \overline{Y})$
1.	34.5	0.5	7.33	−2.50	53.78	6.25	−18.33
2.	29.0	1.5	1.83	−1.50	3.36	2.25	−2.75
3.	28.5	2.5	1.33	−0.50	1.78	0.25	−0.67
4.	26.0	3.5	−1.17	0.50	1.36	0.25	−0.58
5.	24.0	4.5	−3.17	1.50	10.03	2.25	−4.75
6.	21.0	5.5	−6.17	2.50	38.03	6.25	−15.42
Sum	163.00	18.00	0.00	0.00	108.33	17.50	−42.50
Average	27.17	3.00					

$$Cov(X, Y) = S_{xy} = \frac{\sum (X - \overline{X})(Y - \overline{Y})}{n}$$

$$= \frac{-42.50}{6} = -7.083$$

$$S_2^x = \frac{\sum (X - \overline{X})^2}{n} = \frac{17.50}{6} = 2.91$$

$$S_2^y = \frac{\sum (Y - \overline{Y})^2}{n} = \frac{108.33}{6} = 18.056$$

$$\therefore r_{xy} = \frac{Cov(X, Y)}{S_X S_y}$$

$$= \frac{0.38}{\sqrt{(21.05 \times 20.78)}} = 0.0183$$

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Estimation of regression parameters:

$$b_{yx} = \frac{S_{xy}}{S_x^2} = \frac{-7.083}{2.91} = -2.429$$

$$b_1 = -2.429$$

$$\begin{aligned}\text{Intercept}(b_0) &= \overline{Y} - b\overline{X} \\ &= 27.17 - (-2.429) \times 3 \\ &= 34.452\end{aligned}$$

$$b_0 = 34.452$$

Hence, the regression equation of the brooding temperature on the age of chicks is

$$Y = 34.452 - 2.429X$$

Example 8.4
The following table gives the information on the number of birds per pen and area of the pen. Find out the relationship of area with the birds per pen:

Birds/pen	25	100	200	500
Area (sq. ft)	88	300	500	1000

Solution *From the given data, let us construct the following table*:

No. of observations	Area (sq. ft) (Y)	Birds/pen (X)	$(X-\overline{X})^2$	$(X-\overline{X})(Y-\overline{Y})$
1.	88	25	32851.56	69600.00
2.	300	100	11289.06	18275.00
3.	500	200	39.06	−175.00
4.	1000	500	86289.06	155100.00
Sum	1888.00	825.00	130468.75	242800.00
Average	472.00	206.25		

$$Cov(X,Y) = S_{xy} = \frac{\sum (X-\overline{X})(Y-\overline{Y})}{n} = \frac{242800}{4} = 60700$$

$$S_x^2 = \frac{\sum (X-\overline{X})^2}{n} = \frac{130468.75}{4} = 32617.19$$

$$b_{yx} = \frac{S_{xy}}{S_x^2} = \frac{60700}{34617.19} = 1.86$$

$$b_1 = 1.86$$

$$\begin{aligned}\text{Intercept}(b_0) &= \overline{Y} - b\overline{X} \\ &= 472.0 - 1.86 \times 206.25 = 88.17\end{aligned}$$

$$b_0 = 88.17$$

Hence, the regression equation of the area on birds/pen of chicks is

$$Y = 88.17 + 1.86X$$

8.5 Properties of Regression Coefficient

8.5.1 Regression Coefficient

Regression coefficient measures the amount of change expected in the dependent variable due to a unit change in the independent variable. Thus, for the above two regression equations of X_1 on X_2,

i.e., $(x_1 - \overline{x}_1) = r_{x_1x_2}\frac{S_{x_1}}{S_{x_2}}(x_2 - \overline{x}_2)$ or

$$\begin{aligned}x_1 &= \overline{x}_1 + r_{x_1x_2}\frac{S_{x_1}}{S_{x_2}}(x_2 - \overline{x}_2) \\ &= \left(\overline{x}_1 - r_{x_1x_2}\frac{S_{x_1}}{S_{x_2}}\overline{x}_2\right) + r_{x_1x_2}\frac{S_{x_1}}{S_{x_2}}x_2 \\ &= a_1 + b_1x_2\end{aligned} \tag{8.4}$$

and X_2 on X_1,

i.e., $(x_2 - \overline{x}_2) = r_{x_1x_2}\frac{S_{x_2}}{S_{x_1}}(x_1 - \overline{x}_1)$

or

$$\begin{aligned}x_2 &= \overline{x}_2 + r_{x_1x_2}\frac{S_{x_2}}{S_{x_1}}(x_1 - \overline{x}_1) \\ &= \left(\overline{x}_2 - r_{x_1x_2}\frac{S_{x_2}}{S_{x_1}}\overline{x}_1\right) + r_{x_1x_2}\frac{S_{x_2}}{S_{x_1}}x_1 \\ &= a_2 + b_2x_1\end{aligned} \tag{8.5}$$

b_1 and b_2 are the two regression coefficients of X_1 on X_2 and X_2 on X_1, respectively. The regression coefficients b_1 and b_2 are also written as $b_1 = r_{x_1x_2}\frac{S_{x_1}}{S_{x_2}} = b_{x_1x_2}$ and $b_2 = r_{x_1x_2}\frac{S_{x_2}}{S_{x_1}} = b_{x_2x_1}$, respectively.

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8.5.2 The Sign of the Regression Coefficient

We know that $r_{x_1x_2}\frac{S_{x_1}}{S_{x_2}} = b_{x_1x_2}$.

Both S_{x_1} and S_{x_2} are positive quantities, being the standard deviations, so the sign of $b_{x_1x_2}$ depends on the sign of $r_{x_1x_2}$. Again the sign of the correlation coefficient depends on the sign of the covariance between the variables. Thus, the sign of the covariance will be the sign of the regression coefficient.

8.5.3 Relation Between Correlation Coefficient and the Regression Coefficients

We have $x_1 = \bar{x}_1 + r_{x_1x_2}\frac{S_{x_1}}{S_{x_2}}(x_2 - \bar{x}_2) = \left(\bar{x}_1 - r_{x_1x_2}\frac{S_{x_1}}{S_{x_2}}\bar{x}_2\right) + r_{x_1x_2}\frac{S_{x_1}}{S_{x_2}}x_2 = a_1 + b_1x_2$ and $x_2 = \bar{x}_2 + r_{x_1x_2}\frac{S_{x_2}}{S_{x_1}}(x_1 - \bar{x}_1) = \left(\bar{x}_2 - r_{x_1x_2}\frac{S_{x_2}}{S_{x_1}}\bar{x}_1\right) + r_{x_1x_2}\frac{S_{x_2}}{S_{x_1}}x_1 = a_2 + b_2x_1$. Thus two regression coefficients b_1 and b_2 and their product would be

$$b_1.b_2 = r_{x_1x_2}\frac{S_{x_1}}{S_{x_2}}x_2.r_{x_1x_2}\frac{S_{x_2}}{S_{x_1}}x_1 = r^2_{x_1x_2}$$
$$\Rightarrow \sqrt{b_1.b_2} = \sqrt{r^2_{x_1x_2}} = r_{x_1x_2}$$

We have already proved that the correlation coefficient and the regression coefficient will have the same sign.

Therefore, r is the geometric mean of the two regression coefficients.

8.5.4 Relation Between Regression Coefficients

We have

$$b_1b_2 = r^2_{x_1x_2} \le 1$$
$$\Rightarrow b_2 \le \frac{1}{b_1} \text{ or, } b_1 \le \frac{1}{b_2}$$

Thus if one of the regression coefficients is greater than the unity, then the other one must be less than the unity.

8.5.5 AM and GM of Regression Coefficients

We know,

$$\left(\sqrt{b_1} - \sqrt{b_2}\right)^2 \ge 0$$
$$\frac{b_1 + b_2}{2} \ge \sqrt{b_1b_2} \ge r$$

The arithmetic mean of the two regression coefficients is greater than or equal to the correlation coefficient between the variables.

8.5.6 Range of Regression Coefficient

The regression coefficient of X_1 on X_2 is given as $r_{x_1x_2}\frac{s_{x_1}}{s_{x_2}}$.

We know $1 \ge r_{xy} \ge -1, \infty \ge S_x \ge 0$ and $\infty \ge S_y \ge 0$.

$$b_{x_1x_2} = r_{x_1x_2}\frac{S_{x_1}}{S_{x_2}} = \pm 1\frac{\infty \ge S_{x_1} \ge 0}{\infty \ge S_{x_2} \ge 0}$$
$$\therefore \infty \ge b_{x_1x_2} \ge -\infty$$

8.5.7 Effect of Change of Origin and Scale on Regression Coefficient

For two variables X_1 and X_2 having means, variances, and covariance $\overline{X}_1$, $\overline{X}_2$ and $S^2_{x_1}$, $S^2_{x_2}$ and $S_{x_1x_2}$, respectively, one can construct two more variables such that

$$U_i = \frac{X_{1i} - p}{m} \Rightarrow X_{1i} = p + mU_i$$

and

$$V_i = \frac{X_{2i} - q}{n} \Rightarrow X_{2i} = q + nV_i$$

where m, n, p, and q are constants.

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Now from 7.3 (iii), we know that

$$Cov(X_1, X_2) = mn.Cov(U, V)$$

and

$S_{X_1}^2 = m^2 S_U^2$

Similarly

$S_{X_2}^2 = n^2 S_V^2$

$$\therefore b_{x_1x_2} = \frac{Cov(X_1, X_2)}{S_{X_2}^2} = \frac{mnCov(U, V)}{n^2 S_V^2} = \frac{m}{n} b_{UV}$$

$$\text{Similarly, } b_{x_2x_1} = \frac{Cov(X_1, X_2)}{S_{X_1}^2} = \frac{\text{mn}Cov(U, V)}{m^2 S_U^2}$$

$$= \frac{n}{m} b_{VU}$$

So, regression coefficient does not depend on change of origin but depends on change of scales of the variables concerned.

8.5.8 Angle Between Two Lines of Regression

For two variables X_1 and X_2, we have two regression lines

$$x_1 = \bar{x}_1 + r_{x_1x_2} \frac{S_{x_1}}{S_{x_2}} (x_2 - \bar{x}_2)$$

$$or\ (x_1 - \bar{x}_1) = r_{x_1x_2} \frac{S_{x_1}}{S_{x_2}} (x_2 - \bar{x}_2)$$

and

$$x_2 = \bar{x}_2 + r_{x_1x_2} \frac{S_{x_2}}{S_{x_1}} (x_1 - \bar{x}_1)$$

$$or\ (x_2 - \bar{x}_2) = r_{x_1x_2} \frac{S_{x_2}}{S_{x_1}} (x_1 - \bar{x}_1)$$

$$or\ (x_1 - \bar{x}_1) = \frac{S_{x_1}}{r_{x_1x_2} S_{x_2}} (x_2 - \bar{x}_2)$$

So the gradient of the regression line of X_1 on X_2 is $b_1 = r_{x_1x_2} \frac{s_{x_1}}{s_{x_2}}$, and the gradient for the regression line of X_2 on X_1 is $b_2 = \frac{s_{x_2}}{r_{x_1x_2} s_{x_1}}$.

Let us suppose the angle between the two lines is θ, so

$$\tan\theta = \frac{b_2 \sim b_1}{1 + b_1 b_2} = \frac{\frac{s_{x_2}}{r_{x_1x_2} s_{x_1}} - r_{x_1x_2} \frac{s_{x_2}}{s_{x_1}}}{1 + \frac{s_{x_2}}{s_{x_1}} \frac{s_{x_2}}{s_{x_1}}} = \frac{\frac{s_{x_2} - r_{x_1x_2}^2 s_{x_2}}{r_{x_1x_2} s_{x_1}}}{\frac{s_{x_1}^2 + s_{x_2}^2}{s_{x_1}^2}} = \frac{\frac{s_{x_2}\left(1 - r_{x_1x_2}^2\right)}{r_{x_1x_2} s_{x_1}}}{\frac{s_{x_1}^2 + s_{x_2}^2}{s_{x_1}^2}} = \frac{s_{x_2} s_{x_1}\left(1 - r_{x_1x_2}^2\right)}{\left(s_{x_1}^2 + s_{x_2}^2\right) r_{x_1x_2}}$$

$$\therefore \theta = \tan^{-1}\left[\frac{\left(1 - r_{x_1x_2}^2\right)}{r_{x_1x_2}} \frac{s_{x_2} s_{x_1}}{\left(s_{x_1}^2 + s_{x_2}^2\right)}\right]$$

Putting $r = \pm 1$, we have $\theta = 0$, i.e., the two regression lines coincide with each other, and when $r = 0$, $\theta = 90^\circ$, i.e., the regression lines are perpendicular to each other.

Thus as the value of the correlation coefficient between the variables approaches to $\pm$ 1, the angle between them gets reduced.

8.5.9 Regression with Zero Intercept

If the variables are measured from their respective means, then the regression equation passes through the origin. We have the regression equation of X_1 on X_2 as

$$x_1 = \bar{x}_1 + r_{x_1x_2} \frac{S_{x_1}}{S_{x_2}} (x_2 - \bar{x}_2)$$

$$Or\ (x_1 - \bar{x}_1) = r_{x_1x_2} \frac{S_{x_1}}{S_{x_2}} (x_2 - \bar{x}_2)$$

$$Or\ x_1' b_{x_1x_2} x_2' \ \left(\text{where } x_1' = x_1 - \bar{x}_1 \text{ and } x_2' = x_2 - \bar{x}_2\right)$$

Thus, by measuring the variables from their respective means, the intercept term from the regression equation can be removed.

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Example 8.5
Using the same information provided in Example 8.2, find out the regression equations measuring the variables from their respective means:

X_1	1.83	1.56	1.85	1.9	1.7	1.8	1.85	1.73	1.95	1.67	1.82	1.84	1.74	1.68	1.62	1.82	1.91	1.61	1.64	1.85
X_2	13	10	12	14	12	13	12	10	14	13	16	14	11	12	11	15	15	12	13	15
X_3	12	10	11	11	12	11	11	10	11	12	14	14	9	8	9	13	13	9	10	13

Solution Using the deviations of the variables from their respective means, let us construct the following table.

Observation	X_1	X_2	X_3	$x_1 = X_{1i} - \overline{X}_1$	$x_2 = X_{2i} - \overline{X}_2$	$x_3 = X_{3i} - \overline{X}_3$	${x_2}^2$	${x_3}^2$	x_1x_2	x_1x_3
1.	1.83	13.00	12.00	0.061	0.150	0.850	0.023	0.722	0.009	0.052
2.	1.56	10.00	10.00	−0.209	−2.850	−1.150	8.123	1.323	0.596	0.240
3.	1.85	12.00	11.00	0.081	−0.850	−0.150	0.722	0.023	−0.069	−0.012
4.	1.90	14.00	11.00	0.131	1.150	−0.150	1.323	0.023	0.151	−0.020
5.	1.70	12.00	12.00	−0.069	−0.850	0.850	0.722	0.722	0.059	−0.059
6.	1.80	13.00	11.00	0.031	0.150	−0.150	0.023	0.023	0.005	−0.005
7.	1.85	12.00	11.00	0.081	−0.850	−0.150	0.722	0.023	−0.069	−0.012
8.	1.73	10.00	10.00	−0.039	−2.850	−1.150	8.123	1.323	0.111	0.045
9.	1.95	14.00	11.00	0.181	1.150	−0.150	1.323	0.023	0.208	−0.027
10.	1.67	13.00	12.00	−0.099	0.150	0.850	0.023	0.722	−0.015	−0.084
11.	1.82	16.00	14.00	0.051	3.150	2.850	9.923	8.123	0.161	0.145
12.	1.84	14.00	14.00	0.071	1.150	2.850	1.323	8.123	0.082	0.202
13.	1.74	11.00	9.00	−0.029	−1.850	−2.150	3.423	4.623	0.054	0.062
14.	1.68	12.00	8.00	−0.089	−0.850	−3.150	0.722	9.923	0.076	0.280
15.	1.62	11.00	9.00	−0.149	−1.850	−2.150	3.423	4.623	0.276	0.320
16.	1.82	15.00	13.00	0.051	2.150	1.850	4.623	3.423	0.110	0.094
17.	1.91	15.00	13.00	0.141	2.150	1.850	4.623	3.423	0.303	0.261
18.	1.61	12.00	9.00	−0.159	−0.850	−2.150	0.722	4.623	0.135	0.342
19.	1.64	13.00	10.00	−0.129	0.150	−1.150	0.023	1.323	−0.019	0.148
20.	1.85	15.00	13.00	0.081	2.150	1.850	4.623	3.423	0.174	0.150
Total	35.37	257	223				54.550	56.550	2.336	2.125
Average	1.769	12.850	11.150							

From the table above, we have
$\sum x_2^2 = 54.550$; $\sum x_3^2 = 56.550$; $\sum x_1x_2 = 2.336$; $\sum x_1x_3 = 2.125$
In the deviation form, we have

$$b_{x_1x_2} = \frac{\sum x_2x_1}{\sum x_2^2} = \frac{2.336}{54.550} = 0.042$$

Hence the regression line of X_1 on X_2 is given by
$x_1 = 0.042x_2$; transforming back to original variables, we have

$$(X_1 - \overline{X}_1) = (X_2 - \overline{X}_2)0.042$$

$$\text{or } (X_1 - 1.769) = (X_2 - 12.850)0.042$$
$$= 0.042X_2 - 0.539$$

$$\text{or } X_1 = 1.769 + 0.042X_2 - 0.539$$

$$\therefore X_1 = 1.230 + 0.042X_2$$

$$b_{x_1x_3} = \frac{\sum x_3x_1}{\sum x_3^2} = \frac{2.125}{56.550} = 0.037$$

Hence the regression line of X_1 on X_3 is given by

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$x_1 = 0.039x_3$; transforming back to original variables, we have

$$(X_1 - \overline{X}_1) = (X_3 - \overline{X}_3)0.037$$

$$\text{or } (X_1 - 1.769) = (X_3 - 11.150)0.037$$
$$= 0.037X_3 - 0.412$$

$$\text{or } X_1 = 1.769 + 0.037X_3 - 0.412$$

$$\therefore X_1 = 1.357 + 0.037X_3$$

Example 8.6
The following table gives the information on the number of birds per pen and area of the pen. Find out the relationship of area with the birds per pen and vice versa. Also find out the angle between the two lines of regression:

Birds/pen	25	100	200	500
Area (sq. ft)	88	300	500	1000

Solution From the given data, let us construct the following table:

No. of observations	Area (sq. ft) (Y)	Birds/pen (X)	$(X-\overline{X})^2$	$(Y-\overline{Y})^2$	$(X-\overline{X})(Y-\overline{Y})$
1.	88	25	32851.56	147456	69600.00
2.	300	100	11289.06	29584	18275.00
3.	500	200	39.06	784	−175.00
4.	1000	500	86289.06	278784	155100.00
Sum	1888.00	825.00	130468.75	456608	242800.00
Average	472.00	206.25	32617.19	114152	60700

$$Cov(X,Y) = S_{xy} = \frac{\sum (X-\overline{X})(Y-\overline{Y})}{n}$$
$$= \frac{242800}{4} = 60700$$

$$S_x^2 = \frac{\sum (X-\overline{X})^2}{n} = \frac{130468.75}{4} = 32617.19$$

$$S_y^2 = \frac{\sum (Y-\overline{Y})^2}{n} = \frac{456608}{4} = 114152$$

$$b_{yx} = \frac{S_{xy}}{S_x^2} = \frac{60700}{34617.19} = 1.86$$

$$b_1 = 1.86$$

$$b_{xy} = \frac{S_{xy}}{S_x^2} = \frac{60700}{114152} = 0.5317 \qquad b_1' = 0.5317$$

$$\text{Intercept}(b_0) = \overline{Y} - b\overline{X}$$
$$= 472.0 - 1.86 \times 206.25 = 88.17$$

$$b_0 = 88.17$$

$$\text{Intercept}\left(b_0'\right) = \overline{X} - b_1'\overline{Y}$$
$$= 206.25 - 0.5317 \times 472.0$$
$$= -44.7124$$

Hence the regression equations are

$$Y = 88.17 + 1.86X \text{ and}$$

$$X = -44.7124 + 0.5317Y$$

$$\tan\theta = \frac{b_1 \sim b_1'}{1 + b_1 b_1'}$$

$$\therefore \theta = \tan^{-1}\frac{1.86 - 0.5317}{1 + 1.86 \times 0.5317} = 0.6678 = 0.58$$

8.6 Identification of the Regression Equations

Sometimes it becomes very difficult to identify the dependent and independent variables from the given relationship. But to know the structure of dependency is one of the most important objectives of the regression analysis. One can find out the dependent and independent variables following the steps given below:

Step1: Express the equations in terms of two different dependent variables as per your own conception or choice.

Step 2: Identify the regression coefficients (say b_1 and b_2) from the two equations noted in the previous step.

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Step 3: Check whether $b_1 \times b_2 \leq 1$ or not; (i) if $b_1 \times b_2 \leq 1$, then the two equations have been identified correctly, because we have noted that (Sect. 8.5.4) $b_1 \times b_2 = r_{12}^2 \leq 1$; (ii) if $b_1 \times b_2 > 1$, then the regression equations are not correctly assumed; one has to reverse the process once again.

Example 8.7

Suppose two regression equations are given as follows: $2X_1 - 1.2X_2 - 20 = 0$ and $1.6X_1 - 0.8X_2 + 10 = 0$. The problem is to identify the regression equations, i.e., the regression equation of X_1 on X_2 and that of X_2 on X_1.

Solution Let $2X_1 - 1.2X_2 - 20 = 0$ be the regression equation of X_1 on X_2. So we can write

$$X_1 = 10 + 0.6X_2 \tag{8.1}$$

and let

$1.6X_1 - 0.8X_2 + 10 = 0$ be the regression equation of X_2 on X_1. So

$$X_2 = 10/0.8 + 1.6/0.8X_1 = 1.25 + 2X_1 \tag{8.2}$$

Thus from (1) we have $b_{12} = 0.6$ and from (2) $b_{21} = 2$.

We know that $b_{12} \times b_{21} = r^2 \leq 1$.

For our example, $b_{12} \times b_{21} = 0.6 \times 2 = 1.2 > 1$, not satisfying the relationship of regression coefficients and the correlation coefficient.

Therefore, we have not assumed the regression equations correctly.

Now let us assume the reverses.

Let $2X_1 - 1.2X_2 - 20 = 0$ be the regression equation of X_2 on X_1:

$$\begin{aligned} \therefore X_2 &= \frac{2}{1.2}X_1 - \frac{20}{1.2} \\ &= 1.67X_1 - 1.67 \end{aligned} \tag{8.3}$$

and $1.6X_1 - 0.8X_2 + 10 = 0$ be the regression equation of X_1 on X_2:

$$\begin{aligned} \therefore X_1 &= \frac{0.8}{1.6}X_2 - \frac{10}{1.6} \\ &= 0.5X_2 - 6.25 \end{aligned} \tag{8.4}$$

Thus, we have $b_{21} = 1.67$ and $b_{12} = 0.5$.

So, $b_{12} \times b_{21} = 1.67 \times 0.5 = 0.835 < 1$, satisfying the relationship of regression coefficients and the correlation coefficient.

So this time the assumptions of the regression equation were correct. Thus we conclude that $1.6X_1 - 0.8X_2 + 10 = 0$ is the regression equation of X_1 on X_2 and $2X_1 - 1.2X_2 - 20 = 0$ is the regression equation of X_2 on X_1.

8.7 Expectations and Variances of the Regression Parameters

As we are dealing with samples and are to infer about the population based on the sample on hand, so the inferences are based on estimators b_0, the intercept and b_1, the regression coefficient. As such one should know the properties of the estimators and their expectations and variances. Let us assume that X_1 and X_2 are the dependent and independent variables respectively. The expectations of b_0 and b_1 are given as $E(b_0) = \beta_0$ and $E(b_1) = \beta_1$. Then corresponding variances of the estimators are given as

$\mathrm{Var}(b_0) = \sigma_{b_0}^2 = \sigma^2\left(\frac{1}{n} + \frac{\bar{x}_2}{ss_{x2}}\right)$, and $\mathrm{Var}(b_1) = \sigma_{b_1}^2 = \frac{\sigma^2}{ss_{x2}}$ where σ^2 is the error variance of the regression model.

Under the normality assumption of the dependent variable and as both the regression estimators are linear functions of the dependent variable, so these are also assumed to behave like a normal variate. As the estimator of σ^2 is s^2, thus, by replacing σ^2 in the above variance estimates, we have

$$\mathrm{Var}(b_0) = \sigma_{b_0}^2 = \sigma^2\left(\frac{1}{n} + \frac{\bar{x}_2}{ss_{x2}}\right) = s^2\left(\frac{1}{n} + \frac{\bar{x}_2}{ss_{x2}}\right)$$

and $\mathrm{Var}(b_1) = \sigma_{b_1}^2 = \frac{\sigma^2}{ss_{x2}} = \frac{s^2}{ss_{x2}}$, and the corresponding standard errors are the square roots of the variances. Here S^2 is the residual mean sum of squares and is given as $\frac{\sum_{i=1}^{n}(x_{1i} - \hat{x}_1)^2}{d.f.}$, and x_1 is the dependent variable; d.f. is the number of observations – no. of parameters estimated in the model – for simple regression equation model, d.f. would be $n-2$.

It should be noted that the variance of residuals is not equal to the error variance, $\mathrm{Var}(e_i) \neq \sigma^2$. The residual variance depends on the independent variable x_2. But when the sample size is large, $\mathrm{Var}(e_i) \approx \sigma^2$, which is estimated by s^2, that is, $E(s^2) = \sigma^2$.

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8.8 Test of Significance for the Regression Coefficient

When there are changes in the dependent variable due to the change in the independent variable, then we assume that the regression line has a slope; that means the slope coefficient is different from zero. In order to test the same, we have the following null and alternative hypotheses, respectively:

$H_0: \beta_1 = 0$
$H_1: \beta_1 \neq 0$

Assuming that the dependent variable follows normal distribution, we have the following test statistic under the given hypotheses:

$$t = \frac{b_1 - 0}{SE(b_1)} = \frac{b_1}{\sqrt{\frac{S^2}{SS_{x_2}}}} = \frac{b_1}{S}\sqrt{SS_{x_2}} \quad \text{with} \quad (n-2)$$

degrees of freedom. At α level of significance, the null hypothesis H_0 is rejected if the computed value of $|t| \geq t_{\alpha/2,(n-2)}$, where $t_{\alpha/2,(n-2)}$ is a critical value of t-distribution with $(n-2)$ degrees of freedom under H_0.

8.9 Multiple Linear Regression Analysis

As has already been mentioned that in multiple regression analysis, we presume that the dependent variable is no longer dependent on only one independent variable, rather it is dependent on many independent variables. The production of a crop in a country is dependent on the area under crop and per hectare productivity of the crop for constituting states of the country. Thus one can have the regression equation production of a crop in a country on the area and productivity of the crop, taking different states under a country. Again the productivity of any crop (say paddy) is influenced by many yield components like number of hills per square meter, number of effective tillers per hill, length of panicle, number of grains per panicle, number of chaffy grains per panicle, weight of 100 grains, etc. So one can very well frame a multiple regression equation of yield on such yield components. Thus, multiple linear regression equation is a more general case in regression analysis, and simple linear regression equation may be considered as a particular case of multiple linear regression equation in which only two variables are considered at a time.

Extending our idea of simple linear regression problem explained in Sect. 8.4 to more than one independent variable, one can estimate the parameters of the regression equation. Suppose we have k number of variables $X_1, X_2, \ldots\ldots\ldots, X_k$ of which X_1 is the dependent variable and others are independent variables. So we are to frame an equation $X_1 = \beta_1 + \beta_2 X_2 + \ldots\ldots\ldots\ldots + \beta_k X_k$. But instead of the population, we are provided with a sample, so from sample observations we are to work out a linear regression equation of the form $X_1 = b_1 + b_2 X_2 + \ldots\ldots\ldots\ldots + b_k X_k$ using the sets of values for $X_1, X_2, \ldots\ldots\ldots, X_K$. We have also seen that if the variables are measured from their respective means, then the intercept term b_1 does not appear in the regression equation. Let the above regression equation with variables measured from their respective means be denoted as $x_1 = b_2 x_2 + \ldots\ldots\ldots\ldots + b_k x_k$. This equation is also true for all sets of observation where variables are measured from their respective means; that means

Observtion	x_1	x_2	x_3	x_K
1	x_{11}	x_{21}	x_{31}	x_{k1}
2	x_{12}	x_{22}	x_{32}	x_{k2}
3	x_{13}	x_{23}	x_{33}	x_{k3}
.....				
.....				
.....				
i	x_{1i}	x_{2i}	x_{3i}	x_{ki}
.....				
.....				
.....				
n	x_{1n}	x_{2n}	x_{3n}	x_{kn}

(8.6)

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Now multiplying both sides of the above equation $x_1 = b_2x_2 + \ldots\ldots\ldots\ldots + b_kx_k$ by x_2, x_3, ..., x_k, respectively, and taking the sum, we get the following k equations, known as normal equations:

$$\left.\begin{array}{l}
\sum x_1x_2 = b_2\sum x_2^2 + b_3\sum x_2x_3 + b_4\sum x_2x_4 \ldots\ldots\ldots\ldots + b_k\sum x_2x_k \\
\sum x_1x_3 = b_2\sum x_2x_3 + b_3\sum x_3^2 + b_4\sum x_3x_4 \ldots\ldots\ldots\ldots + b_k\sum x_3x_k \\
\sum x_1x_4 = b_2\sum x_2x_4 + b_3\sum x_3x_4 + b_4\sum x_4^2 \ldots\ldots\ldots\ldots + b_k\sum x_4x_k \\
\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \\
\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \\
\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \\
\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \\
\sum x_1x_k = b_2\sum x_2x_k + b_3\sum x_3x_k + b_4\sum x_4x_k \ldots\ldots\ldots\ldots + b_k\sum x_k^2
\end{array}\right\} \quad (8.7)$$

Now these b_2, b_3, ……..., b_k are the estimates of the β_2, β_k,....., β_k.

Solving the above $k-1$ equations, $k-1$ regression coefficients can be obtained.

8.10 Multiple Linear Regression Equation Taking Three Variables

In multiple linear regression analysis with three variables at a time, one is dependent variable (say X_1) and two independent variables (say X_2 and X_3). From the above sets normal equations for a particular case of three variables, the normal equations would be

$$\left.\begin{array}{l}
\sum x_1x_2 = b_2\sum x_2^2 + b_3\sum x_3x_2 \\
\sum x_1x_3 = b_2\sum x_1x_3 + b_3\sum x_3^2
\end{array}\right\} \quad (8.8)$$

Solving the above two Eq. in (8.8), we shall get

$$\frac{\sum x_3^2\sum x_1x_2 - \sum x_2x_3\sum x_1x_3}{\sum x_2^2\sum x_3^2 - \sum x_2x_3} = b_2 \text{ and}$$

$$\frac{\sum x_2^2\sum x_1x_3 - \sum x_2x_3\sum x_1x_2}{\sum x_2^2\sum x_3^2 - \sum x_2x_3} = b_3$$

Example 8.8

The following table gives data pertaining to 20 *units for three variables* X_1, X_2, *and* X_3. *Find out the linear regression equation of* X_1 *on* X_2 *and* X_3:

Observation	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
X_1	1.83	1.56	1.85	1.9	1.7	1.8	1.85	1.73	1.95	1.67	1.82	1.84	1.74	1.68	1.62	1.82	1.91	1.61	1.64	1.85
X_2	13	10	12	14	12	13	12	10	14	13	16	14	11	12	11	15	15	12	13	15
X_3	12	10	11	11	12	11	11	10	11	12	14	14	9	8	9	13	13	9	10	13

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Solution

Observation	X_1	X_2	X_3	$x_1 = X_{1i} - \overline{X}_1$	$x_2 = X_{2i} - \overline{X}_2$	$x_3 = X_{3i} - \overline{X}_3$	${x_1}^2$	${x_2}^2$	${x_3}^2$	x_1x_2	x_1x_3	x_2x_3
1.	1.83	13.00	12.00	0.061	0.150	0.850	0.004	0.023	0.722	0.009	0.052	0.128
2.	1.56	10.00	10.00	−0.209	−2.850	−1.150	0.044	8.123	1.323	0.596	0.240	3.278
3.	1.85	12.00	11.00	0.081	−0.850	−0.150	0.007	0.722	0.023	−0.069	−0.012	0.128
4.	1.90	14.00	11.00	0.131	1.150	−0.150	0.017	1.323	0.023	0.151	−0.020	−0.173
5.	1.70	12.00	12.00	−0.069	−0.850	0.850	0.005	0.722	0.722	0.059	−0.059	−0.722
6.	1.80	13.00	11.00	0.031	0.150	−0.150	0.001	0.023	0.023	0.005	−0.005	−0.023
7.	1.85	12.00	11.00	0.081	−0.850	−0.150	0.007	0.722	0.023	−0.069	−0.012	0.128
8.	1.73	10.00	10.00	−0.039	−2.850	−1.150	0.002	8.123	1.323	0.111	0.045	3.278
9.	1.95	14.00	11.00	0.181	1.150	−0.150	0.033	1.323	0.023	0.208	−0.027	−0.173
10.	1.67	13.00	12.00	−0.099	0.150	0.850	0.010	0.023	0.722	−0.015	−0.084	0.128
11.	1.82	16.00	14.00	0.051	3.150	2.850	0.003	9.923	8.123	0.161	0.145	8.978
12.	1.84	14.00	14.00	0.071	1.150	2.850	0.005	1.323	8.123	0.082	0.202	3.278
13.	1.74	11.00	9.00	−0.029	−1.850	−2.150	0.001	3.423	4.623	0.054	0.062	3.978
14.	1.68	12.00	8.00	−0.089	−0.850	−3.150	0.008	0.722	9.923	0.076	0.280	2.678
15.	1.62	11.00	9.00	−0.149	−1.850	−2.150	0.022	3.423	4.623	0.276	0.320	3.978
16.	1.82	15.00	13.00	0.051	2.150	1.850	0.003	4.623	3.423	0.110	0.094	3.978
17.	1.91	15.00	13.00	0.141	2.150	1.850	0.020	4.623	3.423	0.303	0.261	3.978
18.	1.61	12.00	9.00	−0.159	−0.850	−2.150	0.025	0.722	4.623	0.135	0.342	1.828
19.	1.64	13.00	10.00	−0.129	0.150	−1.150	0.017	0.023	1.323	−0.019	0.148	−0.173
20.	1.85	15.00	13.00	0.081	2.150	1.850	0.007	4.623	3.423	0.174	0.150	3.978
Total	35.37	257	223				0.237	54.550	56.550	2.336	2.125	42.450
Average	1.769	12.850	11.150									

From the above table, we have

$\sum x_1^2 = 0.237;\ \sum x_2^2 = 54.550;\ \sum x_3^2 = 56.550;\ \sum x_1x_2 = 2.336;\ \sum x_1x_3 = 2.125;\ \sum x_2x_3 = 42.450;\ \left(\sum x_2x_3\right)^2 = 1802.003$

We Know that

$$b_1 = \frac{\sum x_3^2 \sum x_2x_1 - \sum x_2x_3 \sum x_3x_1}{\sum x_2^2 \sum x_3^2 - \left(\sum x_2x_3\right)^2}$$

$$= \frac{56.550 \times 2.336 - 42.450 \times 2.125}{54.550 \times 56.550 - 1802.003}$$

$$= \frac{132.100 - 90.206}{3084.803 - 1802.003} = \frac{41.894}{1282.799} = 0.032$$

$$b_2 = \frac{\sum x_2^2 \sum x_3x_1 - \sum x_2x_3 \sum x_2x_1}{\sum x_2^2 \sum x_3^2 - \left(\sum x_2x_3\right)^2}$$

$$= \frac{54.550 \times 2.125 - 42.450 \times 2.336}{54.550 \times 56.550 - 1802.003}$$

$$= \frac{115.918 - 99.163}{3084.803 - 1802.003} = \frac{16.755}{1282.799} = 0.013$$

Hence the linear regression of x_1 on x_2 and x_3 will be $x_1 = 0.032x_2 + 0.013x_3$; transforming back to original variables, we have

$$\left(X_1 - \overline{X}_1\right) = \left(X_2 - \overline{X}_2\right)0.032 + \left(X_3 - \overline{X}_3\right)0.013;$$ putting the value of $\overline{X}_1$, $\overline{X}_2$, and $\overline{X}_3$, we have

$$(X_1 - 1.769) = (X_2 - 12.850)0.032 + (X_3 - 11.150)0.013$$

$$X_1 = 1.769 + 0.032X_2 - 0.411 + 0.013X_3 - 0.144$$

$$X_1 = 1.214 + 0.032X_2 + 0.013X_3$$

8.11 Estimation of the Parameters of Linear Regression Model Using OLS Technique in the Matrix Form

General linear regression equation of X_1 on X_2, X_3, ..., X_k in their deviation form is given as

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$X_{1i} = \beta_2 X_{2i} + \beta_3 X_{3i} + \ldots\ldots\ldots + \beta_k X_{ki} + \varepsilon_i$, ($i = 1, 2, 3, \ldots\ldots\ldots, n-1, n$; number of observation). For each set of observations on $X_1, X_2, X_3, \ldots\ldots\ldots, X_k$, we have

Observation	x_1	x_2	x_3	x_K	u
1	x_{11}	x_{21}	x_{31}	x_{k1}	u_1
2	x_{12}	x_{22}	x_{32}	x_{k2}	u_2
3	x_{13}	x_{23}	x_{33}	x_{k3}	u_3
.....					
.....					
.....					
i	x_{1i}	x_{2i}	x_{3i}	x_{ki}	u_i
.....					
.....					
.....					
n	x_{1n}	x_{2n}	x_{3n}	x_{kn}	u_n

(8.9)

i.e.,

$$
\begin{aligned}
&1\ x_{11} = \beta_2 x_{21} + \beta_3 x_{31} + \ldots\ldots\ldots + \beta_k x_{k1} + u_1 \\
&2\ x_{12} = \beta_2 x_{22} + \beta_3 x_{32} + \ldots\ldots\ldots + \beta_k x_{k2} + u_2 \\
&3\ x_{13} = \beta_2 x_{23} + \beta_3 x_{33} + \ldots\ldots\ldots + \beta_k x_{k3} + u_3 \\
&\ldots\ldots\ldots \\
&\ldots\ldots\ldots \\
&\ldots\ldots\ldots \\
&i\ x_{1i} = \beta_2 x_{2i} + \beta_3 x_{3i} + \ldots\ldots\ldots + \beta_k x_{ki} + u_i \\
&\ldots\ldots\ldots \\
&\ldots\ldots\ldots \\
&\ldots\ldots\ldots \\
&n\ x_{1n} = \beta_2 x_{2n} + \beta_3 x_{3n} + \ldots\ldots\ldots + \beta_k x_{kn} + u_n
\end{aligned}
\tag{8.10}
$$

where u_is are the error terms associated with each set of observations.

In matrix notation the above can be written as

$$
\underset{\sim}{X}_1 = \underset{\sim}{X}\,\underset{\sim}{\beta} + \underset{\sim}{U}
\tag{8.11}
$$

$$
\begin{bmatrix} x_{11} \\ x_{12} \\ x_{13} \\ \\ \\ x_{1i} \\ \\ x_{1n} \end{bmatrix}
=
\begin{bmatrix}
x_{21} & x_{31} & x_{41} & \ldots\ldots\ldots & x_{k1} \\
x_{22} & x_{32} & x_{42} & \ldots\ldots\ldots & x_{k2} \\
x_{23} & x_{33} & x_{43} & \ldots\ldots\ldots & x_{k3} \\
\ldots\ldots & & & & \\
\ldots\ldots & & & & \\
x_{2i} & x_{3i} & x_{4i} & \ldots\ldots\ldots & x_{ki} \\
\ldots\ldots & & & & \\
x_{2n} & x_{3n} & x_{4n} & \ldots\ldots\ldots & x_{kn}
\end{bmatrix}
\begin{bmatrix} \beta_2 \\ \beta_3 \\ \beta_4 \\ \\ \\ \beta_j \\ \\ \beta_k \end{bmatrix}
+
\begin{bmatrix} u_2 \\ u_3 \\ u_4 \\ \\ \\ u_i \\ \\ u_n \end{bmatrix}
$$

$n \times 1$ $\quad$ $n \times \overline{k-1}$ $\quad$ $\overline{k-1} \times 1$ $\quad$ $n \times 1$

Thus, one can write $\underset{\sim}{X}_1 = \underset{\sim}{X}\underset{\sim}{\beta} + \underset{\sim}{u}$.

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The basic idea of ordinary least square technique is to minimize the sum of squares due to errors, (u^s). So we want to minimize

$$L = \underset{\sim}{u}'\underset{\sim}{u} = \left(\underset{\sim}{X}_1 - \underset{\sim}{X}\underset{\sim}{\beta}\right)'\left(\underset{\sim}{X}_1 - \underset{\sim}{X}\underset{\sim}{\beta}\right)$$
$$= \underset{\sim}{X}_1{}'\underset{\sim}{X}_1 - 2\,\underset{\sim}{\beta}'\underset{\sim}{X}'\underset{\sim}{X}_1 + \underset{\sim}{\beta}'\,\underset{\sim}{X}'\underset{\sim}{X}\underset{\sim}{\beta} \qquad (8.12)$$

if $\underset{\sim}{b}$ be the least square estimates of $\underset{\sim}{\beta}$, then

$\frac{\partial L}{\partial \underset{\sim}{\beta}} = 0$, and writing $\underset{\sim}{b}$ for

$\underset{\sim}{\beta}$, we have $2\underset{\sim}{X}'\underset{\sim}{X}_1 - 2\underset{\sim}{X}'\underset{\sim}{X}\underset{\sim}{b} = \quad 0$ or $\underset{\sim}{X}'\underset{\sim}{X}\underset{\sim}{b} = \underset{\sim}{X}'\underset{\sim}{X}_1$

$or\ \underset{\sim}{b} = \left(\underset{\sim}{X}'\underset{\sim}{X}\right)^{-1}\underset{\sim}{X}'\underset{\sim}{X}_1,\ if\ \left(\underset{\sim}{X}'\underset{\sim}{X}\right)^{-1}\ exists,$

where $\left(\underset{\sim}{X}'\underset{\sim}{X}\right) =$

$$\begin{pmatrix} \sum x_{2i}^2 & \sum x_{2i}x_{3i} & \ldots\ldots\ldots & \sum x_{2i}x_{Ki} \\ \sum x_{2i}x_{3i} & \sum x_{3i}^2 & \ldots\ldots\ldots & \sum x_{3i}x_{Ki} \\ \ldots\ldots\ldots & \ldots\ldots\ldots & \ldots\ldots\ldots & \ldots\ldots\ldots \\ \sum x_{2i}x_{Ki} & \sum x_{3i}x_{Ki} & \ldots\ldots\ldots & \sum x^2{}_{Ki} \end{pmatrix}$$

and $\underset{\sim}{X}'\underset{\sim}{X}_1$

$$= \begin{pmatrix} x_{21} & x_{22} & \ldots\ldots\ldots & x_{2n} \\ x_{31} & x_{32} & \ldots\ldots\ldots & x_{3n} \\ \ldots\ldots\ldots & \ldots\ldots\ldots & \ldots\ldots\ldots & \ldots\ldots\ldots \\ x_{k1} & x_{k2} & \ldots\ldots\ldots & x_{kn} \end{pmatrix}\begin{pmatrix} x_{11} \\ x_{12} \\ . \\ x_{1n} \end{pmatrix}$$

$$= \begin{pmatrix} \sum x_{2i}x_{1i} \\ \sum x_{3i}x_{1i} \\ \\ \\ \sum x_{ki}x_{1i} \end{pmatrix}$$

$$\underset{\sim}{b} = \begin{pmatrix} b_2 \\ b_3 \\ . \\ b_k \end{pmatrix}$$

8.12 Estimation of Regression Coefficients from Correlation Coefficients

Readers may please note that $(\underset{\sim}{X}'\underset{\sim}{X})$ and $\underset{\sim}{X}'\underset{\sim}{X}_1$ are nothing but the variance–covariance matrix of the independent variables and the covariance matrix between the dependent variable and the independent variable, respectively. Thus, using the formula for the correlation coefficient, the above two matrices can very well be presented in the form of correlation matrices. That's why, if correlation matrices are known, one can find out the regression equation also. In fact by knowing the correlation coefficients and variance–covariance, one can find out the regression coefficients. In the following section, we would show the calculation regression coefficients from the correlation matrix without going details into the derivation.

Let $\mathfrak{R}$ be the correlation matrix for k number of variables $X_1, X_2, X_3, X_4, \ldots\ldots\ldots, X_k$:

$$\mathfrak{R} = \begin{bmatrix} r_{11}\ r_{12}\ r_{13}\ r_{14}\ .\ \ldots\ldots\ldots\ldots\ldots\ r_{1k} \\ r_{21}\ r_{22}\ r_{23}\ r_{24}\ .\ \ldots\ldots\ldots\ldots\ldots r_{2k} \\ r_{31}\ r_{32}\ r_{33}\ r_{34}.\ \ldots\ldots\ldots\ldots\ r_{3k} \\ \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \\ \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \\ r_{k1}\ r_{k2}\ r_{k3}\ .\ \ldots\ldots\ldots\ldots\ r_{kk} \end{bmatrix}$$

$$= \begin{bmatrix} 1\ r_{12}\ r_{13}\ r_{14}\ .\ \ldots\ldots\ldots\ldots\ r_{1k} \\ r_{21}\ 1\ r_{23}\ r_{24}\ .\ \ldots\ldots\ldots\ldots\ldots r_{2k} \\ r_{31}\ r_{32}\ 1\ r_{34}.\ \ldots\ldots\ldots\ldots\ r_{3k} \\ \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \\ \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \\ r_{k1}\ r_{k2}\ r_{k3}\ .\ \ldots\ldots\ldots\ldots\ldots 1 \end{bmatrix}$$

So the minor of any element of the above matrix is the determinant of the above square matrix after deleting the row and column of the concerned element of the matrix, and the cofactor of the same element is the $(-1)^{r+c}$ minor of the element. Thus, if one wants to know the cofactor (A_{ij}) of the (i,j) element from the above square matrix, then it is the $(-1)^{i+j}\,M_{ij}$, where M_{ij} is the determinant of the above matrix after eliminating the ith row and jth column from the matrix. Given the above correlation matrix, the regression coefficients can be worked out using the formula

$b_{ii'} = -\frac{S_i\,\omega_{ii'}}{S_{i'}\,\omega_{ii}}$, where ω_{ii} and $\omega_{ii'}$ are the cofactors of ii and ii' elements, respectively, and S_i and $S_{i'}$ are the standard deviationof ith and i'th variables, respectively.

Thus, for k variable regression equation of X_1 on $X_2, X_3, \ldots\ldots, X_k$, we have the regression equation $X_1 = -\frac{S_1}{S_2}\frac{\omega_{12}}{\omega_{11}}X_2 - \frac{S_1}{S_3}\frac{\omega_{13}}{\omega_{11}}X_3 - \ldots\ldots\ldots\ldots$

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$-\frac{S_1}{S_k}\frac{\omega_{1k}}{\omega_{11}}X_k$. In particular, the regression equation of X_1 on X_2 and X_3 will be $X_1 = -\frac{S_1}{S_2}\frac{\omega_{12}}{\omega_{11}}X_2 - \frac{S_1}{S_3}\frac{\omega_{13}}{\omega_{11}}X_3$. One can easily find out the $\omega's$ from the correlation matrix:

$$\Re = \begin{bmatrix} 1 & r_{12} & r_{13} \\ r_{21} & 1 & r_{23} \\ r_{31} & r_{32} & 1 \end{bmatrix}$$

$$\therefore \omega_{11} = (-1)^{1+1}\begin{vmatrix} 1 & r_{23} \\ r_{23} & 1 \end{vmatrix} = (-1)^{1+1}\left(1 - r_{23}^2\right) = \left(1 - r_{23}^2\right)$$

$$\therefore \omega_{12} = (-1)^{1+2}\begin{vmatrix} r_{21} & r_{23} \\ r_{31} & 1 \end{vmatrix} = (-1)^{1+2}(r_{21} - r_{23}.r_{31}) = -(r_{21} - r_{23}.r_{31})$$

$$\therefore \omega_{13} = (-1)^{1+3}\begin{vmatrix} r_{21} & 1 \\ r_{31} & r_{32} \end{vmatrix} = (-1)^{1+3}(r_{21}.r_{32} - r_{31}) = (r_{21}.r_{32} - r_{31})$$

$$\therefore X_1 = -\frac{S_1}{S_2}\frac{\omega_{12}}{\omega_{11}}X_2 - \frac{S_1}{S_3}\frac{\omega_{13}}{\omega_{11}}X_3 = -\frac{S_1}{S_2}\frac{-(r_{21} - r_{23}.r_{31})}{\left(1 - r_{23}^2\right)}X_2 - \frac{S_1}{S_3}\frac{(r_{21}.r_{32} - r_{31})}{\left(1 - r_{23}^2\right)}X_3$$

$$= \frac{S_1}{S_2}\frac{(r_{21} - r_{23}.r_{31})}{\left(1 - r_{23}^2\right)}X_2 + \frac{S_1}{S_3}\frac{(r_{31} - r_{21}.r_{32})}{\left(1 - r_{23}^2\right)}X_3$$

Now replacing the values of S_1, S_2, S_3, r_{12}, r_{13}, and r_{23} in the above relationship, one can very well work out the regression equation.

Example 8.9

Find the correlation coefficients for all possible combinations of the variables. Hence find out the correlation matrix of the variables, and work out the regression equation of body weight (Y) on feed intake X_1 and age (X_2) using the correlation matrix:

Body weight (kg)	(Y)	453	481	580	640	720	820	860	900	1000	1040	1090	1130	1180	1220	1270	1320	1360
Feed (kg)	(X_1)	3.85	4.5	4.5	4.6	4.6	4.6	4.9	5	5.4	5.7	5.7	5.9	5.9	6.1	6.1	6.3	6.5
Age (fortnight)	(X_2)	39	43.5	53	60	67	74	81	88	95	102	109	116	123	130	137	144	151

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Solution Let us construct the following tables so as to facilitate the calculation of correlation coefficients:

Sn	Y	X_1	X_2	$(x_1 = X_1 - \overline{X}_1)$	$(x_2 = X_2 - \overline{X}_2)$	$(y = Y - \overline{Y})$	x_1y	x_2y	x_1x_2	${x_1}^2$	${x_2}^2$	y^2
1.	453.00	3.85	39.00	−1.45294	−55.8529	−491.941	714.7616	27476.36	150.15	2.111038	3119.551	242006.1
2.	481.00	4.50	43.50	−0.80294	−51.3529	−463.941	372.5175	23824.74	195.75	0.644715	2637.125	215241.4
3.	580.00	4.50	53.00	−0.80294	−41.8529	−364.941	293.0263	15273.86	238.5	0.644715	1751.669	133182.1
4.	640.00	4.60	60.00	−0.70294	−34.8529	−304.941	214.3557	10628.1	276	0.494126	1214.728	92989.12
5.	720.00	4.60	67.00	−0.70294	−27.8529	−224.941	158.1204	6265.273	308.2	0.494126	775.7863	50598.53
6.	820.00	4.60	74.00	−0.70294	−20.8529	−124.941	87.8263	2605.391	340.4	0.494126	434.8452	15610.3
7.	860.00	4.90	81.00	−0.40294	−13.8529	−84.9412	34.2263	1176.685	396.9	0.162362	191.904	7215.003
8.	900.00	5.00	88.00	−0.30294	−6.85294	−44.9412	13.61453	307.9792	440	0.091773	46.9628	2019.709
9.	1000.00	5.40	95.00	0.097059	0.147059	55.05882	5.343945	8.096886	513	0.00942	0.021626	3031.474
10.	1040.00	5.70	102.00	0.397059	7.147059	95.05882	37.74394	679.391	581.4	0.157656	51.08045	9036.18
11.	1090.00	5.70	109.00	0.397059	14.14706	145.0588	57.59689	2052.156	621.3	0.157656	200.1393	21042.06
12.	1130.00	5.90	116.00	0.597059	21.14706	185.0588	110.491	3913.45	684.4	0.356479	447.1981	34246.77
13.	1180.00	5.90	123.00	0.597059	28.14706	235.0588	140.3439	6616.215	725.7	0.356479	792.2569	55252.65
14.	1220.00	6.10	130.00	0.797059	35.14706	275.0588	219.2381	9667.509	793	0.635303	1235.316	75657.36
15.	1270.00	6.10	137.00	0.797059	42.14706	325.0588	259.091	13700.27	835.7	0.635303	1776.375	105663.2
16.	1320.00	6.30	144.00	0.997059	49.14706	375.0588	373.9557	18433.04	907.2	0.994126	2415.433	140669.1
17.	1360.00	6.50	151.00	1.197059	56.14706	415.0588	496.8498	23304.33	981.5	1.43295	3152.492	172273.8
Sum	16064.00	90.15	1612.50				3589.103	165932.9	8989.1	9.872353	20242.88	1375735
Avg	944.94	5.30	94.85									

$$Cov(X_1, Y) = S_{x_1y} = \frac{\sum x_1y}{n} = \frac{3589.103}{17} = 211.1237$$

$$S^2{}_{x_1} = \frac{\sum x_1^2}{n} = \frac{9.8723}{17} = 0.5807; S_{x_1} = 0.762$$

$$S^2{}_y = \frac{\sum y^2}{n} = \frac{1375734.941}{17} = 80925.5847;\ S_y = 284.474,$$

$$\therefore r_{x_1y} = \frac{Cov(X_1, Y)}{S_{x_1}S_y} = \frac{211.1237}{\sqrt{(0.5807 \times 80925.5847)}} = 0.973908$$

The correlation between body weight and feed is 0.973908:

$$Cov(X_2, Y) = S_{x_2y} = \frac{\sum x_2y}{n} = \frac{165932.85}{17} = 9760.756$$

$$S_{x_2}^2 = \frac{\sum x_2^2}{n} = \frac{2242.88}{17} = 1190.757; S_{x_2} = 34.507$$

$$\therefore r_{x_2y} = \frac{Cov(X_2, Y)}{S_{x_2}S_y} = \frac{9760.7561}{\sqrt{(1190.757 \times 80925.58)}} = 0.994326$$

The correlation between body weight and age is 0.994:

$$Cov(X_1, X_2) = S_{x_1x_2} = \frac{\sum x_1x_2}{n} = \frac{438.11}{17} = 25.77102$$

$$\therefore r_{x_1x_2} = \frac{Cov(X_1, X_2)}{S_{x_1}S_{x_2}} = \frac{25.77102}{\sqrt{(0.5807 \times 1190.758)}} = 0.980018$$

The correlation between feed and age is 0.980018.

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From the above, let us construct the following correlation matrix:

$$\Re = \begin{bmatrix} 1 & r_{yx_1} & r_{yx_2} \\ r_{yx_1} & 1 & r_{x_1x_2} \\ r_{yx_2} & r_{x_1x_2} & 1 \end{bmatrix} = \begin{bmatrix} 1.000000 & 0.973908 & 0.994326 \\ 0.973908 & 1.000000 & 0.980018 \\ 0.994326 & 0.980018 & 1.000000 \end{bmatrix}$$

$$\therefore \omega_{yy} = (-1)^{1+1}\begin{vmatrix} 1 & r_{x_1x_2} \\ r_{x_1x_2} & 1 \end{vmatrix} = (-1)^{1+1}\left(1 - r^2_{x_1x_2}\right) = \left(1 - r^2_{x_1x_2}\right) = 1 - 0.980018^2 = 0.039564$$

$$\therefore \omega_{yx_1} = (-1)^{1+2}\begin{vmatrix} r_{yx_1} & r_{x_1x_2} \\ r_{yx_2} & 1 \end{vmatrix} = (-1)^{1+2}\left(r_{yx_1} - r_{x_1x_2}.r_{yx_2}\right) = -\left(r_{yx_1} - r_{x_1x_2}.r_{yx_2}\right)$$

$$= -(0.973908 - 0.980018 \times 0.994326) = -(-0.000549) = 0.000549$$

$$\therefore \omega_{yx_2} = (-1)^{1+3}\begin{vmatrix} r_{yx_1} & 1 \\ r_{yx_2} & r_{x_1x_2} \end{vmatrix} = (-1)^{1+3}\left(r_{yx_1}.r_{x_1x_2} - r_{31}\right) = \left(r_{yx_1}.r_{x_1x_2} - r_{yx_2}\right)$$

$$= (0.973908 \times 0.980018 - 0.994326) = -0.039878$$

$$\therefore y = -\frac{S_y\,\omega_{yx_1}}{S_{x_1}\,\omega_{yy}}x_1 - \frac{S_y\,\omega_{yx_2}}{S_{x_2}\,\omega_{yy}}x_2 = -\frac{S_y}{S_{x_1}}\frac{(0.000549)}{0.039564}x_1 - \frac{S_y}{S_{x_2}}\frac{(-0.039878)}{0.039564}x_2$$

$$= -\frac{284.474(0.000549)}{0.761 \quad 0.039564}x_1 - \frac{284.474}{34.507}\frac{(-0.039878)}{0.039564}x_2$$

$$= -5.18350x_1 + 8.30928x_2$$

∴Transforming back to original variables, we

$$Y - \overline{Y} = -5.18350\left(X_1 - \overline{X}_1\right) + 8.30928(X_2 - X_2)$$

$$or\ Y = 944.94 - 5.18350(X_1 - 5.30) + 8.30928(X_2 - 94.85)$$

$$= 944.94 - 5.18350\,X_1 + 5.18350 \times 5.30 + 8.30928X_2 - 8.309288 \times 94.85$$

$$= 944.94 + 27.47255 - 788.1359668 - 5.18350X_1 + 8.038X_2$$

$$= 184.27658\text{-}5.18350X_1 + 8.038X_2$$

Example 8.10

Using the same three-variable data set as given in example 8.2, find out the multiple linear regression equation of X_1 on X_2 and X_3:

X_1	1.83	1.56	1.85	1.9	1.7	1.8	1.85	1.73	1.95	1.67	1.82	1.84	1.74	1.68	1.62	1.82	1.91	1.61	1.64	1.85
X_2	13	10	12	14	12	13	12	10	14	13	16	14	11	12	11	15	15	12	13	15
X_3	12	10	11	11	12	11	11	10	11	12	14	14	9	8	9	13	13	9	10	13

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Solution The dependent variable is X_1 and X_2 and X_3 are the two independent variables. We want to construct the regression equation of the form $X_1 = b_1 + b_2X_2 + b_3X_3$. From the above information, the following matrices are constructed.

The $\underset{\sim}{X}$ and $\underset{\sim}{X}_1$ matrices for the data can be obtained as

$$\underset{\sim}{X} = \begin{bmatrix} 1 & 13.00 & 12.00 \\ 1 & 10.00 & 10.00 \\ . & . & . \\ . & . & . \\ 1 & 15.00 & 13.00 \end{bmatrix} \text{ and } \underset{\sim}{X}_1 = \begin{bmatrix} 1.83 \\ 1.53 \\ . \\ . \\ 1.85 \end{bmatrix}$$

We know that

$$\widehat{\beta} = \begin{bmatrix} b_1 \\ b_2 \\ b_3 \end{bmatrix} = \left(\underset{\sim}{X}^1\underset{\sim}{X}\right)^{-1}\left(\underset{\sim}{X}^1\underset{\sim}{X}_1\right)$$

$$= \left[\begin{bmatrix} 1 & 1 & . & . & 1 \\ 13.00 & 10.00 & . & . & 15.00 \\ 12.00 & 10.00 & . & . & 13.00 \end{bmatrix} \times \begin{bmatrix} 1 & 13.00 & 12.00 \\ 1 & 10.00 & 10.00 \\ . & . & . \\ . & . & . \\ 1 & 15.00 & 13.00 \end{bmatrix}\right]^{-1}$$

$$\times \left[\begin{bmatrix} 1 & 1 & . & . & 1 \\ 13.00 & 10.00 & . & . & 15.00 \\ 12.00 & 10.00 & . & . & 13.00 \end{bmatrix} \times \begin{bmatrix} 1.83 \\ 1.53 \\ . \\ . \\ 1.85 \end{bmatrix}\right]$$

$$= \begin{bmatrix} 20 & 257 & 223 \\ 257 & 3357 & 2908 \\ 223 & 2908 & 2543 \end{bmatrix}^{-1} \begin{bmatrix} 35.37 \\ 456.84 \\ 396.50 \end{bmatrix}$$

$$\widehat{\beta}^{\sim} = \begin{bmatrix} 1.203 \\ 0.032 \\ 0.013 \end{bmatrix} = \begin{bmatrix} b_1 \\ b_2 \\ b_3 \end{bmatrix}$$

Hence the required regression equation is

$$X_1 = 1.203 + 0.032X_2 + 0.013X_3$$

8.13 Multiple Correlations

Under multiple-variable situation, the correlation coefficient between the dependent variable and the joint effect of the independent variables is known as the multiple correlation coefficient. Suppose we have k variables X_1, X_2,..... X_k' of which X_1 is the dependent variable and others are independent variables. The joint effects of the independent variables X_2, X_3, X_4,....., X_k on X_1 is the estimated value of the dependent variable X_1, i.e., $\hat{X}_1$, from the regression equation

$X_1 = b_1 + b_2X_2 + b_3X_3 + ... + b_kX_k$,
where b_1, b_2, $b_3, ..., b_k$ are the estimates of the population regression coefficients β_1, β_2, $\beta_3, ..., \beta_k$, respectively.

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Following the usual formula for the calculation of the correlation coefficient, the multiple correlation coefficient can be written as

$$R_{X_1.X_2X_3X_4....X_k} = \frac{Cov(X_1, \hat{X}_1)}{\sqrt{V(X_1)}\sqrt{V(\hat{X}_1)}}$$

We know that $Cov(X_1, \hat{X}_1) = Cov(\hat{X}_1 + u, \hat{X}_1)$ $\quad [\because X_1 = \hat{X}_1 + u$ and u is the error$]$

$= V(\hat{X}_1) + Cov(\hat{X}_1, e)$ $\quad (\because Cov(\hat{X}_1, e) = 0$, by assumption$)$

$= V(\hat{X}_1)$

$$\therefore R_{X_1.X_2X_3X_4....X_k} = \frac{Cov(X_1, \hat{X}_1)}{\sqrt{V(X_1)}\sqrt{V(\hat{X}_1)}} = \frac{V(\hat{X}_1)}{\sqrt{V(X_1)}\sqrt{V(\hat{X}_1)}} = \sqrt{\frac{V(\hat{X}_1)}{V(X_1)}}$$

Squaring both the sides, we get $R^2_{X_1.X_2X_3X_4....X_k} = \frac{V(\hat{X}_1)}{V(X_1)}$, which is known as the **coefficient of determination**. From the formula it is clear that it is nothing but the ratio of the explained variance to that of the total variance in the dependent variable of the regression analysis. *Thus, the coefficient of determination is a measure of the proportion of variance of the dependent variable explained by the joint effects of the independent variables,* i.e., by the regression equation framed. In the following section, we shall discuss more about the coefficient of determination.

Example 8.11

Using the following data on observed and expected values from a multiple regression analysis, find out the multiple correlation coefficient:

X_1	1.83	1.56	1.85	1.9	1.7	1.8	1.85	1.73	1.95	1.67	1.82	1.84	1.74	1.68	1.62	1.82	1.91	1.61	1.64	1.85
$\hat{X}_1$	1.78	1.65	1.73	1.79	1.74	1.76	1.73	1.65	1.79	1.78	1.90	1.83	1.67	1.69	1.67	1.85	1.85	1.70	1.75	1.85

$$n \text{ Var}(\hat{X}_1) = \sum (\hat{X}_1 - \overline{\hat{X}}_1)^2 = 0.106036$$

$$n \text{ Var}(X_1) = \sum (X_1 - \overline{X}_1)^2 = 0.249532$$

$$R = \sqrt{\frac{V(\hat{X}_1)}{V(X_1)}} = \sqrt{\frac{0.106036}{0.249532}} = \sqrt{0.4249}$$

$$R^2 = 0.6518$$

8.14 The Coefficient of Determination (R^2)

Suppose we are dealing with k variables, X_1, X_2,....., X_k situation, where X_1 is the dependent variable and others, i.e., X_2, X_3, X_4,....., X_k are independent variables; that means we have framed a regression equation of X_1 on X_2, X_3, X_4,....., X_k. e know that the total variation in X_1

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can be represented as $\frac{1}{n}\sum_{i=1}^{n}(X_{1i}-\overline{X}_1)^2$. Thus, the total sum of squares due to X_1 is given as $\sum_{i=1}^{n}(X_{1i}-\overline{X}_1)^2$:

So,

$$\begin{aligned}TSS &= \sum_{i=1}^{n}(X_{1i}-\overline{X}_1)^2 \\ &= \sum_{i=1}^{n}(X_{1i}-\hat{X}_{1i}+\hat{X}_{1i}-\overline{X}_1)^2 \\ &= \sum_{i=1}^{n}\left((X_{1i}-\hat{X}_{1i})+(\hat{X}_{1i}-\overline{X}_1)\right)^2 \\ &= \sum_{i=1}^{n}(X_{1i}-\hat{X}_{1i})^2+\sum_{i=1}^{n}(\hat{X}_{1i}-\overline{X}_1)^2 \\ &\quad +2\sum(X_{1i}-\hat{X}_{1i})(\hat{X}_{1i}-\overline{X}_1) \\ &= RSS+RgSS+2\sum_{i=1}^{n}u_i(\hat{X}_{1i}-\overline{X}_1)\end{aligned}$$

where $RgSS$ and RSS are sums of squares due to regression and residual, respectively

$$\begin{aligned}&= RSS+RgSS+2\sum_{i=1}^{n}u_i\hat{X}_{1i}-2\overline{X}_1\sum_{i=1}^{n}u_i \\ &= RSS+RgSS+0+0 \text{ (by assumptions)} \\ &= RSS+RgSS\end{aligned}$$

$$\therefore TSS = RgSS+RSS$$

$$\text{or } \frac{TSS}{TSS}=\frac{RgSS}{TSS}+\frac{RSS}{TSS}$$

$$or\ \frac{\sum_{i=1}^{n}(X_{1i}-\overline{X}_1)^2}{\sum_{i=1}^{n}(X_{1i}-\overline{X}_1)^2}=\frac{\sum_{i=1}^{n}(\hat{X}_{1i}-\overline{X}_1)^2}{\sum_{i=1}^{n}(X_{1i}-\overline{X}_1)^2}+\frac{\sum_{i=1}^{n}(X_{1i}-\hat{X}_{1i})^2}{\sum_{i=1}^{n}(X_{1i}-\overline{X}_1)^2}$$

$$or\ 1=\frac{V(\hat{X}_1)}{V(X_1)}+\frac{V(u)}{V(X_1)}$$

$$= R^2+\frac{V(u)}{V(X_1)} \therefore R^2 = 1-\frac{V(u)}{V(X_1)}$$

$$= 1-\frac{RSS}{TSS}$$

The RSS being the sum of squares, it can take only the positive value including zero, i.e., $RSS \geq 0$. Moreover as $TSS = RgSS + RSS$, so RSS can have a maximum value equal to TSS. Thus, $TSS \geq RSS \geq 0$

$\therefore$ When $RSS = 0$, then $R^2 = 1$; again when $RSS = TSS$, then $R^2 = 0$

$\therefore 1 \geq R^2 \geq 0$.

When $R^2 = 1$, then it implies perfect fittings that total variation of the dependent variable has been explained by its linear relationship with the independent variables. Again, when $R^2 = 0$, then it implies no fittings; that means zero percent of the total variation of the dependent variable has been explained by its linear relationship with the independent variables.

8.14.1 Interpretation of R^2

Suppose, after framing a regression equation of X_1 on X_2, X_3, X_4, ..., X_k, we have calculated $R^2 = 0.9$; this means 90 % of the variations in the dependent variable have been explained by its linear relationship with the independent variables, leaving 10 % unexplained.

Note Readers may note that as simple linear regression equation is a special case of multiple linear regression equation, so the properties of R^2 also hold good for simple linear regression equation. Also, in simple linear regression case, the R^2, the coefficient of determination, is equivalent to the square of the correlation coefficient between the variables.

Thus the value of R^2 measures the explaining power of the linear regression equation.

An experimenter is always in search of a relationship which can explain the dependent variable to the greatest possible extent. As such the experimenter tries to include more and more number of variables in the linear regression equation with an aim to get as much R^2 as possible, so that the relationship could explain more and more variation in the dependent variable. Sometimes, with the aim of maximizing R^2, the experimenter includes such variables which might not have significant contribution toward the objective of the study. Thus, the process of maximizing R^2 by

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including more and more number of variables in the regression model is known as "game of maximization of R^2." As we have already pointed out that the number of variables and the variables to be included in the regression equation is not guided by the statistical theory but by the subject on hand and relevance of the variables under given conditions, it does not matter how much is the value of the R^2, in the process!

8.14.2 Adjusted R^2

Scientists were in search of a better measure, which should not be the non-decreasing function of number of variables in the regression equation, like R^2. *Adjusted* R^2 is such a measure developed, which is *not* a non-decreasing function of number of variables in the regression equation, like R^2. Adjusted R^2 is defined as

$$\begin{aligned}\overline{R}^2_{X_1.X_2X_3X_4.....X_k} &= 1 - \frac{RMS}{TMS} \\ &= 1 - \frac{(TSS - RgSS)/(n-k)}{TSS/(n-1)} = 1 - \frac{(n-1)}{(n-k)} + \frac{(n-1)}{(n-k)}\frac{RgSS}{TSS} \\ &= 1 - \frac{(n-1)}{(n-k)}\left(1 - R^2\right)\end{aligned}$$

Thus adjusted R^2 is taking into consideration the associated degrees of freedom.

In any regression model, we have $K \geq 2$ thereby indicating that $\overline{R}^2 < R^2$; that means as the number of independent variables increases, $\overline{R}^2$ increases lesser than R^2.

Again when $R^2 = 1, \overline{R}^2 = 1 - \frac{n-1}{n-k}\left(1 - R^2\right) = 1$.

When $R^2 = 0$, then $\overline{R}^2 = 1 - \frac{n-1}{n-k}(1-0) = \frac{n-k-n+1}{n-k} = \frac{1-k}{n-k}$

Now, $k \geq 2$, so $\overline{R}^2$ is negative.

Thus though $R^2 \geq 0, \overline{R}^2$ *can be less than zero.*

Example 8.12

Using the following information, the regression equation of X_1 on X_2 and X_3 was worked out as $X_1 = 1.203 + 0.032X_2 + 0.013X_3$:

X_1	1.83	1.56	1.85	1.9	1.7	1.8	1.85	1.73	1.95	1.67	1.82	1.84	1.74	1.68	1.62	1.82	1.91	1.61	1.64	1.85
X_2	13	10	12	14	12	13	12	10	14	13	16	14	11	12	11	15	15	12	13	15
X_3	12	10	11	11	12	11	11	10	11	12	14	14	9	8	9	13	13	9	10	13

Using the above information, find out the multiple correlation coefficient, the coefficient of determination, and also the adjusted coefficient of determination**.**

Solution Using the given regression equation and the values of the variable, let us first construct the expected value of the dependent variables corresponding to each and every set of values of the variables. The expected values of the dependent variable are as follows:

Expected X_1 **values**:

1.775	1.653	1.73	1.794	1.743	1.762	1.73	1.653	1.794	1.775	1.897	1.833	1.672	1.691	1.672	1.852	1.852	1.704	1.749	1.852

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Now find out the variances from both the observed and expected values of the dependent variable X_1.

The $Var(X_1) = 0.0125$ and the $\mathrm{Var}(\hat{X}_1) = 0.0005$:

$$\therefore R = \sqrt{\frac{V(\hat{X}_1)}{V(X_1)}} = \sqrt{\frac{0.0005}{0.0125}} = \sqrt{0.4249} = 0.6518$$

$R^2 = 0.4249$ and

$$\overline{R}^2_{X_1.X_2X_3} = 1 - \frac{(n-1)}{(n-k)}(1 - 0.4249) = 1 - \frac{(20-1)}{(20-3)}(0.5751) = 1 - \frac{19}{17}(0.5751) = 0.3572$$

8.15 Partial Correlation

In Chap. 7 we have discussed about the correlation coefficient between two variables, taking two variables at a time. Now the question is, will the correlation coefficient between two variables remain the same under more than two-variable situation? To answer this query, we are to examine the relationships among the variables under the given situation. If the variables are interrelated with each other, definitely the correlation coefficient between the two variables will be subjected by the relationship of other variables with both these variables. Thus, under multiple-variable situation, simple correlation coefficient may not provide the actual picture. A better measure for the degree of linear associationship under such situation would be the *partial correlation coefficient*. *The partial correlation coefficient measures the degree of linear associationship between the two variables after eliminating the effects of the other variables on both these variables*. If we are dealing with a k variable $X_1, X_2, X_3, \ldots\ldots\ldots, X_k$ situation and we want to know the degrees of linear relationship between X_1 and X_2, simple correlation coefficient between X_1 and X_2 may not provide a good picture of the strength of their linear associationship, because both X_1 and X_2 may be individually linearly related with other variables. As such these $X_3, \ldots\ldots\ldots, X_k$ variables may have a certain degree of influence on both of these two variables. So, instead of finding the simple linear relationship between X_1 and X_2, it will be better to have the partial correlation coefficient between these two after eliminating the effects of other variables on both these variables.

Suppose we are considering the correlation coefficient between height and weight of students under the known situation of ages of the students. As we know, both height and weight depends on the age of the students, as such age might have influenced the degree of linear associationship between height and weight. So one should be interested in getting the correlation coefficient between height and weight after eliminating the effect of age on both height and weight.

Suppose there are k number of variables $X_1, X_2, X_3, \ldots\ldots\ldots, X_k$ in the system; we want to find out the partial correlation coefficient between X_1 and X_2. The linear relationship of X_1 and X_2 separately with $X_3, X_4, \ldots\ldots\ldots, X_k$ can be written as $X_1 = b_{13}X_3 + b_{14}X_4 + \ldots\ldots\ldots\ldots + b_{1k}X_k$ and $X_2 = b_{23}X_3 + b_{24}X_4 + \ldots\ldots\ldots\ldots + b_{2k}X_k$.

Thus after eliminating the joint effects of $X_3, X_4, \ldots\ldots\ldots X_k$ variables from both the variables, we have

$$X_1 - (b_{13}X_3 + b_{14}X_4 + \ldots\ldots\ldots\ldots + b_{1k}X_k)$$

$$\text{i.e. } X_1 - \hat{X}_1 = u_{1.3,4,5,\ldots.k} \text{ and}$$

$$X_2 - (b_{23}X_3 + b_{24}X_4 + \ldots\ldots\ldots\ldots + b_{2k}X_k)$$

$$\text{i.e. } X_2 - \hat{X}_2 = u_{2.3,4,5,\ldots.k}$$

Now, according to the definition of the partial correlation coefficient, the partial correlation coefficient between X_1 and X_2 is actually the simple correlation coefficient between $u_{1.3,4,\ldots..,k}$ and $u_{2.3,4,\ldots..,k}$. Thus, the partial correlation coefficient between X_1 and X_2 is given as

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$$r_{12.3,4,\ldots,k} = \frac{Cov(u_{1.3,4,5,\ldots.k}, u_{2.3,4,5,\ldots.k})}{\sqrt{Var(u_{1.3,4,5,\ldots.k})Var(u_{2.3,4,5,\ldots.k})}}$$

Now, from the properties of the regression coefficients, we know that the correlation coefficient is the geometric mean of the two regression coefficients $b_{12.3,4,\ldots\ldots,k}$ and $b_{21.3,4,\ldots\ldots,k}$. Again we know that

$$b_{12.3,4,\ldots\ldots,k} = (-)^{1+2}\frac{S_1\omega_{12}}{S_2\omega_{11}} \text{ and}$$

$$b_{21.3,4,\ldots\ldots,k} = (-)^{2+1}\frac{S_2\omega_{21}}{S_1\omega_{22}}$$

$$\therefore r^2_{12.3,4,\ldots\ldots,k} = b_{12.3,4,\ldots\ldots,k} \times b_{21.3,4,\ldots\ldots,k}$$

$$= \left(-\frac{S_1\omega_{12}}{S_2\omega_{11}}\right)\left(-\frac{S_2\omega_{21}}{S_1\omega_{22}}\right) = \frac{\omega^2_{12}}{\omega_{11}\omega_{22}}$$

$$\therefore r_{12.3,4,\ldots\ldots,k} = \sqrt{\frac{\omega^2_{12}}{\omega_{11}\omega_{22}}}$$

$$= -\frac{\omega_{12}}{\sqrt{\omega_{11}\omega_{22}}} (\text{negative sign is}$$

because of the sign of ω_{12})

Generalizing the above one can write $r_{ij.i'j'} = (-1)^{i+j}\frac{\omega_{ij}}{\sqrt{\omega_{ii}\omega_{jj}}}$.

It may be noted that being a simple correlation coefficient, the partial correlation coefficient also ranges between ± 1.

Depending upon the number of variables for which effects are eliminated during the calculation of partial correlation coefficients, partial correlation coefficients are of first order, i.e., $r_{12.3}$ (the effect of one variable is eliminated from both the variables); second order, i.e., $r_{12.34}$ (the effect of two variables is eliminated from both the variables); third order, i.e., $r_{12.345}$ (the effect of three variables is eliminated from both the variables); and so on.

In this context readers may note that the variables which strongly influence the correlation between other two variables are known as *lurking variable*. It is our common experience that two variables may be highly correlated, but may not be because of the existence of true linear associationship between them but because of the strong influence of other variables on both the variables. Such a variable which influences the degree of associationship between other two variables is known as lurking variable.

Example 8.13

The following table gives the milk yield per lactation (y), age at the first calving (x_1), and weight at the first calving (x_2) for six different types of milch cows. Find out the first-order partial correlation coefficients of the variables, eliminating the effect of other variables from both the variables:

	Milk yield/ lactation	Age at the first calving	Weight at the first calving
Sindhi	1600	43	320
Sahiwal	1900	42	380
Gin	1900	47.3	350
Haryana	1600	46.7	331
Tharparkar	1600	43.8	367
Ongole	1200	36.8	400

Solution Using the above information, let us first construct the following table:

$$Cov(x_1, y) = S_{x_1y} = \frac{\sum x_1 y}{n} = \frac{3416.67}{6} = 569.44$$

$$S^2_{x_1} = \frac{\sum x_1^2}{n} = \frac{71.83}{6} = 11.97$$

$$S^2_{y} = \frac{\sum y^2}{n} = \frac{333333.33}{6} = 55555.56$$

$$\therefore r_{x_1y} = \frac{Cov(X_1, Y)}{S_{x_1}S_y}$$

$$= \frac{569.44}{\sqrt{(11.97 \times 55555.56)}} = 0.698$$

The correlation between milk yield per lactation and age at the first calving is 0.698:

$$Cov(x_2, y) = S_{x_2y} = \frac{\sum x_2 y}{n} = \frac{-12600}{6}$$

$$= -2100$$

$$S^2_{x_2} = \frac{\sum x_2^2}{n} = \frac{4566.00}{6} = 761$$

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	Milk yield/ lactation Y	Age at the first calving X_1	Weight at the first calving X_2	$x_1 = X_1 - \overline{X}_1$	$x_2 = X_2 - \overline{X}_2$	$y = Y - \overline{Y}$	x_1y	x_2y	x_1x_2	${x_1}^2$	${x_2}^2$	y^2
	1600	43	320	−0.27	−38.00	−33.33	−426.67	−60800.00	10.13	0.07	1444.00	1111.11
	1900	42	380	−1.27	22.00	266.67	−2406.67	41800.00	−27.87	1.60	484.00	71111.11
	1900	47.3	350	4.03	−8.00	266.67	7663.33	−15200.00	−32.27	16.27	64.00	71111.11
	1600	46.7	331	3.43	−27.00	−33.33	5493.33	−43200.00	−92.70	11.79	729.00	1111.11
	1600	43.8	367	0.53	9.00	−33.33	853.33	14400.00	4.80	0.28	81.00	1111.11
	1200	36.8	400	−6.47	42.00	−433.33	−7760.00	50400.00	−271.60	41.82	1764.00	187777.78
Sum	9800.00	259.60	2148.00	0.00	0.00	0.00	3416.67	−12600.00	−409.50	71.83	4566.00	333333.33
Avg	1633.33	43.27	358.00									

$$\therefore r_{x_2y} = \frac{Cov(X_2, Y)}{S_{x_2} S_y} = \frac{-2100}{\sqrt{(761 \times 55555.56)}} = -0.330$$

The correlation between milk yield per lactation and weight at the first calving is −0.323:

$$Cov(x_1, x_2) = S_{x_1x_2} = \frac{\sum x_1x_2}{n} = \frac{-409.50}{6} = -68.25$$

$$\therefore r_{x_1x_2} = \frac{Cov(X_1, X_2)}{S_{x_1} S_{x_2}} = \frac{-68.25}{\sqrt{(11.972 \times 761)}} = -0.715$$

The correlation between age and water intake is −0.715.

Partial Correlation

1. The partial correlation between milk yield per lactation (Y) and age at the first calving (X_1) $= r_{yx_1.x_2} = -\frac{\omega_{yx_1}}{\sqrt{\omega_{yy}\omega_{x_1x_1}}} \frac{r_{yx_1} - r_{yx_2}r_{x_1x_2}}{\sqrt{\left(1-r^2_{yx_2}\right)\left(1-r^2_{x_1x_2}\right)}} = \frac{0.698-(-0.323)\times(-0.715)}{\sqrt{\left(1-(-0.323)^2\right)\left(1-(-0.715)^2\right)}} = 0.706$
2. The partial correlation between milk yield per lactation (Y) and weight at the first calving (X_2) $= r_{yx_2.x_1} = (-1)^{1+2}\frac{\omega_{12}}{\sqrt{\omega_{11}\omega_{22}}} = \frac{r_{yx_2} - r_{y1}r_{x_1x_2}}{\sqrt{\left(1-r^2_{yx_2}\right)\left(1-r^2_{x_1x_2}\right)}} = \frac{-0.323-0.698\times(-0.715)}{\sqrt{\left(1-0.698^2\right)\left(1-(-0.715)^2\right)}} = 0.352$
3. The partial correlation between age at the first calving (X_1) and weight at the first calving (X_2) $=$

$$r_{x_1x_2.y} = (-1)^{2+3}\frac{\omega_{x_1x_2}}{\sqrt{\omega_{x_1x_1}\omega_{x_2x_2}}} = \frac{r_{x_1x_2} - r_{x_1y}r_{x_2y}}{\sqrt{\left(1-r^2_{x_1y}\right)\left(1-r^2_{x_2y}\right)}} = \frac{-0.715 - 0.698 \times (-0.323)}{\sqrt{\left(1-0.698^2\right)\left(1-0.323^2\right)}} = -0.723$$

8.16 Some Other Measures of Association

8.16.1 Biserial Correlation

Biserial correlation is defined as the correlation between a continuous and a dichotomous but assumed to represent a continuous normal variable.

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Thus, the ingredient of biserial correlation is the $2 \times m$ contingency table of one qualitative and a quantitative variate. Let $p =$ probability of the qualitative variable taking level 1 and $q = 1 - p =$ probability of the qualitative variable taking level 0. Let $z_p =$ the normal ordinate of the z score associated with p. Then, $r_{bi} = \frac{(pq)(\bar{y}_2 - \bar{y}_1)}{z_p S_y}$, where $\bar{y}_2$ and $\bar{y}_1$ are the mean level 1 and level 0, respectively.

8.16.2 Tetrachoric Correlation

Tetrachoric correlation is a special case of polychoric correlation worked out from an mxn table of frequencies. In both the cases, the assumption is that the ratings are continuous and the underlying distribution is bivariate normal.

8.16.3 Part Correlation

The partial correlation, defined in earlier section, is the correlation coefficient between the two variables after eliminating the effects of other variables from both of the variables. But in many cases, both the variables may not be influenced by the other variables. So the correlation coefficient between the variables is worked out after eliminating the effect of other variables from the variable being influenced by the other variables. Suppose in a set of k variables X_1, X_2, X_3, ..., X_k, the variable X_2 is being influenced by the variables X_3, ..., X_k but not the variable X_1. Let the regression equation of X_2 on $X_3, X_4, \ldots\ldots, X_k$ be

$$X_2 = b_3X_3 + b_4X_4 + \ldots\ldots + B_kX_k$$

So after eliminating the effect of $X_3, X_4 \ldots . X_k$ on X_2, we have $X_2 - b_3X_3 + b_4X_4 + \ldots\ldots + B_kX_k$

$$= X_2 - \hat{X}_2 = u_{2.3,4,5,\ldots,k}\,(say)$$

Now, the correlation between X_1 and $u_{2\cdot 3,4,5,\ldots\ldots k}$ is termed as the part correlation between X_1 and X_2 and is denoted as $r_{1(2.3,4,\ldots\ldots,k)\cdot}$

8.17 Worked-Out Example Using the Usual Method of Calculation and with the Help of the Software Packages

The following table gives the energy per 100 gm of the food and the percentage of moisture, protein, and lipid and carbohydrate content. Find out (a) all possible simple correlation coefficients among the variables, and (b) find out the relationship of energy content with the constituent of food:

Observation	Energy (K cal) Y	Moisture X_1	Protein X_2	Lipid X_3	Carbohydrate X_4
1.	163	73.70	12.90	11.50	0.90
2.	191	70.40	13.30	14.50	0.70
3.	185	70.40	13.90	13.30	1.50
4.	170	72.80	13.50	12.00	0.80
5.	170	72.80	13.80	12.00	0.80
6.	161	73.70	13.10	11.10	1.00
7.	170	72.60	13.10	11.80	1.70
8.	173	70.12	13.20	12.46	0.90
9.	178	71.23	13.60	12.76	0.87
10.	167	73.21	12.97	11.97	0.77
11.	182	70.02	13.76	13.78	1.34
12.	184	69.12	13.77	13.98	1.23
13.	174	70.07	13.34	12.45	0.45
14.	168	73.23	12.98	11.77	0.77
15.	162	74.12	12.77	11.34	0.87
16.	182	69.77	13.77	13.57	1.45
17.	191	68.12	13.98	14.54	1.77
18.	161	74.77	12.87	11.22	0.95
19.	164	74.27	12.99	12.34	0.97
20.	185	71.23	13.87	13.65	1.17

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8.17.1 Calculation of All Possible Correlation Coefficients

(a) *Calculation of correlation coefficients following the usual method of calculation:*

From the given table, we can have the following calculation:

Obs.	Y	X_1	X_2	X_3	X_4	Y^2	X_1^2	X_2^2	X_3^2	X_4^2	X_1Y	X_2Y	X_3Y	X_4Y
1.	163.00	73.70	12.90	11.50	0.90	26569.00	5431.69	166.41	132.25	0.81	12013.10	2102.70	1874.50	146.70
2.	191.00	70.40	13.30	14.50	0.70	36481.00	4956.16	176.89	210.25	0.49	13446.40	2540.30	2769.50	133.70
3.	185.00	70.40	13.90	13.30	1.50	34225.00	4956.16	193.21	176.89	2.25	13024.00	2571.50	2460.50	277.50
4.	170.00	72.80	13.50	12.00	0.80	28900.00	5299.84	182.25	144.00	0.64	12376.00	2295.00	2040.00	136.00
5.	170.00	72.80	13.80	12.00	0.80	28900.00	5299.84	190.44	144.00	0.64	12376.00	2346.00	2040.00	136.00
6.	161.00	73.70	13.10	11.10	1.00	25921.00	5431.69	171.61	123.21	1.00	11865.70	2109.10	1787.10	161.00
7.	170.00	72.60	13.10	11.80	1.70	28900.00	5270.76	171.61	139.24	2.89	12342.00	2227.00	2006.00	289.00
8.	173.00	70.12	13.20	12.46	0.90	29929.00	4916.81	174.24	155.25	0.81	12130.76	2283.60	2155.58	155.70
9.	178.00	71.23	13.60	12.76	0.87	31684.00	5073.71	184.96	162.82	0.76	12678.94	2420.80	2271.28	154.86
10.	167.00	73.21	12.97	11.97	0.77	27889.0.0	5359.70	168.22	143.28	0.59	12226.07	2165.99	1998.99	128.59
11.	182.00	70.02	13.76	13.78	1.34	33124.00	4902.80	189.34	189.89	1.80	12743.64	2504.32	2507.96	243.88
12	184.00	69.12	13.77	13.98	1.23	33856.00	4777.57	189.61	195.44	1.51	12718.08	2533.68	2572.32	226.32
13.	174.00	70.07	13.34	12.45	0.45	30276.00	4909.80	177.96	155.00	0.20	12192.18	2321.16	2166.30	78.30
14.	168.00	73.23	12.98	11.77	0.77	28224.00	5362.63	168.48	138.53	0.59	12302.64	2180.64	1977.36	129.36
15.	162.00	74.12	12.77	11.34	0.87	26244.00	5493.77	163.07	128.60	0.76	12007.44	2068.74	1837.08	140.94
16.	182.00	69.77	13.77	13.57	1.45	33124.00	4867.85	189.61	184.14	2.10	12698.14	2506.14	2469.74	263.90
17.	191.00	68.12	13.98	14.54	1.77	36481.00	4640.33	195.44	211.41	3.13	13010.92	2670.18	2777.14	338.07
18.	161.00	74.77	12.87	11.22	0.95	25921.00	5590.55	165.64	125.89	0.90	12037.97	2072.07	1806.42	152.95
19.	164.00	74.27	12.99	12.34	0.97	26896.00	5516.03	168.74	152.28	0.94	12180.28	2130.36	2023.76	159.08
20.	185.00	71.23	13.87	13.65	1.17	34225.00	5073.71	192.38	186.32	1.37	13177.55	2565.95	2525.25	216.45
Total	3481.000	1435.680	267.470	252.030	20.910	607769.00	103131.44	3580.11	3198.69	24.19	249547.81	46615.23	44066.78	3668.30
Mean	174.050	71.784	13.374	12.602	1.046									

$$\overline{Y} = \frac{1}{20}\sum_{i=1}^{20} Y_i = \frac{1}{20} \times 3481.000 = 174.050$$

$$\overline{X}_1 = \frac{1}{20}\sum_{i=1}^{20} X_{1i} = \frac{1}{20} \times 1435.680 = 71.784$$

$$\overline{X}_2 = \frac{1}{20}\sum_{i=1}^{20} X_{2i} = \frac{1}{20} \times 267.470 = 13.374$$

$$\overline{X}_3 = \frac{1}{20}\sum_{i=1}^{20} X_{3i} = \frac{1}{20} \times 252.030 = 12.602$$

$$\overline{X}_4 = \frac{1}{20}\sum_{i=1}^{20} X_{4i} = \frac{1}{20} \times 20.910 = 1.046$$

$$s_Y^2 = \frac{1}{n}\sum_{i=1}^{n} \left(Y_i - \overline{Y}\right)^2 = \frac{1}{n}\sum_{i=1}^{n} Y_i^2 - \overline{Y}^2$$

$$= \frac{1}{20} \times 607769.00 - 174.050^2 = 95.048$$

$$s_{X_1}^2 = \frac{1}{n}\sum_{i=1}^{n} \left(X_{1i} - \overline{X}_1\right)^2 = \frac{1}{n}\sum_{i=1}^{n} X_{1i}^2 - \overline{X}_1^2$$

$$= \frac{1}{20} \times 103131.44 - 71.784^2 = 3.630$$

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$$s_{X_2}^2 = \frac{1}{n}\sum_{i=1}^{n}\left(X_{2i} - \overline{X}_2\right)^2 = \frac{1}{n}\sum_{i=1}^{n}X_{2i}^2 - \overline{X}_2{}^2$$
$$= \frac{1}{20} \times 3580.11 - 13.374^2 = 0.155$$

$$s_{X_3}^2 = \frac{1}{n}\sum_{i=1}^{n}\left(X_{3i} - \overline{X}_3\right)^2 = \frac{1}{n}\sum_{i=1}^{n}X_{3i}^2 - \overline{X}_3{}^2$$
$$= \frac{1}{20} \times 3198.69 - 12.602^2 = 1.137$$

$$s_{X_4}^2 = \frac{1}{n}\sum_{i=1}^{n}\left(X_{4i} - \overline{X}_4\right)^2 = \frac{1}{n}\sum_{i=1}^{n}X_{4i}^2 - \overline{X}_4{}^2$$
$$= \frac{1}{20} \times 24.19 - 1.046^2 = 0.116$$

$$\mathrm{Cov}(X,Y) = \frac{1}{n}\sum_{i=1}^{n}\left(X_i - \overline{X}\right)\left(Y_i - \overline{Y}\right)$$

$$\mathrm{Cov}(X_1,Y) = \frac{1}{n}\sum_{i=1}^{n}\left(X_{1i} - \overline{X}\right)\left(Y_i - \overline{Y}\right)$$
$$= \frac{1}{20}\sum_{i=1}^{n}X_{1i}Y_i - \overline{X}_1\overline{Y}$$
$$= \frac{1}{20} \times 249547.81 - 71.784 \times 174.050 = -16.615$$

$$\mathrm{Cov}(X_2,Y) = \frac{1}{n}\sum_{i=1}^{n}\left(X_{2i} - \overline{X}\right)\left(Y_i - \overline{Y}\right)$$
$$= \frac{1}{20}\sum_{i=1}^{n}X_{2i}Y_i - \overline{X}_2\overline{Y}$$
$$= \frac{1}{20} \times 46615.23 - 13.374 \times 174.050 = 3.104$$

$$\mathrm{Cov}(X_3,Y) = \frac{1}{n}\sum_{i=1}^{n}\left(X_{3i} - \overline{X}\right)\left(Y_i - \overline{Y}\right)$$
$$= \frac{1}{20}\sum_{i=1}^{n}X_{3i}Y_i - \overline{X}_3\overline{Y}$$
$$= \frac{1}{20} \times 44066.78 - 12.602 \times 174.050 = 10.048$$

$$\mathrm{Cov}(X_4,Y) = \frac{1}{n}\sum_{i=1}^{n}\left(X_{4i} - \overline{X}\right)\left(Y_i - \overline{Y}\right)$$
$$= \frac{1}{20}\sum_{i=1}^{n}X_{4i}Y_i - \overline{X}_4\overline{Y}$$
$$= \frac{1}{20} \times 3668.30 - 1.046 \times 174.050 = 1.446$$

Now, we know that

$$r_{XY} = \frac{Cov(X,Y)}{\sqrt{S_X S_Y}}$$

$$\therefore r_{X_1Y} = \frac{Cov(X_1,Y)}{\sqrt{s_{X_1} \times s_Y}} = \frac{-16.615}{\sqrt{3.630 \times 95.048}} = -0.895$$
$$r_{X_2Y} = \frac{Cov(X_2,Y)}{\sqrt{s_{X_2} \times s_Y}} = \frac{3.104}{\sqrt{0.155 \times 95.048}} = 0.809$$
$$r_{X_3Y} = \frac{Cov(X_3,Y)}{\sqrt{s_{X_3} \times s_Y}} = \frac{10.048}{\sqrt{1.137 \times 95.048}} = 0.967$$
$$r_{X_4Y} = \frac{Cov(X_4,Y)}{\sqrt{s_{X_4} \times s_Y}} = \frac{1.446}{\sqrt{0.116 \times 95.048}} = 0.435$$

(b) *Calculation of correlation coefficients using MS Excel:*

Step 1: Showing the entered or transferred data and selection of *Correlation Analysis* menu from the Data Analysis tool pack in MS Excel workbook.

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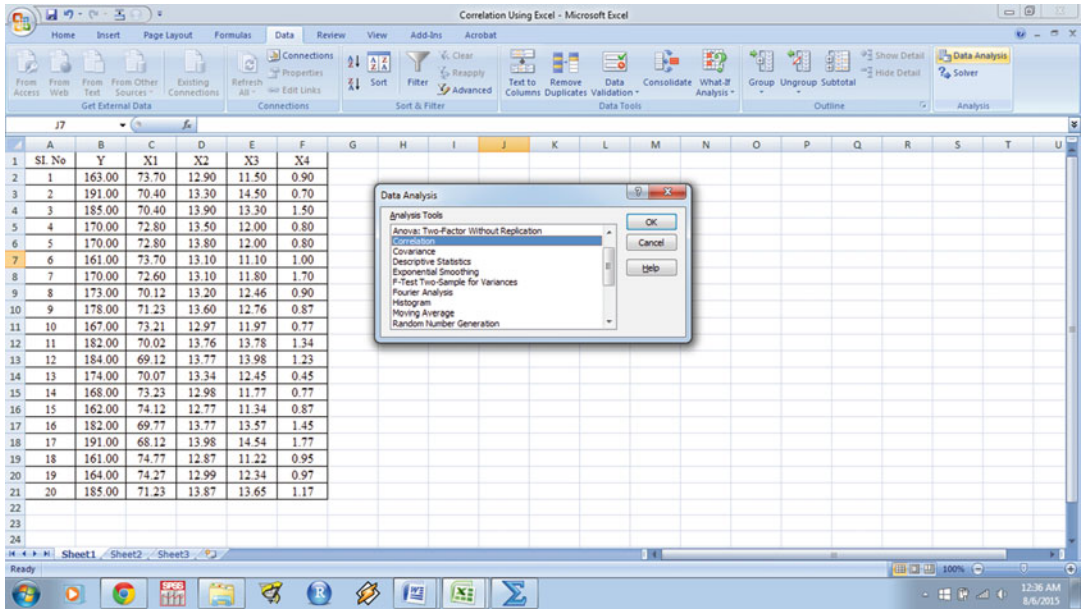
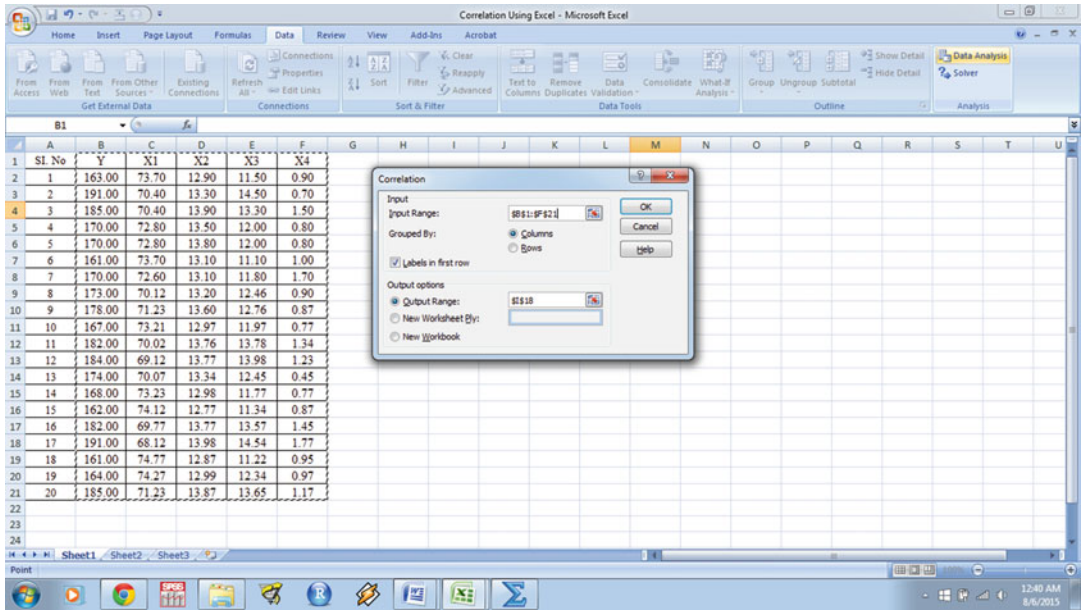


Step 2: Showing the entered or transferred data and selection of data range and other required commands in *Correlation Analysis* menu in MS Excel.



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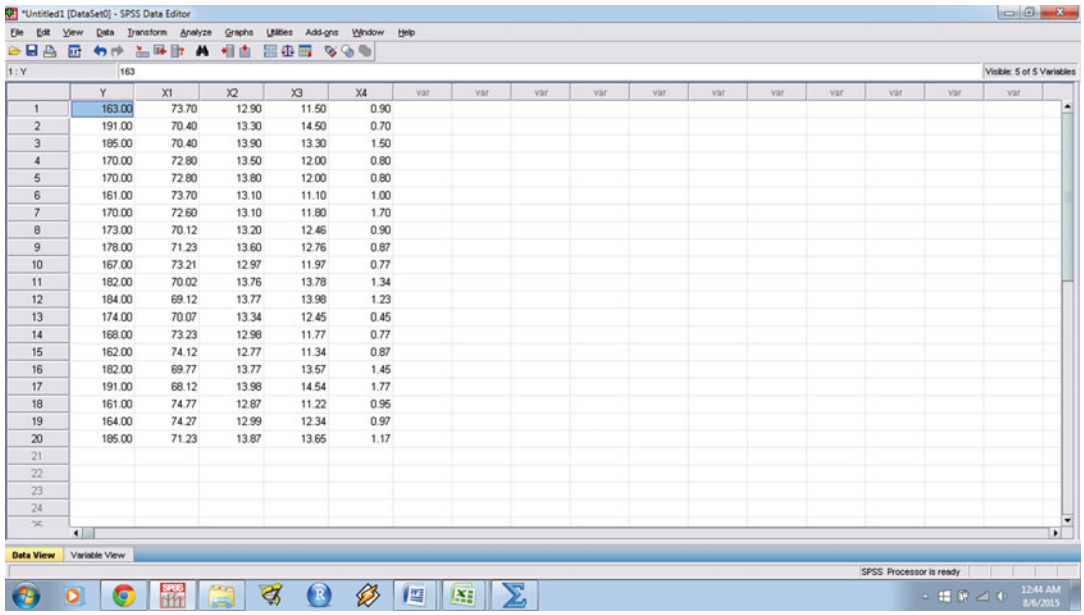
Step 3: Showing the output from Correlation Analysis menu in MS Excel:

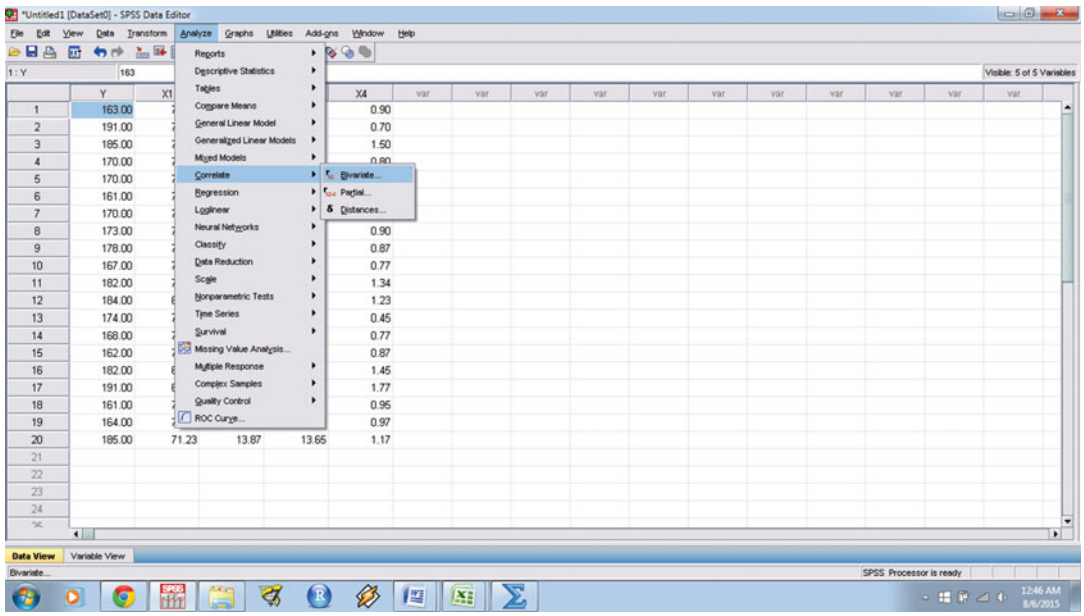
	Y	X_1	X_2	X_3	X_4
Y	1.000				
X_1	−0.895	1.000			
X_2	0.809	−0.770	1.000		
X_3	0.967	−0.868	0.755	1.000	
X_4	0.435	−0.411	0.480	0.419	1.000

(c) *Calculation of correlation coefficients using SPSS:*

Step 1: Using the usual procedure of import, transfer the data to SPSS from Excel, or copy and paste the data into the SPSS data editor. Data imported for correlation analysis through SPSS will be as below.



Step 2: Go to Analysis → Correlate → Click on Bivariate as shown below.



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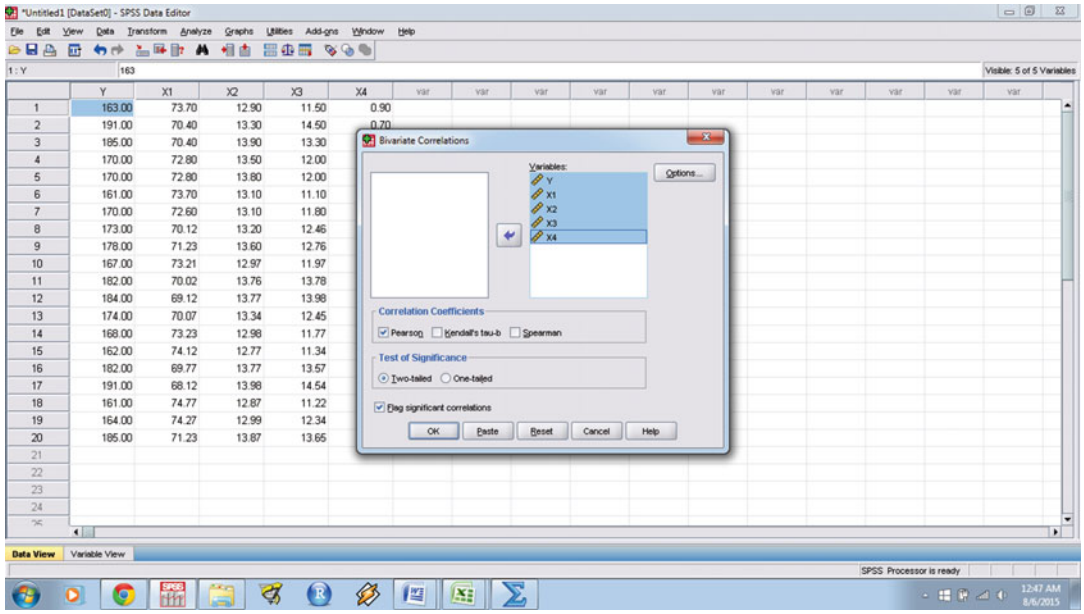
Step 3: Select the required variables, and move these to the right-hand panel as shown below and then click on OK.



Step 4: SPSS output will be displayed as given below:

Correlations

		Y	X_1	X_2	X_3	X_4
Y	Pearson correlation	1	−.895[a]	.809[a]	.967[a]	.435
	Sig. (two tailed)		.000	.000	.000	.055
	N	20	20	20	20	20
X_1	Pearson correlation	−.895[a]	1	−.770[a]	−.868[a]	−.411
	Sig. (two tailed)	.000		.000	.000	.072
	N	20	20	20	20	20
X_2	Pearson correlation	.809[a]	−.770[a]	1	.755[a]	.480[b]
	Sig. (two tailed)	.000	.000		.000	.032
	N	20	20	20	20	20
X_3	Pearson correlation	.967[a]	−.868[a]	.755[a]	1	.419
	Sig. (two tailed)	.000	.000	.000		.066
	N	20	20	20	20	20
X_4	Pearson correlation	.435	−.411	.480[b]	.419	1
	Sig. (two tailed)	.055	.072	.032	.066	
	N	20	20	20	20	20

[a]The correlation is significant at the 0.01 level (two tailed)
[b]The correlation is significant at the 0.05 level (two tailed)

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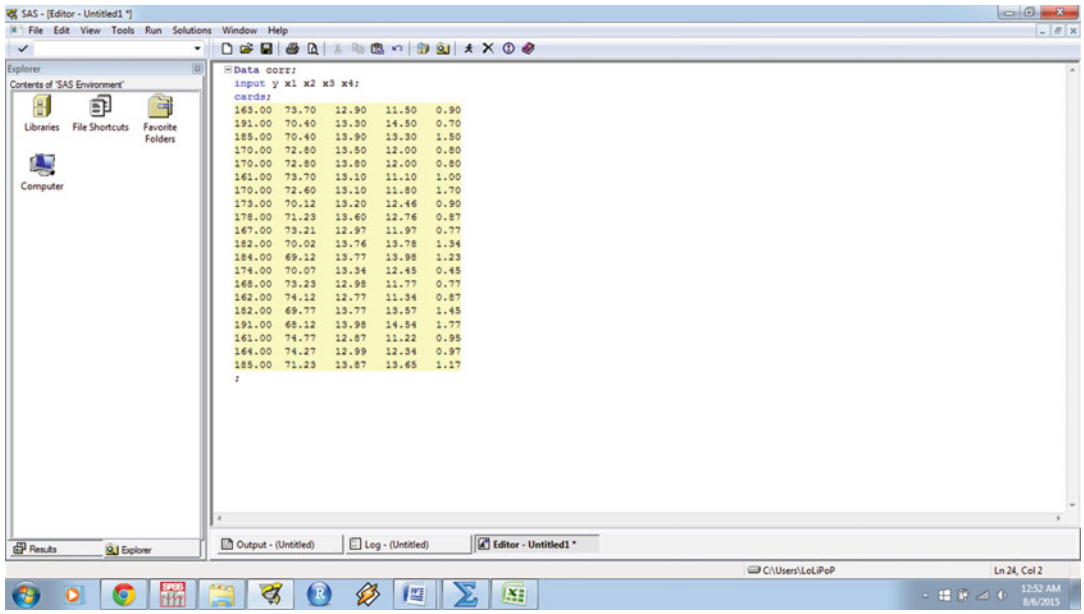
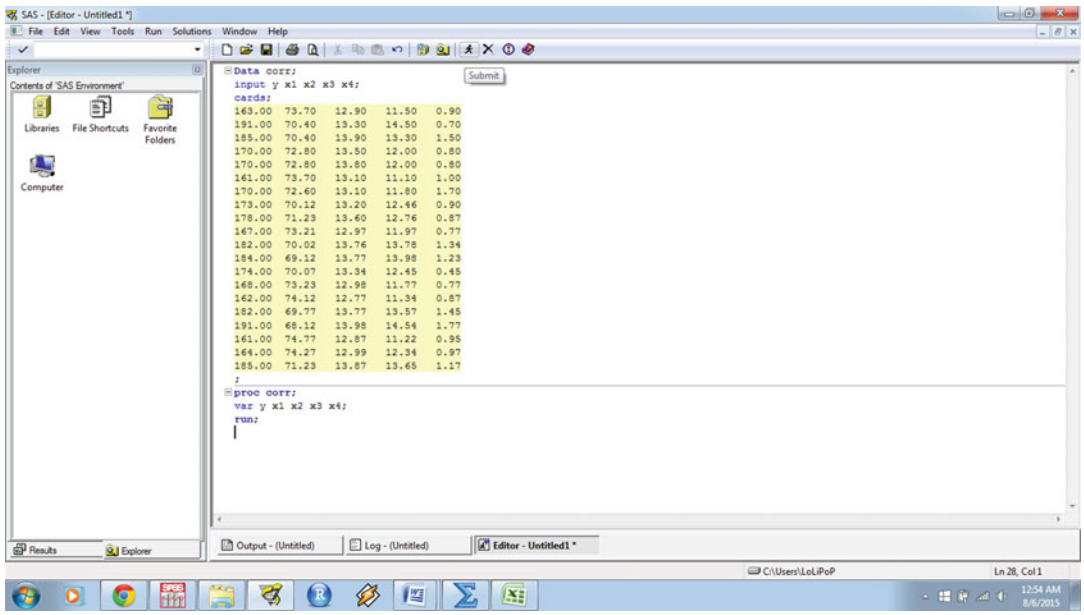
(d) *Calculation of correlation coefficients using SAS:*

Using the SAS, the same analysis can be done as follows:

Step 1: Showing the data input for correlation analysis using the SAS.



Step 2: Showing the data and the command to perform the correlation analysis using SAS.



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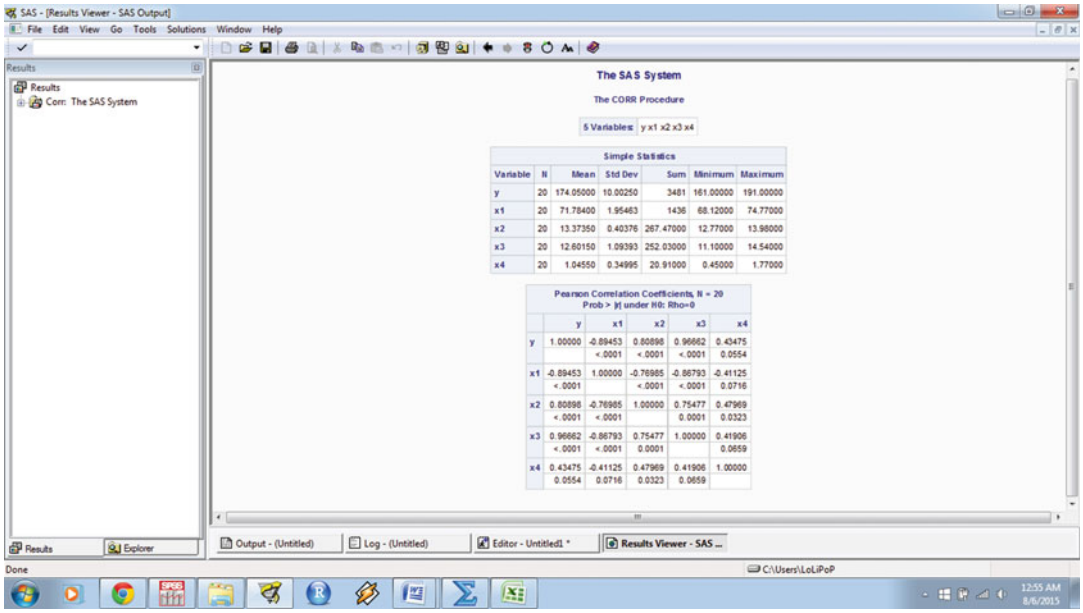
Step 3: Click on the submit button to have the output as below.



Readers may note the differences among the outputs from different software. Additional outputs like the mean, SD of the variables, and probability level at which the correlation coefficients are significant are given in the output through SPSS and SAS, but these were not available either through manual calculation or through MS Excel.

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8.17.2 Calculation of Partial Correlation Coefficients

Observation	Energy (K cal)	Moisture	Protein	Lipid
	Y	X_1	X_2	X_3
1.	163	73.70	12.90	11.50
2.	191	70.40	13.30	14.50
3.	185	70.40	13.90	13.30
4.	170	72.80	13.50	12.00
5.	170	72.80	13.80	12.00
6.	161	73.70	13.10	11.10
7.	170	72.60	13.10	11.80
8.	173	70.12	13.20	12.46
9.	178	71.23	13.60	12.76
10.	167	73.21	12.97	11.97
11.	182	70.02	13.76	13.78
12.	184	69.12	13.77	13.98
13.	174	70.07	13.34	12.45
14.	168	73.23	12.98	11.77
15.	162	74.12	12.77	11.34
16.	182	69.77	13.77	13.57
17.	191	68.12	13.98	14.54
18.	161	74.77	12.87	11.22
19.	164	74.27	12.99	12.34
20.	185	71.23	13.87	13.65

To calculate the partial correlation, first we need to calculate the correlation coefficient between all the given variables using the usual procedure.

For the above example, the correlation matrix will be as given below:

	Y	X_1	X_2	X_3
Y	1			
X_1	−0.895	1		
X_2	0.809	−0.770	1	
X_3	0.967	−0.868	0.755	1

(a) *Calculation of partial correlation coefficients following the usual method of calculation:*

The partial correlation between energy (Y) and moisture (X_1) by eliminating the effects of all the other variables (X_2 and X_3) from both the variables X_1 and Y can be calculated using the formula

$$r_{YX_1.X_2X_3} = \frac{r_{YX_1.X_3} - r_{YX_2.X_3} r_{X_1X_2.X_3}}{\sqrt{\left(1 - r^2_{YX_2.X_3}\right)\left(1 - r^2_{X_1X_2.X_3}\right)}}$$

So, we need to calculate the first-order partial correlation between Y and X_1 by eliminating the effect of X_3 and Y and X_2 and X_1 and X_2 by eliminating the effect of X_3 in both the cases, which can be calculated by using the formula as below:

$$r_{YX_1.X_3} = \frac{r_{YX_1} - r_{YX_3} r_{X_1X_3}}{\sqrt{\left(1 - r^2_{YX_3}\right)\left(1 - r^2_{X_1X_3}\right)}} = \frac{-0.0556}{\sqrt{0.01600}} = -0.439$$

$$r_{YX_2.X_3} = \frac{r_{YX_2} - r_{YX_3} r_{X_2X_3}}{\sqrt{\left(1 - r^2_{YX_3}\right)\left(1 - r^2_{X_2X_3}\right)}} = \frac{0.0789}{\sqrt{0.0160}} = 0.472$$

$$r_{X_1X_2.X_3} = \frac{r_{X_1X_2} - r_{X_1X_3} r_{X_2X_3}}{\sqrt{\left(1 - r^2_{X_1X_3}\right)\left(1 - r^2_{X_2X_3}\right)}} = \frac{-0.1146}{\sqrt{0.3256}} = -0.352$$

$$\therefore r_{YX_1.X_2X_3} = \frac{r_{YX_1.X_3} - r_{YX_2.X_3} r_{X_1X_2.X_3}}{\sqrt{\left(1 - r^2_{YX_2.X_3}\right)\left(1 - r^2_{X_1X_2.X_3}\right)}} = \frac{-0.2734}{0.8249} = -0.331$$

In similar way we can calculate the partial correlation for the following combinations:

$$r_{YX_2.X_1X_3} = \frac{r_{YX_2.X_3} - r_{YX_1.X_3} r_{X_1X_2.X_3}}{\sqrt{\left(1 - r^2_{YX_1.X_3}\right)\left(1 - r^2_{X_1X_2.X_3}\right)}} = 0.378$$

$$r_{YX_3.X_1X_2} = \frac{r_{YX_3.X_2} - r_{YX_1.X_2} r_{X_1X_3.X_2}}{\sqrt{\left(1 - r^2_{YX_1.X_2}\right)\left(1 - r^2_{X_1X_3.X_2}\right)}} = 0.850$$

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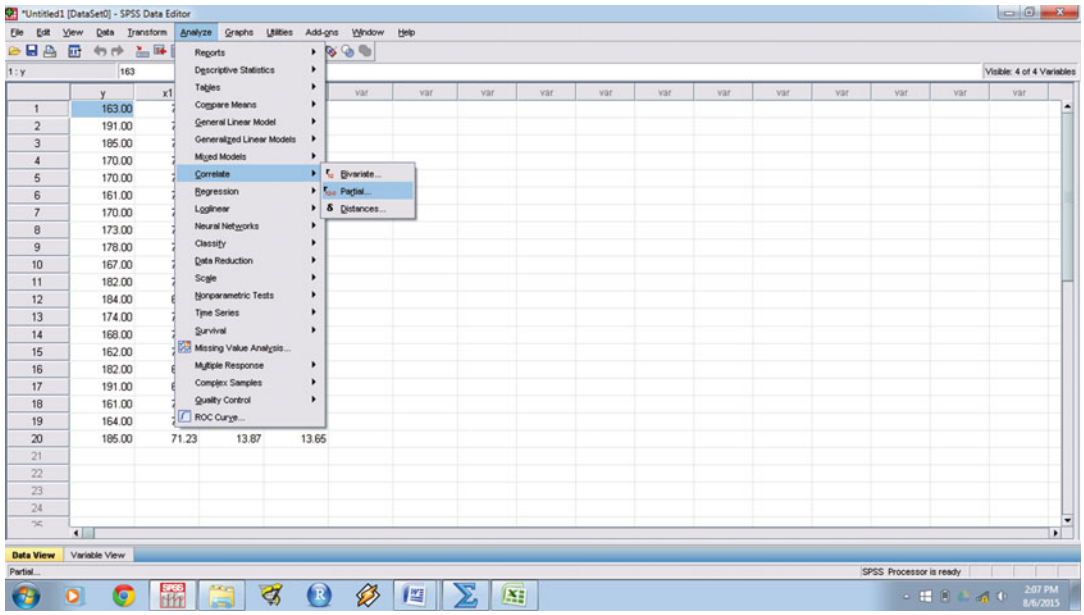
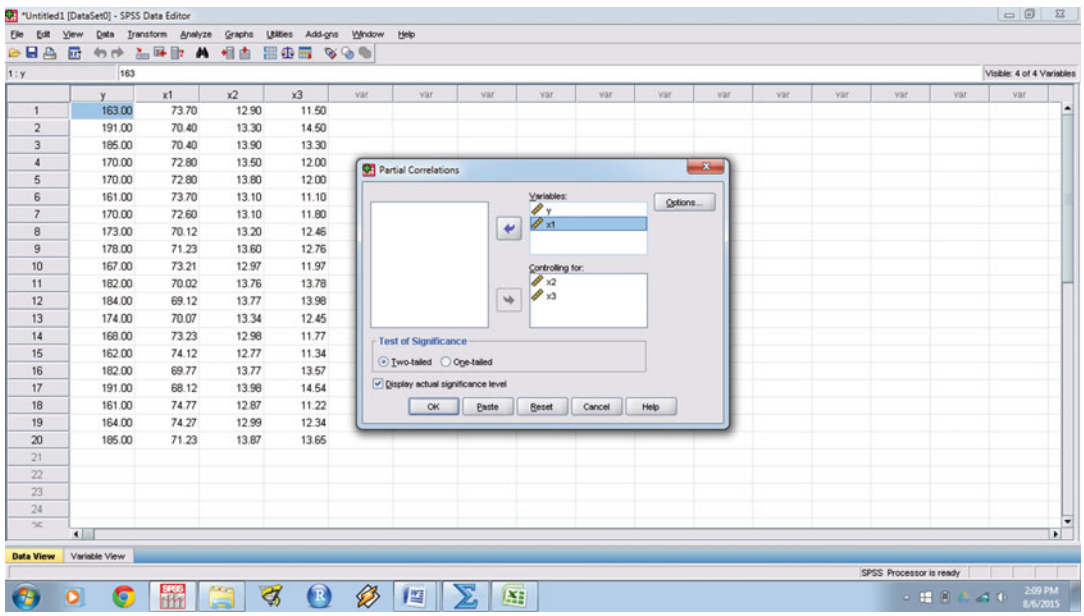
(b) *Calculation of partial correlation coefficients using the SPSS:*

For the problem given above, calculate the partial correlation coefficient between Y and X_1 by eliminating the effect of X_2 and X_3 using SPSS**:**

Step 1: After importing the data to the SPSS editor, go to Analysis, followed by Correlate and then to Partial, as shown below.



Step 2: Select the variables for which the partial correlation is to be calculated and the variables for which effects are to be eliminated as shown below.



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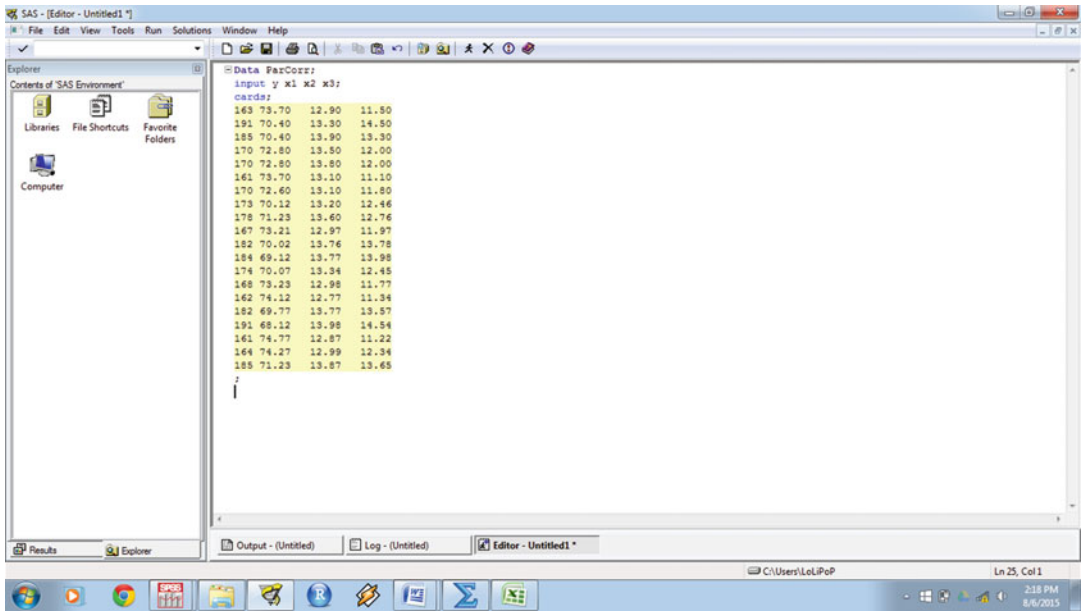
Step 3: Click on OK to get the following output:

Correlations				
Control variables			y	x_1
x_2 and x_3	y	Correlation	1.000	−.328
		Significance (two tailed)	.	.184
		d.f.	0	16
	x_1	Correlation	−.328	1.000
		Significance (two tailed)	.184	.
		d.f.	16	0

In similar way, by changing the variables as in step 2, one can have different combinations of partial correlation coefficients among the variables.

(c) *Calculation of partial correlation coefficients using SAS:*

Step 1: Showing the data input for partial correlation analysis using the SAS.



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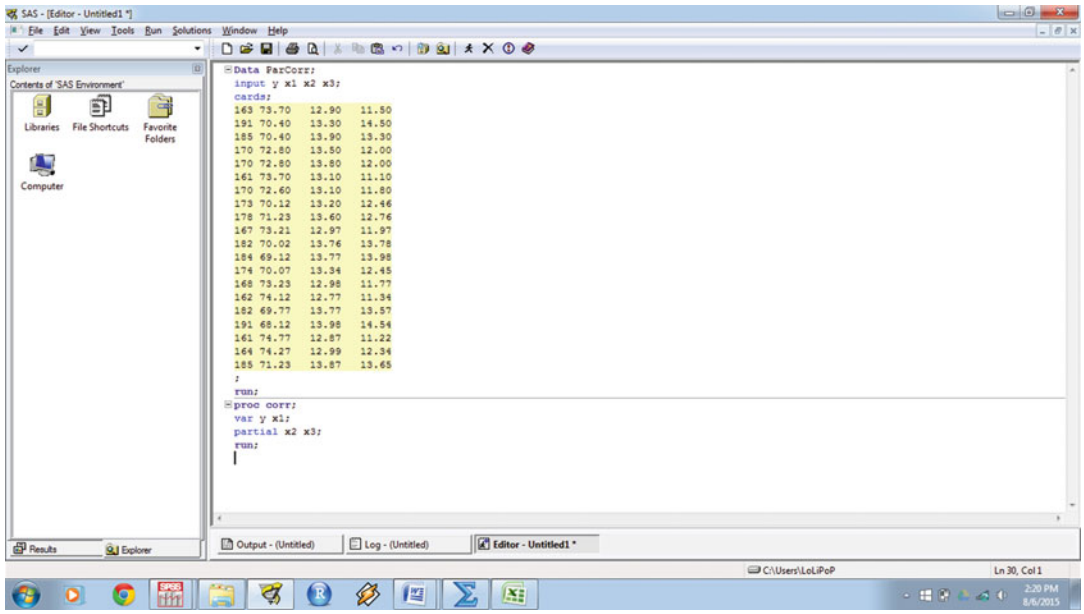
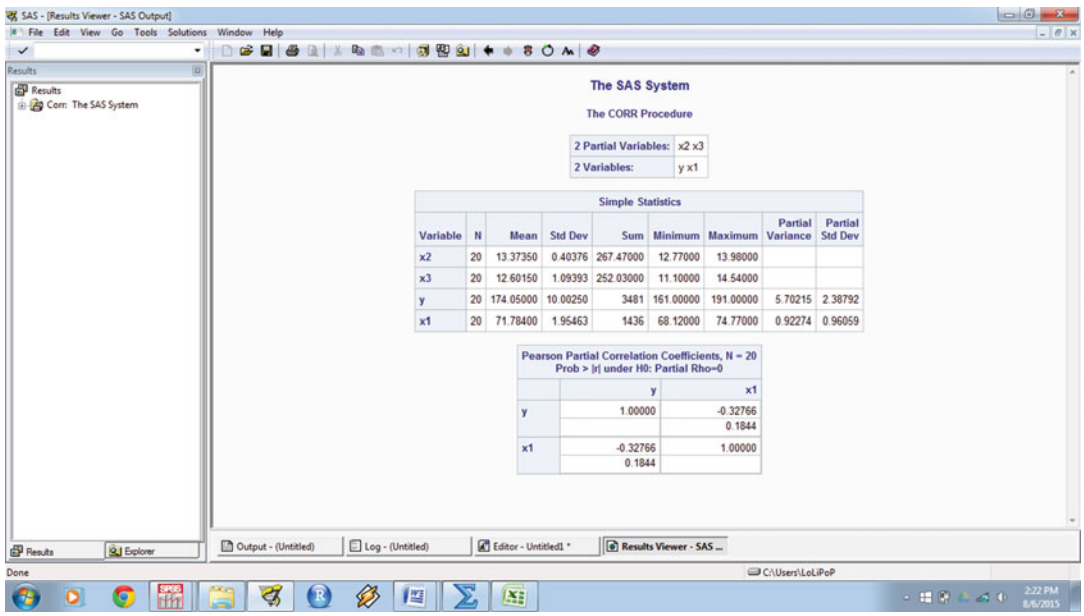
Step 2: Showing the data and the command to perform the partial correlation analysis using SAS.



Step 3: Click on the submit button to have the output as below.



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In similar way we can perform the partial correlation analysis for other combinations of variables by changing the variable name in code.

8.17.3 Estimation of Simple Linear Regression

For the following data, find the regression equation for Y on X_1:

Observation	Energy (K cal)	Moisture
	Y	X_1
1.	163	73.70
2.	191	70.40
3.	185	70.40
4.	170	72.80
5.	170	72.80
6.	161	73.70
7.	170	72.60
8.	173	70.12
9.	178	71.23
10.	167	73.21
11.	182	70.02
12.	184	69.12
13.	174	70.07
14.	168	73.23
15.	162	74.12
16.	182	69.77
17.	191	68.12
18.	161	74.77
19.	164	74.27
20.	185	71.23

Solution

(a) *Estimation of simple linear regression equation following the usual method of calculation:*

We have no. of observations "n" = 20, and the mean, variances, and covariance can be calculated as elaborated in the previous section:

$\overline{Y} = 174.050$; $\overline{X}_1 = 71.784$; $S_Y^2 = 95.048$; $s_{X_1}^2 = 3.630$; $\mathrm{Cov}(X_1, Y) = -16.615$, and $r_{X_1Y} = -0.895$

Now the regression equation of Y on X_1 is given by

$$(Y-\overline{Y}) = b_{yx}(X_1-\overline{X}_1)$$

$$\Rightarrow (Y-174.050) = \frac{Cov(X_1,Y)}{S_{x_1}^2}(X_1-71.784)$$

$$= \frac{-16.615}{3.630}(X_1-71.784) = -4.577(X_1-71.784)$$

$$= -4.577X_1+328.555$$

$$\Rightarrow Y = 174.050-4.577X_1+328.555$$

$$\Rightarrow Y = 502.605-4.577X_1$$

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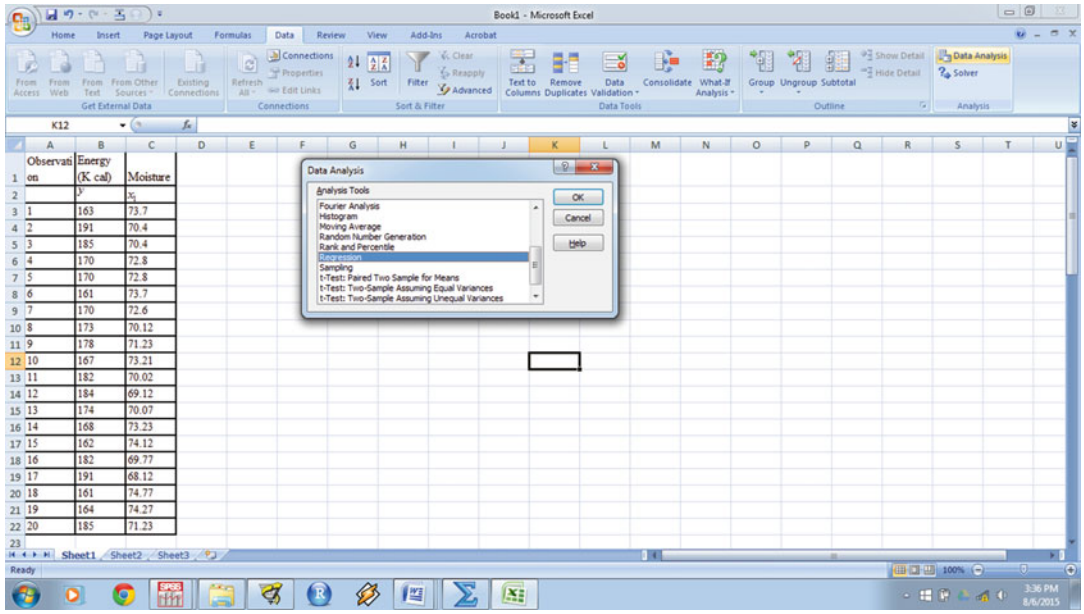
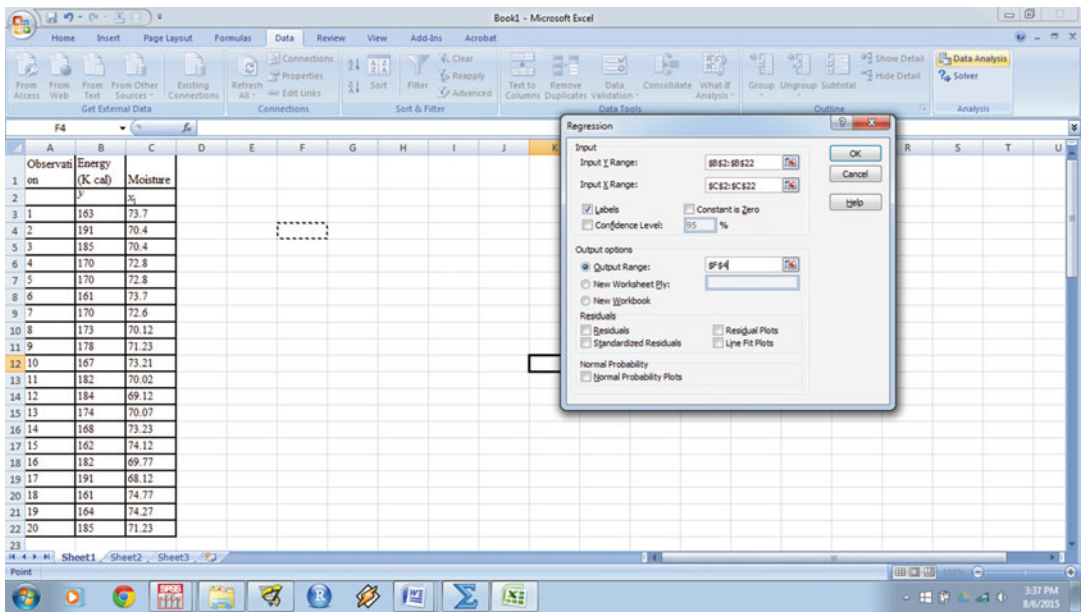
(b) *Estimation of simple linear regression equation using MS Excel:*

Step 1: Showing the data entry and the selection of the Regression Analysis menu using MS Excel.



Step 2: Showing the data and the selection of data range and other submenus in regression analysis using MS Excel.



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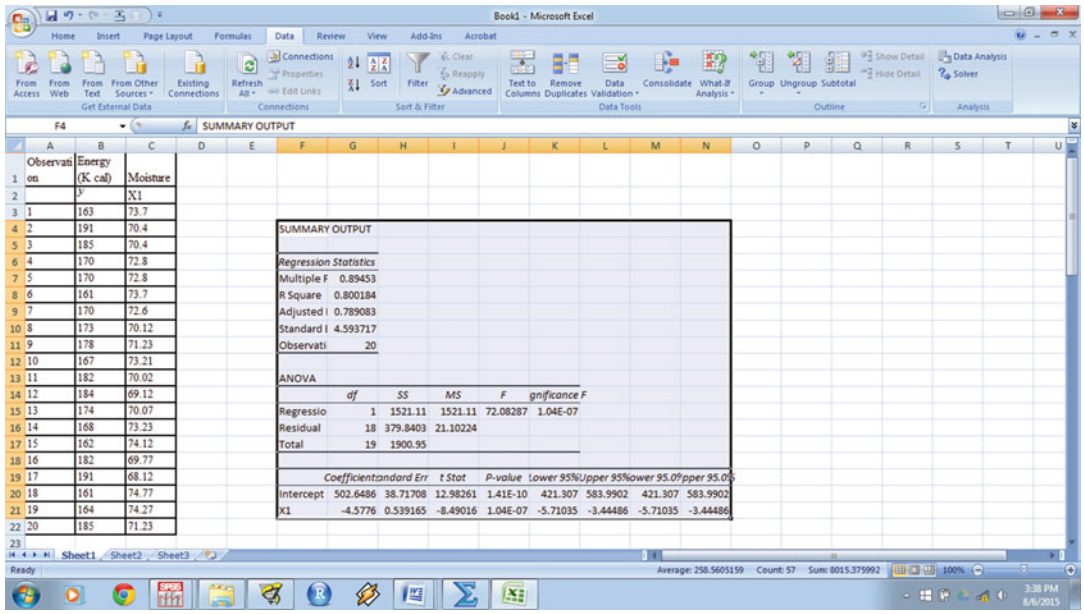
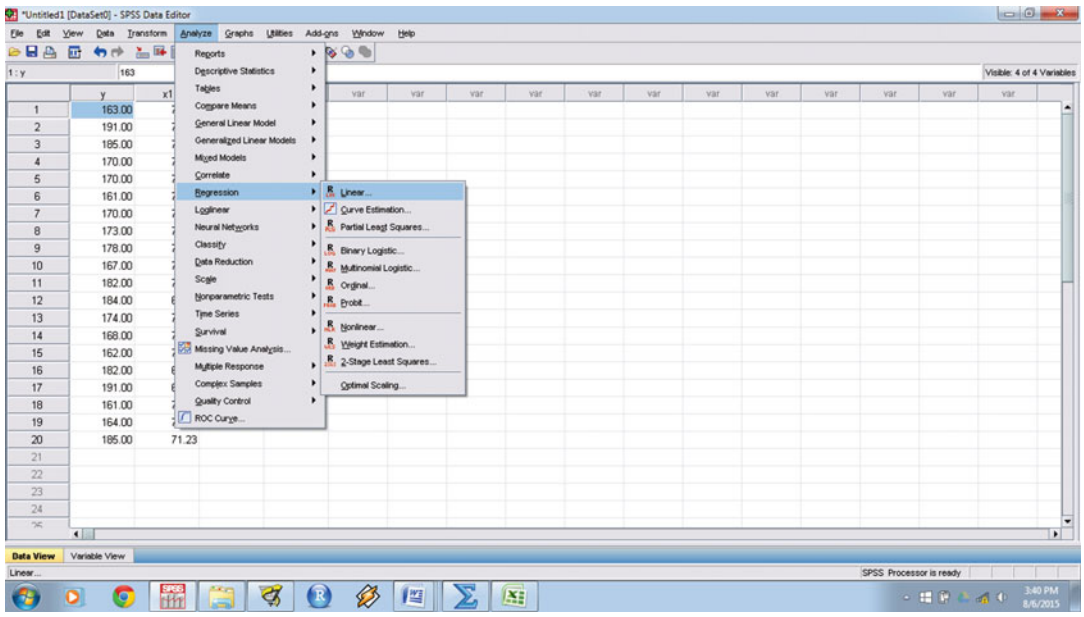
Step 3: Showing the output generated for regression analysis using MS Excel.



(c) *Estimation of simple linear regression equation using SPSS:*

Step 1: After importing the data to the SPSS editor, go to Analysis menu, followed by Regression and then to Linear, as shown below.



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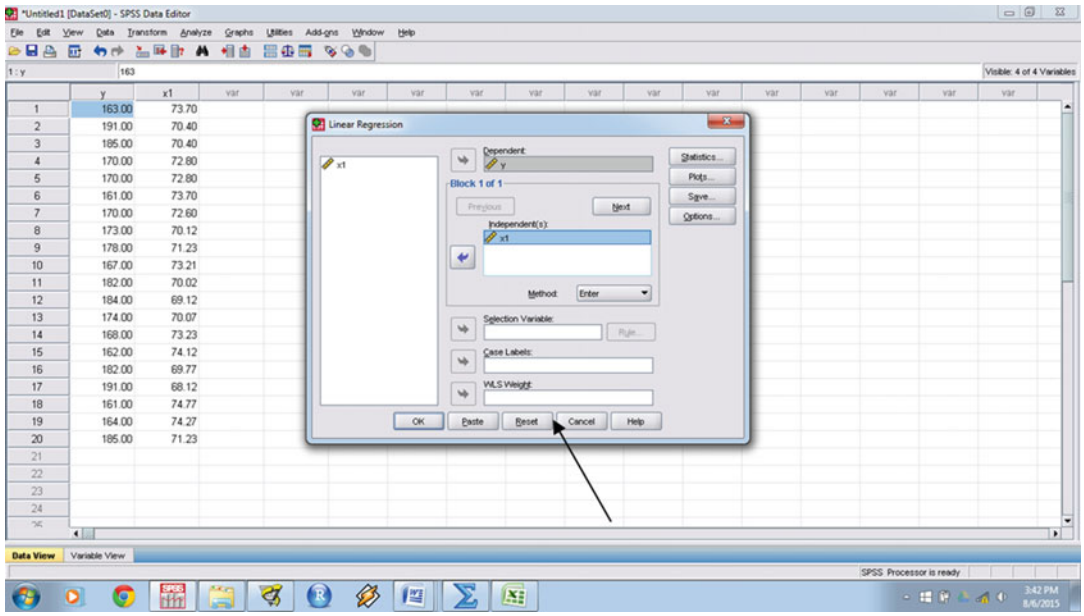
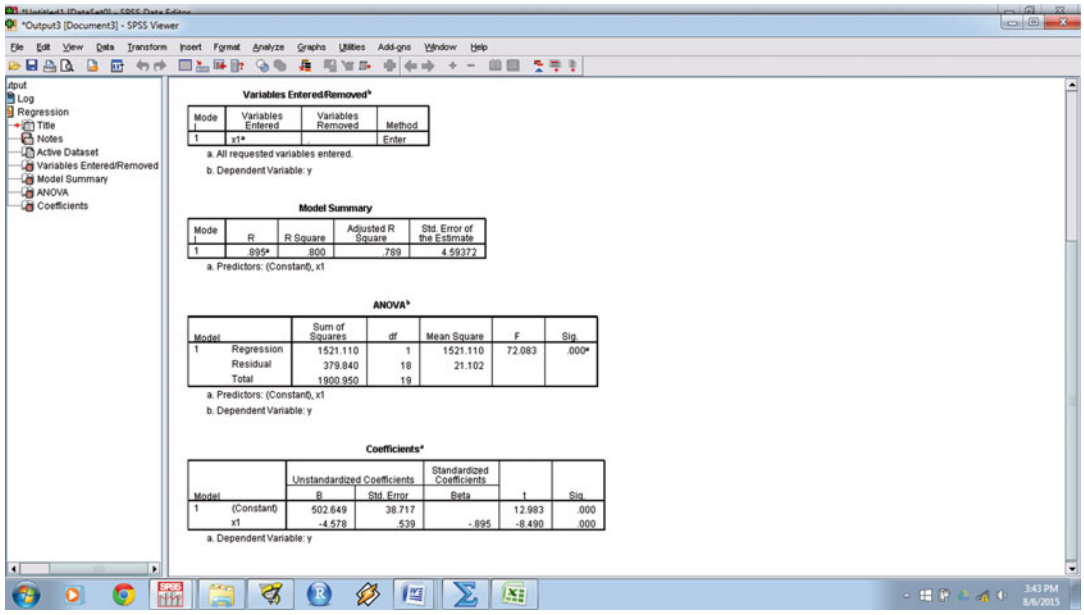
Step 2: Select the dependent and independent variables for which regression analysis is to be performed as shown below.



Step 3: Click on OK in Liner Regression menu to get the output as below.



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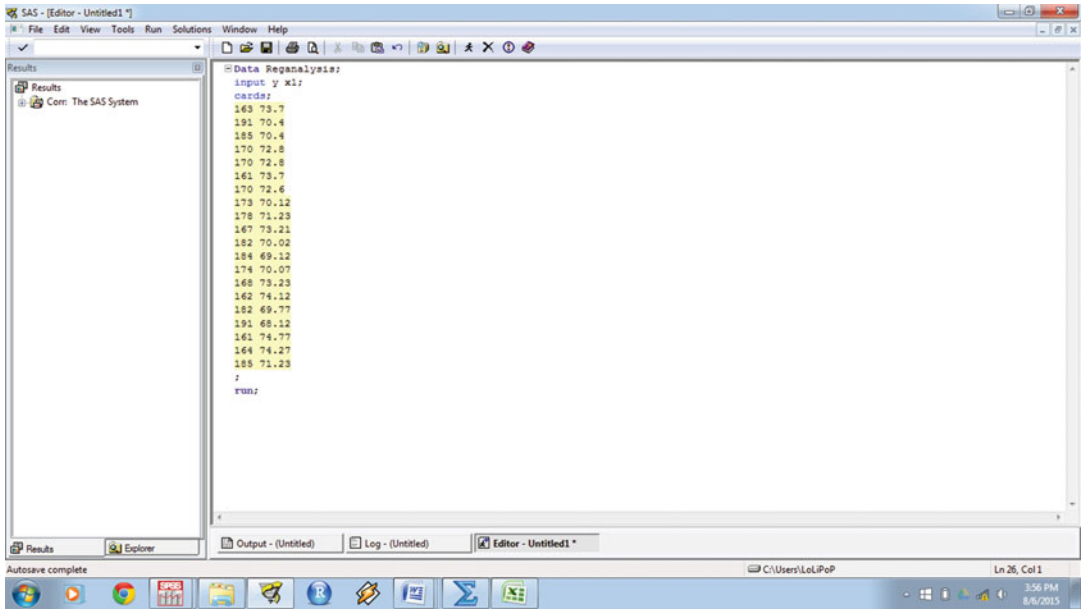
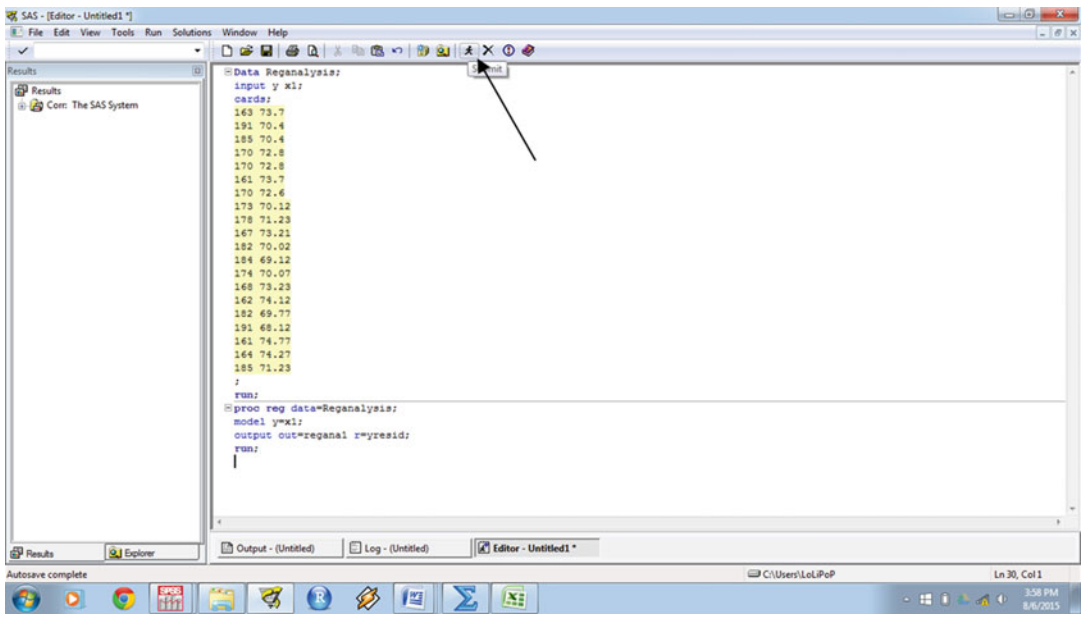
(d) *Estimation of simple linear regression equation using SAS:*

Step 1: Showing the data input to perform the regression analysis using the SAS.



Step 2: Showing the data and the command to perform the regression analysis using SAS.



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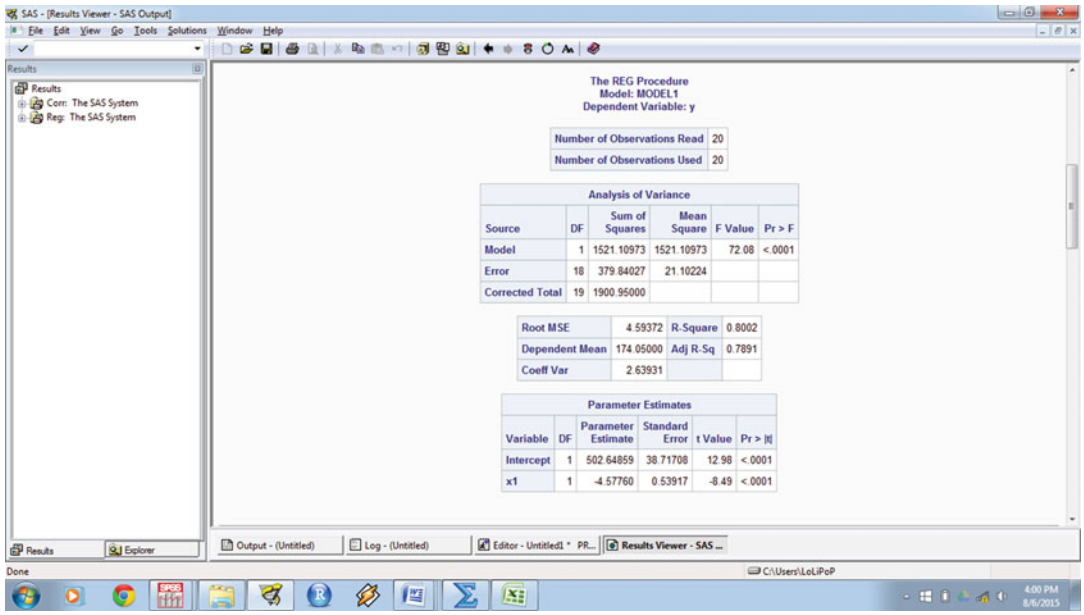
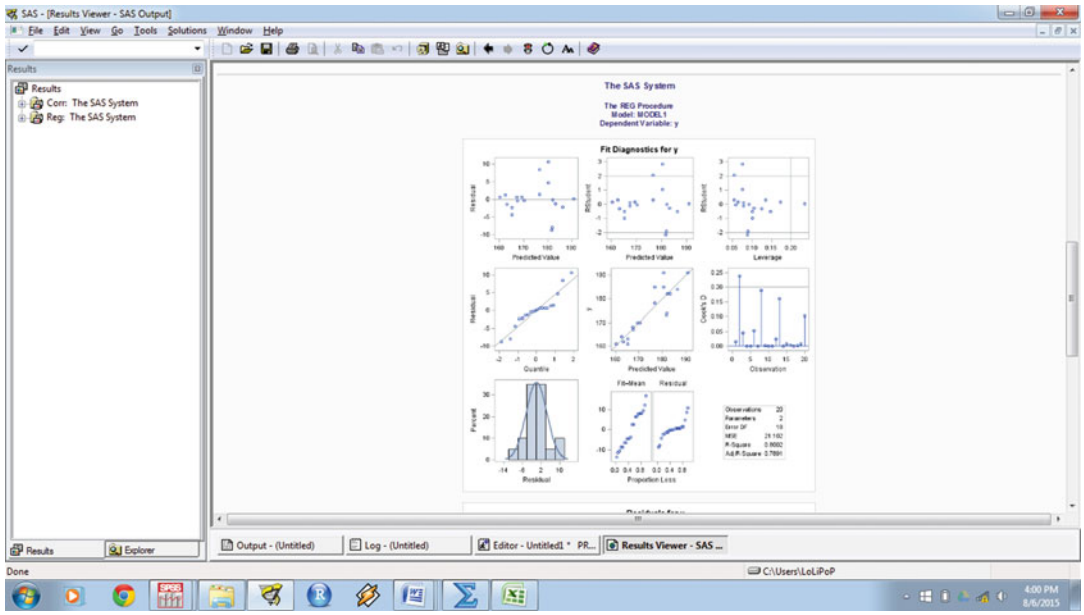
Step 3: Click on the submit button to have the output as below.





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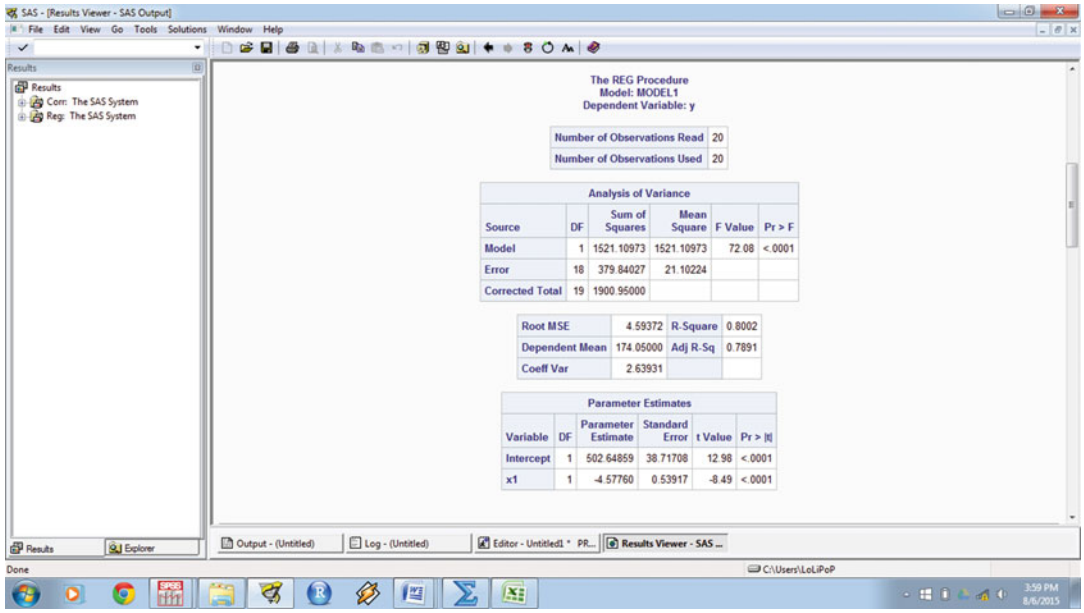


SAS - [Results Viewer - SAS Output]

File Edit View Go Tools Solutions Window Help

Results

Results
Corr: The SAS System
Reg: The SAS System

The REG Procedure
Model: MODEL1
Dependent Variable: y

Number of Observations Read	20
Number of Observations Used	20

Analysis of Variance

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	1	1521.10973	1521.10973	72.08	<.0001
Error	18	379.84027	21.10224		
Corrected Total	19	1900.95000			

Root MSE	4.59372	R-Square	0.8002
Dependent Mean	174.05000	Adj R-Sq	0.7891
Coeff Var	2.63931		

Parameter Estimates

Variable	DF	Parameter Estimate	Standard Error	t Value	Pr > |t|
Intercept	1	502.64859	38.71708	12.98	<.0001
x1	1	-4.57760	0.53917	-8.49	<.0001

Results Explorer

Output - (Untitled) Log - (Untitled) Editor - Untitled1 * PR... Results Viewer - SAS ...

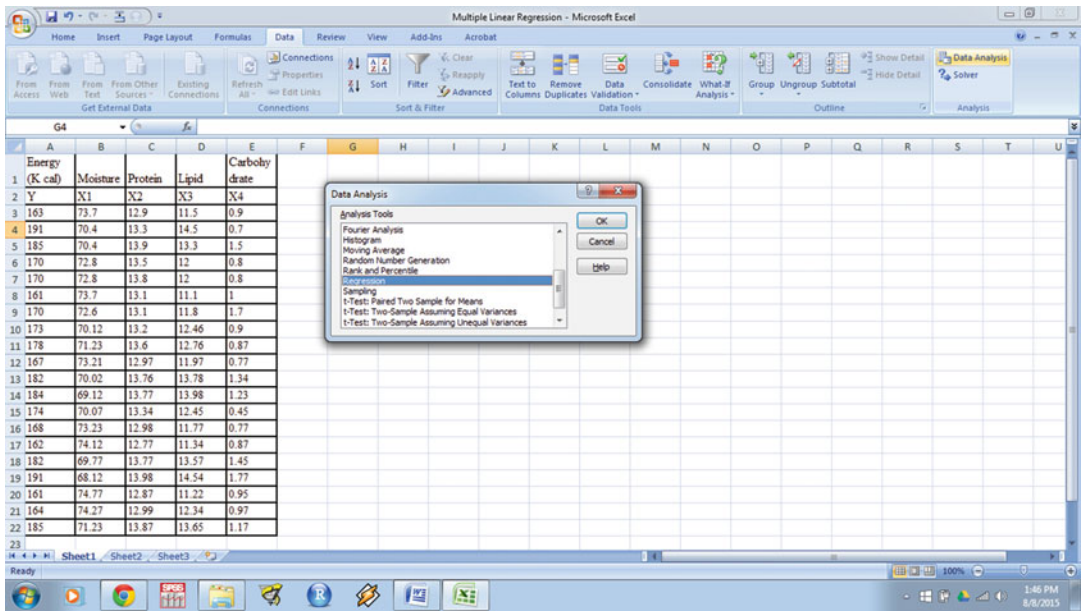
Done C:\Users\LoLiPoP

3:59 PM 8/6/2015

8.17.4 Estimation of Multiple Linear Regression Equation

(a) *Estimation of multiple linear regression equation using MS Excel*

Step 1: Showing the data structure and selection of Regression submenu from the Data Analysis toolbar in MS Excel.



Multiple Linear Regression - Microsoft Excel

Home Insert Page Layout Formulas Data Review View Add-Ins Acrobat

Get External Data Connections Sort & Filter Data Tools Outline Analysis

G4

	A	B	C	D	E
1	Energy (K cal)	Moisture	Protein	Lipid	Carbohydrate
2	Y	X1	X2	X3	X4
3	163	73.7	12.9	11.5	0.9
4	191	70.4	13.3	14.5	0.7
5	185	70.4	13.9	13.3	1.5
6	170	72.8	13.5	12	0.8
7	170	72.8	13.8	12	0.8
8	161	73.7	13.1	11.1	1
9	170	72.6	13.1	11.8	1.7
10	173	70.12	13.2	12.46	0.9
11	178	71.23	13.6	12.76	0.87
12	167	73.21	12.97	11.97	0.77
13	182	70.02	13.76	13.78	1.34
14	184	69.12	13.77	13.98	1.23
15	174	70.07	13.34	12.45	0.45
16	168	73.23	12.98	11.77	0.77
17	162	74.12	12.77	11.34	0.87
18	182	69.77	13.77	13.57	1.45
19	191	68.12	13.98	14.54	1.77
20	161	74.77	12.87	11.22	0.95
21	164	74.27	12.99	12.34	0.97
22	185	71.23	13.87	13.65	1.17
23					

Data Analysis

Analysis Tools
Fourier Analysis
Histogram
Moving Average
Random Number Generation
Rank and Percentile
Regression
Sampling
t-Test: Paired Two Sample for Means
t-Test: Two-Sample Assuming Equal Variances
t-Test: Two-Sample Assuming Unequal Variances

OK Cancel Help

Sheet1 Sheet2 Sheet3

Ready 100%

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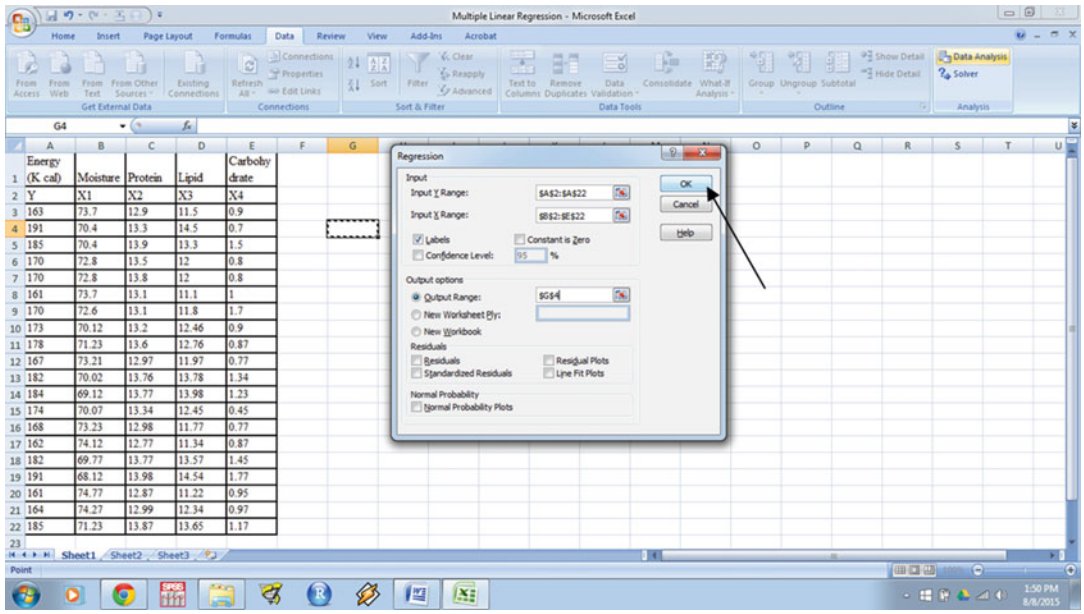
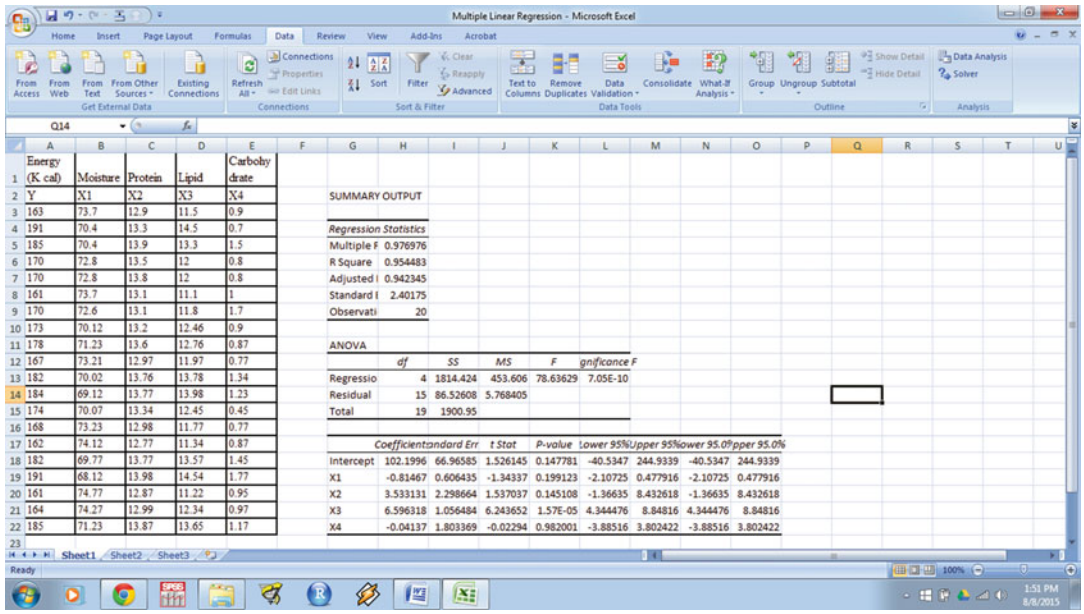
Step 2: Showing the data structure and selection of data range and other options in Regression submenu from the Data Analysis toolbar of MS Excel.



Step 3: Click on the OK button in Regression submenu to get the output as below.



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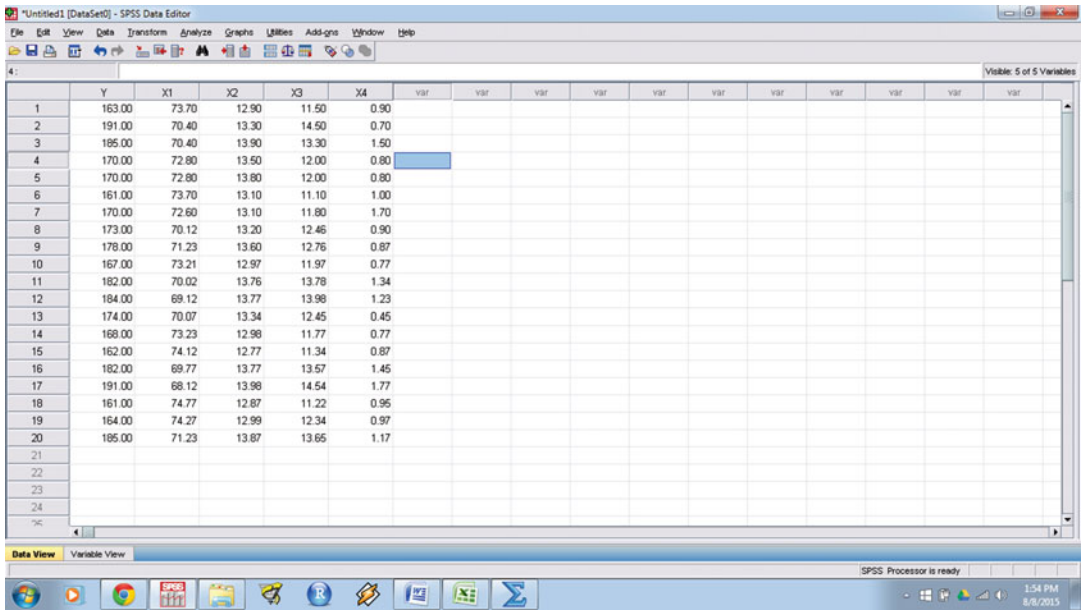
Thus, the above regression equation is found to be

$$y = 102.199 - 0.814x_1 + 3.533x_2 + 6.596x_3 - 0.041x_4$$

(b) *Estimation of multiple linear regression equation using SPSS:*

Step 1: Showing the data structure to perform the regression analysis in data editor menu of SPSS.



	Y	X1	X2	X3	X4
1	163.00	73.70	12.90	11.50	0.90
2	191.00	70.40	13.30	14.50	0.70
3	185.00	70.40	13.90	13.30	1.50
4	170.00	72.80	13.50	12.00	0.80
5	170.00	72.80	13.80	12.00	0.80
6	161.00	73.70	13.10	11.10	1.00
7	170.00	72.60	13.10	11.80	1.70
8	173.00	70.12	13.20	12.46	0.90
9	178.00	71.23	13.60	12.76	0.87
10	167.00	73.21	12.97	11.97	0.77
11	182.00	70.02	13.76	13.78	1.34
12	184.00	69.12	13.77	13.98	1.23
13	174.00	70.07	13.34	12.45	0.45
14	168.00	73.23	12.98	11.77	0.77
15	162.00	74.12	12.77	11.34	0.87
16	182.00	69.77	13.77	13.57	1.45
17	191.00	68.12	13.98	14.54	1.77
18	161.00	74.77	12.87	11.22	0.95
19	164.00	74.27	12.99	12.34	0.97
20	185.00	71.23	13.87	13.65	1.17
21					
22					
23					
24					

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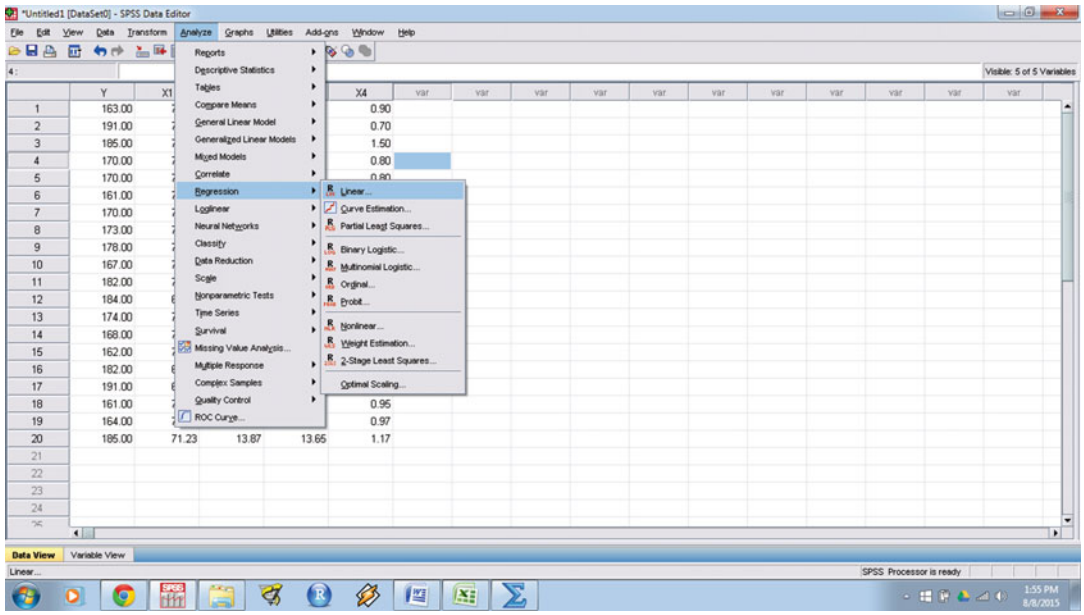
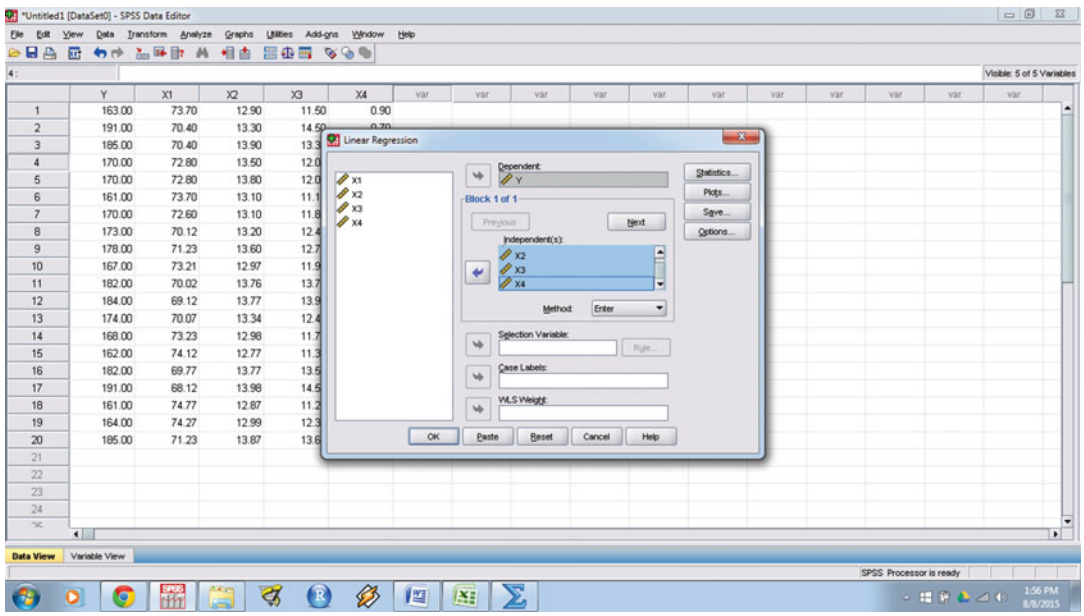
Step 2: Showing the data structure and selection of appropriate options in analysis menu of SPSS.



Step 3: Showing the data structure and variable selection of regression analysis using SPSS.



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Step 4: Click on OK button; out of regression analysis will be displayed in the output window of SPSS:

Variables entered/removed[b]

Model	Variables entered	Variables removed	Method
1	X_4, X_1, X_2, X_3[a]		Enter

[a]All requested variables entered
[b]Dependent variable: Y

Model summary

Model	R	R square	Adjusted R square	Std. error of the estimate
1	.977[a]	.954	.942	2.40175

[a]Predictors: (constant) X_4, X_1, X_2, X_3

ANOVA[b]

Model		Sum of squares	d.f.	Mean square	F	Sig.
1	Regression	1814.424	4	453.606	78.636	.000[a]
	Residual	86.526	15	5.768		
	Total	1900.950	19			

[a]Predictors: (constant) X_4, X_1, X_2, X_3
[b]Dependent variable: Y

Coefficients[a]

Model		Unstandardized coefficients		Standardized coefficients		
		B	Std. error	Beta	t	Sig.
1.	(Constant)	102.200	66.966		1.526	.148
	X_1	−.815	.606	−.159	−1.343	.199
	X_2	3.533	2.299	.143	1.537	.145
	X_3	6.596	1.056	.721	6.244	.000
	X_4	−.041	1.803	−.001	−.023	.982

[a]Dependent variable: Y

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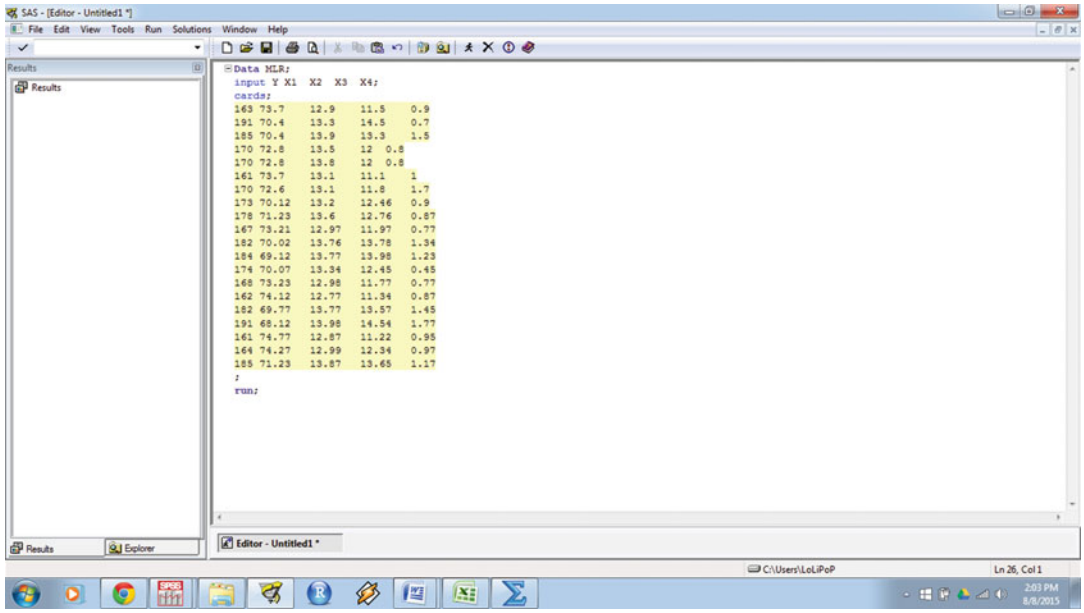
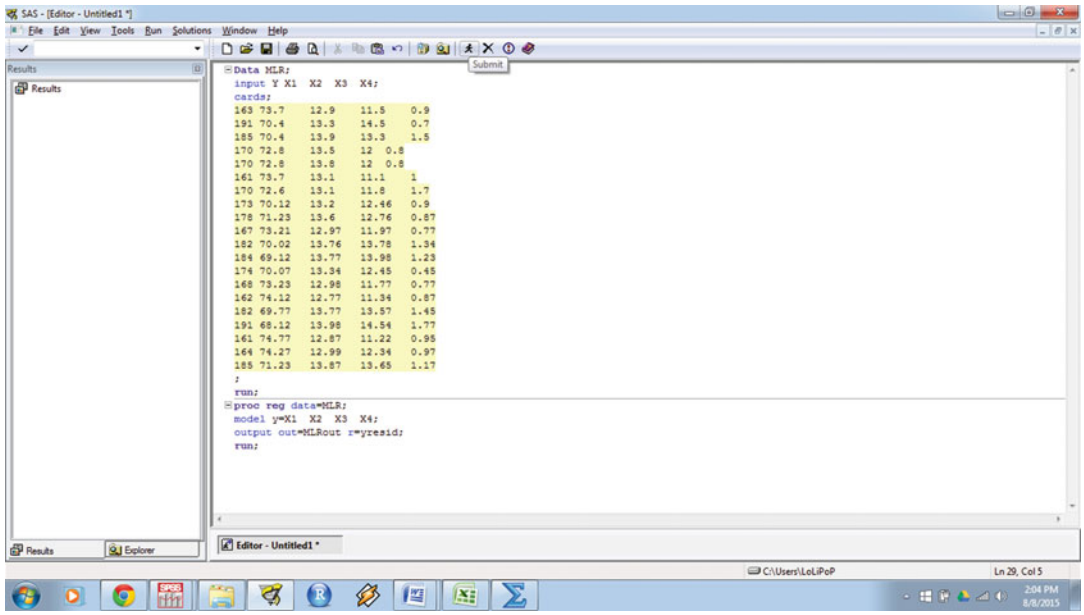
(c) *Estimation of multiple linear regression equation using SAS:*

Step 1: Showing the data input to perform multiple regression analysis using the SAS.



Step 2: Showing the data and the command to perform the regression analysis using SAS.



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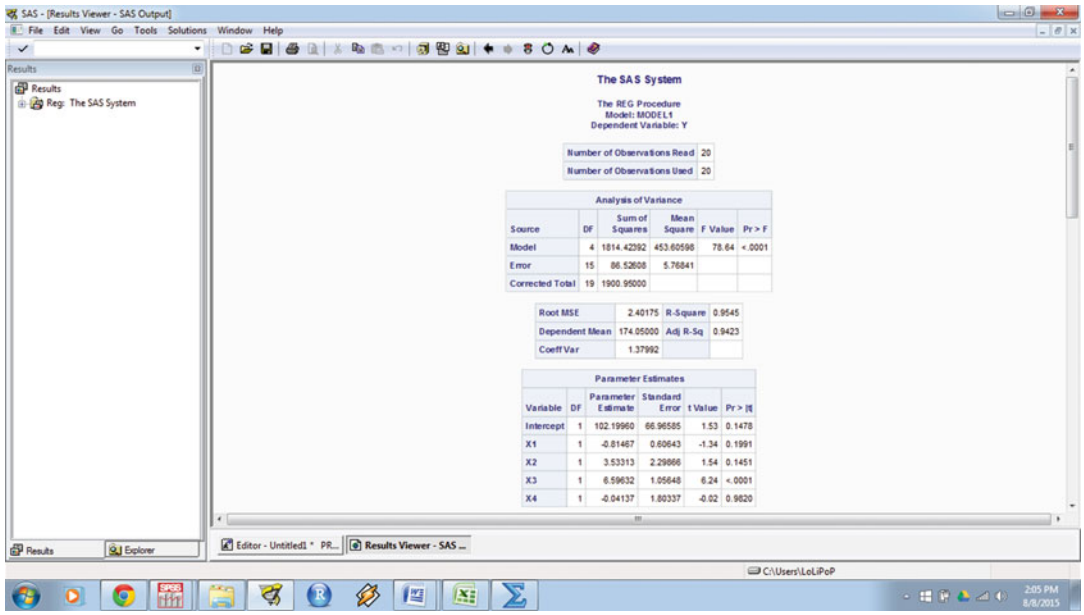
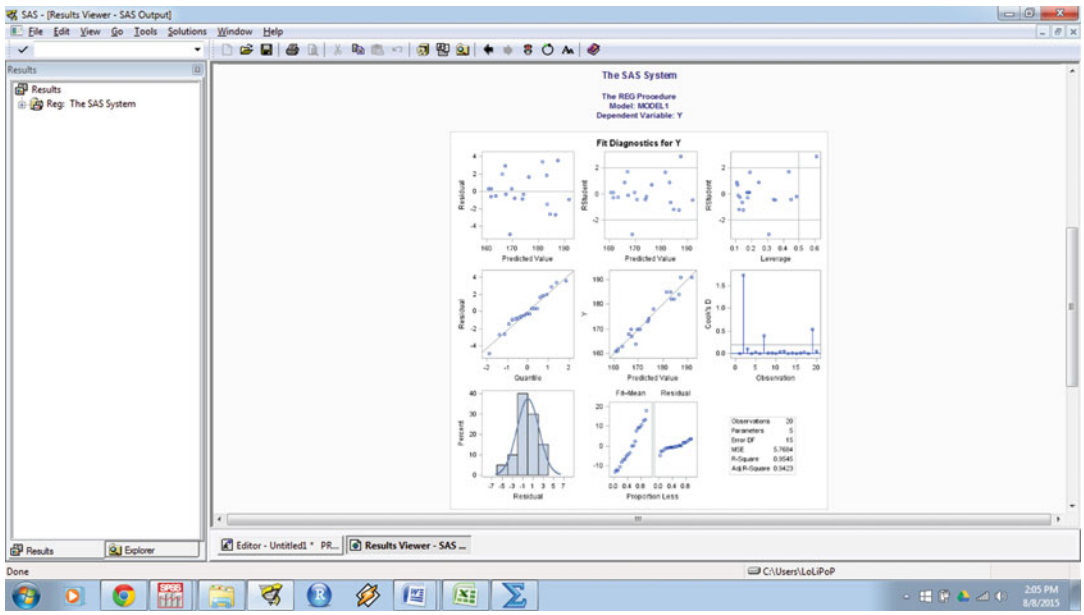
Step 3: Click on the submit button to have the output as below.





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Analysis of Variance

9

9.1 Introduction

One of the many uses of statistics in agriculture and allied sciences is its use in testing the hypothesis of differences between two or more population means or variances. Generally, one tries to infer about the differences among two or more categorical or quantitative treatment groups. For example, by applying three vitamins to three distinct groups of animals or by applying five different doses of nitrogen to a particular variety of paddy or by applying three different health drinks to three groups of students of the same age, three, five, or three populations are defined, respectively. In the first case, each population is made up of those animals that will be subjected to those three types of vitamins. Similarly, the five populations of paddy are constituted of plants of plots subjected to five different doses of nitrogen. Three populations of students are administered with three different health drinks that constitute the three populations.

Now if we want to compare the means of three groups in the first example, then we are to perform ${}^{3}C_{2} = 3$ sets of mean tests using either Z tests or t tests depending upon the situations. Similarly, for five populations in the second example and again three population means in the third example, we are to perform ${}^{5}C_{2} = 10$ and ${}^{3}C_{2} = 3$ sets of mean tests, respectively. Analysis of variance is used to determine whether these three animal populations in the first example differ with respect to some response characteristics like gain in body weight, resistance to diseases or stress tolerance, etc. Similarly, with the help of analysis of variance, one can ascertain whether the five doses of nitrogen are equally effective in growth or grain yield of paddy. In the third example, one can conclude whether three health drinks are equally effective in developing body composition, stress tolerance, disease resistance, etc.

In statistical studies, variability and measures of variability are the major focal points of attention. *Analysis of variance is a systematic approach towards partitioning the variance of a variable into assignable and non-assignable parts*. The analysis of variance partitions the total variability to different sources, viz., among the groups versus that remaining within groups, and analyzes the significance of the explained variability. Analysis of variance is used for testing differences among group means by comparing explained variability due to differences among groups (populations), with the variability measured among the units within groups. If explained variability is much greater than the variability measured among the units within groups, then it is concluded that the treatments or groups have significantly influenced the variability and the population means are significantly different from each other.

In testing differences among populations, models are used to describe measurements or

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P.K. Sahu, *Applied Statistics for Agriculture, Veterinary, Fishery, Dairy and Allied Fields*,
DOI 10.1007/978-81-322-2831-8_9

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observations with a dependent variable and the way of grouping by an independent variable. As already discussed, the independent variable may be qualitative, categorical, classification variable or quantitative and is often called a factor. Depending upon the nature, type of data and classification of data, analysis of variance is developed for one-way classified data, two-way classified data with one observation per cell, two-way classified data with more than one observation per cell, etc. Before taking up the analysis of variance in detail, let us discuss about linear model which is mostly being used in analysis of variance.

9.2 Linear Analysis of Variance Model

It has already been mentioned that the analysis of variance partitions the total variability to its sources, viz., among the groups versus that remaining within groups. Each value of the response variables can be assumed to be composed of two parts, viz., its true value and the error part which may be because of chance factor. The true part is because of assignable sources, whereas the error part is due to non-assignable part, which cannot be ascribed to any cause. Thus, if y be a particular value of the response variable Y, then it can be decomposed as $y = \beta + e$, where β is the true value of the variable Y (i.e., due to assignable causes) and e is the error (i.e., due to non-assignable cause). This β again may be a linear combination of "k" sources of variations having α_1, α_2,....., α_k effects, respectively. Thus, $\beta = a_1\alpha_1 + a_2\alpha_2 + \ldots\ldots + a_k\alpha_k$. Where $a_j\ (j = 1, 2, \ldots\ldots, k)$ are the constants and take the value 0 or 1. Thus, for ith observation of the dependent variable Y, we have the linear model $y_i = a_{i1}\alpha_1 + a_{i2}\alpha_2 + \ldots\ldots + a_{ik}\alpha_k + e_i$

A linear model in which all the α_js are unknown constants (known as parameters) is termed as *fixed effect model*. The effects of groups are said to be fixed because they are specifically chosen or defined by some nonrandom process. The effect of the particular group is fixed for all observations in that group. Differences among observations within group are random. These inferences about the populations are made based on random samples drawn from those populations. On the contrary, a linear model in which α_js are random variables excepting the general mean or general effect is known as *variance component model or random effect model*. A linear model in which at least one α_j is a random variable and at least one α_j is a constant (other than general effect or general mean) is called a *mixed effect model*. Let the number of groups be m, and in each group there are n number of subjects put under experimentation, thereby a total of $N = (m\,n)$ subjects divided into m groups of size n. A model that has an equal number of observations in each group is called *balanced*, while in *unbalanced* model, there is an unequal number of observations per group, n_i denotes the number of observations in group i, and then the total number of observations is $N = \sum_{i=1}^{m} n_i\ (i = 1, \ldots, m)$.

9.3 Assumptions in Analysis Variance

The analysis of variance is based on the following assumptions:

(i) *The effects are additive in nature*. Two independent factors are said to be additive in nature if the effect of one factor remains constant over the levels of other factor. On the contrary, when effects of one factor remains constant by certain percentage over the levels of other factors, then the factors are multiplicative or nonadditive in nature:
$y_{ij} = \mu + \alpha_i + \beta_j + e_{ij}$ (additive model)
$y_{ij} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + e_{ij}$ (multiplicative model)

(ii) *The observations are independent*.

(iii) *The variable concerned must be normally distributed*.

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(iv) *Variances of all populations from which samples have been drawn must be the same*. In other words, all samples should be drawn from normal populations having common variance with the same or different means.

The interpretation of analysis of variance is valid only when the assumptions are met. A larger deviation from these assumptions affects the level of significance and the sensitivity of F and t test.

9.4 One-Way Classified Data

Let us suppose there are $n = \sum_{i=1}^{k} n_i$ observations grouped into k classes with y_{ij} (i =1,2,3,....k; j = 1, 2,3,3.....n_i) that are given as follows:

1	2	……..i…….	k
y_{11}	y_{21}	y_{i1}	y_{k1}
y_{12}	y_{22}	y_{i2}	y_{k2}
⋮	⋮	⋮	⋮
⋮	⋮	⋮	⋮
$y_1 n_1$	$y_2 n_2$	$y_i n_i$	$y_k n_k$

The fixed effect model can be written as $y_{ij} = \mu_i + e_{ij}$, where μ_i is fixed effect due to ith group and e_{ij}s are the error component associated with jth observation of ith group and are independently distributed as $N(0, \sigma^2)$. This μ_i can be regarded as the sum of two components, viz., μ, the overall mean across the groups and a component due to the ith specific group. Thus we can write

$$\mu_i = \mu + (\mu_i - \mu)$$
$$or, \mu_i = \mu + \alpha_i$$

Thus the mathematical model will be:

$$y_{ij} = \mu + \alpha_i + e_{ij}$$

where

μ = general mean across all observations
α_i = additional effect due to ith group
e_{ij} = error components associated with jth observation of ith group and $e_{ij} \sim$ iid$N(0, \sigma^2)$ and $\sum_{i=1}^{k} n_i \alpha_i = 0$

We want to test the equality of the additional population means, i.e.,

$H_0 : \alpha_1 = \alpha_2 = \alpha_3 = ... = \alpha_k = 0$ against the alternative hypothesis.

$H_0 : \alpha_i \neq \alpha_{i'}$ for at least one pair of (i, i') the additional means are not equal

The least square estimators of μ and α_i are obtained by minimising

$$S = \sum_{i=1}^{k} \sum_{j=1}^{n_i} (y_{ij} - \mu - \alpha_i)^2$$

The normal equations are:

$$\frac{\partial S}{\partial \mu} = -2 \sum_i \sum_j (y_{ij} - \mu - \alpha_i) = 0 \text{ and}$$
$$\frac{\partial S}{\partial \alpha_i} = -2 \sum_i \sum_j (y_{ij} - \mu - \alpha_i) = 0$$

From these equations, we have

$$\sum_{i,j} y_{ij} = n\mu + \sum_i n_i \alpha_i$$
$$\text{or}, \hat{\mu} = \bar{y}_{..} \left[\because \sum_i n_i \alpha_i = 0 \right] \text{and}$$
$$\sum_j y_{ij} = n_i \mu + n_i \alpha_i$$
$$\text{or}, \hat{\alpha}_i = \bar{y}_{i.} - \bar{y}_{..}$$

where,

$\bar{y}_{..} = \frac{1}{n} \sum_i \sum_j y_{ij}$ is the mean of all n observations and $\bar{y}_{i.} = \frac{1}{n_i} \sum_j y_{ij}$ is the mean of all observations for ith class

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Thus, the linear model becomes $y_{ij} = \overline{y}_{..} + (\overline{y}_{i.} - \overline{y}_{..}) + (y_{ij} - \overline{y}_{i.})$.

The error terms e_{ij} being so chosen that both sides are equal.

$$\therefore y_{ij} - \overline{y}_{..} = (\overline{y}_{i.} - \overline{y}_{..}) + (y_{ij} - \overline{y}_{i.})$$

Squaring and taking sum for both the sides over i and j we have

$$\begin{aligned}
\sum_i \sum_j \left(y_{ij} - \overline{y}_{..}\right)^2 &= \sum_i \sum_j \left[(\overline{y}_{i.} - \overline{y}_{..}) + (y_{ij} - \overline{y}_{i.})\right]^2 \\
&= \sum_i \sum_j (\overline{y}_{i.} - \overline{y}_{..})^2 + \sum_i \sum_j (y_{ij} - \overline{y}_{i.})^2 + 2\sum_i \sum_j (\overline{y}_{i.} - \overline{y}_{..})(y_{ij} - \overline{y}_{i.}) \\
&= \sum_i \sum_j (\overline{y}_{i0} - \overline{y}_{00})^2 + \sum_i \sum_j (y_{ij} - \overline{y}_{i.})^2 + 2\sum_i (\overline{y}_{i.} - \overline{y}_{..}) \sum_j (y_{ij} - \overline{y}_{i.}) \\
&= \sum_i n_i (\overline{y}_{i0} - \overline{y}_{00})^2 + \sum_i \sum_j (y_{ij} - \overline{y}_{i.})^2 \left[\because \sum_j (y_{ij} - \overline{y}_{i.}) = 0\right]
\end{aligned}$$

$SS(\text{Total}) = SS(\text{group}) + SS(\text{res})$

$SS_{\text{Tot}} = SS_{Gr} + SS_{Er}$

Thus, the total sum of squares is partitioned into sum of squares due to groups and sum of squares due to error.

Similarly, the degrees of freedom can be partitioned into:

Total	=	**Group or treatment**	+	**Residual or Error**
$(n-1)$	=	$(k-1)$	+	$(n-k)$

where

n = the total number of observations
k = the number of groups or treatments

Sums of squares can be calculated using a shortcut calculation presented here in five steps:

1. Total sum = sum of all observations:

$$\sum_{i=1}^{k} \sum_{j=n_1}^{n_k} y_{ij} = GT$$

2. Correction for the mean:

$$\frac{\left[\sum_{i=1}^{k} \sum_{j=n_1}^{n_k} y_{ij}\right]^2}{\sum_{i=1}^{k} n_i} = \frac{(GT)^2}{n}$$

$$= CF(\text{ Correction factor})$$

3. Total (corrected) sum of squares:

$$SS_{\text{Tot}} = \left[\sum_{i=1}^{k} \sum_{j=n_1}^{n_k} y_{ij}^2\right] - CF$$

4. Group or treatment sum of squares:

$$SS_{Gr} = \frac{\sum_{i=1}^{k} y_{i.}^2}{n_i} - CF$$

5. Residual/error sum of squares:

$$SSEr = SS_{\text{Tot}} - SS_{Gr}$$

Mean sum of squares due to different sources of variations can be obtained by dividing *SSs* by the respective d.f.

Thus, $MS_{Gr} = \dfrac{SS_{Gr}}{k-1}$ = Mean sum of squares due to groups

$MS_{Er} = \dfrac{SS_{Er}}{n-k}$ = Mean sum of squares due to error.

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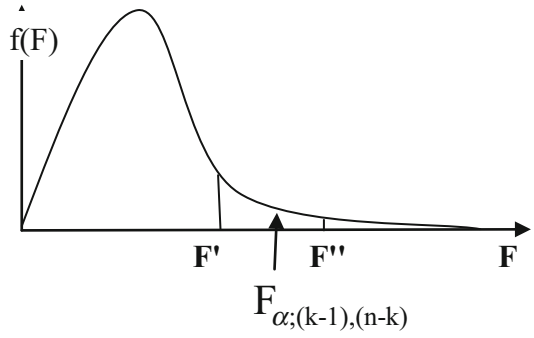
The test statistic under H_0 is given by $F = \frac{MS_{Gr}}{MS_{Er}}$ with $(k-1)$ and $(n-k)$ d.f. If the calculated value of $F > F_{\alpha;k-1,n-k}$, then H_0 is rejected, otherwise it cannot be rejected. In the following figure, if the calculated value of $F = F'$, then H_0 cannot be rejected.



The estimates of population means $\mu_i's$ are the respective means of the groups or treatments, i.e., $y_{i.}$

Now taking help of the central limit theorem, we can assume that estimators of the means are normally distributed with mean μ_i and $s_{y_i} = \sqrt{\frac{MS_{Er}}{n_i}}$; MS_{Er} is the error mean square, which is an estimate of the population variance; and n_i is the number of observations in i treatment/group. Generally, the standard deviation of estimators of the mean is called the standard error of the mean. Confidence intervals at $100(1-\alpha)\%$ for the means are calculated by using a student t-distribution with n–k degrees of freedom and is given by $\overline{y}_{i.} \pm \sqrt{\frac{MS_{Er}}{n_i}}\, t_{\alpha/2,\text{Err}.d.f.}$

In the event of rejection of null hypothesis, that means if the equality population means are rejected against at least one pair of unequal population means, we are to find out the pairs of population means from the sampled data, which are significantly different from each other, and which population is the best population with respect to the characteristic under consideration. That means we are to compare multiple number of means, i.e., multiple comparison of means. There are a few tests like least significant difference (*LSD*) or critical difference (*CD*) method, Bonferroni, Newman-Keuls, Duncan, Dunnet, Tukeys test, etc. found in literature. Here we shall discus *LSD* or *CD* to accomplish this task. If the difference between any pair of means is greater than the critical difference value at specified level of significance, then the means under comparison differ significantly. The critical difference (*CD*) or least significant difference (*LSD*) value is calculated using the following formula for one-way analysis of variance:

$$LSD_\alpha \text{ or } CD_\alpha = \sqrt{MS_{Er}\left(\frac{1}{r_i} - \frac{1}{r_{i'}}\right)}\, t_{\alpha/2,\text{Err}.d.f.}$$

where, r_i and $r_{i'}$ are the number of observations under i and i'th treatments respectively and $t_{\alpha/2,Err.d.f.}$ is the table value of t distribution at α level of siginificance (for both sided test) at error degrees of freedom. $\sqrt{MS_{Er}\left(\frac{1}{r_i} - \frac{1}{r_{i'}}\right)}$ is known as standard error of difference (SED) between pair of means. The advantage of the *CD*/*LSD* is that it has a low level of type II error and will most likely detect a difference if a difference really exists. A disadvantage of this procedure is that it has a high level of type I error.

Example 9.1

An experiment was conducted to investigate the effects of four different diets D_1, D_2, D_3, and D_4 on daily gains (g) in weight of six chicks of 6 weeks old. The following data are related to gain in weights. Analyze the data and test whether all the four diet treatments are equally efficient and if not which diet is the best:

D_1	D_2	D_3	D_4
30	32	34	36
27	28	25	30
23	27	26	28
25	29	27	33
23	26	25	32
26	29	29	30

Solution This is a fixed effect model and can be written as $y_{ij} = \mu + \alpha_i + e_{ij}$

Thus, null hypothesis is

$H_0 : \alpha_1 = \alpha_2 = \alpha_3 = \alpha_4 = 0$ against the $H_1 : \alpha'$sare not equal,

where α_i is the effect of ith (i =1,2, 3,4) diet
Let the level of significance be 0.05.

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We calculate the following quantities from the given information:

	D_1	D_2	D_3	D_4
	30	32	34	36
	27	28	25	30
	23	27	26	28
	25	29	27	33
	23	26	25	32
	26	29	29	30
Total	154	171	166	189
Average	25.67	28.50	27.67	31.50

$$GT = 30 + 27 + \ldots\ldots\ldots\ldots + 29 + 30 = 680$$
$$CF = GT^2/n = 680^2/24 = 19266.67$$

$$TSS = 30^2 + 27^2 + \ldots\ldots\ldots + 29^2 + 30^2 - CF = 261.333$$

$$SS\ (dDiet) = \left(154^2 + 171^2 + 166^2 + 189^2\right)/6 - CF = 105.667$$

$$ErSS = TSS - SS\ (dDiet) = 155.667$$

ANOVA table					
Source of variation	d.f.	SS	MS	F	Tab F
Diet	3	105.667	35.22222	4.525339	3.10
Error	20	155.667	7.783333		
Total	23	261.333			

The table value of $F_{0.05;3,20} = 3.10$, i.e., $F_{cal} > F_{tab}$. So the test is significant at 5 % level of significance, and we reject the null hypothesis. Thus, we can conclude that the all four diets are not equally efficient.

Now we are to find out which diet is the best among four diets given. To compare the diets, we calculate the mean ($\overline{y}_i$) of the observations of four diets, and the means are arranged in decreasing order. Thus, we get:

Diet no.	4	2	3	1
Mean	31.50	28.50	27.67	25.67

Now we find the critical difference value which is given by

$$\begin{aligned} \text{LSD/CD}(0.05) &= \sqrt{MSE\left(\frac{1}{r_i} + \frac{1}{r_i}\right)} \times t_{0.025,\text{err}.df.} \\ &= \sqrt{7.783\left(\frac{2}{r_i}\right)} \times t_{0.025,20.} \\ &= \sqrt{7.783\left(\frac{2}{6}\right)} \times 2.086 = 3.359 \end{aligned}$$

where r_i is the number of observations of the ith diet in comparison; here all the diets are repeated six number of times. Thus, for comparing the diets, we have the following critical difference and mean difference values.

Conclusion

Mean difference		Remarks	Conclusion
Diet 4 and diet 2	3	<CD (0.05)	Diet 4 and diet 2 are at per
Diet 4 and diet 3	3.83	>CD (0.05)	Diet 4 is significantly greater than diet 3
Diet 4 and diet 1	5.83	>CD (0.05)	Diet 4 is significantly greater than diet 1
Diet 2 and diet 3	0.83	<CD (0.05)	Diet 2 and diet 3 are at per
Diet 2 and diet 1	2.83	<CD (0.05)	Diet 2 and diet 1 are at per
Diet 3 and diet 1	2.00	<CD (0.05)	Diet 3 and diet 1 are at per

It is found from the above table that though diet 4 and diet 2 are statistically at par, diet 4 is having higher gain in body weight. As such, we conclude that diet 4 is the best diet, so far about the increase in body weight of chicks is concerned.

Example 9.2

Thirty-two animals were fed with four different feeds. The following figures give the gain in body weight after 2 months. Analyze the data and draw your conclusion: (i) whether all the

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four feeds are equally efficient and which feed is the best feed:

Feed 1	*Feed 2*	Feed 3	*Feed 4*
12.5	13.7	11.6	14.8
12	13.8	11.8	14.5
12.3	13.9	11.9	14.9
13.4	13.8	12.2	15
13.5	14	11.8	14.7
13.6	12.9	12.1	14.5
11.9	13.5	12.4	14.9
12.7		11.9	14.8
12.8		11.9	
12.4			
13.2			

Solution This is a fixed effect model and can be written as

$$y_{ij} = \mu + \alpha_i + e_{ij}$$

The null hypothesis is

$H_0 : \alpha_1 = \alpha_2 = \alpha_3 = \alpha_4 = 0$ against the $H_1 : \alpha'$s are not all equal, where, α_i is the effect of ith ($i = 1,2,3,4$) feed.

From the above information, we are to test the null hypothesis.

From the above information, let us construct the following table:

	Feed 1	Feed 2	Feed 3	Feed 4	Total
	12.50	13.70	11.60	14.80	
	12.00	13.80	11.80	14.50	
	12.30	13.90	11.90	14.90	
	13.40	13.80	12.20	15.00	
	13.50	14.00	11.80	14.70	
	13.60	12.90	12.10	14.50	
	11.90	13.50	12.40	14.90	
	12.70		11.90	14.80	
	12.80		11.90		
	12.40				
	13.20				
$GT=$	140.30	95.60	107.60	118.10	461.60
Means	12.75	13.66	11.96	14.76	
$CF =$	6087.84				
$SS_{\text{Tot}} =$	42.22				
$SS_F =$	37.11				
$SS_{Er} =$	5.11				

$$GT = 12.5 + 12.0 + 12.3 + \ldots\ldots\ldots.. + 14.5 + 14.9 + 14.8 = 461.60$$

$$CF = GT^2/n = 461.60^2/35 = 6087.84$$

$$SS_{\text{Tot}} = 12.5^2 + 12.0^2 + 12.3^2 + \ldots\ldots.. + 14.5^2 + 14.9^2 + 14.8^2 - CF = 42.22$$

$$SS_{(\text{Feed})} = \frac{140.30^2}{11} + \frac{95.60^2}{7} + \frac{107.60^2}{9} + \frac{118.1^2}{8} - CF = 37.11$$

$$SS_{Er} = TSS - FSS = 5.11$$

ANOVA for one-way analysis of variance

SOV	d.f.	SS	MSS	F ratio
Feed	3	37.11	12.37	75.11
Error	31	5.11	0.16	
Total	34	42.22		

The table value of $F_{0.05;3,31} = 2.91$, i.e., $F_{Cal} > F_{Tab}$. So the test is significant at 5 % level of significance, and we reject the null hypothesis. Thus, we can conclude that the feeds are not equally efficient.

Next task is to find out which pair of feeds differ significantly and which is the best feed. To compare the feeds, we calculate the means ($\bar{y}_i$) of the observations of four schools, and the means are arranged in decreasing order. Thus, we get

Feed	4	2	1	3
Mean ($\bar{y}_i$)	14.76	13.66	12.75	11.96

Now we find the critical difference value which is given by

$$\sqrt{MSE\left(\frac{1}{r_i} + \frac{1}{r_{i'}}\right)} \times t_{0.025,\text{err}.df.}$$
$$= \sqrt{0.16\left(\frac{1}{r_i} + \frac{1}{r_{i'}}\right)} \times t_{0.025,31.}$$
$$= \sqrt{0.16\left(\frac{1}{r_i} + \frac{1}{r_{i'}}\right)} \times 2.04$$

where r_i and r_j are the number of observations of the two diets in comparison. Thus, for comparing the diets, we have the following critical

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difference and mean difference values among the feeds:

CD values		Mean difference	
LSD/CD(0.05) (feed 1–feed 2)	0.395	Difference between feed 1 and feed 2	0.9026
LSD/CD (0.05) (feed 1–feed 3)	0.367	Difference between feed 1 and feed 3	0.7990
LSD/CD (0.05) (feed 1–feed 4)	0.379	Difference between feed 1 and feed 4	2.0080
LSD/CD (0.05) (feed 2–feed 3)	0.411	Difference between feed 2 and feed 3	1.7016
LSD/CD (0.05) (feed 2–feed 4)	0.422	Difference between feed 2 and feed 4	1.1054
LSD/CD (0.05) (feed 3–feed 4)	0.397	Difference between feed 3 and feed 4	2.8069

It is found from the above table that all the values of the mean differences are greater than the respective LSD/CD values at 5 % level of significance. So all the four feeds differ among themselves with respect to change in body weight. Among the four feeds, the feed 4 has increased the body weight most; as such, the feed 4 is the best feed.

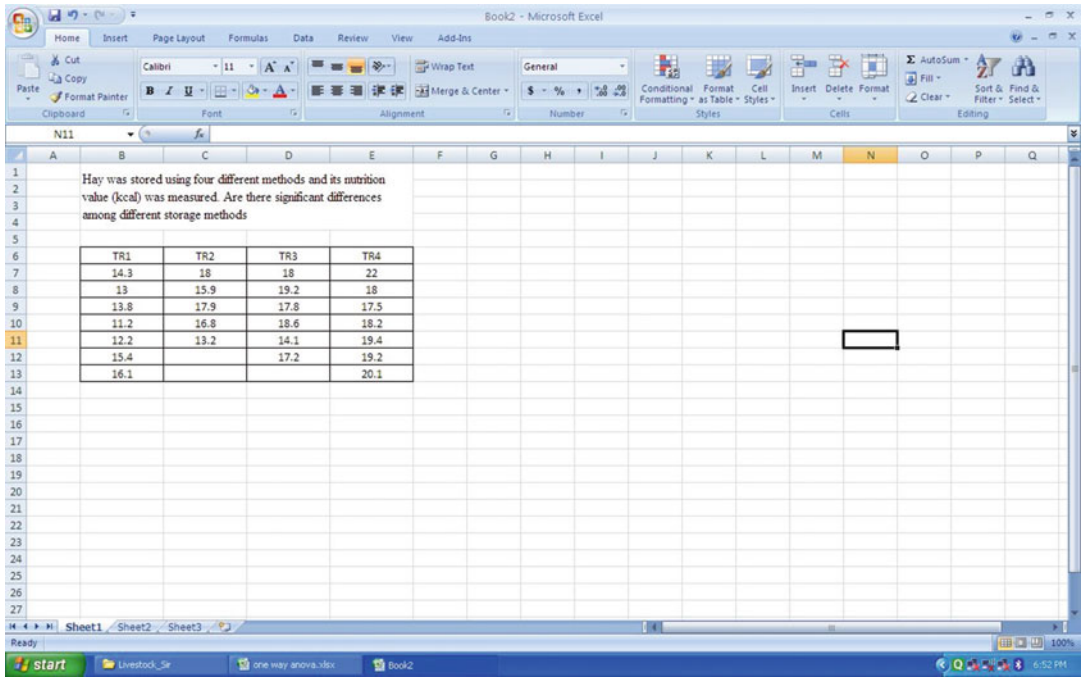
9.4.1 Analysis of One-Way Classified Data Using MS Excel

Example 9.3

Hay was stored using four different methods, and its nutritional value (kcal) was measured. Are there significant differences among different storage methods?

TR1	TR2	TR3	TR4
14.3	18	18	22
13	15.9	19.2	18
13.8	17.9	17.8	17.5
11.2	16.8	18.6	18.2
12.2	13.2	14.1	19.4
15.4		17.2	19.2
16.1			20.1

(i) Enter the data as given above in MS Excel work sheet.
(ii) Go to Data Analysis menu under Data.



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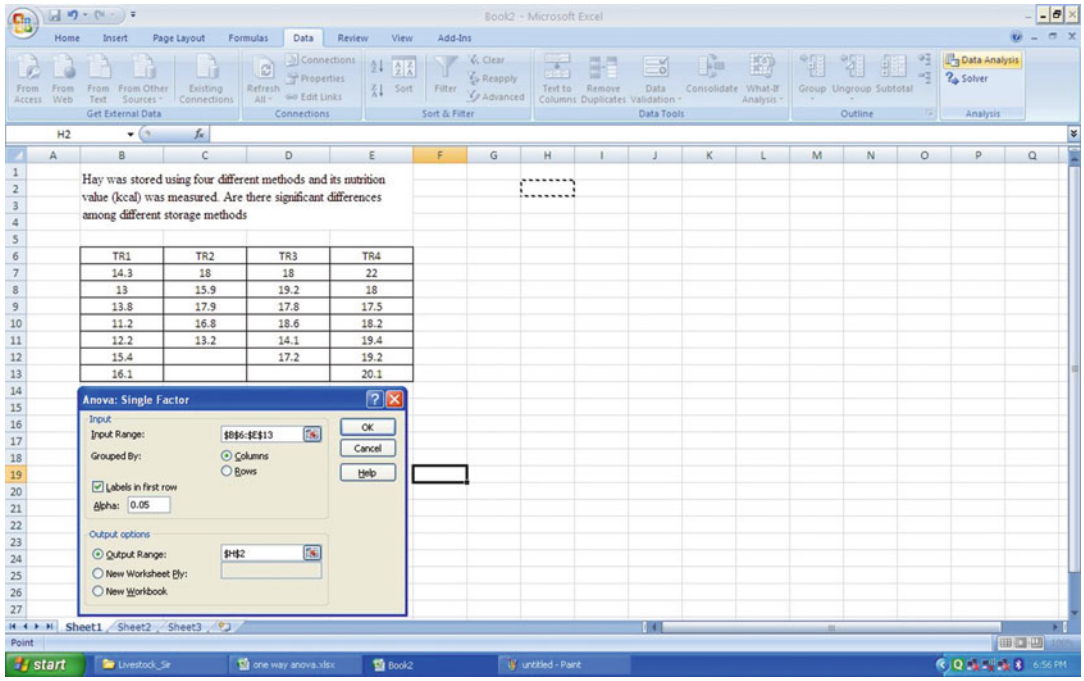
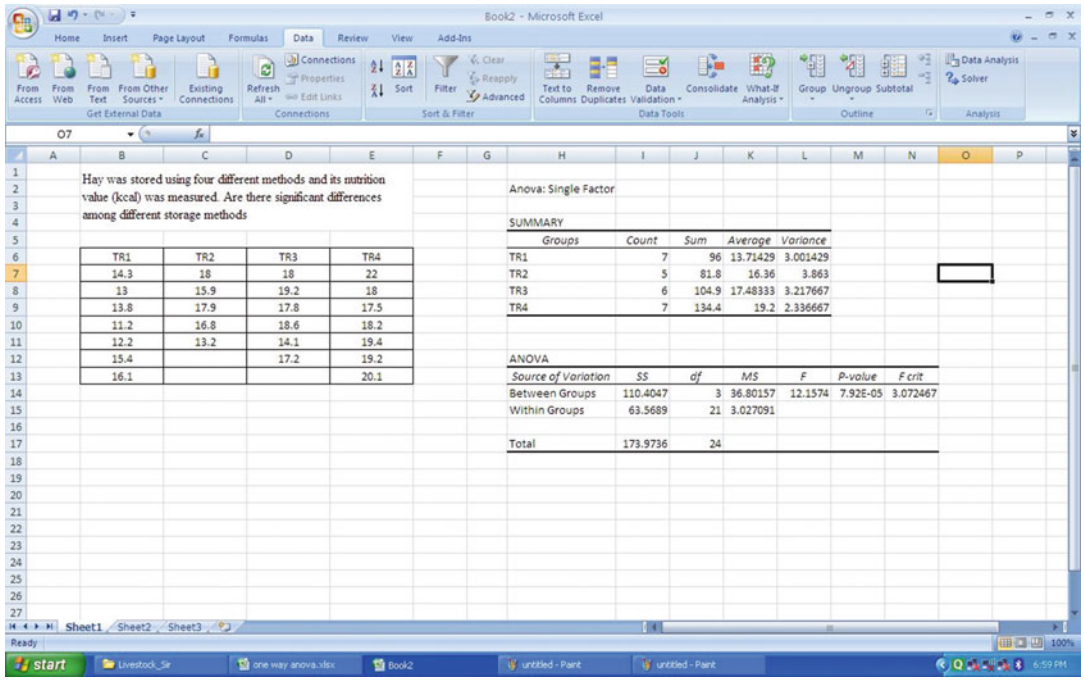
(iii) Select "Anova Single Factor" option.



(iii) Select the input range including the labels in the first row of the data.

(iv) Select the level of significance alpha (α) at desired level (generally, 0.05 or 0.01).

(v) Select the output range i.e. the starting cell for writing output of the analysis.



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(vi) Get the above results as shown in the figure.

(vii) If the P-value given in the ANOVA is less than the desired level of significance, then the test is significant, and we can reject the null hypothesis of equality of effect of different types of storage conditions. That means all the storage methods are not equally effective for maintaining nutritional value.

(viii) If the probability (P level) given in the ANOVA is less than the desired level of significance, then the test is significant, and there exists significant differences among the groups. Hence arises the need for finding the groups or treatments (here storage types) which are significantly different from each other and also the best treatment or group (storage type). For that one has worked out the CD/LSD value at desired level of significance. For the above example, CD is calculated with the help of the following formula, and conclusion is drawn accordingly:

$$\sqrt{MSE\left(\frac{1}{r_1}+\frac{1}{r_2}\right)} \times t_{0.05,\text{err}.df.}$$
$$= \sqrt{3.02\left(\frac{1}{r_1}+\frac{1}{r_2}\right)} \times t_{0.05,21.}$$
$$= \sqrt{3.02\left(\frac{1}{r_1}+\frac{1}{r_2}\right)} \times 2.07$$

where r_1 and r_2 are the replications of the two groups or treatments under consideration.

Thus, to compare storage method 1 and storage method 2, we have CD (0.05)

$$= \sqrt{3.02\left(\frac{1}{7}+\frac{1}{5}\right)} \times 2.07 = 2.11$$

The difference between the means of storage method 1 and storage method 2, 16.76-13.71 = 2.65 is more than CD (0.05) = 2.11. So these two feeds are different, and storage method 2 is better than storage method 1. Likewise, we are to calculate other CD values for comparing means of different storage method having different observation:

Difference between	Mean difference	CD value
Storage method 1 and storage method 2	2.65	2.12
Storage method 1 and storage method 3	3.77	2.19
Storage method 1 and storage method4	5.49	1.93
Storage method 2 and storage method 3	1.12	2.19
Storage method 2 and storage method 4	2.84	2.19
Storage method 3 and storage method 4	1.72	2.01

In this example, storage method 3 and 4 and storage method 2 and 3 are equally efficient as mean difference between treatment means are less than corresponding calculated CD values. Overall, storage method 4 is more efficient for maintaining nutritional value of feed.

9.5 Two-Way Classified Data

The problem with one-way analysis of variance is that one can accommodate one factor at a time, but in many practical cases, we need to accommodate more than one factor at a time. Subjects are required to be classified on the basis of two grouping characteristics simultaneously. In this type of classification, each of the grouping factors may have different levels, and each level may have one or more observations. Let us take an example, suppose an experimenter wants to test the efficacy of three different feeds (F1, F2, F3) on two different types of fish *Catla catla* (viz., local and hybrid). Thus, we have two factors, viz., feed and type of fish; for the first factor, i.e., feed, we have three levels, viz., F1, F2, and F3, and for the second factor type of fish, we have two levels, viz., local and hybrid. So we have different levels for the two factors, but the level of factors may be the same also. Thus, altogether we have $3 \times 2 = 6$ treatment combinations as follows:

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	Feed		
Type	F1	F2	F3
Local(L)	(F1L)	(F2L)	(F3L)
Hybrid(H)	(F1H)	(F2H)	(F3H)

This idea that can be generalized using two factors has A and B having *i* and *j* levels (*i* and *j* can take different or same values) with *i.j* treatment combinations, and the treatment combinations will be as follows:

Two way classification with one observation per cell

A	B				
	B1	B2	.....	Bj	.....
A1	(A1B1)	(A1B2)	.....	(A1Bj)	.....
A2	(A2B1)	(A2B2)	.....	(A2Bj)	.....
:	.....	.....	.....	:	.....
:				:	.....
Ai	(AiB1)	(AiB2)	.....	(AiBj)	.....
:	:	:	.....	:	.....
:	:	:	.....	:	.....

In the above arrangement, if all the treatment combinations are repeated more than once, then the shape of the above table will be as follows:

Two way classification with more than one observation per cell

A	B				
	B1	B2	.....	Bj	.....
A1	(A1B1)1 (A1B1)2 (A1B1)3	(A1B2)1 (A1B2)2 (A1B2)3	....	(A1Bj)1 (A1Bj)2 (A1Bj)3	....
A2	(A2B1)1 (A2B1)2 (A2B1)3	(A2B2)1 (A2B2)2 (A2B2)3	....	(A2Bj)1 (A2Bj)2 (A2Bj)3	....
:	.....	.....	.....	:	.....
:				:	.....
Ai	(AiB1)1 (AiB1)2 (AiB1)3	(AiB2)1 (AiB2)2 (AiB2)3	....	(AiBj)1 (AiBj)2 (AiBj)3	....
:	:	:	.....	:	.....
:	:	:	.....	:	.....

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Number of repetition may or may not vary from treatment to treatment combination.

9.5.1 Two-Way Classified Data with One Observation per Cell

Let us consider fixed effect models for two-way classified data for two factors, A and B, with m and n levels, respectively, and no repetition of any of the treatment combinations. If y_{ij} be the response recorded corresponding to ith level of the factor A and jth level of the factor B, the observations can be presented as follows:

	B_1	B_2	.....	B_j	.....	B_n
A_1	y_{11}	y_{12}	.....	y_{1j}	.....	y_{1n}
A_2	y_{21}	y_{22}	.....	y_{2j}	.....	y_{2n}
:	:	:		:		:
:	:	:		:		:
A_i	y_{i1}	y_{i2}	.....	y_{ij}	.....	y_{in}
:	:	:		:		:
:	:	:		:		:
A_m	y_{m1}	y_{m2}	.....	y_{mj}	.....	y_{mn}

If we consider a fixed effect model, then following the same procedure of one-way classified data, we can have

$$\begin{aligned} y_{ij} &= \mu_{ij} + e_{ij} \\ &= \mu + (\mu_{i0} - \mu) + (\mu_{0j} - \mu) \\ &\quad + (\mu_{ij} - \mu_{i0} - \mu_{0j} + \mu) + e_{ij} \\ &= \alpha_i + \mu + \beta_j + \gamma_{ij} + e_{ij} \\ &= \mu + \alpha_i + \beta_j + e_{ij} \end{aligned}$$

[The interaction effect γ_{ij} can not be estmated by a single value, since there is only one value per cell. So we take $\gamma_{ij} = 0$ and hence the model],

where $i = 1, 2, \ldots\ldots, m$; $j = 1, 2, \ldots..., n$:

y_{ij} = value of the observation corresponding to the ith level of the factor A and jth level of the factor B.

μ = general effect.

α_i = additional effect due to ith level of factor A.

β_j = additional effect due to jth level of factor B.

e_{ij} = errors associated with ith level of the factor A and jth level of the factor B and are i.i.d N(0, σ^2) and $\sum_{i=1}^{m} \alpha_i = \sum_{j=1}^{n} \beta_j = 0$

It may be noted that in case of two-way classified data only, one observation per cell interaction effect cannot be estimated.

The least square estimates μ, α_i and β_j are obtained by minimizing the sum of squares due to error:

$$S = \sum_i \sum_j e_{ij}^2 = \sum_i \sum_j \left(y_{ij} - \mu - \alpha_i - \beta_j\right)^2$$

The normal equations obtained are

$$\frac{\partial S}{\partial \mu} = -2\sum_{i}^{m}\sum_{j}^{n}\left(y_{ij} - \mu - \alpha_i - \beta_j\right) = 0$$

$$\frac{\partial S}{\partial \alpha_i} = -2\sum_{j=1}^{n}\left(y_{ij} - \mu - \alpha_i - \beta_j\right) = 0$$

$$\frac{\partial S}{\partial \alpha_i} = -2\sum_{i=1}^{m}\left(y_{ij} - \mu - \alpha_i - \beta_j\right) = 0$$

Solving the above equations, we have

$$\hat{\mu} = \bar{y}_{..}$$
$$\hat{\alpha}_i = \bar{y}_{i.} - \bar{y}_{..}$$
$$\hat{\beta}_j = \bar{y}_{.j} - \bar{y}_{..}$$

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where, $\bar{y}_{..} = \frac{1}{mn}\sum_{i,j} y_{ij}, \bar{y}_{i.} = \frac{1}{n}\sum_{j} y_{ij}, \bar{y}_{.j} = \frac{1}{m}\sum_{i} y_{ij}$

Thus,

$$y_{ij} = \bar{y}_{..} + (\bar{y}_{i.} - \bar{y}_{..}) + (\bar{y}_{.j} - \bar{y}_{..}) + (y_{ij} - \bar{y}_{i.} - \bar{y}_{.j} + \bar{y}_{..})$$

or

$$\sum_i \sum_j y_{ij}^2 = mn\bar{y}_{..}^2 + n\sum_i (\bar{y}_{i.} - \bar{y}_{..})^2 + m\sum_j (\bar{y}_{.j} - \bar{y}_{..})^2 + \sum_i \sum_j (y_{ij} - \bar{y}_{i.} - \bar{y}_{.j} + \bar{y}_{..})^2$$

[Note: All product terms vanish because of the fact $\sum_i (y_{i.} - y_{..}) = \sum_j (\bar{y}_{.j} - \bar{y}_{..}) = \sum_i \sum_j (y_{ij} - \bar{y}_{i.} - \bar{y}_{.j} + \bar{y}_{..}) = 0$]

or

$$\sum_i \sum_j (y_{ij} - \bar{y}_{..}) = n\sum_i (\bar{y}_{i.} - \bar{y}_{..})^2 + m\sum_j (\bar{y}_{.j} - \bar{y}_{..}) + \sum_i \sum_j (y_{ij} - \bar{y}_{i.} - \bar{y}_{.j} + \bar{y}_{..})^2$$

Or $SS_{\text{Tot}} = SS(A) + SS(B) + SS_{Er}$

The corresponding partitioning of the total d.f. is as follows:

Total d.f. = d.f. due to Factor A + d.f. due to Factor B + d.f. due to Error

$$mn - 1 = (m-1) + (n-1) + (m-1)(n-1)$$

Our objective is to test the following two hypotheses:

$H_{01} : \alpha_1 = \alpha_2 = \alpha_3 = ...\alpha_m = 0$ and
$H_{02} : \beta_1 = \beta_2 = \beta_3 = ...\beta_n = 0$

For practical purposes, the various sums of squares are calculated from the following table and using the following formulae:

	B_1	B_2	.....	B_j	.....	B_n	Total	Mean
A_1	y_{11}	y_{12}	.....	y_{1j}	.....	y_{1n}	$y_{1.}$	$\bar{y}_{1.}$
A_2	y_{21}	y_{22}	.....	y_{2j}	.....	y_{2n}	$y_{2.}$	$\bar{y}_{2.}$
:	:	:		:		:	:	:
:	:	:		:		:	:	:
A_i	y_{i1}	y_{i2}	.....	y_{ij}	.....	y_{in}	$y_{i.}$	$\bar{y}_{i.}$
:	:	:		:		:	:	:
:	:	:		:		:	:	:
A_m	y_{m1}	y_{m2}	.....	y_{mj}	.....	y_{mn}	$y_{m.}$	$\bar{y}_{m.}$
Total	$y_{.1}$	$y_{.2}$	.....	$y_{.j}$	.....	$y_{.n}$	$y_{..}$	
Mean	$\bar{y}_{.1}$	$\bar{y}_{.2}$	.....	$\bar{y}_{.j}$	.....	$\bar{y}_{.n}$		$\bar{y}_{..}$

Step 1: G = Grand total $= \sum_{i=1}^{m}\sum_{j=1}^{n} y_{ij}$

Step 2: Correction factor $(CF) = \frac{G^2}{mn}$,

Step 3: Total Sum of Squares (SS_{Tot})
$= \sum_{\text{i}} \sum_{\text{j}} (y_{ij} - \bar{y}_{..})^2$
$= \sum_i \sum_j y_{ij}^2 - CF$

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Step 4: Sum of Squares(A) $= SS_{\mathrm{A}}$

$$= n\sum_i (\overline{y}_{i.} - \overline{y}_{..})^2$$

$$= n\left[\sum_i \overline{y}_{i.}^2 - m\overline{y}_{..}^2\right]$$

$$= n\sum_i \left(\frac{\sum_{j=1}^{n}\overline{y}_{ij}}{n}\right)^2 - nm\overline{y}_{00}^2$$

$$= \frac{1}{n}\sum_i y_{i0}^2 - CF, \text{ where, } y_{i0} = \sum_{j=1}^{n} y_{ij} \text{ is the}$$

sum of observations for ith level of the factor A.
Step 5: Sum of Squares(B) $= SS_B$

$$= m\sum_j (\overline{y}_{.j} - \overline{y}_{..})^2$$

$$= \frac{1}{m}\sum_j y_{.j}^2 - CF, \text{where, } y_{0j} = \sum_{i=1}^{m} y_{ij} \text{ is the}$$

sum of observations for jth level of the factor B.
Step 6: $ErSS = SS_{\mathrm{Tot}} - SS_{\mathrm{A}} - SS_{\mathrm{B}}$

Dividing these sums of squares by their respective degrees of freedom, we will get the mean sum of square, i.e., mean sum of square due to factor A, factor B, and error mean sum of square.

We have the following ANOVA table for two-way classification with one observation per cell:

SOV	*d.f.*	*SS*	*MS*	*F*
Factor A	$m-1$	SS_A	$MS_A = SS_A/m-1)$	MS_A/MS_{Er}
Factor B	$n-1$	SS_B	$MS_B = SS_B/(n-1)$	MS_B/MS_{Er}
Error	$(m-1)(n-1)$	SS_{Er}	$MS_{Er} = SS_{Er}/(m-1)(n-1)$	
Total	$mn-1$	SS_{Tot}		

In the event of rejection of any or both null hypotheses, that means if the equality of population means are rejected against at least one pair of unequal population means, we are to find out the pairs of population means from the sampled data, which are significantly different from each other, and which population is the best population with respect to the characteristic under consideration. That means we are to compare multiple number of means, i.e., multiple comparison of means. This is followed as per the formula given in for one-way ANOVA, but there will be two corrections:

(a) A number of observations are equal for all treatment combinations.
(b) Corresponding to rejection of each null hypothesis, there would be one LSD or CD value to be calculated.

Thus, we are to get two CD values corresponding to factor A and factor B, respectively, using the formulae given below:

$$\mathrm{LSD/CD}(0.05) \text{ for factor A}$$

$$= \sqrt{\frac{2MSE}{\text{levels of factor B}}} \times t_{0.025,\,\mathrm{err}.df.}$$

$$= \sqrt{\frac{2MSE}{n}} \times t_{0.025,\,\mathrm{err}.d.f.}$$

$$\mathrm{LSD/CD}(0.05) \text{ for factor B}$$

$$= \sqrt{\frac{2MSE}{\text{levels of factor A}}} \times t_{0.025,\,\mathrm{err}.df.}$$

$$= \sqrt{\frac{2MSE}{m}} \times t_{0.025,\,\mathrm{err}.d.f.}$$

Example 9.3
Four different breeds of cows were treated with five vitamins for improving milk production. Type of breed was criteria for assigning cows in four different blocks. Each block is assigned with four cows. The effect of these vitamins on milk production was tested by weekly milk production (liter) after treatment. Analyze the data using two-way ANOVA:

Vitamin	Breed 1	Breed 2	Breed 3	Breed 4
V1	42	54	72	88
V2	44	57	76	92
V3	45	52	78	86
V4	42	60	73	93
V5	41	61	78	92
V6	46	65	82	99

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This is a fixed effect model $y_{ij} = \mu + \alpha_i + \beta_j + e_{ij}$, where $i = 1, 2, \ldots\ldots, 6$; $j = 1, 2, 3, 4$:

y_{ij} = value of the observation corresponding to the ith vitamin and jth type of breed.
μ = general mean effect
α_i = additional effect due to ith vitamin.
β_j = additional effect due to jth type of breed.
e_{ij} = errors with associated with ith vitamin and jth type of breed.

Under the given condition, the null hypotheses are

$H_{01} : \alpha_1 = \alpha_2 = \alpha_3 = \alpha_4 = \alpha_5 = \alpha_6 = 0$ against

$H_{11} : \alpha'$s are not equal and

$H_{02} : \beta_1 = \beta_2 = \beta_3 = \beta_4 = 0$ against

$H_{12} : \beta'$s are not equal

This is a problem of two-way analysis of variance with one observation per cell.

We calculate the following quantities:

Vitamin	Breed 1	Breed 2	Breed 3	Breed 4	Total $\sum y_{i.}$	Mean $\bar{y}_{i.}$
V1	42	54	72	88	256	64.00
V2	44	57	76	92	269	67.25
V3	45	52	78	86	261	65.25
V4	42	60	73	93	268	67.00
V5	41	61	78	92	272	68.00
V6	46	65	82	99	292	73.00
Total $\sum y_{.j}$	260	349	459	550	1618	
Mean $\left(\bar{y}_{.j}\right)$	43.33	58.17	76.50	91.67		

Total number of observations $= N = mn = 24$
(m = no. of vitamins and n = no. of breeds)

$$G = 42 + 44 + \ldots\ldots\ldots + 92 + 99 = 1618$$
$$CF = G^2/N = 1618^2/24 = 109080.17$$

$$TSS = 42^2 + 44^2 + 45^2 + \ldots\ldots\ldots + 93^2 + 92^2 + 99^2 - CF = 8319.83$$

$$Tr\ SS = SS\ (\text{Vitamin}) = \frac{256^2}{4} + \frac{269^2}{4} + \frac{261^2}{4} + \frac{268^2}{4} + \frac{272^2}{4} + \frac{292^2}{4} - CF = 192.33$$

$$Ty\ SS = SS(\text{Breed}) = \frac{260^2}{6} + \frac{349^2}{6} + \frac{459^2}{6} + \frac{550^2}{6} - CF = 8016.83$$

$$Er\ SS = SS_{Er} = TSS - SS_V - SS_{Br} = 110.66$$

ANOVA table

Source of variation	d.f.	SS	MS	F	Table F
Breed	3	8016.83	2672.28	362.21	2.90
Vitamin	5	192.33	38.47	5.21	3.29
Error	15	110.67	7.38		
Total	23	8319.83			

Let the level of significance $\alpha = 0.05$.

The table value corresponding to the effect of breed, i.e., $F_{0.05;3,15} = 2.90$. From the analysis, we have $F_{\text{Cal}} > F_{\text{Tab}}$; so the test is significant, and the hypothesis of equality of breeds is rejected.

On the other hand, the table value corresponding to the effect of vitamin, i.e., $F_{0.05;5,15} = 3.29$, From the analysis, we have $F_{\text{Cal}} > F_{\text{Tab}}$; so the test is significant, and the hypothesis of equality vitamins is also rejected. We conclude that there exists significant difference among the effects of breeds as well as vitamins with respect to milk production (liter).

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Thus, the next task is to find out the best breed and the best vitamin to produce maximum milk per cow. For this, we calculate critical differences for both breeds and vitamins separately and then compare the respective mean effects using the following formulae:

$$LSD/CD(0.05) \text{ for Breed} = \sqrt{\frac{2ErMS}{V}} \times t_{0.025,\text{err}.df.} = \sqrt{\frac{2 \times 7.38}{6}} \times t_{0.025,15.} = \sqrt{\frac{2 \times 7.38}{6}} \times 2.13 = 3.34$$

$$LSD/CD(0.05) \text{ for Vitamin} = \sqrt{\frac{2 \times ErMS}{B}} \times t_{0.025,\text{err}.df.} = \sqrt{\frac{2 \times 7.38}{4}} \times t_{0.025,15.} = \sqrt{\frac{2 \times 7.38}{4}} \times 2.13 = 4.09$$

Ordered breed mean milk yield			
B4	B3	B2	B1
91.67	76.50	58.17	43.33

Comparison of breeds with respect to per day milk production

Mean difference		Remarks	Conclusion
Breed 4 and breed 3	15.17	>CD (0.05) = 3.34	Breed 4 and breed 3 are significantly different from each other
Breed 4 and breed 2	33.50	>CD (0.05) = 3.34	Breed 4 and breed 2 are significantly different from each other
Breed 4 and breed 1	48.33	>CD (0.05) = 3.34	Breed 4 and breed 1 are significantly different from each other
Breed 3 and breed 2	18.33	>CD (0.05) = 3.34	Breed 3 and breed 2 are significantly different from each other
Breed 3 and breed 1	33.17	>CD (0.05) = 3.34	Breed 3 and breed 1 are significantly different from each other
Breed 2 and breed 1	14.8	>CD (0.05) = 3.34	Breed 2 and breed 1 are significantly different from each other

From the above table, it is clear that all the breeds differ significantly among themselves with respect to milk production per day. Among the breeds, breed 4 is the significantly higher yielder than other breeds.

Comparison of vitamins with respect to per day milk production

Ordered vitamin mean milk yield (*l*)					
V6	V5	V2	V4	V3	V1
73	68	67.25	67	65.25	64

The mean comparison as followed for breeds will be laborious and clumsy as the number of levels increases. As such for the purpose of comparing the mean differences among the vitamins w.r.t. milk yield per day, let us construct the following mean difference matrix w.r.t. milk yield per day as given below from the above-ordered means:

Mean difference matrix w.r.t. milk yield per day (*l*)					
	V5	V2	V4	V3	V1
V6	5.0	5.8	6.0	7.8	9.0
V5		0.8	1.0	2.8	4.0
V2			0.3	2.0	3.3
V4				1.8	3.0
V3					1.3

It is clear from the above two tables that the highest milk yielder per day is vitamin six and

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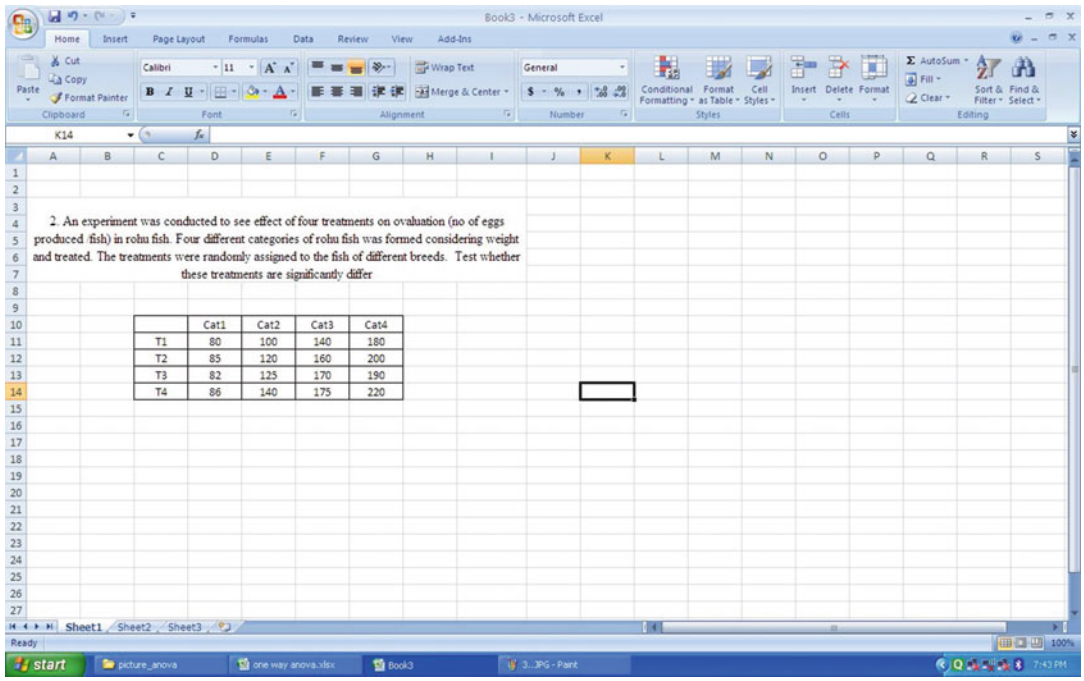
the difference of milk yield due to application of vitamin six with that of the milk yield from any other vitamin is greater than the LSD value at 5 % level of significance (i.e., 4.09).Thus, vitamin six is the best vitamin compared to other vitamin w.r.t. milk yield per day (l)

9.5.2 Analysis of Two-Way Classified Data with One Observation per Cell Using MS Excel

Example 9.4

An experiment was conducted to see the effect of four treatments on ovulation (no. of eggs produced/fish in thousands) in rohu (*Labeo rohita*) fish. Four different categories of rohu fish was formed considering weight and treatment. The treatments were randomly assigned to the fish of different breeds. Test whether these treatments significantly differ or not:

	Cat1	Cat2	Cat3	Cat4
T1	80	100	140	180
T2	85	120	160	200
T3	82	125	170	190
T4	86	140	175	220



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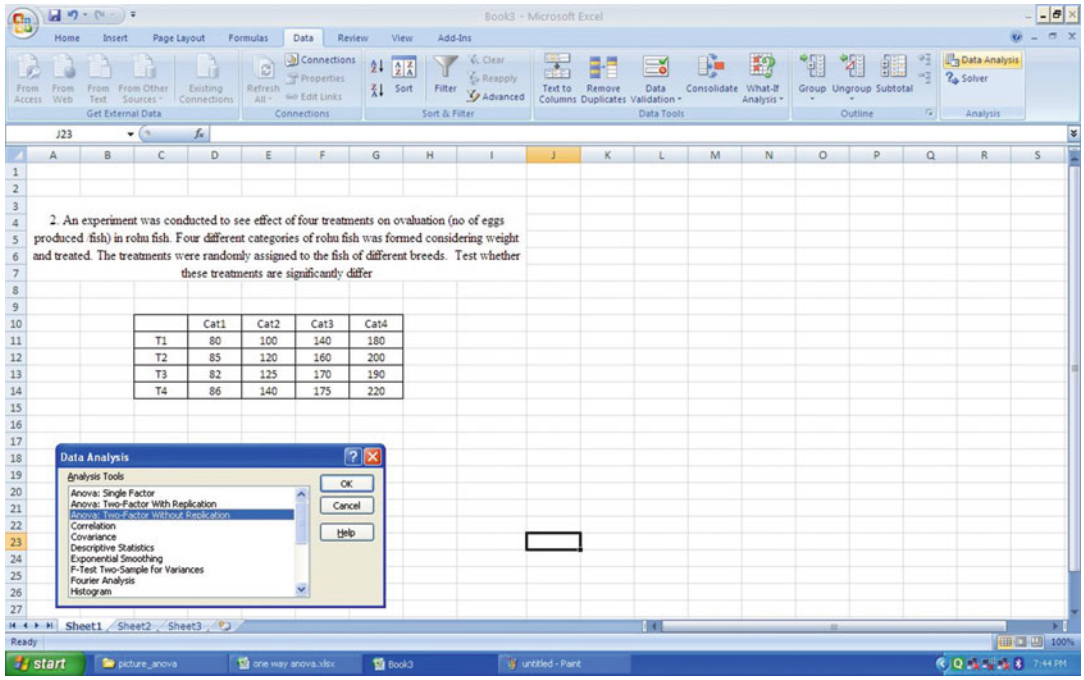
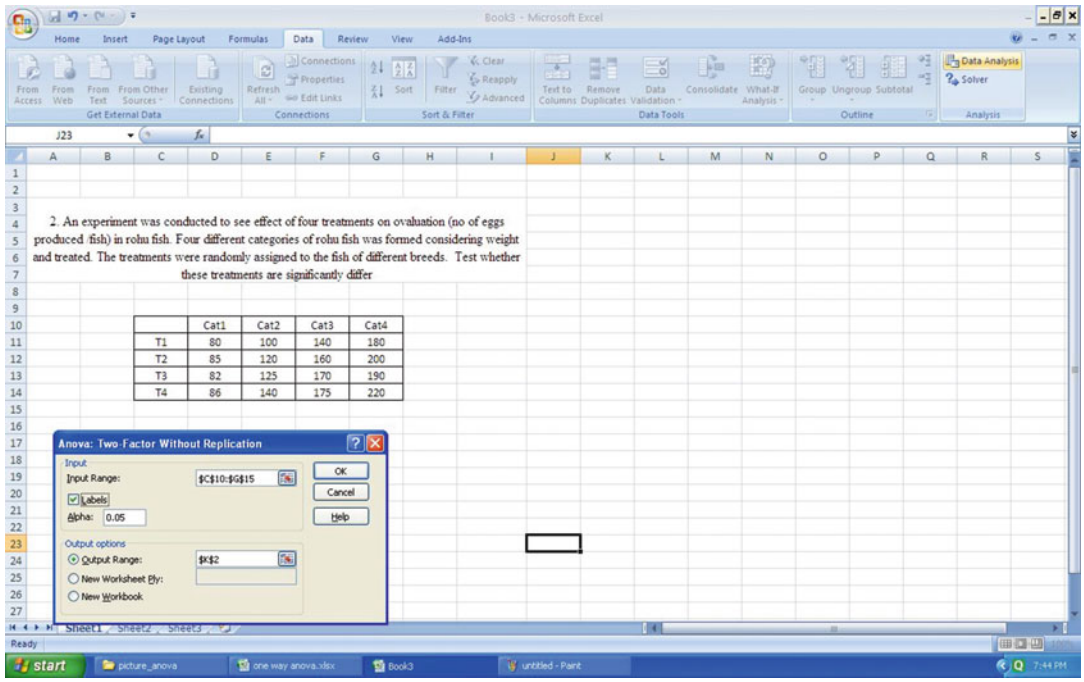
Step 1: Go to data analysis of Tools menu.



Step 2: Select Anova – two factor without replication.



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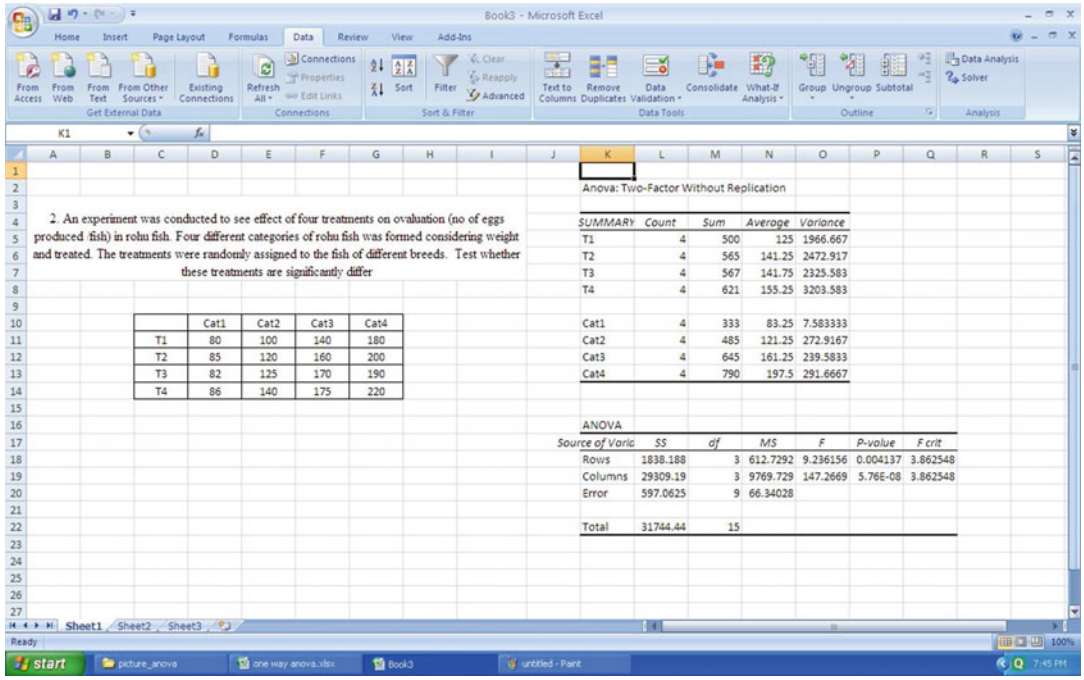
Step 3: Select the options as given above.



Step 4: Get the results as given above. Here rows are the treatments, and columns are the categories.

Step 5: From the above table, we see that both the factors (treatment and categories of rohu fish) are significant at $p = 0.05$. So we need to calculate the CD/LSD values to identify the pair of category of fish means and pairs of treatment means which are significantly different from each other and also to identify the best method of treatment as well as the category of fish weight to have high ovulation. CD values are calculated as follows:

$$CD_{0.05}(\text{treatments}) = \sqrt{\frac{2MSE}{r}} \times t_{0.025,\text{err}.df}.$$
$$= \sqrt{\frac{2 \times 66.346}{4}} \times t_{0.025,9.}$$
$$= \sqrt{\frac{2 \times 66.34}{4}} \times 2.26 = 13.02$$

and

$$CD_{0.05}(\text{category}) = \sqrt{\frac{2MSE}{m}} \times t_{0.025,\text{err}.df}.$$
$$= \sqrt{\frac{2 \times 66.34}{4}} \times t_{0.025,9.}$$
$$= \sqrt{\frac{2 \times 66.34}{4}} \times 2.26 = 13.02$$

Where r and m are the categories of fish used as block and number of treatments, respectively. From the values of CD, it is clear that (i) all the categories of fish and treatments are significantly different with respect to ovulation and T4 treatment is the best method for increasing ovulation in rohu fish. Treatment 2 and treatment 3 are statistically at par (ii). All categories of fish with respect to weight are statistically different in ovulation, while weight of category 4 fish found best to increase ovulation in rohu.

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9.6 Two-Way Classified Data with More Than One Observation per Cell

Let us consider fixed effect models for two-way classified data for two factors, A and B, with m and n levels, respectively, and l repetitions of the treatment combination. If y_{ijk} be the response recorded corresponding to kth observation of ith level of the factor A and jth level of the factor B, the observations can be presented as follows:

	B_1	B_2	.....	B_j	.....	B_n
A_1	y_{111} y_{112} : : y_{11l}	y_{121} y_{122} : : y_{12l}	....	y_{1j1} y_{1j2} : : y_{1jl}	....	y_{1n1} y_{1n2} : : y_{1nl}
A_2	y_{211} y_{212} : : y_{21l}	y_{221} y_{222} : : y_{22l}	....	y_{2j1} y_{2j2} : : y_{2jl}	....	y_{2n1} y_{2n2} : : y_{2nl}
:	:	:		:		:
:	:	:		:		:
A_i	y_{i11} y_{i12} : : y_{i1l}	y_{i21} y_{i22} : : y_{i2l}	....	y_{ij1} y_{ij2} : : y_{ijl}	....	y_{in1} y_{in2} : : y_{inl}
:	:	:	:	:	:	:
:	:	:	:	:	:	:
A_m	y_{m11} y_{m12} : : y_{m1l}	y_{m21} y_{m21} : : y_{m21}	....	y_{mj1} y_{mj1} : : y_{mj1}	....	y_{mn1} y_{mn1} : : y_{mn1}

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In the above analysis of variance for two-way classified data with one observation per cell, it was not possible to estimate the interaction effect of the factors. In the present case with two-way classified data having l observations per cell, one can work out the interaction effects. The model will be

$y_{ijk} = \mu + \alpha_i + \beta_j + \gamma_{ij} + e_{ijk}$,

where $i = 1, 2, \ldots\ldots, m$; $j = 1, 2, \ldots..., n$;

$k = 1, 2, \ldots..., l$

μ = general effect.

α_i = additional effect due to ith group of factor A.

β_j = additional effect due to jth group of factor B.

γ_{ij} = interaction effect due to ith group of factor A and jth group of factor B.

e_{ijk} = errors with associated with kth observation of ith group of factor A and jth group of factor B and are i.i.d $N(0, \sigma^2)$;

$$\sum_i \alpha_i = \sum_j \beta_j = \sum_i \gamma_{ij} = 0$$

The least square estimates are obtained by minimizing

$$\sum_i \sum_j \sum_k \left(y_{ijk} - \mu - \alpha_i - \beta_j - \gamma_{ij}\right)^2 \text{ for all } i \text{ and } j$$

To get

$$\hat{\mu} = \bar{y}_{...}$$
$$\hat{\alpha}_i = \bar{y}_{i..} - \bar{y}_{...}$$
$$\hat{\beta}_j = \bar{y}_{.j.} - \bar{y}_{...}$$
$$\hat{\gamma}_{ij} = \bar{y}_{ij.} - \bar{y}_{i..} - \bar{y}_{.j.} + \bar{y}_{...}$$

where, $\bar{y}_{...} = \frac{1}{mnl}\sum_i \sum_j \sum_k y_{ijk}$ = mean of all observations

$\bar{y}_{i..} = \frac{1}{nl}\sum_j \sum_k y_{ijk}$ = mean of ith level of A

$\bar{y}_{.j.} = \frac{1}{ml}\sum_i \sum_k y_{ijk}$ = mean of jth level of B

$\bar{y}_{ij.} = \frac{1}{l}\sum_k y_{ijk}$ = mean of the observations for ith level of A and jth level of B

$\hat{\gamma}_{ij} = \bar{y}_{ij.} - \bar{y}_{i..} - \bar{y}_{.j.} + \bar{y}_{...}$

Thus, the linear model becomes

$$y_{ijk} = \bar{y}_{...} + (\bar{y}_{i..} - \bar{y}_{...}) + (\bar{y}_{.j.} - \bar{y}_{...}) + (\bar{y}_{ij.} - \bar{y}_{i..} - \bar{y}_{.j.} + \bar{y}_{...}) + (y_{ijk} - y_{ij.})$$

Transferring $y_{...}$ to the left, squaring both the sides and summing over i,j,k, we get

$$\sum_i^m \sum_j^n \sum_k^l \left(y_{ijk} - \bar{y}_{...}\right)^2 = nl\sum_i (\bar{y}_{i..} - \bar{y}_{...})^2 + ml\sum_j \left(\bar{y}_{.j.} - \bar{y}_{...}\right)^2 + l\sum_i \sum_j \left(\bar{y}_{ij.} - \bar{y}_{i..} - \bar{y}_{.j.} + \bar{y}_{...}\right)^2 + \sum_i \sum_j \sum_k \left(y_{ijk} - \bar{y}_{ij.}\right)^2$$

[product terms vanishes as usual]

$$\textbf{or } SS_{\textbf{Tot}} = SS_A + SS_B + SS_{AB} + SS_{Er}.$$

Corresponding partitioning of the total d.f. is as follows:

$$\text{d.f. for } SS_{\text{Tot}} = \text{d.f. for } SS_A + \text{d.f. for } SS_B + \text{d.f. for } SS_{AB} + \text{d.f. for } SS_{Er}$$

$$lmn - 1 = (m-1) + (n-1) + (m-1)(n-1) + mn(l-1)$$

Hypotheses to be tested are as follows:

$H_{01}: \alpha_1 = \alpha_2 = \alpha_3 = \ldots\ldots\ldots\alpha_m = 0,$
$H_{02}: \beta_1 = \beta_2 = \beta_3 = \ldots\ldots\ldots\beta_n = 0$ and
$H_{03}: \gamma_{ij} = 0 \forall i,j$ (for all i and j)

Against the alternative hypotheses,

H_{11}: All α 's are not equal,
H_{12}: All β ' s are not equal and
H_{13}: All γ_{ij}' s are not equal, $\forall\, i,j$(for all i and j)

Dividing the sum of squares by their corresponding d.f. will result in corresponding *MSs*, and the ANOVA table structure will be as follows:

ANOVA table for two-way classified data with m l(>1) observations per cell

SOV	d.f.	SS	MS	F
Factor A	$m-1$	SS_A	$MS_A = SS_A/(m-1)$	MS_A/MS_{Er}
Factor B	$n-1$	SS_B	$MS_B = SS_B/(n-1)$	MS_B/MS_{Er}
Interaction (A × B)	$(m-1)(n-1)$	SS_{AB}	$MS_{AB} = SS_{AB}/(m-1)(n-1)$	MS_{AB}/MS_{Er}
Error	By subtraction = $mn(l-1)$	SS_{Er}	$MS_{Er} = SS_{Er}/mn(l-1)$	
Total	$mn\,l-1$	SS_{Tot}		

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For practical purposes, different sums of squares are calculated by using the following formulae:

$$\text{Step 1: Grand Total} = G = \sum_{i}^{m}\sum_{j}^{n}\sum_{k}^{l} y_{ijk}$$

$$\text{Step 2: Correction Factor} = CF = \frac{G^2}{mnl}$$

$$\text{Step 3: Treatment Sum of Squares} = SS_{Tr} = \sum_{i}^{m}\sum_{j}^{n}\sum_{k}^{l}\left(y_{ijk} - \bar{y}_{...}\right)^2 = \sum_{i}^{m}\sum_{j}^{n}\sum_{k}^{l}\left(y_{ijk}\right)^2 - CF$$

$$\text{Step 4: Sum of Squares due to A} = SS_A = nl\sum_{i}(\bar{y}_{i..} - \bar{y}_{...})^2 = nl\left[\sum_{i}\bar{y}_{i..}^2 - m\bar{y}_{...}^2\right] = nl\sum_{i}\left(\frac{\sum_{j}\sum_{k} y_{ijk}}{nl}\right)^2 - CF = \frac{1}{nl}\sum_{i} y_{i..}^2 - CF$$

$$\text{Step 5: Sum of Squares due to B} = SS_B = ml\sum_{j}\left(\bar{y}_{.j.} - \bar{y}_{...}\right)^2 = \frac{1}{ml}\sum_{i} y_{j.}^2 - CF$$

$$\text{Step 6: Sum of Squares due to AB} = 1\sum_{\text{i}}\sum_{j}\left(\bar{y}_{ij.} - \bar{y}_{i..} - \bar{y}_{.j.} + \bar{y}_{...}\right)^2$$

$$= 1\sum_{i}\sum_{j}\left(\bar{y}_{ij.} - \bar{y}_{...} - (\bar{y}_{i..} - \bar{y}_{...}) - \left(\bar{y}_{.j.} - \bar{y}_{...}\right)\right)^2$$

$$= l\left[\sum_{i}\sum_{j}\left(\bar{y}_{ij.} - \bar{y}_{...}\right)^2 - n\sum_{i}(\bar{y}_{i..} - \bar{y}_{...})^2\right.$$

$$\left. -m\sum_{j}\left(\bar{y}_{.j.} - \bar{y}_{...}\right)^2\right.$$

$$= l\sum_{i}\sum_{j}\left(\bar{y}_{ij.} - \bar{y}_{...}\right)^2 - SS_A - SS_B$$

$$= 1\left[\sum_{i}^{m}\sum_{j}^{n}\mathrm{y}_{ij.}^2 - mny_{...}^2\right] - SS_A - SS_B$$

$$= \sum_{i}^{m}\sum_{j}^{n}\frac{y_{ij.}^2}{1} - CF - SS_A - SS_B$$

$$= SS_{Tr} - SS_A - SS_B$$

$$\therefore ErSS = SS_{\text{Tot}} - SS_{Tr} = SS_{\text{Tot}} - (SS_A + SS_B + SS_{AB}) = SS_{\text{Tot}} - SS_A - SS_B - SS_{AB}$$

In the event of rejection of any or all the null hypotheses, that means if the equality of population means are rejected against at least one pair of unequal population means, we are to find out the pairs of population means from the sampled data, which are significantly different from each other, and which population considering all the factors separately and their interaction is the best population with respect to the characteristic under consideration. That means we are to compare multiple number of means, i.e., multiple comparison of means. This is followed as per the formula given in for one-way ANOVA, but there will be two corrections:

(a) Number of observations are equal for all treatment combinations.
(b) Corresponding to rejection of each null hypothesis, there would one LSD or CD value to be calculated.

Thus, we are to get three CD values corresponding to factor A, factor B, and their interaction, respectively, using the formulae given below:

(1) $LSD/CD(0.05)$ for factor A

$$= \sqrt{\frac{2MSE}{\text{No of repetition} \times \text{levels of factor B}}} \times t_{0.025,\text{err}.df.} = \sqrt{\frac{2MSE}{l.\text{n}}} \times t_{0.025,\text{err}.d.f.}$$

(2) $LSD/CD(0.05)$ for factor B

$$= \sqrt{\frac{2MSE}{\text{No of repetition} \times \text{levels of factor A}}} \times t_{0.025,\text{err}.df.} = \sqrt{\frac{2MSE}{l.\text{m}}} \times t_{0.025,\text{err}.d.f.}$$

(3) $LSD/CD(0.05)$ for interaction of factor A and B

$$= \sqrt{\frac{2MSE}{\text{No of repetition}}} \times t_{0.025,\text{err}.df.} = \sqrt{\frac{2MSE}{l}} \times t_{0.025,\text{err}.d.f.}$$

Example 9.5

An experiment was conducted to determine the effect of three diet treatments ($T1$, $T2$, and $T3$) on daily gain in body weight (g/d) of pigs. Pigs of five different breeds were selected. In each breed, there were six animals to which each treatment was randomly assigned to two animals. There-

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fore, a total of 30 animals were used. Analyze the data and draw conclusions on whether:

(a) There exists significant difference between three different breeds of pigs with respect to weight gain.
(b) Three different treatments significantly differ with respect to weight gain.
(c) There exists any interaction effect between the breed and diet or not:

	Pig breed 1	Pig breed 2	Pig breed 3	Pig breed 4	Pig breed 5
T1	240	290	510	320	420
	250	275	520	340	410
T2	170	265	470	330	375
	180	260	480	300	380
T3	190	255	500	310	390
	210	265	490	290	395

The problem can be visualized as the problem of two-way analysis of variance with two observations per cell. The linear model is

$$y_{ijk} = \mu + \alpha_i + \beta_j + \gamma_{ij} + e_{ijk}$$

where,

y_{ijk} is the gain in weight associated with kth observation of ith level of treatment(diet) and jth level of breed
α_i is the effect of ith level of treatment(diet); i=1,2,3
β_j is the effect of jth level of breed; j=1,2,3,4,5
γ_{ij} is the interaction effect of ith level of treatment(diet) and jth level of breed
e_{ijk} is the error component associated with $k$thobservation of $i$ith level of treatment(diet) and jth level of breed

We want to test the following null hypotheses:

$H_{01} : \alpha_1 = \alpha_2 = \alpha_3 = 0$ against H_{11}: α' s are not equal
$H_{02} : \beta_1 = \beta_2 = \beta_3 = \beta_4 = \beta_5 = 0$ against H_{12}: β' s are not equal
$H_{03} : \gamma_{ij}'s = 0$ for all i, j against H_{13}: γ_{ij}' s are not equal

Let us construct the following table of totals ($y_{ij.}$):

	Pig breed 1	Pig breed 2	Pig breed 3	Pig breed 4	Pig breed 5	Total ($y_{i..}$)	Mean ($\bar{y}_{i..}$)
T1	490	565	1030	660	830	3575	715
T2	350	525	950	630	755	3210	642
T3	400	520	990	600	785	3295	659
Total ($y_{.j.}$)	1240	1610	2970	1890	2370	10,080	
Mean $\left(\bar{y}_{.j.}\right)$	413.33	536.67	990.00	630.00	790.00		

Total number of observations $= mnl$
$= 3 \times 5 \times 2 = 30 = N$ (say)

$$G = 240 + 250 + 170 + 180 + \ldots\ldots\ldots + 330 + 300 + 310 = 10080$$

$$CF = GT^2/N = 10080^2/30 = 3386880$$

$$TSS = 240^2 + 250^2 + \ldots\ldots\ldots.. + 330^2 + 300^2 + 310^2 - CF = 314170$$

$$TrSS = \frac{3575^2}{10} + \frac{3210^2}{10} + \frac{3295^2}{10} - CF = 7295$$

$$BSS = \frac{1240^2}{6} + \frac{1610^2}{6} + \frac{2970^2}{6} + \frac{1890^2}{6} - CF = 303053.33$$

$$\text{Table } SS = 1/2\left(490^2 + 350^2 + \ldots.. + 755^2 + 785^2\right) - CF = 312620$$

$$SS\ (Tr \times B) = \text{Table } SS - TrSS - -BSS = 312,620 - 7295 - 303053.33 = 2271.67$$

$$Er\ SS = TSS - Tr\ SS - BSS - SS\ (Tr \times xB) = 314170 - 7295 - 303053.33 - 2271.67 = 1550$$

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ANOVA table for two-way analysis of variance with three observations per cell

ANOVA table					
Source of variation	d.f.	SS	MS	Cal F	Tab F
Breed	4	303053.33	75763.33	733.19	3.06
Diet	2	7295.00	3647.50	35.30	3.68
Breed × diet	8	2271.67	283.96	2.75	2.64
Error	15	1550.00	103.33		
Total	29	314170.00			

Let the level of significance $\alpha = 0.05$.

The table value of $F_{0.05;4,15} = 3.06$, $F_{0.05;2,15} = 3.68$, and $F_{0.05;8,15} = 2.64$, i.e., $F_{\text{Cal}} > \text{F}_{\text{Tab,}}$ in all the cases, i.e., breed, diet, and breed × diet interaction are having significant effects on gain in body weights of pig. So the tests are significant, and we reject the null hypotheses and conclude that there exists significant difference among the effects of diet, breeds, and their interactions with respect to the weight gain.

Now, we are interested to identify the best diet, best breed, and the breed × diet combination providing best weight gain.

To accomplish this task, we calculate critical difference values for diet, breed, and interaction separately as follows:

$$\begin{aligned} LSD_{0.05}/CD_{0.05}(\text{Diet}) &= \sqrt{\frac{2MSE}{l \times n}} \times t_{0.025,\text{err}.df.} \\ &= \sqrt{\frac{2 \times 103.33}{2 \times 5}} \times t_{0.025,15.} \\ &= \sqrt{\frac{2 \times 103.33}{2 \times 5}} \times 2.131 \\ &= 9.687 \end{aligned}$$

Ordered diet effect on gain in body weight		
T1	T3	T2
715	659	642

It is clear from the above table that T1 diet has resulted in maximum gain in body weight and which is also significantly different from the effects of other two diets. *Thus, diet one is the best diet:*

$$\begin{aligned} LSD_{0.05}/CD_{0.05}(\text{Breed}) &= \sqrt{\frac{2MSE}{l \times m}} \times t_{0.025,\text{err}.df.} \\ &= \sqrt{\frac{2 \times 103.33}{2 \times 3}} \times t_{0.025,15.} \\ &= \sqrt{\frac{2 \times 103.33}{2 \times 3}} \times 2.131 \\ &= 12.506 \end{aligned}$$

Ordered breed effect on gain in body weight				
B3	B5	B4	B2	B1
990.00	790.00	630.00	536.67	413.33

Comparing the mean differences among the breeds from the above table with the corresponding LSD value of breed, it is clear that all the breeds significantly differ from each other w.r.t. gain in body weight of pigs. From the above table, it is also clear that breed 3 is the best breed w.r.t. gain in body weight of pigs:

$$\begin{aligned} LSD_{0.05}/CD_{0.05}(D \times B) &= \sqrt{\frac{2MSE}{l}} \times t_{0.025,\text{err}.df.} \\ &= \sqrt{\frac{2 \times 103.33}{2}} \times t_{0.025,15.} \\ &= \sqrt{\frac{2 \times 103.33}{2}} \times 2.131 \\ &= 21.662 \end{aligned}$$

Ordered treatment combination effect towards gain in body weight of pigs														
T1B3	T3B3	T2B3	T1B5	T3B5	T2B5	T1B4	T2B4	T3B4	T1B2	T2B2	T3B2	T1B1	T3B1	T2B1
1030	990	950	830	785	755	660	630	600	565	525	520	490	400	350
Mean differences among the treatment combinations w.r.t. gain in body weight of pigs														
	T3B3	T2B3	T1B5	T3B5	T2B5	T1B4	T2B4	T3B4	T1B2	T2B2	T3B2	T1B1	T3B1	T2B1
T1B3	40	80	200	245	275	370	400	430	465	505	510	540	630	680
T3B3		40	160	205	235	330	360	390	425	465	470	500	590	640
T2B3			120	165	195	290	320	350	385	425	430	460	550	600

(continued)

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T1B5				45	75	170	200	230	265	305	310	340	430	480
T3B5					30	125	155	185	220	260	265	295	385	435
T2B5						95	125	155	190	230	235	265	355	405
T1B4							30	60	95	135	140	170	260	310
T2B4								30	65	105	110	140	230	280
T3B4									35	75	80	110	200	250
T1B2										40	45	75	165	215
T2B2											5	35	125	175
T3B2												30	120	170
T1B1													90	140
T3B1														50

From the above table, it can be seen that difference between any pair of treatment combination means is greater than the LSD value for interaction effects excepting the difference between T2B2 and T3B2 combinations. Among the treatment combinations, T1B3 is resulting in significantly higher gain in body weight than any other treatment combination. Therefore, one can conclude that breed 3 with diet 1 can produce maximum gain in body weight of pigs under experimentation.

Thus, from the analysis, we draw conclusions that:

1. The diets differ significantly among themselves, and the best diet is T_1.
2. The breeds differ significantly among themselves, and the best breed is the B_3.
3. The diet T_1 along with breed B_3 produces significantly higher weight gain than any other combination.

9.6.1 Analysis of Two-Way Classified Data with More than One Observation per Cell Using MS Excel

Example 9.6

The yield (q/ha) of three different varieties of forage sorghum with application of three nitrogen doses is given below. Analyze the data to show whether:

(a) There exists significant differences in yield of three varieties of forage sorghum.
(b) Nitrogen doses are significantly different with respect to production.
(c) The varieties have performed equally under different doses of nitrogen or not:

Treatment	Variety 1	Variety 2	Variety 3
T1	8.90	9.00	12.00
	9.20	10.20	11.50
	9.70	11.10	11.80
T2	8.50	9.10	10.50
	9.00	8.50	11.80
	9.20	8.80	12.00
T3	11.70	12.20	14.50
	11.55	12.50	14.20
	11.50	12.80	15.00

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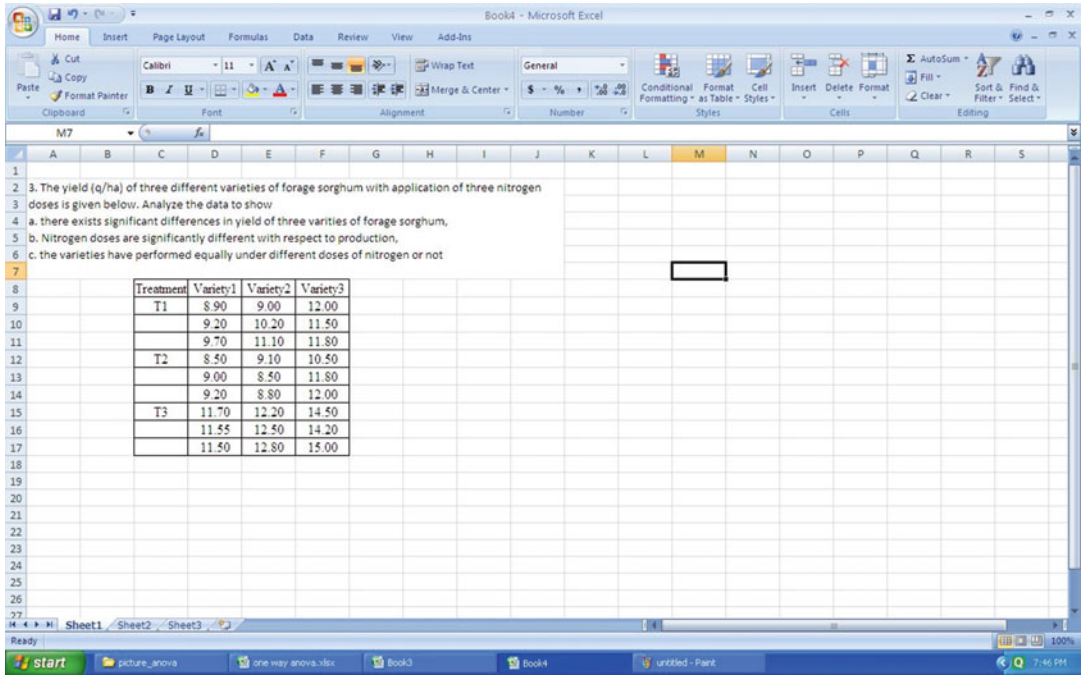
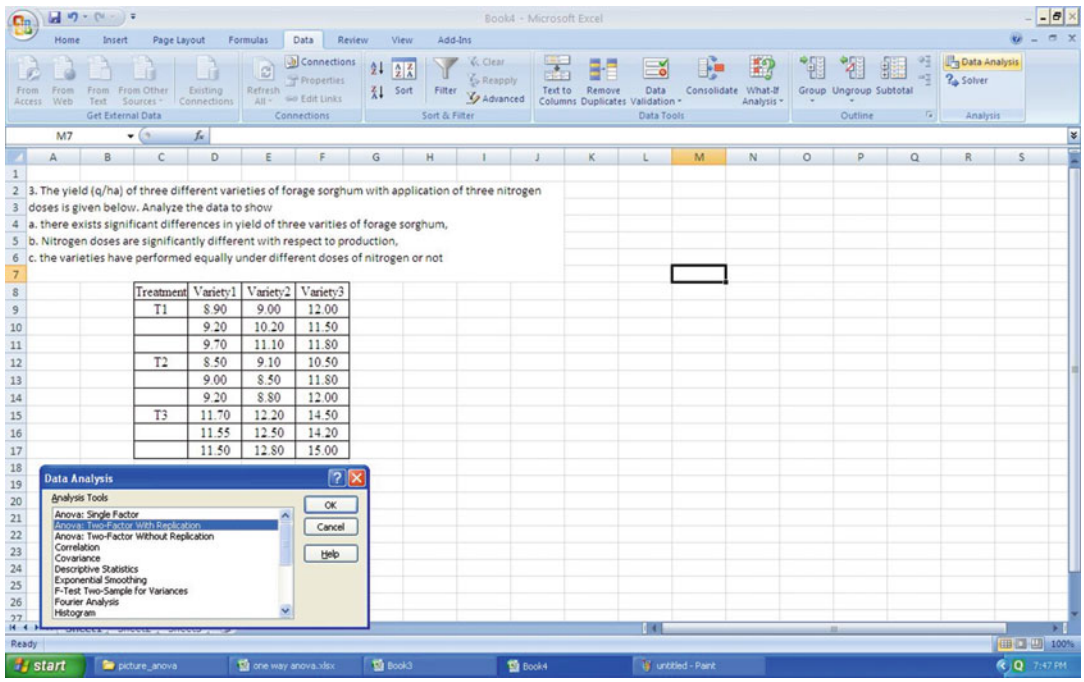


Step 1: Go to data analysis of Tools menu.

Step 2: Select ANOVA – two factor with replication



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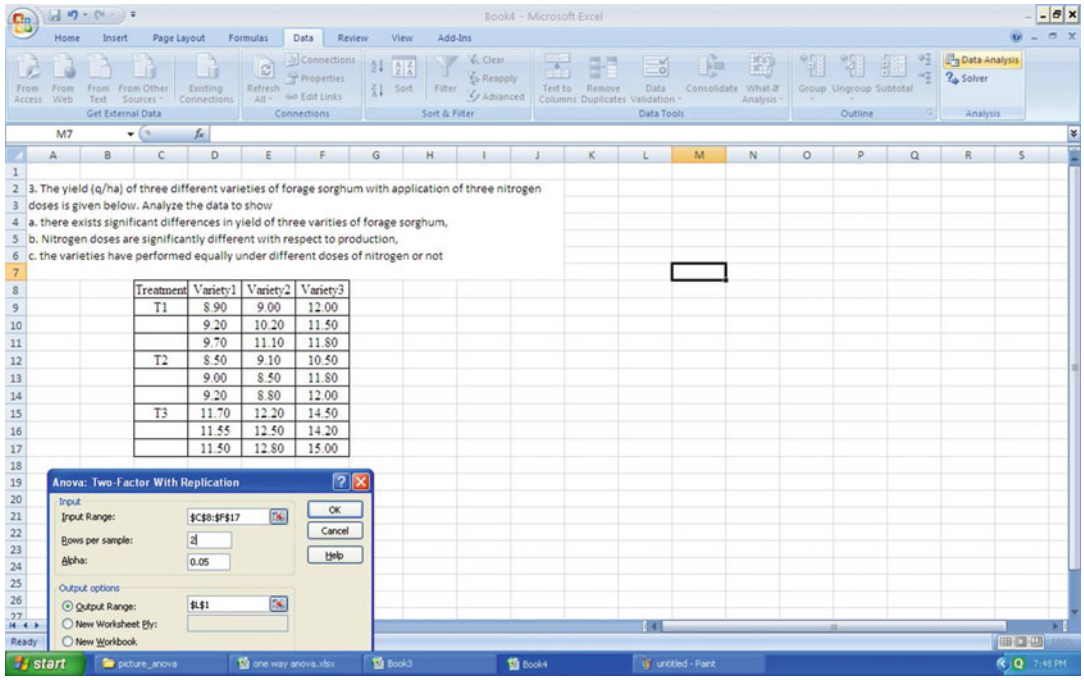
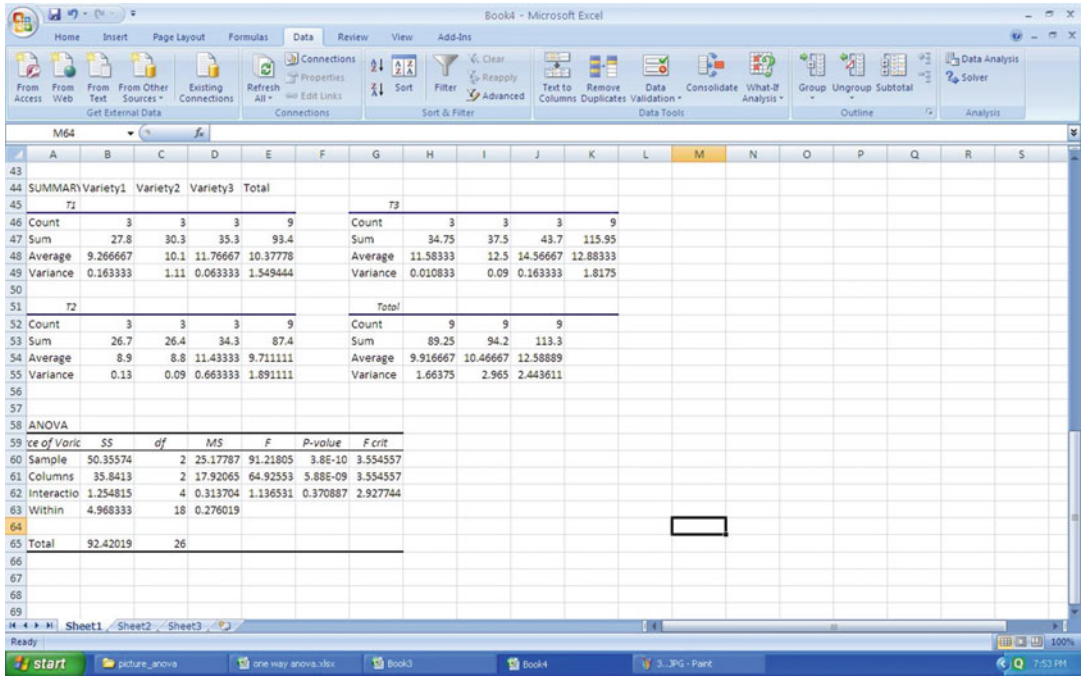


Treatment	Variety1	Variety2	Variety3
T1	8.90	9.00	12.00
	9.20	10.20	11.50
	9.70	11.10	11.80
T2	8.50	9.10	10.50
	9.00	8.50	11.80
	9.20	8.80	12.00
T3	11.70	12.20	14.50
	11.55	12.50	14.20
	11.50	12.80	15.00

Step 3: Select the options as given above.



SUMMARY	Variety1	Variety2	Variety3	Total
T1				
Count	3	3	3	9
Sum	27.8	30.3	35.3	93.4
Average	9.266667	10.1	11.76667	10.37778
Variance	0.163333	1.11	0.063333	1.549444
T2				
Count	3	3	3	9
Sum	26.7	26.4	34.3	87.4
Average	8.9	8.8	11.43333	9.711111
Variance	0.13	0.09	0.663333	1.891111

T3				
Count	3	3	3	9
Sum	34.75	37.5	43.7	115.95
Average	11.58333	12.5	14.56667	12.88333
Variance	0.010833	0.09	0.163333	1.8175
Total				
Count	9	9	9	
Sum	89.25	94.2	113.3	
Average	9.916667	10.46667	12.58889	
Variance	1.66375	2.965	2.443611	

ANOVA

ce of Varic	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Sample	50.35574	2	25.17787	91.21805	3.8E-10	3.554557
Columns	35.8413	2	17.92065	64.92553	5.88E-09	3.554557
Interactio	1.254815	4	0.313704	1.136531	0.370887	2.927744
Within	4.968333	18	0.276019			
Total	92.42019	26				

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Step 4: Get the result as given above. Here, samples are the types and columns are the seasons.

Step 5: From the above table, we see that both the factors are significant at $p = 0.05$ and their interaction effects are nonsignificant at 5 % level. So we need to calculate the *CD*/*LSD* values to identify the pair of varieties of forage sorghum means and pair of nitrogen dose means which are significantly different from each other. Corresponding *CD* values are calculated as follows:

$$LSD_{0.05}/CD_{0.05}(\text{Varieties}) = \sqrt{\frac{2MSE}{r \times s}} \times t_{0.025,\text{err}.df.}$$
$$= \sqrt{\frac{2 \times 0.276}{3 \times 3}} \times t_{0.025,26.}$$
$$= \sqrt{\frac{2 \times 0.276}{3 \times 3}} \times 2.10$$
$$= 1.56$$

$$LSD_{0.05}/CD_{0.05}(\text{Fertilizer}) = \sqrt{\frac{2MSE}{r \times s}} \times t_{0.025,\text{err}.df.}$$
$$= \sqrt{\frac{2 \times 0.276}{3 \times 3}} \times t_{0.025,26.}$$
$$= \sqrt{\frac{2 \times 0.276}{3 \times 3}} \times 2.10$$
$$= 1.56$$

Comparing calculated CD value with difference in means of varieties and treatment, variety 3 is the best variety, and treatment 3 is the best treatment for increasing forage sorghum yield.

Problem 9.1

Following information are pertaining to the gain in weight (g) per month of five groups of fishes administered with five different feeds. Analyze the data and test whether there exists any difference in effects of feeds on body weight of fishes or not. If yes, then find out the best feed:

Feed 1	Feed 2	Feed 3	Feed 4	Feed 5
109	94	160	110	75
104	87	155	125	78
111	81	135	117	70
117	81	142	18	75
105	95	155	120	80
135	105	155	132	80
142	105		135	55
	115			60

Problem 9.2 The following data gives number of fruits per plant under four types of growth regulator treatments in 3 years. Analyze the data to show which growth regulator and which year have resulted maximum fruits per plant:

Method	Year 1	Year 2	Year 3
GR1	145	135	150
GR2	195	200	210
GR3	355	375	385
GR4	240	225	275

Problem 9.3 The following data give the weight (q) of mango per plant for four different types of mango in 3 different years. Analyze the data, and comment (i) which type of mango is the best, (ii) which year has produced maximum mango per plant, and (iii) which type-year combination has produced highest fruit per plant:

Method	Year 1	Year 2	Year 3
V 1	4.52	5.46	4.75
	4.61	5.65	4.66
	4.45	5.50	4.85
V 2	8.55	10.0	7.50
	8.05	9.50	7.48
	8.10	8.75	7.12
V 3	3.56	6.58	4.15
	4.08	6.66	4.65
	4.25	6.00	4.65
V 4	5.65	5.08	4.01
	6.05	5.20	4.20
	5.59	5.40	4.35

9.7 Violation of Assumptions in ANOVA

The results from analysis of variance are acceptable so long the assumptions of the ANOVA are maintained properly. Failure to meet the assumption that the effects (treatments and the environmental) additive in nature and experimental errors are i.i.d. N (0, σ^2) adversely affects both the sensitivity of *F* and *t* test as well as the level of significance. So, before analysis data needs to be checked, data which are suspected to be

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deviated from one or more of the assumptions required to be corrected before taking up the analysis of variance. The violations of additivity can be detected by the fact that the effects of two or more factors are additive only when these are expressed in percentage. The multiplicative effect is common in case of design of experiment relating to the incidence of diseased pests. The normality assumption is needed only during the process of estimation and inference phase. The estimator and their variances remain valid even under nonnormality conditions. The independence of error assumptions is maintained with the use of proper randomization technique. Heteroscedasticity does not make the estimator biased. The remedial measure for handling the heterogeneous variance is either through construction of a new model to which the available data could be fit or through correction of available data in such a way that corrected data follow the assumptions of the analysis of variance. Development of new model is the task of the statisticians. But for a practitioner, transformation of data is the most commonly used practice to overcome the problems of violations of assumptions in analysis of variance.

Though there are certain nonparametric methods to bypass the problems of violation or assumption in analysis of variance, but for each and every analysis of variance model, we may not have the appropriate nonparametric procedure. Moreover, the parametric methods are the superior over the nonparametric method, if available and applied properly. Thus, data transformation is by far the most widely used procedure for the data violating the assumptions of analysis of variance.

Data Transformation Depending upon the nature of the data, different types of transformation are generally used to make the data corrected for analysis of variance, viz., logarithmic transformation, square root transformation, angular transformation, etc.

9.7.1 Logarithmic Transformation

Logarithmic transformation is used when the data are having multiplicative effects, i.e., when the variance/range is proportional to the mean. The number of parasitic insects per animal, number of egg mass per unit area, number of larvae per unit area, etc. are the typical examples where logarithmic transformation can be used effectively. The procedure is to take simply the logarithm of each and every observation and carry out the analysis of variance following usual procedure with the transformed data. However, if in the data set small values (less than 10) are recorded, then instead of taking log(x), it will be better take $\log(x + 1)$. The final results or inference should be drawn on the basis of transformed mean values and on the basis of calculations made through transformed data. While presenting the mean table, it will be appropriate to recalculate the means by taking the antilog of the transform data. In practice, the treatment means are calculated from the original data because of simplicity of calculations, but statistically the procedure of converting transformed mean to original form is more appropriate. If there is a mismatch in the two procedures, the procedure of converting the transformed mean with the help of antilogarithm is preferred over the other procedure.

Example 9.7

In fish breeding improvement program, five chemical treatments are given to four varieties of fish and tested for number of eggs viable (lakh). Verify the relationship between the mean effects of the treatments and the respective variance to use suitable transformation and analyze the data:

	C. catla	*C. rohita*	*C. mrigala*	*C. carpio*
T1	2.2	1.4	1.8	2.1
T2	2.9	1.9	2.1	2.4
T3	2.5	1.5	1.8	2.2
T4	2.4	1.8	1.9	2.2
T5	2.3	1.4	1.7	1.9

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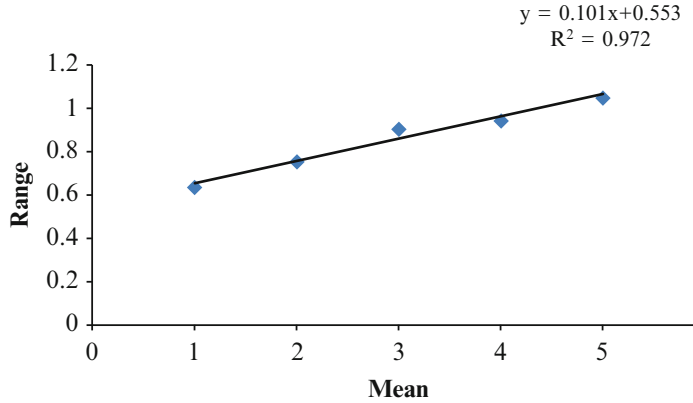
Solution As because this experiment is related with count data, so violation of the assumption of ANOVA is suspected. So from the above table, we first make the following table to get an idea about the relationship between the mean of the treatments and the ranges:

	C. catla	*C. rohita*	*C. mrigala*	*C. carpio*	Total	Average	Range
T1	2.2	1.4	1.8	2.1	7.47	1.87	0.75
T2	2.9	1.9	2.1	2.4	9.25	2.31	0.94
T3	2.5	1.5	1.8	2.2	7.94	1.99	1.05
T4	2.4	1.8	1.9	2.2	8.43	2.11	0.64
T5	2.3	1.4	1.7	1.9	7.31	1.83	0.91



By plotting the treatment means with range, it is found that there exists a linear relationship between the range and the mean; range increases proportionately with mean. Thus, a logarithmic transformation is necessary before taking up the analysis.

The following table presents the transformed data. It may be noted that as all observations are below 10, we apply $\log(X + 1)$ transformation instead of $\log(X)$.

	C. catla	*C. rohita*	*C. mrigala*	*C. carpio*
T1	0.5021	0.3844	0.4452	0.4882
T2	0.5873	0.4658	0.4878	0.5301
T3	0.5454	0.3912	0.4491	0.4991
T4	0.5371	0.4483	0.4680	0.5111
T5	0.5141	0.3732	0.4374	0.4690

Using the MS Excel program (as described in Example 9.5) with the transformed data, we analyze the above data to get the following ANOVA table:

ANOVA						
Source of variation	d.f.	SS	MS	F	P-value	F crit
Treatments	4	0.012789	0.003197	16.96906	7.01E-05	3.259167
Types	3	0.043310	0.014437	76.62135	4.28E-08	3.490295
Error	12	0.002261	0.000188			
Total	19	0.058360				

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The *LSD* value at 5 % level of significance is given by

$$LSD_{(0.05)}(\text{Treat.}) = \sqrt{\frac{2ErMS}{Type}} \times t_{0.025,12}$$
$$= \sqrt{\frac{2 \times 0.000188}{4}} \times 2.179$$
$$= 0.021$$
$$LSD_{(0.05)}(\text{Type.}) = \sqrt{\frac{2ErMS}{\text{Treat.}}} \times t_{0.025,12}$$
$$= \sqrt{\frac{2 \times 0.000188}{5}} \times 2.179$$
$$= 0.019$$

From the *LSD* values, it is clear that all the treatments as well as the types are significantly different from each other with respect to egg viability.

By arranging the treatment means in descending order, we find that treatment 2 is the best treatment with respect to egg viability:

Treatment means		
	Transformed	Original
T5	0.448414	1.83
T1	0.454986	1.87
T3	0.471205	1.99
T4	0.491147	2.11
T2	0.51777	2.31

By arranging the type means in descending order, we find that treatment 2 is the best treatment with respect to egg viability:

Type means		
	Transformed	Original
C. rohita	0.4126	1.60
C. mrigala	0.4575	1.86
C. carpio	0.4995	2.16
C. catla	0.5372	2.46

Problem 9.4 The following data gives the number of panicle per hill as a result of application of seven different flower initiating regulator in a field trial. Verify the relationship between the mean effect of the treatments and the respective variances to use suitable transformation, and analyze the data using suitable model:

Growth regulator	R 1	R 2	R 3
GR1	3	12	14
GR 2	4	5	6
GR 3	5	7	13
GR 4	3	10	4
GR 5	9	18	15
GR 6	2	16	25
GR 7	5	1	2

9.7.2 Square Root Transformation

When count data are consisting of small whole numbers and the percentage data arising out of count data where the data ranges either between 0 and 30 % or between 70 and 100 %, then square root transformation is used. This type of data generally follows a Poison distribution in which the variance/range tends to be proportional to the mean. Data obtained from counting the rare events like number of death per unit time, number of infested leaf per plant, number of call received in a telephone exchange, or the percentage of infestation (disease or pest) in a plot (either 0–30 % or 70–100 %) are the examples where square root transformation can be useful before taking up analysis of variance to draw a meaningful conclusion or inference. If most of the values in a data set are small (less than 10) coupled with the presence of 0 values, instead of using $\sqrt{x}$ transformation, it is better to use $\sqrt{(x+0.5)}$. The analysis of variance to be conducted with the transformed data and the mean table should be made from the transformed data instead of taking the mean from original data.

Example 9.8
The following information is pertaining to the number of insects per plot after application of six different insecticides in forage maize. Analyze the data to work out the most efficient herbicide:

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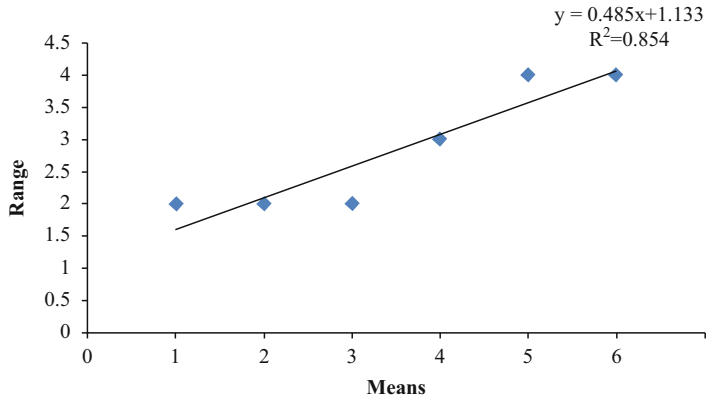
Pesticides	Replication 1	Replication 2	Replication 3	Replication 4
I1	2	3	6	3
I2	4	4	3	5
I3	5	7	6	5
I4	12	9	10	11
I5	7	8	9	8
I6	0	5	3	3

Solution The information given in this problem is in the form of small whole numbers, and plotting the data, one can find a relationship between the range and the treatment means:

Insecticides	Replication 1	Replication 2	Replication 3	Replication 4	Average	Range
I1	2	3	6	3	3.50	4.00
I2	4	4	3	5	4.00	2.00
I3	5	7	6	5	5.75	2.00
I4	12	9	10	11	10.50	3.00
I5	7	8	9	8	8.00	2.00
I6	0	5	3	3	2.75	5.00



Hence, a square root transformation will be appropriate before taking up the analysis of variance.

So from the given data table, we first make the following table by taking square roots of the given observations. It may be noted that the data set contains small whole number (<10); instead of $\sqrt{X}$, we have taken $\sqrt{(X+0.5)}$:

	R 1	R 2	R 3	R 4
I1	1.581139	1.870829	2.54951	1.870829
I2	2.12132	2.12132	1.870829	2.345208
I3	2.345208	2.738613	2.54951	2.345208
I4	3.535534	3.082207	3.24037	3.391165
I5	2.738613	2.915476	3.082207	2.915476
I6	0.707107	2.345208	1.870829	1.870829

Using the MS Excel program with the transformed data, we analyze the above data to get the following ANOVA table:

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ANOVA						
Source of variation	d.f.	SS	MS	F	P-value	F crit
Replication	3	0.49834	0.166113	1.338214	0.29932	3.287382
Insecticide	5	7.451084	1.490217	12.00524	8.3E-05	2.901295
Error	15	1.861958	0.124131			
Total	23	9.811382				

The *LSD* value at 5 % level of significance is given by

$$LSD_{(0.05)} = \sqrt{\frac{2ErMS}{r}} \times t_{0.05,15}$$
$$= \sqrt{\frac{2 \times 0.1241}{4}} \times 2.489 = 0.6203$$

Arranging the treatment means in ascending order, we find that insecticide 4 one is the best treatment recording minimum number of insects per plot:

Treatment means		
	Transformed	Original
I6	1.698493	2.75
I1	1.968076	3.50
I2	2.114669	4.00
I3	2.494635	5.75
I5	2.912943	8.00
I4	3.312319	10.50

Problem 9.5 The following information is pertaining to the number of insects per plant in six different treatment in an insecticidal trial. Analyze the data to work out the most efficient insecticide:

Insecticides	Replication 1	Replication 2	Replication 3	Replication 4
I1	3	4	3	3
I2	2	4	6	4
I3	4	7	5	5
I4	4	4	4	5
I5	7	7	10	9
I6	10	10	9	10

9.7.3 Angular Transformation

Proportion or percentage data *arising out of count data* are subjected to angular transformation or arcsine transformation before taking up analysis of variance. But the percentage data like percentage of carbohydrate, protein, sugar etc., percentage of marks, percentage of infections etc. which *are not arising out of count data* ($\frac{m}{n} \times 100$) *should not be put under arcsine transformation. Again, not all percentage data arising out of count data are to be subjected to arcsine transformation before analysis of variance, for example:*

(i) Percentage data arising out of count data and ranging between either 0 and 30 % or 70–100 % but not both, square root transformation should be used.
(ii) Percentage data arising out of count data and ranging between 30 and 70 %, no transformation is required.
(iii) Percentage data arising out of count data and which overlaps both the above two situations should only be put under arcsine transformation before taking up analysis of variance.

Thus, a percentage data set arising out of count data and having range (i) 0 *to more than* 30 %*, (ii) less than* 70–100 %*, and (iii)* 0–100 % *should be put under arcsine transformation.*

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The actual procedures is to convert the percentage data into proportions and transformed it into $\sin^{-1}\sqrt{p}$, where p = proportions $= \frac{m}{n}$; m is the number in favor of an event, and n is the total number. If the data set contains zero value, it should be substituted by $\frac{1}{4n}$, and the values of 100 % are changed to $100 - \frac{1}{4n}$, where n is the total number of counts on which proportions or percentages are work out. The principle of arcsine transformation is to convert the percentage data into angles measured in degrees meaning transformation 0–100 % data into 0 to 90° angles. Ready-made tables are available for different percentage values with their corresponding transformed values. However, in MS Excel using the following functional form "= degrees (asin(sqrt(p/100)))," where p is the percentage data, arcsine transformation of data could be made.

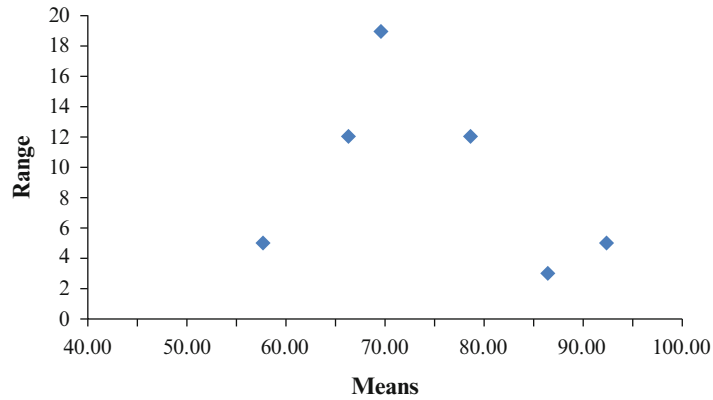
Analysis of variance is to be taken up on the transformed data, and inferences are made accordingly. However, to get the original mean retransformation of transformed means is preferred over the means from original data.

Example 9.9

The following table gives the percent fertilization rate for six breeds of fish in breeding improvement program. Analyze the data to find out the best breed with respect to fertilization rate:

	Replication 1	Replication 2	Replication 3
F1	55	60	58
F2	61	68	80
F3	73	78	85
F4	86	88	85
F5	90	95	92
F6	60	67	72

Solution From the given information, it is clear that (a) the data can be analyzed as per the analysis of two-way classified data and (b) the data relates to percentage data arising out of count data and the percentage ranges from 55 to 95 %. Thus, there is a chance of heterogeneous variance. In fact, by plotting the range values against the mean data, we get the picture of heterogeneous variance as shown below.



So we opt for *arcsine transformation* before taking up the analysis of variance.

The transformed data are presented in the following table:

Variety	Replication 1	Replication 2	Replication 3
F1	47.86959	50.76848	49.60345
F2	51.35452	55.5501	63.43495
F3	58.69355	62.0279	67.2135
F4	68.02724	69.7321	67.2135
F5	71.56505	77.07903	73.57006
F6	50.76848	54.93844	58.05194

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Next, we take up the analysis of variance with these transformed data as per the analysis of two classified data.

The analysis of variance table is as follows:

ANOVA					
Source of variation	d.f.	SS	MS	Cal F	Tab F
Replication	2	83.66922	41.83461	5.344039	4.102821
Breeds	5	1261.174	252.2347	32.22099	3.325835
Error	10	78.28275	7.828275		
Total	17	1423.126			

Thus, as the calculated value of F (32.22) exceeds the table value (3.32) of F statistic at 5 % level of significance, the test is significant, and the null hypothesis of equality of breed effect w.r.t. fertilization rate is rejected. That means the breeds differ significantly among themselves w.r.t. germination rate.

Now the problem lies in identifying the best fish breed w.r.t. fertilization rate. For the same, we work out the LSD (CD) value at 5 % level of significance as given below:

$$LSD_{(0.05)} = \sqrt{\frac{2ErMS}{r}} \times t_{0.025,10}$$
$$= \sqrt{\frac{2 \times 7.8282}{3}} \times 2.28 = 5.090$$

We arrange the breed means in ascending order and compare with them in relation to the above CD value, as presented below:

Treatment means		
	Transformed	Original
F1	49.4138	57.67
F6	54.5863	66.33
F2	56.7799	69.67
F3	62.6450	78.67
F4	68.3243	86.33
F5	74.0714	92.33

Thus, from the above table, it is clear that all the breeds significantly differ from each other with respect to fertilization rate excepting breed 6 and breed 2 which are statistically at par, because the mean difference of these two breeds is less than the *CD* value. Breed five is the best breed having 92 % fertilization rate followed by breed 4, breed 3, and so on. On the other hand, the lowest fertilization rate of only 57.67 % is recorded in breed 1. Hence, fish breed 5 is the best breed with respect to fertilization rate.

Problem 9.6 The following table gives the percentage grains per panicle affected by grain pest in seven different varieties of wheat in field trial. Analyze the data to find out the best variety of wheat against stored grain pest:

Variety	Replication 1	Replication 2	Replication 3
W1	75	72	70
W2	55	48	62
W3	86	88	85
W4	23	12	18
W5	65	66	68
W6	90	95	92
W7	16	28	20

9.8 Effect of Change in Origin and Scale on Analysis of Variance

In real-life situation, the experimenter encounters varied range of data sets; for example, some data are measured in part of million and some data are measured in million units, thereby posing a real problem in handling such data. Before analyzing such data, these are required to be transformed into suitable manageable units. Thus, the need for change in origin/scale/origin and scale both is felt necessary. Now

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the question is what are the impacts of such changes on analysis of variance? Analysis of variance, as has been mentioned earlier, is nothing but the partitioning of variance due to assignable causes and non-assignable causes. As such ANOVA is essentially an exercise with variance. We know that variance does not depend on change of origin but depends on change of scale. So if we add or subtract a constant quantity to each and every observation of the data set, the analysis of variance should not be affected by such mathematical exercise of origin. But we know that variance depends on change of scale, so one can expect an effect on analysis of variance due to change of scale. Let us take an example and examine how the change in origin and scale is affecting the analysis of variance vis-à-vis general conclusion from it.

Example 9.10 The following table gives monthly milk yield (liter) of four breeds of cows. We shall analyze the data (i) with original data, (ii) by changing origin to 120, (iii) by changing scale to 1/10 of the original data, and (iv) by changing both origin and scale to 120 and 1/10, respectively, with the help of MS Excel:

Breed 1	Breed 2	Breed 3	Breed 4
174	200	210	120
177	202	209	135
175	203	212	125
195	212	229	141
217	250	253	155
193	215	230	140
194	213	227	142
218	245	252	145
216	252	254	152

i) Anova: Single Factor with original data

Breed 1	**Breed 2**	**Breed 3**	**Breed 4**
174	200	210	120
177	202	209	135
175	203	212	125
195	212	229	141
217	250	253	155
193	215	230	140
194	213	227	142
218	245	252	145
216	252	254	152

SUMMARY

Groups	*Count*	*Sum*	*Average*	*Variance*
Breed 1	9	1759	195.4444	327.7778
Breed 2	9	1992	221.3333	460.5000
Breed 3	9	2076	230.6667	345.0000
Breed 4	9	1255	139.4444	130.7778

ANOVA

SOV	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Breeds	45362.78	3	15120.93	47.84893	6.25E-12	2.90112
Error	10112.44	32	316.0139			
Total	55475.22	35				

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ii) Anova: Single Factor with change of origin to 100 $(X' = X - 100)$

Breed 1	Breed 2	Breed 3	Breed 4
74	100	110	20
77	102	109	35
75	103	112	25
95	112	129	41
117	150	153	55
93	115	130	40
94	113	127	42
118	145	152	45
116	152	154	52

SUMMARY

Groups	*Count*	*Sum*	*Average*	*Variance*
Breed 1	9	859	95.444	327.778
Breed 2	9	1092	121.333	460.500
Breed 3	9	1176	130.667	345.000
Breed 4	9	355	39.444	130.778

ANOVA

SOV	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Breeds	45362.78	3	15120.9259	47.8489	0.0000	2.9011
Error	10112.44	32	316.0139			
Total	55475.22	35				

iii) Anova: Single Factor with change of scale to 1/10, $\left(X' = \frac{X}{10}\right)$

Breed 1	Breed 2	Breed 3	Breed 4
17.40	20.00	21.00	12.00
17.70	20.20	20.90	13.50
17.50	20.30	21.20	12.50
19.50	21.20	22.90	14.10
21.70	25.00	25.30	15.50

SUMMARY

Groups	*Count*	*Sum*	*Average*	*Variance*
Breed 1	9	175.900	19.544	3.278
Breed 2	9	199.200	22.133	4.605
Breed 3	9	207.600	23.067	3.450
Breed 4	9	125.500	13.944	1.308

ANOVA

SOV	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Breeds	453.6278	3	151.2093	47.8489	0.0000	2.9011
Error	101.1244	32	3.1601			
Total	554.7522	35				

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iv) Anova: Single Factor with change of origin and scale both, $X' = \frac{X - 100}{10}$

Breed 1	Breed 2	Breed 3	Breed 4
7.40	10.00	11.00	2.00
7.70	10.20	10.90	3.50
7.50	10.30	11.20	2.50
9.50	11.20	12.90	4.10
11.70	15.00	15.30	5.50
9.30	11.50	13.00	4.00
9.40	11.30	12.70	4.20
11.80	14.50	15.20	4.50
11.60	15.20	15.40	5.20

SUMMARY

Groups	*Count*	*Sum*	*Average*	*Variance*
Breed 1	9	85.900	9.544	3.278
Breed 2	9	109.200	12.133	4.605
Breed 3	9	117.600	13.067	3.450
Breed 4	9	35.500	3.944	1.308

ANOVA

SOV	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Breeds	453.6278	3	151.2093	47.8489	0.0000	2.9011
Error	101.1244	32	3.1601			
Total	554.7522	35				

From the above analyses, the following points are noted:

1. Mean values change in all the cases with change of origin or scale or both.
2. Sum of squares and mean sum of squares values are different with transformation.
3. Error mean square remains the same in the first and second cases but differs in the third and fourth cases.
4. F ratios and the significance level do not change under any case.

Thus, with the change of origin and or scale, the basic conclusion from ANOVA does not change. But due to changes in means and mean squares under different transformation situation, while comparing the means, care should be taken to adjust the mean values and the critical difference values accordingly.

Table for transformed values of percentages as arcsine $\sqrt{\text{Percentage}}$

Percent (%)	Trans-formed	Percent (%)	Trans-formed	Percent (%)	Trans-formed	Percent (%)	Trans-formed	Percent (%)	Trans-formed
0.0	0.00	4.1	11.68	8.2	16.64	12.3	20.53	16.4	23.89
0.1	1.81	4.2	11.83	8.3	16.74	12.4	20.62	16.5	23.97
0.2	2.56	4.3	11.97	8.4	16.85	12.5	20.70	16.6	24.04
0.3	3.14	4.4	12.11	8.5	16.95	12.6	20.79	16.7	24.12
0.4	3.63	4.5	12.25	8.6	17.05	12.7	20.88	16.8	24.20
0.5	4.05	4.6	12.38	8.7	17.15	12.8	20.96	16.9	24.27

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Percent (%)	Trans-formed	Percent (%)	Trans-formed	Percent (%)	Trans-formed	Percent (%)	Trans-formed	Percent (%)	Trans-formed
0.6	4.44	4.7	12.52	8.8	17.26	12.9	21.05	17.0	24.35
0.7	4.80	4.8	12.66	8.9	17.36	13	21.13	17.1	24.43
0.8	5.13	4.9	12.79	9.0	17.46	13.1	21.22	17.2	24.50
0.9	5.44	5.0	12.92	9.1	17.56	13.2	21.30	17.3	24.58
1.0	5.74	5.1	13.05	9.2	17.66	13.3	21.39	17.4	24.65
1.1	6.02	5.2	13.18	9.3	17.76	13.4	21.47	17.5	24.73
1.2	6.29	5.3	13.31	9.4	17.85	13.5	21.56	17.6	24.80
1.3	6.55	5.4	13.44	9.5	17.95	13.6	21.64	17.7	24.88
1.4	6.80	5.5	13.56	9.6	18.05	13.7	21.72	17.8	24.95
1.5	7.03	5.6	13.69	9.7	18.15	13.8	21.81	17.9	25.03
1.6	7.27	5.7	13.81	9.8	18.24	13.9	21.89	18	25.10
1.7	7.49	5.8	13.94	9.9	18.34	14	21.97	18.1	25.18
1.8	7.71	5.9	14.06	10.0	18.43	14.1	22.06	18.2	25.25
1.9	7.92	6.0	14.18	10.1	18.53	14.2	22.14	18.3	25.33
2.0	8.13	6.1	14.30	10.2	18.63	14.3	22.22	18.4	25.40
2.1	8.33	6.2	14.42	10.3	18.72	14.4	22.30	18.5	25.47
2.2	8.53	6.3	14.54	10.4	18.81	14.5	22.38	18.6	25.55
2.3	8.72	6.4	14.65	10.5	18.91	14.6	22.46	18.7	25.62
2.4	8.91	6.5	14.77	10.6	19.00	14.7	22.54	18.8	25.70
2.5	9.10	6.6	14.89	10.7	19.09	14.8	22.63	18.9	25.77
2.6	9.28	6.7	15.00	10.8	19.19	14.9	22.71	19.0	25.84
2.7	9.46	6.8	15.12	10.9	19.28	15.0	22.79	19.1	25.91
2.8	9.63	6.9	15.23	11.0	19.37	15.1	22.87	19.2	25.99
2.9	9.80	7.0	15.34	11.1	19.46	15.2	22.95	19.3	26.06
3.0	9.97	7.1	15.45	11.2	19.55	15.3	23.03	19.4	26.13
3.1	10.14	7.2	15.56	11.3	19.64	15.4	23.11	19.5	26.21
3.2	10.30	7.3	15.68	11.4	19.73	15.5	23.18	19.6	26.28
3.3	10.47	7.4	15.79	11.5	19.82	15.6	23.26	19.7	26.35
3.4	10.63	7.5	15.89	11.6	19.91	15.7	23.34	19.8	26.42
3.5	10.78	7.6	16.00	11.7	20.00	15.8	23.42	19.9	26.49
3.6	10.94	7.7	16.11	11.8	20.09	15.9	23.50	20.0	26.57
3.7	11.09	7.8	16.22	11.9	20.18	16.0	23.58	20.1	26.64
3.8	11.24	7.9	16.32	12.0	20.27	16.1	23.66	20.2	26.71
3.9	11.39	8.0	16.43	12.1	20.36	16.2	23.73	20.3	26.78
4.0	11.54	8.1	16.54	12.2	20.44	16.3	23.81	20.4	26.85
20.5	26.92	24.6	29.73	28.7	32.39	32.8	34.94	36.9	37.41
20.6	26.99	24.7	29.80	28.8	32.46	32.9	35.00	37.0	37.46
20.7	27.06	24.8	29.87	28.9	32.52	33.0	35.06	37.1	37.52
20.8	27.13	24.9	29.93	29.0	32.58	33.1	35.12	37.2	37.58
20.9	27.20	25.0	30.00	29.1	32.65	33.2	35.18	37.3	37.64
21.0	27.27	25.1	30.07	29.2	32.71	33.3	35.24	37.4	37.70
21.1	27.35	25.2	30.13	29.3	32.77	33.4	35.30	37.5	37.76
21.2	27.42	25.3	30.20	29.4	32.83	33.5	35.37	37.6	37.82
21.3	27.49	25.4	30.26	29.5	32.90	33.6	35.43	37.7	37.88
21.4	27.56	25.5	30.33	29.6	32.96	33.7	35.49	37.8	37.94
21.5	27.62	25.6	30.40	29.7	33.02	33.8	35.55	37.9	38.00
22.0	27.69	25.7	30.46	29.8	33.09	33.9	35.61	38.0	38.06
21.7	27.76	25.8	30.53	29.9	33.15	34.0	35.67	38.1	38.12
21.8	27.83	25.9	30.59	30.0	33.21	34.1	35.73	38.2	38.17
21.9	27.90	26.0	30.66	30.1	33.27	34.2	35.79	38.3	38.23

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Percent (%)	Trans-formed	Percent (%)	Trans-formed	Percent (%)	Trans-formed	Percent (%)	Trans-formed	Percent (%)	Trans-formed
22.0	27.97	26.1	30.72	30.2	33.34	34.3	35.85	38.4	38.29
22.1	28.04	26.2	30.79	30.3	33.40	34.4	35.91	38.5	38.35
22.2	28.11	26.3	30.85	30.4	33.46	34.5	35.97	38.6	38.41
22.3	28.18	26.4	30.92	30.5	33.52	34.6	36.03	38.7	38.47
22.4	28.25	26.5	30.98	30.6	33.58	34.7	36.09	38.8	38.53
22.5	28.32	26.6	31.05	30.7	33.65	34.8	36.15	38.9	38.59
22.6	28.39	26.7	31.11	30.8	33.71	34.9	36.21	39.0	38.65
22.7	28.45	26.8	31.18	30.9	33.77	35.0	36.27	39.1	38.70
22.8	28.52	26.9	31.24	31.0	33.83	35.1	36.33	39.2	38.76
22.9	28.59	27.0	31.31	31.1	33.90	35.2	36.39	39.3	38.82
23.0	28.66	27.1	31.37	31.2	33.96	35.3	36.45	39.4	38.88
23.1	28.73	27.2	31.44	31.3	34.02	35.4	36.51	39.5	38.94
23.2	28.79	27.3	31.50	31.4	34.08	35.5	36.57	39.6	39.00
23.3	28.86	27.4	31.56	31.5	34.14	35.6	36.63	39.7	39.06
23.4	28.93	27.5	31.63	31.6	34.20	35.7	36.69	39.8	39.11
23.5	29.00	27.6	31.69	31.7	34.27	35.8	36.75	39.9	39.17
23.6	29.06	27.7	31.76	31.8	34.33	35.9	36.81	40.0	39.23
23.7	29.13	27.8	31.82	31.9	34.39	36.0	36.87	40.1	39.29
23.8	29.20	27.9	31.88	32.0	34.45	36.1	36.93	40.2	39.35
23.9	29.27	28.0	31.95	32.1	34.51	36.2	36.99	40.3	39.41
24.0	29.33	28.1	32.01	32.2	34.57	36.3	37.05	40.4	39.47
24.1	29.40	28.2	32.08	32.3	34.63	36.4	37.11	40.5	39.52
24.2	29.47	28.3	32.14	32.4	34.70	36.5	37.17	40.6	39.58
24.3	29.53	28.4	32.20	32.5	34.76	36.6	37.23	40.7	39.64
24.4	29.60	28.5	32.27	32.6	34.82	36.7	37.29	40.8	39.70
24.5	29.67	28.6	32.33	32.7	34.88	36.8	37.35	40.9	39.76
41.0	39.82	45.1	42.19	49.2	44.54	53.3	46.89	57.4	49.26
41.1	39.87	45.2	42.25	49.3	44.60	53.4	46.95	57.5	49.31
41.2	39.93	45.3	42.30	49.4	44.66	53.5	47.01	57.6	49.37
41.3	39.99	45.4	42.36	49.5	44.71	53.6	47.06	57.7	49.43
41.4	40.05	45.5	42.42	49.6	44.77	53.7	47.12	57.8	49.49
41.5	40.11	45.6	42.48	49.7	44.83	53.8	47.18	57.9	49.55
41.6	40.16	45.7	42.53	49.8	44.89	53.9	47.24	58.0	49.60
41.7	40.22	45.8	42.59	49.9	44.94	54.0	47.29	58.1	49.66
41.8	40.28	45.9	42.65	50.0	45.00	54.1	47.35	58.2	49.72
41.9	40.34	46.0	42.71	50.1	45.06	54.2	47.41	58.3	49.78
42.0	40.40	46.1	42.76	50.2	45.11	54.3	47.47	58.4	49.84
42.1	40.45	46.2	42.82	50.3	45.17	54.4	47.52	58.5	49.89
42.2	40.51	46.3	42.88	50.4	45.23	54.5	47.58	58.6	49.95
42.3	40.57	46.4	42.94	50.5	45.29	54.6	47.64	58.7	50.01
42.4	40.63	46.5	42.99	50.6	45.34	54.7	47.70	58.8	50.07
42.5	40.69	46.6	43.05	50.7	45.40	54.8	47.75	58.9	50.13
42.6	40.74	46.7	43.11	50.8	45.46	54.9	47.81	59.0	50.18
42.7	40.80	46.8	43.17	50.9	45.52	55.0	47.87	59.1	50.24
42.8	40.86	46.9	43.22	51.0	45.57	55.1	47.93	59.2	50.30
42.9	40.92	47.0	43.28	51.1	45.63	55.2	47.98	59.3	50.36
43.0	40.98	47.1	43.34	51.2	45.69	55.3	48.04	59.4	50.42
43.1	41.03	47.2	43.39	51.3	45.74	55.4	48.10	59.5	50.48
43.2	41.09	47.3	43.45	51.4	45.80	55.5	48.16	59.6	50.53
43.3	41.15	47.4	43.51	51.5	45.86	55.6	48.22	59.7	50.59

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Percent (%)	Trans-formed	Percent (%)	Trans-formed	Percent (%)	Trans-formed	Percent (%)	Trans-formed	Percent (%)	Trans-formed
43.4	41.21	47.5	43.57	51.6	45.92	55.7	48.27	59.8	50.65
43.5	41.27	47.6	43.62	51.7	45.97	55.8	48.33	59.9	50.71
43.6	41.32	47.7	43.68	51.8	46.03	55.9	48.39	60.0	50.77
43.7	41.38	47.8	43.74	51.9	46.09	56.0	48.45	60.1	50.83
43.8	41.44	47.9	43.80	52.0	46.15	56.1	48.50	60.2	50.89
43.9	41.50	48.0	43.85	52.1	46.20	56.2	48.56	60.3	50.94
44.0	41.55	48.1	43.91	52.2	46.26	56.3	48.62	60.4	51.00
44.1	41.61	48.2	43.97	52.3	46.32	56.4	48.68	60.5	51.06
44.2	41.67	48.3	44.03	52.4	46.38	56.5	48.73	60.6	51.12
44.3	41.73	48.4	44.08	52.5	46.43	56.6	48.79	60.7	51.18
44.4	41.78	48.5	44.14	52.6	46.49	56.7	48.85	60.8	51.24
44.5	41.84	48.6	44.20	52.7	46.55	56.8	48.91	60.9	51.30
44.6	41.90	48.7	44.26	52.8	46.61	56.9	48.97	61.0	51.35
44.7	41.96	48.8	44.31	52.9	46.66	57.0	49.02	61.1	51.41
44.8	42.02	48.9	44.37	53.0	46.72	57.1	49.08	61.2	51.47
44.9	42.07	49.0	44.43	53.1	46.78	57.2	49.14	61.3	51.53
45.0	42.13	49.1	44.48	53.2	46.83	57.3	49.20	61.4	51.59
61.5	51.65	65.6	54.09	69.7	56.60	73.8	59.21	77.9	61.96
61.6	51.71	65.7	54.15	69.8	56.66	73.9	59.28	78.0	62.03
61.7	51.77	65.8	54.21	69.9	56.73	74.0	59.34	78.1	62.10
61.8	51.83	65.9	54.27	70.0	56.79	74.1	59.41	78.2	62.17
61.9	51.88	66.0	54.33	70.1	56.85	74.2	59.47	78.3	62.24
62.0	51.94	66.1	54.39	70.2	56.91	74.3	59.54	78.4	62.31
62.1	52.00	66.2	54.45	70.3	56.98	74.4	59.60	78.5	62.38
62.2	52.06	66.3	54.51	70.4	57.04	74.5	59.67	78.6	62.44
62.3	52.12	66.4	54.57	70.5	57.10	74.6	59.74	78.7	62.51
62.4	52.18	66.5	54.63	70.6	57.17	74.7	59.80	78.8	62.58
62.5	52.24	66.6	54.70	70.7	57.23	74.8	59.87	78.9	62.65
62.6	52.30	66.7	54.76	70.8	57.29	74.9	59.93	79.0	62.73
62.7	52.36	66.8	54.82	70.9	57.35	75.0	60.00	79.1	62.80
62.8	52.42	66.9	54.88	71.0	57.42	75.1	60.07	79.2	62.87
62.9	52.48	67.0	54.94	71.1	57.48	75.2	60.13	79.3	62.94
63.0	52.54	67.1	55.00	71.2	57.54	75.3	60.20	79.4	63.01
63.1	52.59	67.2	55.06	71.3	57.61	75.4	60.27	79.5	63.08
63.2	52.65	67.3	55.12	71.4	57.67	75.5	60.33	79.6	63.15
63.3	52.71	67.4	55.18	71.5	57.73	75.6	60.40	79.7	63.22
63.4	52.77	67.5	55.24	71.6	57.80	75.7	60.47	79.8	63.29
63.5	52.83	67.6	55.30	71.7	57.86	75.8	60.53	79.9	63.36
63.6	52.89	67.7	55.37	71.8	57.92	75.9	60.60	80.0	63.43
63.7	52.95	67.8	55.43	71.9	57.99	76.0	60.67	80.1	63.51
63.8	53.01	67.9	55.49	72.0	58.05	76.1	60.73	80.2	63.58
63.9	53.07	68.0	55.55	72.1	58.12	76.2	60.80	80.3	63.65
64.0	53.13	68.1	55.61	72.2	58.18	76.3	60.87	80.4	63.72
64.1	53.19	68.2	55.67	72.3	58.24	76.4	60.94	80.5	63.79
64.2	53.25	68.3	55.73	72.4	58.31	76.5	61.00	80.6	63.87
64.3	53.31	68.4	55.80	72.5	58.37	76.6	61.07	80.7	63.94
64.4	53.37	68.5	55.86	72.6	58.44	76.7	61.14	80.8	64.01
64.5	53.43	68.6	55.92	72.7	58.50	76.8	61.21	80.9	64.09
64.6	53.49	68.7	55.98	72.8	58.56	76.9	61.27	81.0	64.16
64.7	53.55	68.8	56.04	72.9	58.63	77.0	61.34	81.1	64.23

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Percent (%)	Trans-formed	Percent (%)	Trans-formed	Percent (%)	Trans-formed	Percent (%)	Trans-formed	Percent (%)	Trans-formed
64.8	53.61	68.9	56.10	73.0	58.69	77.1	61.41	81.2	64.30
64.9	53.67	69.0	56.17	73.1	58.76	77.2	61.48	81.3	64.38
65.0	53.73	69.1	56.23	73.2	58.82	77.3	61.55	81.4	64.45
65.1	53.79	69.2	56.29	73.3	58.89	77.4	61.61	81.5	64.53
65.2	53.85	69.3	56.35	73.4	58.95	77.5	61.68	81.6	64.60
65.3	53.91	69.4	56.42	73.5	59.02	77.6	61.75	81.7	64.67
65.4	53.97	69.5	56.48	73.6	59.08	77.7	61.82	81.8	64.75
65.5	54.03	69.6	56.54	73.7	59.15	77.8	61.89	81.9	64.82
82.0	64.90	86.1	68.11	90.2	71.76	94.3	76.19	98.4	82.73
82.1	64.97	86.2	68.19	90.3	71.85	94.4	76.31	98.5	82.97
82.2	65.05	86.3	68.28	90.4	71.95	94.5	76.44	98.6	83.20
82.3	65.12	86.4	68.36	90.5	72.05	94.6	76.56	98.7	83.45
82.4	65.20	86.5	68.44	90.6	72.15	94.7	76.69	98.8	83.71
82.5	65.27	86.6	68.53	90.7	72.24	94.8	76.82	98.9	83.98
82.6	65.35	86.7	68.61	90.8	72.34	94.9	76.95	99	84.26
82.7	65.42	86.8	68.70	90.9	72.44	95.0	77.08	99.1	84.56
82.8	65.50	86.9	68.78	91.0	72.54	95.1	77.21	99.2	84.87
82.9	65.57	87.0	68.87	91.1	72.64	95.2	77.34	99.3	85.20
83.0	65.65	87.1	68.95	91.2	72.74	95.3	77.48	99.4	85.56
83.1	65.73	87.2	69.04	91.3	72.85	95.4	77.62	99.5	85.95
83.2	65.80	87.3	69.12	91.4	72.95	95.5	77.75	99.6	86.37
83.3	65.88	87.4	69.21	91.5	73.05	95.6	77.89	99.7	86.86
83.4	65.96	87.5	69.30	91.6	73.15	95.7	78.03	99.8	87.44
83.5	66.03	87.6	69.38	91.7	73.26	95.8	78.17	99.9	88.19
83.6	66.11	87.7	69.47	91.8	73.36	95.9	78.32	100	90.00
83.7	66.19	87.8	69.56	91.9	73.46	96.0	78.46		
83.8	66.27	87.9	69.64	92.0	73.57	96.1	78.61		
83.9	66.34	88.0	69.73	92.1	73.68	96.2	78.76		
84.0	66.42	88.1	69.82	92.2	73.78	96.3	78.91		
84.1	66.50	88.2	69.91	92.3	73.89	96.4	79.06		
84.2	66.58	88.3	70.00	92.4	74.00	96.5	79.22		
84.3	66.66	88.4	70.09	92.5	74.11	96.6	79.37		
84.4	66.74	88.5	70.18	92.6	74.21	96.7	79.53		
84.5	66.82	88.6	70.27	92.7	74.32	96.8	79.70		
84.6	66.89	88.7	70.36	92.8	74.44	96.9	79.86		
84.7	66.97	88.8	70.45	92.9	74.55	97.0	80.03		
84.8	67.05	88.9	70.54	93.0	74.66	97.1	80.20		
84.9	67.13	89.0	70.63	93.1	74.77	97.2	80.37		
85.0	67.21	89.1	70.72	93.2	74.88	97.3	80.54		
85.1	67.29	89.2	70.81	93.3	75.00	97.4	80.72		
85.2	67.37	89.3	70.91	93.4	75.11	97.5	80.90		
85.3	67.46	89.4	71.00	93.5	75.23	97.6	81.09		
85.4	67.54	89.5	71.09	93.6	75.35	97.7	81.28		
85.5	67.62	89.6	71.19	93.7	75.46	97.8	81.47		
85.6	67.70	89.7	71.28	93.8	75.58	97.9	81.67		
85.7	67.78	89.8	71.37	93.9	75.70	98.0	81.87		
85.8	67.86	89.9	71.47	94.0	75.82	98.1	82.08		
85.9	67.94	90.0	71.57	94.1	75.94	98.2	82.29		
86.0	68.03	90.1	71.66	94.2	76.06	98.3	82.51		

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Basic Experimental Designs

10

10.1 Introduction

Statistical tolls or techniques are used to extract information, which otherwise remain hidden, from a set of data. As has been mentioned earlier, data can be gathered/collected from existing population (through sample survey technique/census method) or can be collected by conducting experiment as per the objective of the experimenter. In the first case, the researcher has little choice of controlling the external factors while collecting information from the existing population; the maximum the researcher can do is to orient the collected data from a befitting sample so as to explain the objective in mind. This type of data collection is mostly used in social, economical, political, and other fields. On the other hand, in the second option, the researcher has greater control over the data to be collected for specific purpose through experimentation. The researchers can exercise control to the extraneous factors to some extent allowing the desirable factors to vary. To examine the performance of different varieties of paddy with respect to yield, the experimenter can select the varieties as per the objective of the program and put all the varieties essentially under the same protocol so that only the source of variation can be the varieties. In this chapter we are concerned about such experimental procedure, collection of data and their analyses toward meaningful inference about the objectives the experimenter has in mind. In the experimental procedure, a researcher designs a set of activities keeping in mind the objectives and tries to measure the variations on different response variables/entities/objects keeping other variations at minimum level. Let us now try to formalize the definition of experiment or what do we mean by an experiment. *An experiment is a systematic process or series of activities which lead to collection of information on certain aspects to reply to the objectives that the researcher has already in mind.*

Experiments may be conducted to know some absolute measures of the populations like the measures of central tendency, the measures of dispersion (Chap. 3), the measures of associationships, etc. (Chap. 7). Experiments may also be conducted to compare the yields of a set of paddy varieties under a given management protocol, experiments may be conducted for screening of breeds of cattle against a particular disease, and experiments may be conducted to know the relationship between the age of calving and milk yield per calving, to know the degree of linear associationship between the number of hills per square meter and yield, and so on. All these experiments can broadly be classified into two categories, viz., *absolute experiments and comparative experiments.* An *absolute experiment is an experiment in which the experimenter is in search of certain absolute measures like average, variance, median, mode,*

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correlation coefficient, etc. to infer about the population. On the other hand, in comparative experiments *the researcher compares the effects of different objects/entities (treatments) under consideration*. In a comparative experiment, an experimental design is formulated in such a way that the experimenter can compare the objects or entities (treatments) under identical conditions keeping the other sources of variations as minimum as possible. Whatever may be the objective of the study either comparative or absolute, it is generally designed meticulously, and the area of subject statistics which deals with such objectives is known as the design of experiments. The design of experiments mainly has three components, viz., (a) planning of experiment, (b) obtaining the relevant information, and (c) statistical analysis of information and drawing the inference.

An experiment is to be planned in such a way that the future activities could be performed meticulously depending upon the objectives of the experiment. Knowledge about the objective of the experiment, nature of the experiment, experimental place, materials, observations to be recorded, etc. are the most essential feature during the formulation of experiment. Information/observations to be recorded could be subjected to statistical analysis to draw inferences so that the objectives of the study are the major considerations one experimenter should keep in mind. A good, reliable data/information with the help of appropriate statistical tool helps in drawing accurate inference about the population, while faulty/inaccurate information may lead to inaccurate and/or fallacious conclusion, whatever good or accurate statistical theories are applied to it. Thus, along with getting good relevant information, knowledge and application of appropriate statistical theory are most warranted. In the following section, let us discuss about the different terminologies used in the design of experiment:

(i) *Treatment*:

Treatments are mainly associated with comparative experiments. Different objects under comparison in a comparative experiment are known as treatment. Thus the varieties/breeds under comparison may constitute different treatments in the respective experiment. An experiment conducted with different doses to find out the most effective dose of a particular nitrogenous fertilizer in getting maximum yield of a crop forms the treatments. Thus treatments may be qualitative (varieties/breeds) as well as quantitative (doses) in nature.

(ii) *Experimental unit*:

The objects or the units in which treatments are applied are known as subjects. The smallest part/unit of the experimental area/subjects (e.g., plots in field experiment, pots, test tubes, etc. in laboratory experiment, trees in plantation crop experiments, animal, individual students, etc.) in which one applies treatments and from which observations/responses are recorded is called experimental unit.

(ii) *Block*:

The idea of block came into existence to group the homogenous experimental units and is mainly associated with field experiment but can very well be extended to non-field experiments. Experimental units/subjects in a particular experimental field/experiment may vary with respect to fertility, soil structure, texture, age of the plants, nature of animals, etc. (or in other conditions). Thus, there is a need to identify or group the experimental units similar in nature. Blocking is the technique by virtue of which the whole experimental area/units are subdivided into a number of small parts, each having homogeneous experimental units. Thus, *a block is consisted of homogeneous experimental units*. Experimental units within a block are homogeneous in nature but units among the blocks are heterogeneous. In experiments conducted with animals, blocking may be done according to the age, weight, sex, etc. group of animals, where animals of the same age or similar weight or same sex may form the blocks.

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(iii) *Experimental error*:

Experimental information is generally analyzed using the analysis of variance technique as discussed in Chap. 9. The variations in response due to various sources of variations among different experimental units may be ascribed due to:

(i) A systematic part (assignable part)
(ii) A nonsystematic part(non-assignable part)

Systematic variation part is consisting of that part of the variations caused due to known sources of variations like differences in treatments, blocks, etc. But the part of the variation which cannot be assigned to specific reasons or causes, i.e., the nonsystematic part, is termed as the experimental error. Often it is found the homogenous experimental units receiving the same treatments and experimental protocol but providing differential responses. This type of nonsystematic variations in response may be due to extraneous factor and is known as experimental error. So the *variation in responses due to these extraneous factors is termed as experimental error*. While designing and planning of any experiment, a researcher always intends to minimize the experimental error.

(iv) *Precision*:

Often it is of most important point in designing experiments how precisely one is estimating the effects. As such *the precision of an experiment is defined as the reciprocal of the variance of mean*. We know that the sampling distribution of a sample mean has a variance σ^2/n so the precision of the experimental design is $\frac{1}{V(x)} = \frac{1}{\sigma^2/n} = \frac{n}{\sigma^2}$ where X is the variable under consideration, with n and σ^2 as the observations and variance, respectively. The higher the precision, the better is the design.

(v) *Efficiency*:

To fulfill the same objectives, experiments can be conducted in different ways; hence, measuring the efficiency of designs comes into play in comparing the designs framed to fulfill the same objectives. Efficiency is the ratio of the variances of the difference between two treatment means in two different experiments. If we have two designs D_1 and D_2 with error variances ${\sigma_1}^2$ and ${\sigma_2}^2$ and observations r_1 and r_2, respectively, therefore, the variance of the difference between two treatment means is given by $\frac{2\sigma_1^2}{r_1}$ and $\frac{2\sigma_2^2}{r_2}$, respectively. So the efficiency of D_1 with respect to D_2 is $\frac{r_1}{2\sigma_1^2} \div \frac{r_2}{2\sigma_2^2} = \frac{\sigma_2^2}{r_2} \cdot \frac{r_1}{\sigma_1^2} = \frac{r_1}{r_2} \cdot \frac{\sigma_2^2}{\sigma_1^2}$.

(vi) *Experimental reliability*:

Reliability of an experimental procedure/outcome can be measured with the help of the coefficient of variation. The coefficient of variation is defined as

$$\text{CV} = \frac{\text{SD}}{\text{grand mean}} \times 100$$

For all practical purposes, the positive square root of error mean square in the analysis of variance is taken as an estimate of the standard deviation. Thus, from the ANOVA table of the analysis of variance, one can work out the CV% as follows.

$$\text{CV} = \frac{\sqrt{MS_{Er}}}{\text{grand mean}} \times 100$$

The range of the CV for reliability of an experiment is one of the important points. In fact there is no silver line to determine the cut of value of CV% for an experiment to be reliable; it depends on the condition of experiment (laboratory condition, field condition, etc.), type of materials/treatments tested in the experiment, desired level of precision from the experiment, etc. Generally lesser CV% is expected for experiments conducted under laboratory conditions compared to the field experiments. Similarly CV% also depends on the type of field crop, size and shape of experimental units, etc. As a thumb rule, a CV% less than 20 % is regarded as an indication for reliability of the

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field experiments, whereas that should be still less for laboratory experiments. If the CV value is more than 20 %, there is a need to verify the experimental procedure and the observations based on which the CV has been calculated; there is a need for emphasis on the reduction of experimental error.

10.2 Principles of Design

As has already been mentioned, an experiment is conducted to answer specific objectives of the experiment. As such it is formulated and performed in such a way to have valid estimation of the mean and variances of the assignable and non-assignable sources of variation in valid, efficient, economical way, providing due consideration to the constraints and situations provided for the experiment. All these could be achieved by following some basic principles of designing experiments. In the following paragraphs, we shall discuss these principles of the design of experiments. The principles are (a) *replication, (b) randomization, and (c) local control*.

(a) *Replication*:

To have valid and accurate estimation of means and variances due to different sources of variations, one needs to apply the treatments into more than one experimental unit. Thus, *repeated application of treatments under investigation in experimental units is termed as replication*. (i) A treatment is repeated to have a more reliable estimate than what would be possible from a single observation. Thus the average performance (mean) recorded from a number of experimental units is more reliable than the recording from only one experimental unit. Moreover, (ii) replication along with the other principle randomization helps in unbiased estimation of the experimental errors, and (iii) replication along with local control helps in the reduction of experimental error. So providing due importance to the role of replication in the design of experiment, the question is how many replications one should have in a particular experiment? Depending upon the objective of the experiment, the cost involvement in the experiment, the type and variability of the test materials, the size of mean differences, the desired level of accuracy expected, the size of error variance, etc., the number of replications to be adopted in a particular experiment is decided. Required number of replications can be worked out with the help of the following formula:

$$r = \frac{2t^2 s^2}{d^2}$$

where

t = table value of t-distribution at the desired level of significance at error degrees of freedom
d = difference between the means of two treatments
s^2 = error variance taken from the past experience or conducting similar experiment
r = number of replications to be determined

At a given level of significance and with a given coefficient of variation percent, one can find out the number of replications required for a specific percent difference between two means to be significant with the help of the following formula:

$$\frac{\text{Difference} \quad \%}{c\sqrt{2/r}} = 1.96$$

where

c = coefficient of variation among the plots
r = number of replicates

The value of area under normal curve at 5 % level of significance is 1.96.

For example, with CV% of 15 and mean difference of 20 %,

we have $\frac{20}{15\sqrt{2/r}} = 1.96$

or $\sqrt{2/r} = \frac{20}{15\times 1.96}$

or $\frac{2}{r} = \left(\frac{20}{15\times 1.96}\right)^2$

or $r = \frac{2}{\left(\frac{20}{15\times 1.96}\right)^2} = 4.32 \sim 5$

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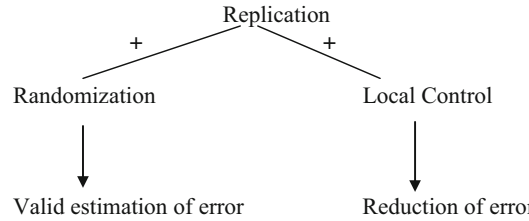
(b) *Randomization*:

One of the mottos in designing experiment is to provide equal opportunity to each and every treatment to exhibit their respective performances that means all the treatments should be put under equal experimental condition. In doing so, treatments are required to be applied unbiasedly among the experimental units. Moreover valid and unbiased estimation of different treatment effects as well as for experimental error is required to be done; the principle of randomization helps in this regard. Randomization is a technique to achieve the independence of errors in experimental design. *Unbiased random allocation of the treatments among the experimental units is known as randomization*. Randomization provides equal opportunity to each and every experimental unit to receive any treatment. Through the adoption of the technique randomization, human biasedness/error is reduced. It not only helps in (i) valid estimation of experimental error, (ii) independence of errors in normality assumption is also achieved. (iii) Randomization also makes the experiment free from systematic errors. In the subsequent sections, we shall see that the process of randomization, i.e., random allocation of treatments among the experimental units, is not same for all types of designs. It should be noted that randomization, by itself, is not sufficient for valid estimation of errors; for valid estimation of error along with randomization, replication is needed.

(c) *Local control*:

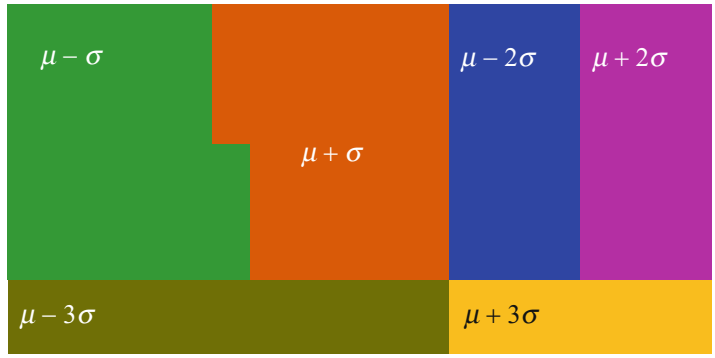
Local control is a principle, mostly applicable for field experiments. As the name suggests, local situations for different experiments vary, and one needs to take care of such variation during experimentation so as to minimize the error. *Local control, simply, is the technique which helps in the reduction of experimental error, providing due consideration to the information available under the local conditions where the actual experiment is conducted*. Using the locally available information like shape of the experimental plot, direction of the field, its fertility gradient, slope, and other conditions nearby the plot designs are to be framed in such a way so as to reduce the experimental error.

Thus replication, randomization, and local control are the three main principles in guiding an experimenter for the conduction of a valid and efficient experiment. R. A. Fisher has diagrammatically presented the importance of these principles as follows.



10.3 Uniformity Trial

An efficient experimental design aims at valid estimation of different effects along with the reduction in experimental error. To achieve these, particularly under field conditions, the experimenter should have clear idea about the area where the experiment is to be conducted. In order to have an idea about the conditions of the proposed experimental area, a trial known as uniformity trial is conducted. Generally a short-duration crop is grown with uniform package of practices (cultivation technique) by dividing the whole area into the smallest units. Sometimes the division of plot into the smallest units is also done before recording the response. Responses are recorded from the basic unit plots. The overall mean response is also worked out. All the experimental units are then grouped into of more or less homogenous units; these groups may be of unit plots bellow and above the specific percentage of mean responses, and a response contour map is drawn by joining the unit plots having under the same group. Thus a fertility contour may be drawn as shown below.



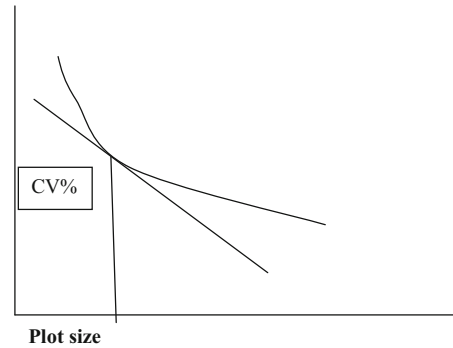
Fertility contour map

Thus, *uniformity trial not only helps us in identifying the nature of the experimental field but also in making blocks of homogenous experimental units*, as can be seen that we can make six blocks of homogenous experimental units in the above experimental field.

10.4 Optimum Size and Shape of Experimental Units

The size and shape of the experimental units play a vital role on the accuracy of the experimental results. Laboratory experiments, where pots, petri dishes, beakers, etc. form the experimental unit, do not pose a serious problem in experimental accuracy. Selection of optimum size and shape of experimental units has varied responses, particularly in field experiments. Generally with the increase in plot size, precision of single-plot response increases, but an increase in plot size results in enlarged blocks and/or experimental area which subsequently increases the variability among plots. Thus there is a need to optimize the size of experimental units. Optimum plot size may not be uniform for all crops under all experimental conditions. It required to be estimated for a particular crop, for a particular experimental situation for a defined objective in mind. Optimum plot size is ascertained through *maximum curvature method or Fairfield Smith method*. Ascertaining optimum plot size is by itself an area of research for specific crops under different situations.

Unit-wise basic information from uniformity trial experiment is used in maximum curvature method. In this method basic units from uniformity trial are joined, row-wise, column-wise, or both, to form experimental units of different sizes. The coefficient of variations corresponding to different sizes of experimental units is computed, and a curve is drawn by plotting the sizes of the experimental units on the x-axis and corresponding coefficient of variations on the y-axis.



Selection of optimum plot size by maximum curvature method

At the point of maximum curvature, one can get the optimum plot size. With the help of the mini-max theory of the calculus, the optimum plot size for which the curvature is maximum can also be worked out from the relationship (nonlinear) between the plot size and the coefficient of variation. H. Fairfield Smith proposed a variance law by taking the results from the uniformity trial experiment. Generally according to this law, an increase in plot size increases the precision of the experiment provided the number of plot remains the same.

The size and shape of the plots are determined on the basis of the experimental area provided, the type of materials to be tested, the type of precision required, etc.; if the plot size is small, the shape may have little or no effect on experimental precision, whereas for large plot sizes, the effects of shape may be considerable. Various experiments have been conducted to fix the optimum size and shape of the plot. By and large long and narrow plots have been found to be relatively more precise. In fact if fertility gradient is known, then arrangement of experimental units is to be made by forming block of homogenous plots. As such the freedom of taking decision on the shape of the experimental units is reduced. In the absence of all these, it is better to have square-shaped plots.

10.5 Layout

Experimental layout forms a very important component in designing and analysis of experimental data. In fact layout varies from design to design and type of experiments. *Systematic arrangement of experimental units in the experimental field and allocation of treatments in experimental units according to the requirement of the specific design is called layout.* Thus layout is mainly concerned in field experimentation. For example, if the whole experimental field is homogeneous in nature, then it is divided into as many numbers of experimental units as the total number of plots required to allot all the treatments with respective number of replication. On the other hand, if the experimental units are heterogeneous in nature, then at the first step of layout, blocks are required to be framed, and then treatments are to be allocated. Above all, each and every experimental design has its own layout as well as analytical procedure.

10.6 Steps in Designing of Experiments

Likewise to that of any statistical procedure, the designing of experiment is also based on certain steps which are to be followed meticulously to fulfill the objectives of the experiments. In the following section, let us discuss these steps in brief, but it should be noted that neither the steps discussed below are exclusive nor are essential and exhaustive in all experiments:

(i) *Identification and statement of the problem and objectives*: What for the experiment? The problem which the experimenter is going to address required be stated, delineating clearly the specific objectives.

(ii) *Formulations of statistical hypothesis*: Hypotheses under the given situation and based on the objectives of the experiment are required to be framed. Careful examination is required in regard to the feasibility of getting necessary information to test the hypothesis from the experiment.

(iii) *Selection of experimental technique vis-à-vis experimental designs*: Depending upon the objective of the study, hypothesis to be tested, etc., it requires to be decided which experimental design is befitting for the purpose.

(iv) *To examine the possible outcomes from the experiment*: From the past records and review, the experimenter should have an idea about the nature of the information that can be obtained from the experiment and whether these are sufficient to fulfill the objective. He has to examine whether the information would be available from the experiment that are sufficient to draw meaningful conclusion with respect to objective or not.

(v) *To settle the statistical tools*: Among the hosts of available statistical tools, the appropriate tools to be used in testing the hypothesis with the help of the information from the experiment to fulfill the objective are to be ascertained.

(vi) *Conducting the experiments*: Following the experimental procedure and protocol and keeping in mind the objective of the study, experiment is to be conducted. A list is prepared for which information are to be collected during the experimental period. In doing so the experimenters

make it sure that the conditions for necessary statistical procedure to be taken up on these information (data) are satisfied.

(vii) *Scrutiny and processing of information:* Before taking up any statistical analysis, data are required to be thoroughly checked for their reliability and authenticity.

(viii) *Applications of statistical technique*: The type of statistical technique to be applied is fixed, and now with the scrutinized data, analysis is taken up toward drawing valid conclusion about the objectives of the study.

(ix) *Evaluation of the whole procedure*: An overall evaluation of the whole process is required to facilitate the same type of experiments in the future, so that the problems and difficulties could be minimized.

10.7 Completely Randomized Design (CRD)

One of the most important and simple experimental designs is the completely randomized design (CRD). When the whole experimental area or all the experimental units are homogenous in nature, then one can think of such design. In this design out of the three basic principles of the design of experiments, only two principles, viz., replication and randomization, have been used. The third principle, i.e., the principle of local control, is not used; as such the minimization of error is not there. The whole experimental area to be divided or the number of experimental units is to be such that there are as many numbers of experimental units as the sum of the number of replications of all the treatments. Suppose we are to test five new varieties (viz., M1, M2, M3, M4, M5) of mustard along with a traditional check (Mt) for their applicability under a particular local situation. Moreover the amount of materials available for each of the new varieties is not sufficient to be replicated equal number of times. Suppose we are provided with material such that there could be 5, 4, 4, 3, 3, and 5 replications for M1, M2, M3, M4, M5, and Mt, respectively. Then the experimental field is required to be divided into 24 (=5 + 4 + 4 + 3 + 3 + 5) experimental plots of equal size and preferably of equal shape. If the experiment is to be conducted in a laboratory condition, then one needs to have 24 experimental units. In general if there be t treatments replicated $r_1, r_2, \ldots\ldots, r_t$ times, respectively, then to accommodate these we need to have $n = \sum_{i=1}^{t} r_i$ number of homogeneous experimental units/plots of equal size.

10.7.1 Randomization and Layout

Randomization and layout of the completely randomized design are demonstrated with the help of the following example and in the following steps. Suppose we have t treatments each replicated r_i times ($i = 1, 2, \ldots\ldots, t$). The problem is to allocate these t treatments each replicated r_i times among the $n = \sum_{i=1}^{t} r_i$ number of experimental units:

Step 1: Divide the whole experimental area into n experimental plots of equal size and preferably of the same shape. For other than field experiment, take n experimental units of homogenous in nature.

Step 2: Number the experimental units 1 to n.

Step 3: Arrange the treatments along with their replications as follows:

Treatment	T_1	T_2		T_{t-1}	T_t
Replication	r_1	r_2		r_{t-1}	r_t
Sl No	1,2,…….r_1	r_{1+1},r_{1+2}……..r_2	……..	$r_{(t-2)+1}$, $r_{(t-2)+2}$,.. $r_{(t-1)}$	$r_{(t-1)+1}$, $r_{(t-1)+2}$, …,r_t
	1,2,3,4,5,6,……n				

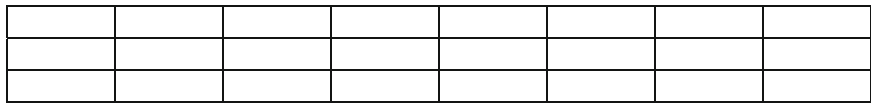
Step 4: Select n random numbers less than or equal to n, without replacement, from the random number table; these random numbers will indicate the plot numbers.

Step 5: Allocate the first treatment the first time to the first random numbered plot, i.e.,T_{1r1}, and then the first treatment the second time to the second random numbered, and continue the process till all the n plots are allotted with one treatment each in such random manner.

Example Let us take an example of experiment with five newly developed varieties of mustard along with standard variety as discussed earlier.

So we have six varieties altogether, M1, M2, M3, M4, M5, and Mt replicated 5, 4, 4, 3, 3, and 5 times, respectively:

Step 1: We need to divide the whole experimental area into 24 experimental plots of equal size and preferably of the same shape.



Step 2: Number the experimental units 1–24:

1	2	3	4	5	6	7	8
9	10	11	12	13	14	15	16
17	18	19	20	21	22	23	24

Step 3: Arrange the treatments along with their replications as follows:

Treatment	M1	M1	M1	M1	M1	M2	M2	M2	M2	M3	M3	M3	M3	M4	M4	M4	M5	M5	M5	M6	M6	M6	M6	M6
S1 no	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

Step 4: Selected 24 random numbers less than or equal to 24, without replacement, from the random number table are

22	17	14	21	4	11	9	18	6	7	19	24	16	1	13	5	12	15	2	23	10	8	3	20

Step 5: The first variety M_1 for the first time is allocated to the first random numbered plot, i.e., M_1 to experimental unit 22, and then the first treatment M_1 the second time to the second random numbered plot, i.e., experimental unit 17, and continue the process till all the 24 plots are allotted with one treatment each in such random manner, and the ultimate layout is as follows:

Plot No	22	17	14	21	4	11	9	18	6	7	19	24	16	1	13	5	12	15	2	23	10	8	3	20
Treatment	M1	M1	M1	M1	M1	M2	M2	M2	M2	M3	M3	M3	M3	M4	M4	M4	M5	M5	M5	Mt	Mt	Mt	Mt	Mt
Sl No	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

Thus, the ultimate layout would be

1 M4	2 M5	3 Mt	4 M1	5 M4	6 M2	7 M3	8 Mt
9 M2	10 Mt	11 M2	12 M5	13 M4	14 M1	15 M5	16 M3
17 M1	18 M2	19 M3	20 Mt	21 M1	22 M1	23 Mt	24 M3

The same procedure could be followed for laboratory experiments with homogenous experimental units.

10.7.2 Statistical Model and Analysis

One can clearly find that the data arrangement is analogous to one-way classified data discussed in Chap. 9. So the model and the analysis will follow exactly as that for one-way classified data. Suppose there are t treatments with r_1, r_2, $r_3 \ldots, r_t$ replications, respectively, to be tested in a completely randomized design. So the model for the experiment will be $y_{ij} = \mu + \alpha_i + e_{ij}$, $i = 1, 2, 3, \ldots, t$ and $j = 1, 2, \ldots, r_i$.

where

y_{ij} = response due to jth observation of the ith treatment

μ = general effect

α_i = additional effect due to ith treatment and $\sum r_i \alpha_i = 0$

e_{ij} = error associated with jth observation of ith treatment and are i.i.d. N(0, σ^2)

Assumption of the Model

(i) Additive model assumed.

(ii) e_{ij}'s ~ i.i.d. N(0, σ^2).

Hypothesis to Be Tested

$H_0 : \alpha_1 = \alpha_2 = \alpha_3 = \ldots\ldots\ldots = \alpha_i = \ldots\ldots\ldots = \alpha_t = 0$ against

H_1: all α are not equal

Let the level of significance be α. So the total number of observations is $n = \sum_{i=1}^{t} r_i$.

Let us arrange the responses recorded from experimental units as follows:

Replication	Treatment					
	1	2	…….	i	…….	t
1	y_{11}	y_{21}	…….	y_{i1}	…….	y_{t1}
2	y_{12}	y_{22}	…….	y_{i2}	…….	y_{t2}
:	:	:	…….	:	…….	:
:	:	:		:		:
:	:	y_{2r2}	…….	:	…….	:
r_i	…….		…….	y_{iri}	…….	:
:	y_{1r1}					:
:						y_{tr_t}
Total	$y_{1.}$	$y_{2.}$	…….	$y_{i.}$	…….	$y_{t.}$
Mean	$\bar{y}_{1.}$	$\bar{y}_{2.}$		$\bar{y}_{i.}$		$\bar{y}_{t.}$

The analysis for this type of data is the same as that of one-way classified data discussed in Chap. 9 Sect. (9.4). From the above table, we calculate the following quantities:

$$\text{Grand total} = \sum_{i=1}^{t} \sum_{j}^{r_i} (\text{observation})$$
$$= y_{11} + y_{21} + y_{31} + \ldots\ldots\ldots + y_{trt}$$
$$= \sum_{i=1}^{t} \sum_{j=1}^{r_t} y_{ij} = G$$

$$\text{Correction factor} = \frac{G^2}{n} = CF$$

$$\text{Total sum of squares } (SS_{\text{Tot}}) = \sum_{i=1}^{t}\sum_{j}^{r_i}(\text{observation})^2 - CF = \sum_{i=1}^{t}\sum_{j=1}^{r_t} y_{ij}^2 - CF$$
$$= y_{11}^2 + y_{21}^2 + y_{31}^2 + \ldots\ldots\ldots + y_{tr_t}^2 - CF$$

Treatment sum of squares (SS_{Tr})

$$= \sum_{i=1}^{t} \frac{y_{i.}^{\ 2}}{r_i} - CF, \text{ where } y_{i.}$$

$$= \sum_{j=1}^{r_i} y_{ij}$$

= sum of the observations for the ith treatment

$$= \frac{y_{1.}^2}{r_1} + \frac{y_{2.}^2}{r_2} + \frac{y_{3.}^2}{r_3} + \ldots\ldots\ldots \frac{y_{i.}^2}{r_i} + \ldots\ldots\ldots \frac{y_{t.}^2}{r_t} - CF$$

Error sum of squares (by subtraction)
$= TSS - TrSS = SS_{Er}$.

ANOVA table for completely randomized design

SOV	d.f.	SS	MS	Tab F
Treatment	$t-1$	SS_{Tr}	$MS_{Tr} = \frac{TrSS}{t-1}$	$\frac{MS_{Tr}}{MS_{Er}}$
Error	$n-t$	SS_{Er}	$MS_{Er} = \frac{ErSS}{n-t}$	
Total	$n-1$	TSS		

The null hypothesis is rejected at α level of significance if the calculated value of F ratio corresponding to the treatment be greater than the table value at the same level of significance with $(t-1),(n-t)$ degrees of freedom that means we reject Ho if Fcal $>$ Ftab $_{\alpha;(t-1),(n-t)}$; otherwise, one cannot reject the null hypothesis. When the test is nonsignificant, we conclude that there exist no significant differences among the treatments which means with respect to the particular characters under consideration, all treatments are statistically at par.

In the event of the test being significant, i.e., when the null hypothesis is rejected, then one should find out which pair of treatments is significantly different from each other and which treatment is the best.

For this we need to calculate the least significant difference (LSD) value at specified level of significance using the following formula:

$$LSD_\alpha = \sqrt{ErMS\left(\frac{1}{r_i} + \frac{1}{r_{i'}}\right)} \times t_{\alpha/2,(n-t)} \text{ where}$$

i and i' are the treatments involved in comparison and t is the table value of t-distribution at α level of significance with $(n-t)$ d.f. Here the table value of t is to be considered at $\frac{\alpha}{2}$ level of significance as we are concerned with a both-sided test.

$\sqrt{ErMS\left(\frac{1}{r_i} + \frac{1}{r_{i'}}\right)}$ is the standard error of difference (SE_d) between the means for treatments i and i'. If the absolute value of the difference between the pair of treatment means exceeds the corresponding LSD value, then the two treatments are significantly different, and the better treatment is the treatment having better value over the other one.

10.7.3 Merits and Demerits of CRD

Merits

(i) CRD is the most simple among all experimental designs.

(ii) CRD is the only basic design where one can have flexibility of adopting different numbers of replications for different treatments. When the experimenter comes across with the problem of varied availability of experimental materials, the flexibility of different replications for different treatments becomes very useful.

(iii) Missing data does not provide potential threat so long there are a few observations corresponding to each and every treatment. This is possible only because of the design flexibility to handle different replications for different treatments.

(iv) Compared to other basic designs, CRD can be used in irregular shaped experimental plot.

Demerits

(i) Though CRD is most suitable for laboratory or greenhouse experimental condition because of homogenous experimental units, it is very difficult to have homogenous experimental units in large number under field condition.

(ii) In CRD only two basic principles of the design of experiment are used. The principle of "local control" is not used in this design which is very efficient in reducing the experimental error. As experimental error is more compared to other basic experimental designs.

(iii) With the increase in number of treatments and/or replications, especially under field condition, it becomes very difficult to get more number of homogeneous experimental units.

Example 10.1: (CRD with Unequal Replications)

An experiment was carried out at the research farm of the BCKV, Mohanpur, India, to know the effect of different levels of mushroom waste feeding on body weight in broiler chickens. The following results were obtained:

Mushroom waste (%)	Body weight after 40 days (in grams)					
1	1802.30	1799.49	1834.98	1723.12	1811.45	
3	1912.23	1934.12	1985.23	1954.31	1987.53	1977.23
5	2143.23	2143.77	2143.23	2193.34	2188.23	
7	2423.55	2453.78	2477.45	2412.54	2423.43	
9	2013.22	2076.23	2098.23	2043.77		

Analyze the data and draw the necessary conclusion.

Solution

This is a problem of completely randomized design with unequal replications. This is a fixed effect model $y_{ij} = \mu + \alpha_i + e_{ij}$, where α_i is the effect of the ith level, $i = 1, 2, 3, 4, 5$. That means the problem is to test

$H_0 : \alpha_1 = \alpha_2 = \ldots = \alpha_5$ against $H_1 : \alpha_i{}' s$ that are not equal.

Let the level of significance be $(\alpha = 0.01)$:

	Mushroom waste				
	1 %	3 %	5 %	7 %	9 %
	1802.30	1912.23	2143.23	2423.55	2013.22
	1799.49	1934.12	2143.77	2453.78	2076.23
	1834.98	1985.23	2143.23	2477.45	2098.23
	1723.12	1954.31	2193.34	2412.54	2043.77
	1811.45	1987.53	2188.23	2423.43	
		1977.23			
Sum (y_{i0})	8971.34	11750.65	10811.80	12190.75	8231.45
Average ($\bar{y}_{i0}$)	1794.27	1958.44	2162.36	2438.15	2057.86

The number of replications for mushroom waste 1 %, 5 %, and 7 % is 5, for 3 % is 6, and for 9 % is 4 so the total number of observations is $n = 3 \times 5 + 6 + 4 = 25$.

$$\begin{aligned} &Grandt Total\ (GT): \\ &= 1802.30 + 1799.49 + 1934.98 \\ &\quad + \ldots\ldots\ldots\ldots\ldots\ldots\ldots \\ &\quad + 2098.23 + 2043.77 = 51955.99 \end{aligned}$$

$$\text{Correction factor } (CF) = \frac{GT^2}{n} = \frac{51955.99^2}{25} = 107976995.90$$

$$\begin{aligned} &\text{Total sum of squares } (SS_{\text{Tot}}) \\ &= 1802.30^2 + 1799.49^2 + 1934.98^2 + \ldots\ldots \\ &\quad + 2098.23^2 + 2043.77^2 - CF \\ &= 1195535.07 \end{aligned}$$

$$\begin{aligned} &\text{Treatment sum of squares } (SS_{Tr}) \\ &= \frac{8971.34^2}{5} + \frac{11750.65^2}{6} + \frac{10811.80^2}{5} \\ &\quad + \frac{12190.75^2}{5} + \frac{12190.75^2}{4} \\ &= 1174028.21 \end{aligned}$$

$$\text{Error sum of squares } (SS_{Er}) = SS_{\text{Tot}} - SS_{Tr}$$

$$= 1195535.07 - 1174028.21 = 21506.86$$

ANOVA table

SOV	d.f.	SS	MS	F
Mushroom waste	4	1174028.21	293507.05	272.94
Error	20	21506.86	1075.34	
Total	24	1195535.07		

The table value of $F_{0.01,4,20} = 4.43$.

Thus F(Cal) > F(Tab)$_{0.01,4,20}$, so the test is significant, and we reject the null hypothesis of equality. We conclude that there exist significant differences among the different levels of mushroom waste feeding on body weight of broiler chicken.

So, the next objective is to find out the level at which the body weight differs significantly or the level/levels give significantly the highest body weight.

To compare the levels, we calculate the critical difference value, which is given as

$$LSD/CD(0.01) = \sqrt{MSE\left(\frac{1}{r_i} + \frac{1}{r_i^{'}}\right)} \times t_{0.01,\text{error}.df}$$

$$LSD/CD(0.01) = \sqrt{1075.34\left(\frac{1}{r_i} + \frac{1}{r_i^{'}}\right)} \times 2.845$$

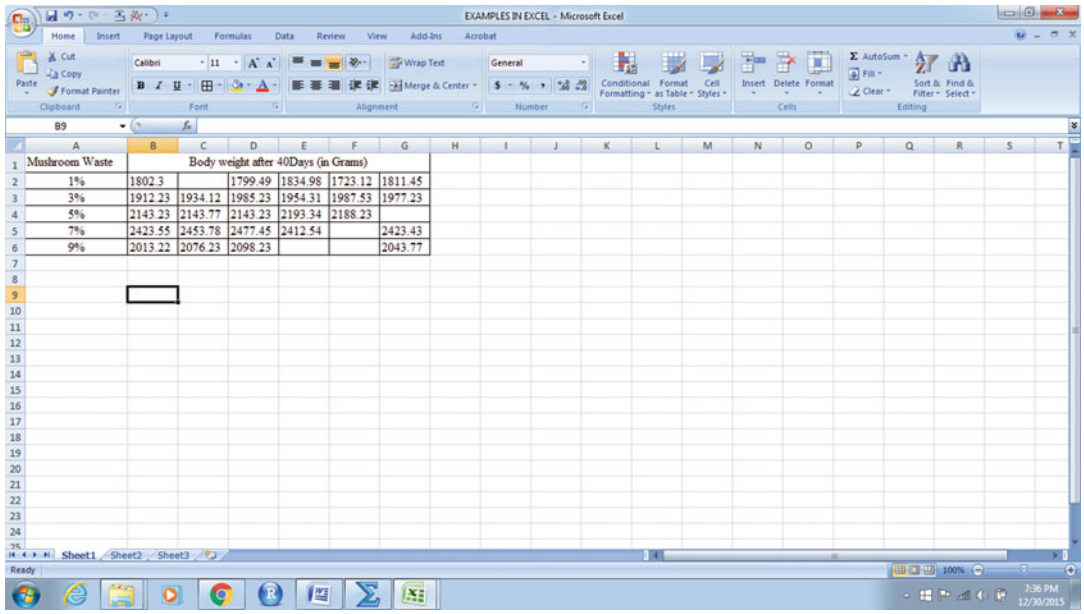
where r_i and $r_i^{'}$ are the number of observations of the two levels of mushroom wastes under comparison. Thus for comparing the levels of mushroom waste feeding, we have the following critical difference and mean difference values among the levels of mushroom feedings:

Comparison (%)	CD (0.01) values	Mean difference $\lvert\overline{y}_{i0} - \overline{y}_{i'0}\rvert$	Inference
1–3	56.490	164.174	Levels of mushroom waste feeding are results in significantly different broiler body weights in all the pairs
1–5	59.012	368.092	
1–7	59.012	643.882	
1–9	62.591	263.595	
3–5	56.499	203.918	
3–7	56.499	479.708	
3–9	62.591	99.420	
5–7	59.012	275.790	
5–9	62.591	104.497	
7–9	62.591	380.290	

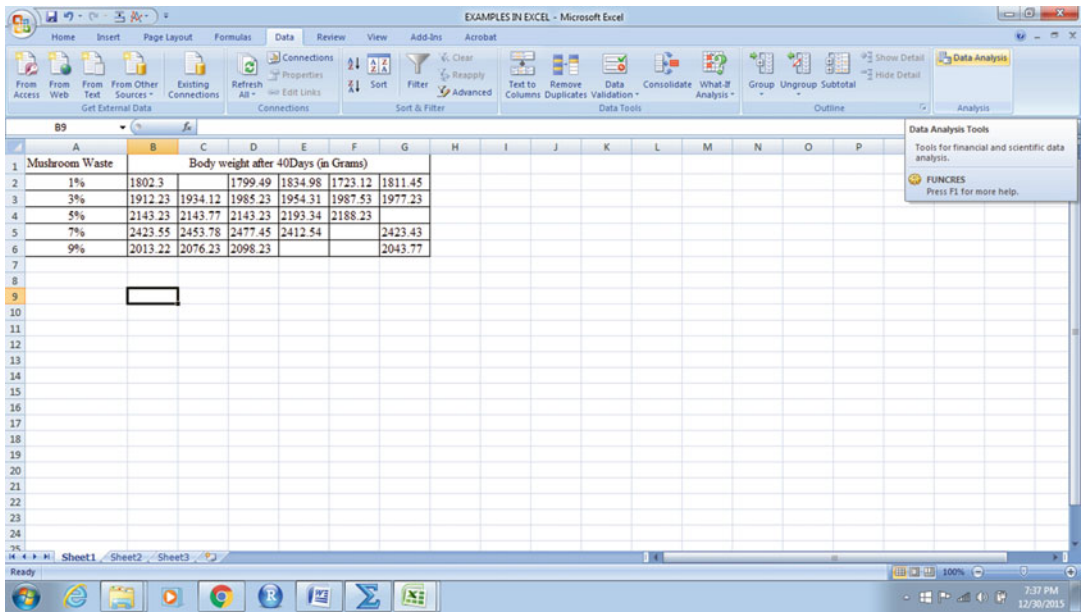
Example 10.1: (Using MS Excel)

Mushroom waste (%)	Body weight after 40 days (in grams)					
1	1802.30	1799.49	1834.98	1723.12	1811.45	
3	1912.23	1934.12	1985.23	1954.31	1987.53	1977.23
5	2143.23	2143.77	2143.23	2193.34	2188.23	
7	2423.55	2453.78	2477.45	2412.54	2423.43	
9	2013.22	2076.23	2098.23	2043.77		

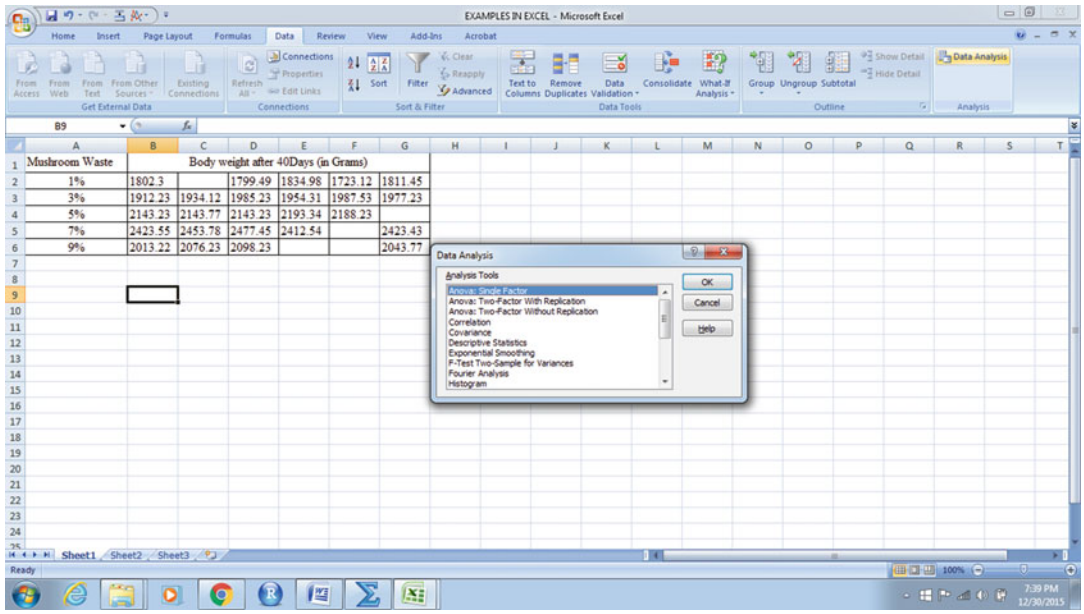
Step 1: Enter the data in the Excel as below.



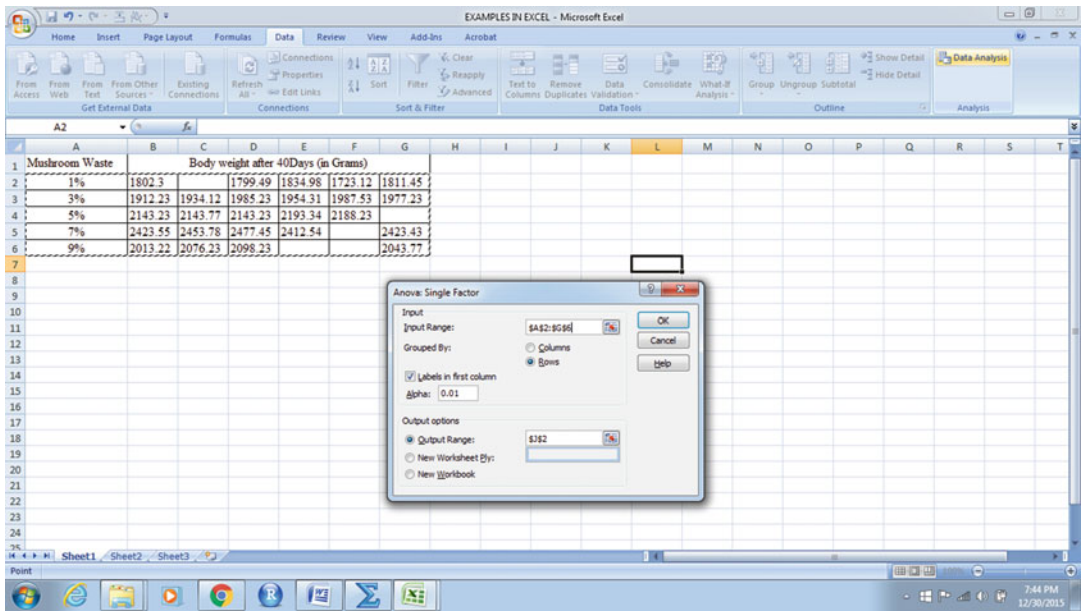
Step 2: Go to Data → click on Data Analysis toolbar.



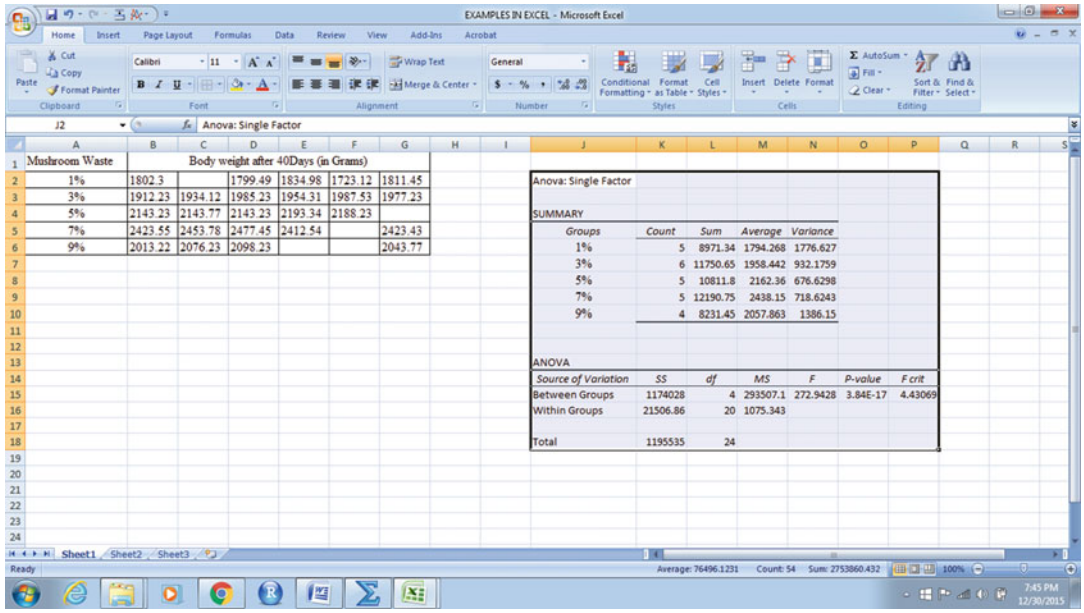
Step 3: Search for the option "Anova: Single" → click on OK.



Step 4: Select the input–output ranges, label etc., and select group by rows as shown below in the figure.



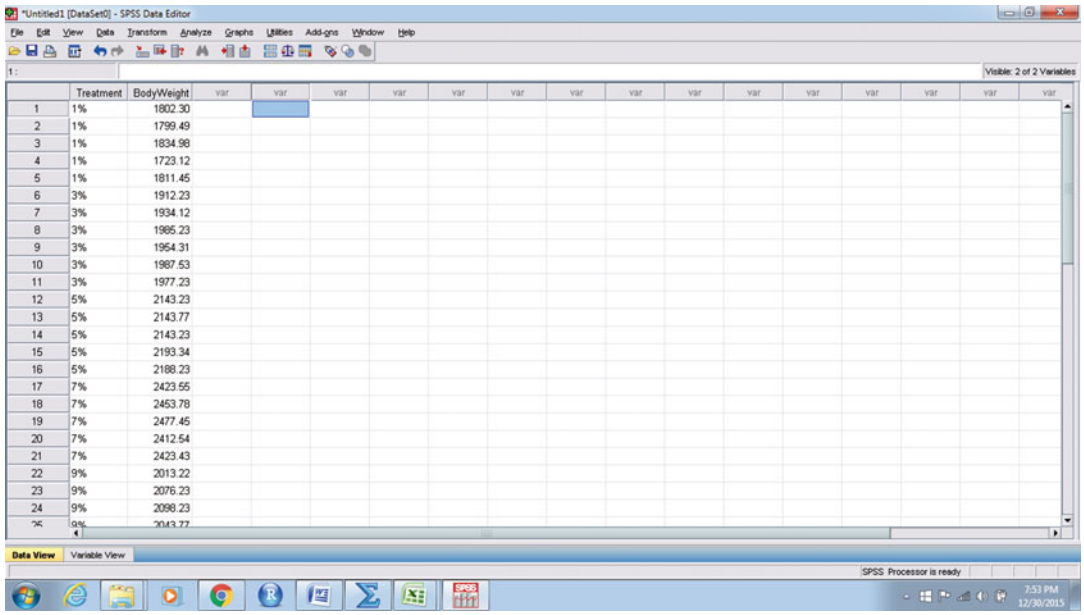
Step 5: Click on OK; then results will appear as shown below.



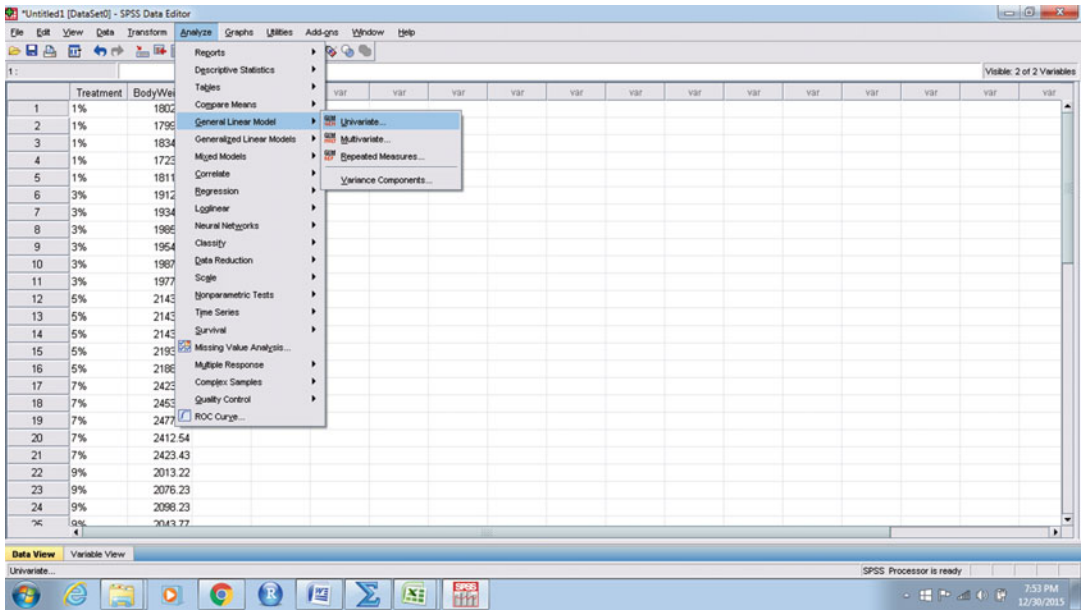
Example 10.1 (Using SPSS)

Mushroom waste (%)	Body weight after 40 days (in grams)					
1	1802.30		1799.49	1834.98	1723.12	1811.45
3	1912.23	1934.12	1985.23	1954.31	1987.53	1977.23
5	2143.23	2143.77	2143.23	2193.34	2188.23	
7	2423.55	2453.78	2477.45	2412.54		2423.43
9	2013.22	2076.23	2098.23			2043.77

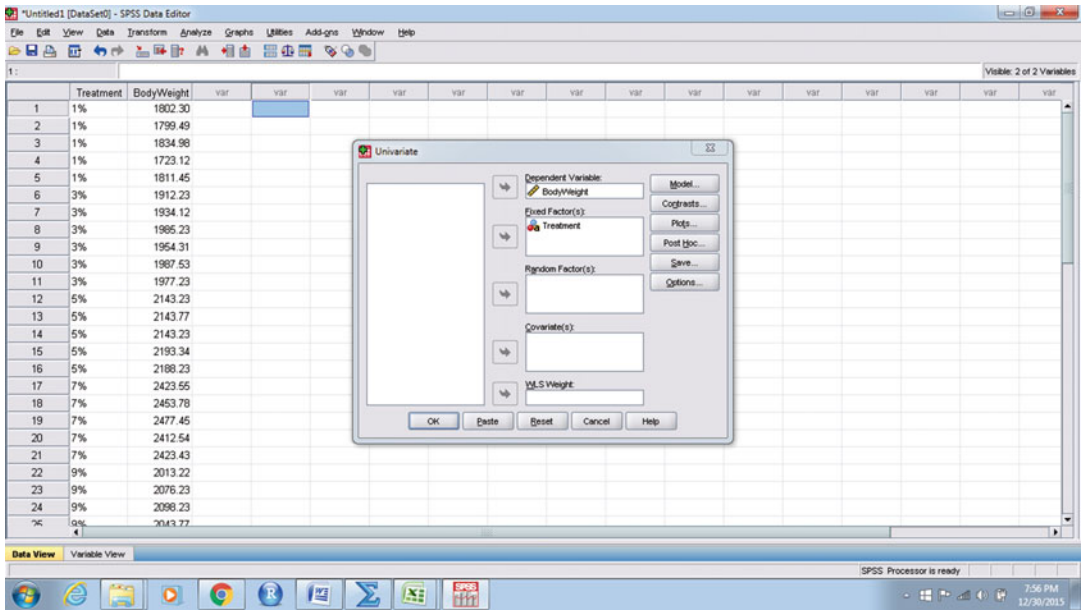
Step 1: Enter the data in SPSS data view as below; change the variable names.



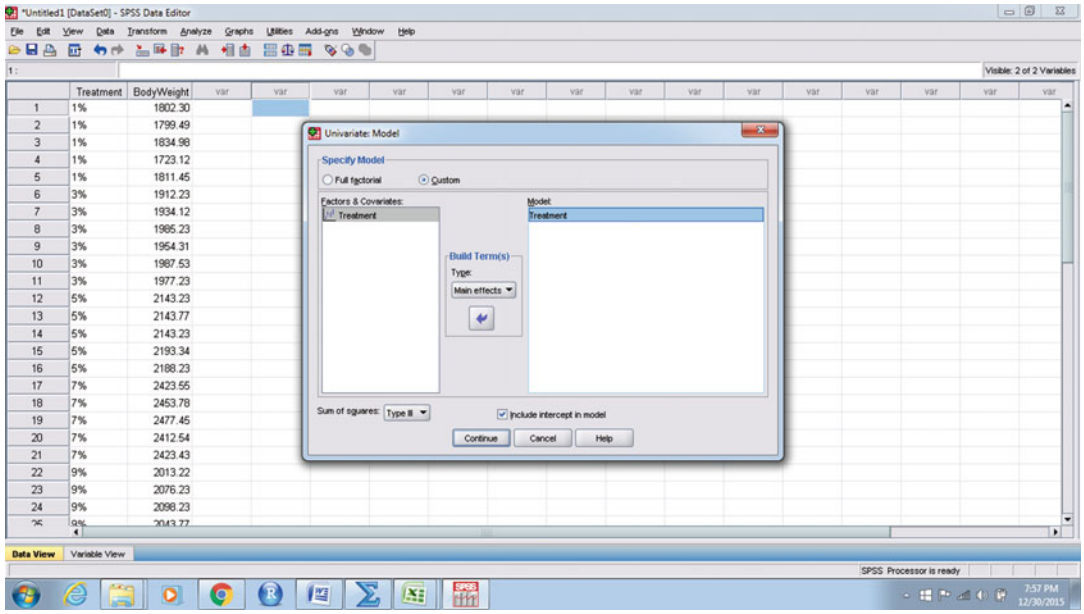
Step 2: Go to Analysis → generalize linear model → click on Univariate as below.



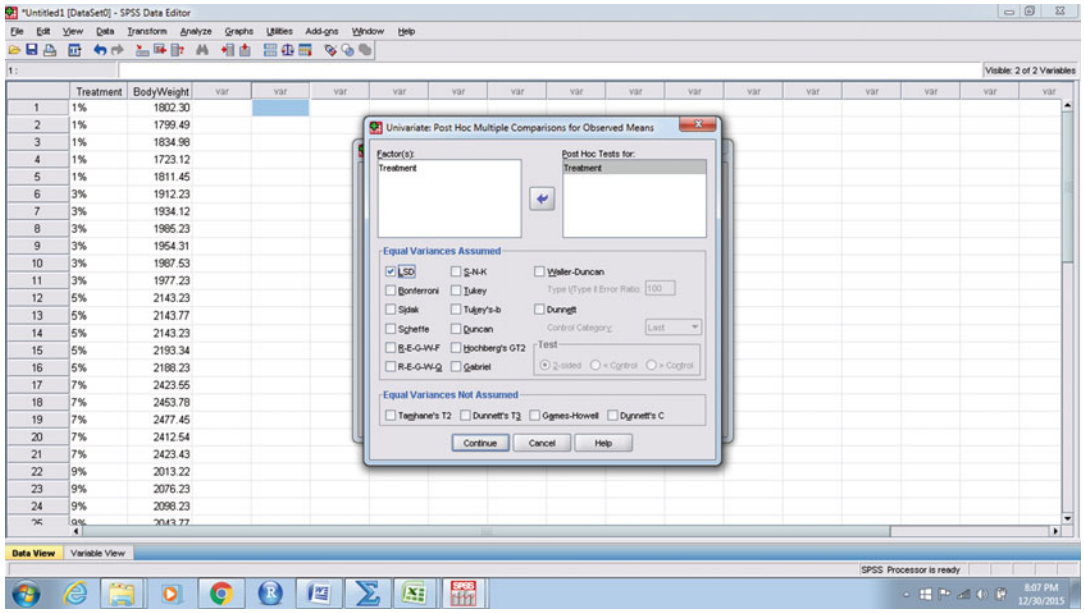
Step 3: Copy the dependent variable (in our case Body weight) into the Dependent variable option and fixed variable into the Fixed variable (in our case Treatment) as below.



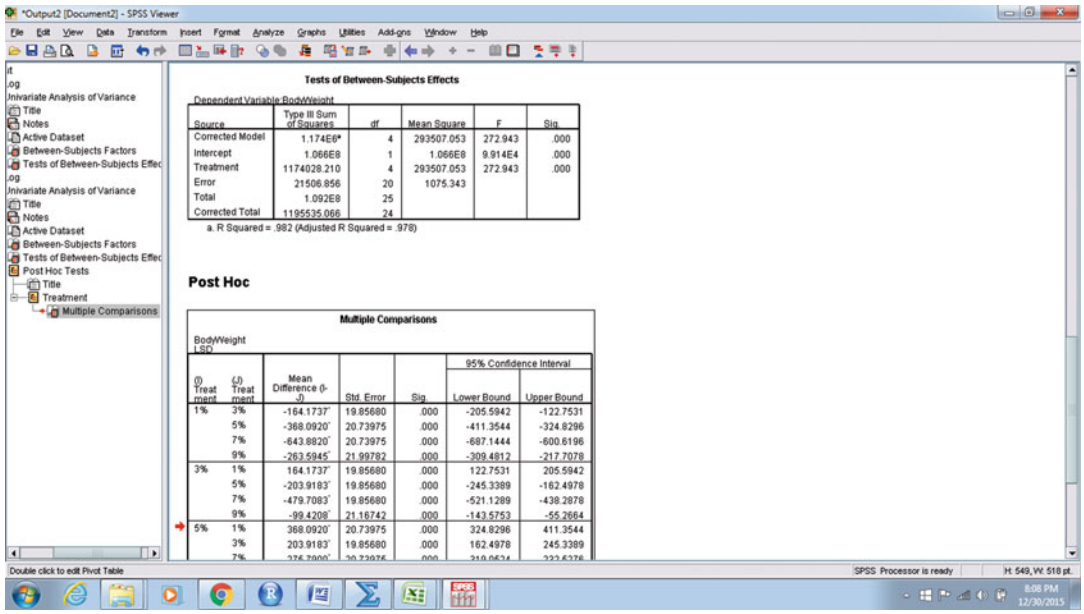
Step 4: Click on Model → change the option to custom → pass the Treatment into the Model → change the Type option to Main effect as below.



Step 5: Now click on Post Hoc; select any one of the Post Hoc options to perform a multiple pairwise comparison procedure as below. (We have to stick onto the LSD.)



Click on Continue and then OK to get the output as below.



Example 10.2: (CRD with an Equal Number of Replications)
In fish breeding improvement program, fishes are subjected to five different light intensities. The following table gives the fish weight (in kg) at the harvest after 90 days. Test whether the different light intensities differ significantly with respect to fish weight:

T1	T2	T3	T4	T5
2.22	1.54	1.8	2.12	2.26
2.32	1.57	1.91	2.41	2.37
2.27	1.65	1.84	2.34	2.43
2.32	1.63	1.97	2.42	2.46
2.24	1.61	1.88	2.33	2.31

Solution The statement shows that the experiment was laid out in completely randomized design with five different light intensities each replicated five times, so the analysis of data will follow one-way analysis of variance.

The model for the purpose is $y_{ij} = \mu + \alpha_i + e_{ij}$ where

$i = 1,2,3,4,5$; $j = 1,2,3,4,5$
$y_{ij} = j$ th observation for the ith light intensity
μ = general effect
α_i = additional effect due to ith light intensity
e_{ij} = errors associated with jth observation in ith light intensity and are i.i.d N(0, σ^2)

$H_0 : \alpha_1 = \alpha_2 = \ldots = \alpha_5$ against H_1 : All $\alpha_i's$ are not equal.

Let the level of significance be $(\alpha) = 0.01$:

	T1	T2	T3	T4	T5
	2.22	1.54	1.80	2.12	2.26
	2.32	1.57	1.91	2.41	2.37
	2.27	1.65	1.84	2.34	2.43
	2.32	1.63	1.97	2.42	2.46
	2.24	1.61	1.88	2.33	2.31
Total (y_{i0})	11.37	8.00	9.40	11.62	11.82
Average ($\bar{y}_{i0}$)	2.27	1.60	1.88	2.32	2.36

$$\text{Grand total } (GT) = 2.22 + 2.32 + 2.27 + \ldots\ldots\ldots\ldots + 2.43 + 2.46 + 2.31 = 52.20$$

$$\text{Correction factor } (CF) = \frac{GT^2}{n} = \frac{52.20^2}{25} = 109.024$$

Total sum of squares (SS_{Tot})

$$= 2.22^2 + 2.32^2 + 2.27^2 + \ldots\ldots\ldots\ldots + 2.43^2 + 2.46^2 + 2.31^2 - CF$$
$$= 2.35$$

Treatment sum of squares (SS_{Tr})

$$= \frac{11.37^2 + 8.00^2 + 9.40^2 + 11.62^2 + 11.82^2}{5} - CF$$
$$= 2.23$$

ANOVA table

SOV	d.f.	SS	MS	F
Treatment	4	2.238	0.559	94.662
Error	20	0.118	0.006	
Total	24	2.356		

Error sum of squares $(SS_{Er}) = TSS - TrSS$
$= 2.35 - 2.23 = 0.12$

The table value of $F_{0.01,4,20} = 4.43$.

Thus, F(Cal) > F(Tab)$_{0.01,4,20}$, so the test is significant and we reject the null hypothesis of equality of fish weight.

So, the next objective is to find out the light intensity which differs significantly among themselves and the light intensity having significantly the highest average fish weight.

To compare the light intensity, we calculate the critical difference value, which is given as

$$CD = \sqrt{MSE\left(\frac{1}{r_i} + \frac{1}{r_i'}\right)} \times t_{0.01,\text{error}.df}$$

$$CD = \sqrt{0.006\left(\frac{1}{r} + \frac{1}{r}\right)} \times t_{0.01,20}$$

$$= \sqrt{0.006\left(\frac{2}{5}\right)} \times 2.84 = 0.31$$

where r_i and r_i' are the number of observations of the two light intensities under comparison, and for this problem all are equal to 5.

We arrange the mean values corresponding to different light intensities in ascending order and compare the differences with CD value as follows:

Treatments (Light intensity)	Mean fish weight (kg)
T2	1.60
T3	1.88
T1	2.27
T4	2.32
T5	2.36

Treatments (light intensity) joined by the same line are statistically at par, i.e., they are not significantly different among themselves. Thus, the light intensities T2 and T3, T1, T4, and T5 are statistically at par. For the above table, it is clear that the T5 is by far the best light intensity giving the highest fish weight followed by T4, which is statistically at par with T1, and the light intensity T2 is the lowest yielder.

This type of problem can also be solved in MS Excel and SPSS following the steps discussed in Example 10.1.

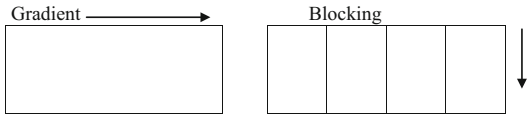
10.8 Randomized Block Design/ Randomized Complete Block Design (RBD/RCBD)

Randomized complete block design or simply randomized block design is the simplest of all field designs which uses all the basic principles, viz., (i) replication, (ii) randomization, and (iii) local control, of designs of experiment. This is the most basic design which takes care of the soil heterogeneity and hence the variability among the experimental units. In fact randomized block design takes care of soil heterogeneity in one direction; it is useful when the experimental units vary in nature in one way. Blocking is done across the fertility gradient, and each block should contain as many experimental units as the number of treatments in the experiment. As each and every block contains all the treatments, the blocks are known to be complete, and as such the design is also known as randomized complete block design (RCBD).

10.8.1 Experimental Layout

Step 1: Depending upon the heterogeneity among the experimental units and the number of treatments to be included in the experiment,

the whole experimental field is divided into number of blocks, perpendicular to the direction of heterogeneity, equal to the types/group of experimental units taking information from the uniformity trial or previous experience, e.g.,



In most of the cases, the number decides the number of replications in the experiment. That means the number of replications and the number of blocks are equal (synonymous) in this type of design. Thus each and every block contains as many numbers of experimental units as the number of treatments in the experiment so that each treatment is repeated equal number of times (equal to the number of blocks/replications) in the whole experiment:

Step 2: Each block is divided into number of experimental units equal to the number of treatments (say t) across the fertility gradient as shown below:

1st experimental unit
2nd experimental unit
:
:
:
:
t-1th experimental unit
tth experimental unit

Step 3: In each block consisting of *t* experimental units, allocate *t* treatments randomly so that no treatment is repeated more than once in any block.

Example Let us suppose we are to conduct an experiment taking six (A, B, C, D, E, F) treatments in three replications (R1, R2, R3). The step-by-step layout is as follows:
Step 1: Fertility gradient:

Step 1: Fertility gradient ⟶

Whole experimental area

Step 2: Blocks are made across the fertility gradient as follows:

R1	R2	R3

Step 3: Each replication/block is divided into six experimental units of equal size:

R1	R2	R3

Step 4: Six treatments are to be allocated randomly among the six experimental units of each block separately. Let us draw six random numbers 1–6 without repetition and suppose the random numbers are 5, 3, 2, 4, 1, and 6. So the treatment A is allotted to the fifth experimental unit, treatment C is allotted to the third experimental unit, and so on. Thus the distribution of treatments among the experimental units of the first replication/block will be as follows:

R1: Replication 1
E
C
B
D
A
F

Step 5: Repeat step 4 with fresh sets of random numbers for other two blocks separately to get the following layout of the design:

R1: Replication 1	R2: Replication 2	R3: Replication 3
E	B	C
C	C	E
B	E	F
D	D	A
A	F	D
F	A	B

10.8.2 Statistical Model and Analysis

From the design and its layout, it is quite evident that the randomized block design is almost similar to that of two-way classification of data with one observation per cell. As such the statistical model and analysis would be similar. Suppose we have a RBD experiment with t treatments, each being replicated r number of times. The appropriate statistical model for RBD will be

$$y_{ij} = \mu + \alpha_i + \beta_j + e_{ij}, i = 1, 2, 3, \ldots\ldots, t; j = 1, 2, \ldots . r$$

where

y_{ij} = response due to jth replication/block of the ith treatment
μ = general effect
α_i = additional effect due to ith treatment and $\sum \alpha_i = 0$
β_j = additional effect due to jth replication/block and $\sum \beta_j = 0$
e_{ij} = error associated with jth replication/block of ith treatment and
e_{ij}'s $\sim$ i.i.d. N$(0, \sigma^2)$

Assumptions of the Model

(i) Additive model assumed.
(ii) e_{ij}'s $\sim$ i.i.d. N$(0, \sigma^2)$.

Let the level of significance be α.

Hypothesis to Be Tested

The null hypotheses to be tested are

$$H_{01}: \alpha_1 = \alpha_2 = \ldots\ldots = \alpha_i = \ldots\ldots = \alpha_t = 0$$
$$H_{02}: \beta_1 = \beta_2 = \ldots\ldots = \beta_j = \ldots\ldots = \beta_r = 0$$

Against the alternative hypotheses,
H_{11}: all α's are not equal
H_{12}: all β's are not equal

In total we have $n = r.t.$ number of plots in the experiment:

Replications/Blocks								
Treatments	**1**	**2**	**....**	**j**	**....**	**r**	**Total**	**Mean**
1	y_{11}	y_{12}	....	y_{1j}	....	y_{1r}	$y_{1.}$	$\overline{y}_{1.}$
2	y_{21}	y_{22}	....	y_{2j}	....	y_{2r}	$y_{2.}$	$\overline{y}_{2.}$
:	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$
i	y_{i1}	y_{i2}	....	y_{ij}	....	y_{ir}	$y_{i.}$	$\overline{y}_{i.}$
:	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$	$\vdots$
t	y_{t1}	y_{t2}	....	y_{tj}	....	y_{tr}	$y_{t.}$	$\overline{y}_{t.}$
Total	$y_{.1}$	$y_{.2}$	....	$y_{.j}$	....	$y_{.r}$	$y_{..}$	
Mean	$\overline{y}_{.1}$	$\overline{y}_{.2}$	....	$\overline{y}_{.j}$	....	$\overline{y}_{.r}$		

From the above table, we calculate the following quantities:

$$\text{Grand total} = \sum_{i,j} y_{ij}$$
$$= y_{11} + y_{21} + y_{31} + \ldots\ldots\ldots + y_{tr}$$
$$= G$$

$$\text{Correction factor} = CF = \frac{G^2}{rt}$$

$$\text{Total sum of squares } (SS_{\text{Tot}}) = \sum_{i,j} y_{ij}^{\,2} - CF$$
$$= y_{11}^2 + y_{21}^2 + y_{31}^2 + \ldots\ldots\ldots + y_{tr}^2 - CF$$

$$\text{Treatment sum of squares } (SS_{Tr})$$
$$= \frac{\sum_{i=1}^{t} y_{i.}^{\,2}}{r} - CF$$
$$= \frac{y_{1.}^2}{r} + \frac{y_{2.}^2}{r} + \frac{y_{3.}^2}{r} + \ldots\ldots\ldots \frac{y_{i.}^2}{r} + \ldots\ldots\ldots \frac{y_{t.}^2}{r} - CF$$

$$\text{Replication sum of squares } (SS_R)$$
$$= \frac{\sum_{j=1}^{r} y_{.j}^{\,2}}{t} - CF$$
$$= \frac{y_{.1}^2}{t} + \frac{y_{.2}^2}{t} + \frac{y_{.3}^2}{t} + \ldots\ldots\ldots \frac{y_{.j}^2}{t} + \ldots\ldots\ldots \frac{y_{.r}^2}{t} - CF$$

$$\text{Error sum of squares (by subtraction)} = SS_{Er}$$
$$= TSS - TrSS - RSS$$

ANOVA table for RBD

SOV	d.f.	SS	MS	Cal F
Treatment	$t-1$	SS_{Tr}	$MS_{Tr} = \frac{SS_{Tr}}{t-1}$	$F_{Tr} = \frac{MS_{Tr}}{MS_{Er}}$
Replication (block)	$r-1$	SS_R	$MS_R = \frac{SS_R}{r-1}$	$F_R = \frac{MS_R}{MS_{Er}}$
Error	$(t-1)(r-1)$	SS_{Er}	$MS_{Er} = \frac{SS_{Er}}{(t-1)(r-1)}$	
Total	$rt-1$	SS_{Tot}		

If the calculated values of F corresponding to treatment and replication be greater than the corresponding table values at the α level of significance with $(t-1)$, $(t-1)(r-1)$ and $(r-1)$, $(t-1)(r-1)$ degrees of freedom, respectively, then the null hypotheses are rejected at α level of significance; otherwise one cannot reject the null hypothesis. When the test(s) is or are non-significant, we conclude that there exist no significant differences among the treatments and among the replications with respect to the particular character under consideration; all treatments are statistically at par so also the replications.

In the event of significance test(s), one rejects the null hypothesis (hypotheses), resulting in the decision that there exist significant differences among the treatments and also among the replications. Thus there is a need to find out which pairs of the treatments are significantly different from each other and which treatment is the best treatment or what is the order of the treatments w.r.t. the particular character under consideration. Similarly there is a need to find

out which pair of replications differs significantly among themselves. For the purpose we need to find out the least significant difference (critical difference) value for treatments and replications separately using the following formulae, respectively, and compare the treatment/replication mean differences with the respective LSD/CD values.

LSD/CD for Replication

$$LSD/CD_{\alpha}(\text{Rep.}) = \sqrt{\frac{2MS_{Er}}{t}} \times t_{\alpha/2;(t-1)(r-1)}$$

where t is the number of treatments and $t_{\alpha/2;(t-1)(r-1)}$ is the table value of t at α level of significance and $(t-1)(r-1)$ degrees of freedom for both-sided test.

The absolute value of difference between any pair of replication means is compared against the above LSD value; if the difference is more than the critical value (LSD/CD value), then the replication means is significantly different from each other, otherwise not.

Note: There are different schools of thought about the effect of the significant tests for replications. The significance of replication test does not hamper the estimation procedure and as such does not pose any serious problem in the inference. There is an argument that the replication(s) which are significantly different from the other should be discarded from the analysis. A counterargument is that if you discard the information from significant replications, then there exist no differences among the replications; then one should analyze the data as per the one-way analysis of variance, CRD, which design has got comparatively more error mean square than the competitive simple designs. And in that case, the basic parameter of adopting RBD that there exists one-way heterogeneity among the experimental units is put under question. Moreover, if one discards one or more replications from the analysis, there may be a shortfall in the minimum required degrees of freedom for error, and the sensitivity of F test and t test will be under question. So it is always better to have more number of replications while planning the experimental design.

LSD/CD for Treatment

$$LSD/CD_{\alpha} = \sqrt{\frac{2MS_{Er}}{r}} \times t_{\alpha/2;(t-1)(r-1)},$$

where r is the number of replications and $t_{\alpha/2;(t-1)(r-1)}$ is the table value of t at α level of significance and $(t-1)(r-1)$ degrees of freedom for both-sided test.

The absolute value of difference between any pair of treatment means is compared against the above LSD value; if the difference is more than the critical value (LSD/CD value), then the treatment means are significantly different from each other; otherwise, they are statistically at par.

10.8.3 Merits and Demerits of RBD

Merits

(i) RBD is the simplest of all block design.
(ii) RBD uses all the three principles of the design of experiments.
(iii) RBD takes care of soil heterogeneity.
(iv) The layout is very simple.
(v) It is more efficient compared to CRD.

Demerits

(i) RBD is a complete block design; each and every block contains all the treatments. Now if the number of treatments increases to a great extent, block size also increases simultaneously. It becomes very difficult to have a greater homogeneous block to accommodate more number of treatments. In practice, the number of treatments in RBD should not exceed 12.
(ii) Each and every treatment is repeated equal number of times in RBD. As such like CRD, the flexibility of using different replications for different treatments is not possible in RBD.
(iii) The missing observation, if any, is to be estimated first and then analysis of data to be taken.
(iv) RBD takes care of heterogeneity of experimental area in only one direction.

Example 10.3 A field experiment was conducted at Central Research Farm, Gayeshpur, Nadia, West Bengal, to study the effect of eight different herbicides on the total weed density (no. m $^{-2}$) in transplanted rice on weed management in rice–lathyrus cropping system. The following are the layout and data pertaining to weed density at 60 days after transplanting. Analyze the data and find out the best herbicide for weed management:

Rep-1	Rep-2	Rep-3
T4 (96)	T1 (180.45)	T6 (197.76)
T3 (145.33)	T3 (140.77)	T8 (339.375)
T5 (196.99)	T8 (335.89)	T3 (147.37)
T7 (79.99)	T4 (95.29)	T5 (196.585)
T6 (197.01)	T6 (193.87)	T4 (98.875)
T2 (169.67)	T2 (174.67)	T7 (87.895)
T8 (338.00)	T7 (86.26)	T2 (174.17)
T1 (182.34)	T5 (187.32)	T1 (184.395)

Solution

It appears from the information that the experiment has been laid out in randomized block design with eight different herbicides in three replications.

So the model for RBD is given by $y_{ij} = \mu + \alpha_i + \beta_j + e_{ij}$

where

$i = 1,2,\ldots, 6$; $j = 1,2,3$.

y_{ij} = effect due to the ith herbicide in jth replication

μ =general effect

α_i =additional effect due to ith herbicide

β_j =additional effect due to jth replication

e_{ij} =errors associated with ith herbicide in jth replication and are i.i.d. N(0, σ^2)

The hypotheses to be tested are

$H_{01} : \alpha_1 = \alpha_2 = \ldots = \alpha_8$ against H_{11}; all α's are not equal

$H_{02} : \beta_1 = \beta_2 = \beta_3$ against H_{12}; all β's are not equal

Let the level of significance be 0.05.

We shall analyze the data in the following steps:

Step.1: Make the following table from the given information:

Replication	T1	T2	T3	T4	T5	T6	T7	T8	Total	Mean
R1	182.34	169.67	145.33	96.00	196.99	197.01	79.99	338.00	**1405.33**	**175.67**
R2	180.45	174.67	140.77	95.29	187.32	193.87	86.26	335.89	**1394.52**	**174.32**
R3	184.40	174.17	147.37	98.88	196.59	197.76	87.90	339.38	**1426.43**	**178.30**
Total	**547.19**	**518.51**	**433.47**	**290.17**	**580.90**	**588.64**	**254.15**	**1013.27**	**4226.28**	
Mean	**182.40**	**172.84**	**144.49**	**96.72**	**193.63**	**196.21**	**84.72**	**337.76**		

Step.2: Calculate the following quantities:

$$\text{Grand total } (GT) = 182.34 + 169.67 + 145.33 + \ldots\ldots\ldots\ldots + 197.76 + 87.90 + 339.38 = 4226.28$$

$$\text{Correction factor } (CF) = \frac{GT^2}{n} = \frac{4226.28^2}{24} = 744225.01$$

$$\text{Total sum of squares } (SS_{\text{Tot}}) = \sum Obs.^2 - CF = 182.34^2 + 169.67^2 + 145.33^2 + \ldots\ldots\ldots\ldots + 197.76^2 + 87.90^2 + 339.38^2 - CF = 127799.89$$

$$\text{Treatment sum of squares } (SS_{Tr}) = \frac{1}{3}\sum_{i=1}^{3} y_{i0}^2 - CF$$

$$= \frac{547.19^2 + 518.51^2 + 433.47^2 + 290.17^2 + 580.90^2 + 588.64^2 + 254.15^2 + 1013.27^2}{3} - CF = 127637.55$$

$$\text{Replication sum of squares}(SS_R) = \frac{1}{8}\sum_{j=1}^{3} y_{0j}^2 - CF = \frac{1405.33^2 + 1394.52^2 + 1426.43^2}{8} - 744225.01 = 65.82$$

Error sum of squares ($ErSS$) = $TSS - TrSS - RSS$ = 127799.89 − 127637.55 − 65.82 = 96.51

Step.3: Construct the ANPVA table as given below:

SV	d.f.	SS	MS	F
Replication	2	65.82	32.91	4.78
Treatment	7	127637.55	18233.94	2644.79
Error	14	96.52	6.89	
Total	23	127799.89		

Step.4: The table value of $F_{0.05,2,14} = 3.75$ and $F_{0.05,7,14} = 2.76$. Thus, we find that the test corresponding to the replication and effect of different herbicides is significant. So the null hypothesis of equality of both replications and herbicidal effect is rejected; that means there exist significant differences among the replications as well as herbicides. But we are interested in the effects of herbicides. So we are to identify the herbicides, which are significantly different from each other and the best herbicide.

Step 5: Calculate the critical difference value using the following formula:

$$CD = \sqrt{\frac{2MSE}{r}} \times t_{0.025,\text{error}.df}$$

$$CD = \sqrt{\frac{2 \times 6.89}{3}} \times 2.14 = 4.598$$

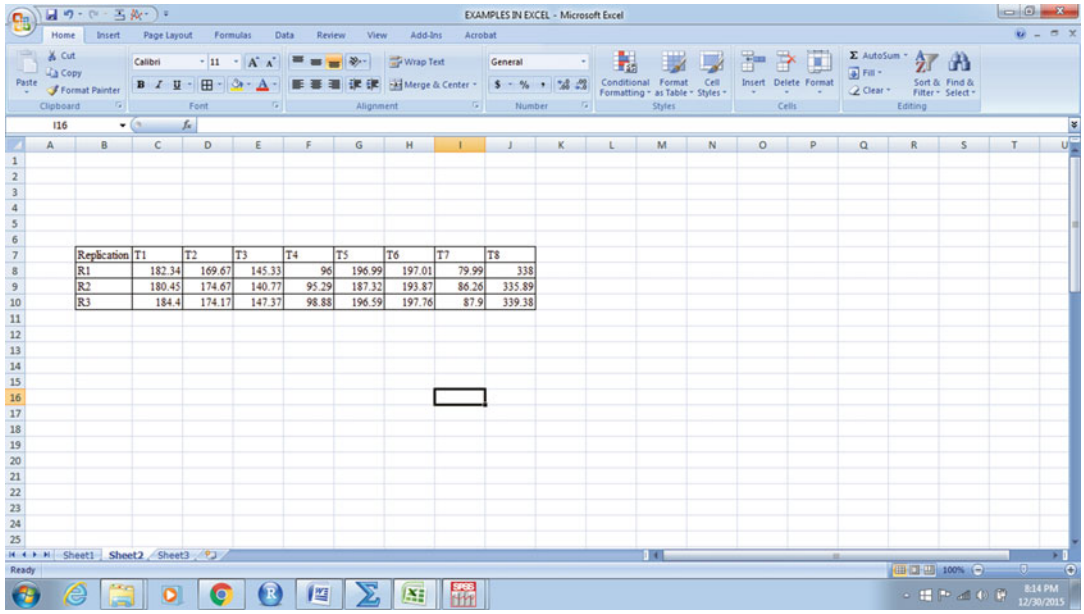
Arrange the weed density mean values in descending order, and compare the difference between any two treatment mean differences with that of the critical difference value. If the critical difference value be greater than the difference of two varietal means, then the treatments are statistically at par; there exists no significant difference among the means under comparison:

Treatment	Mean weed density (no. m^{-2})
T8	337.76
T6	196.21
T5	193.63
T1	182.40
T2	172.84
T3	144.49
T4	96.72
T7	84.72

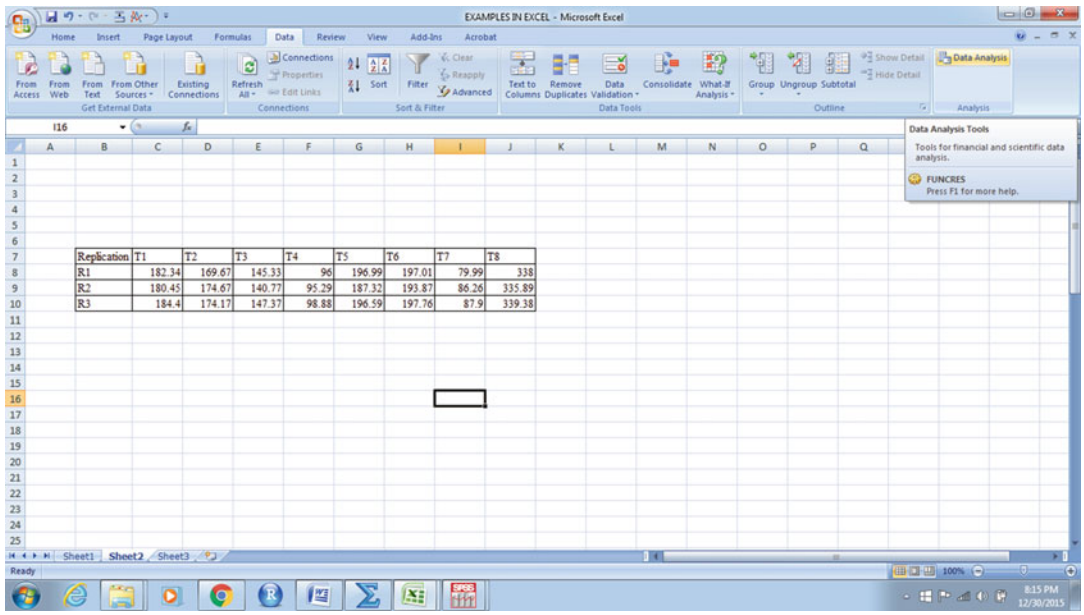
From the above one can find that herbicide 7 is the best herbicide having less weed density followed by 4th, 3rd, and 2nd herbicides and herbicide numbers 6 and 5 are at par with each other.

Example 10.3: (Using MS Excel)

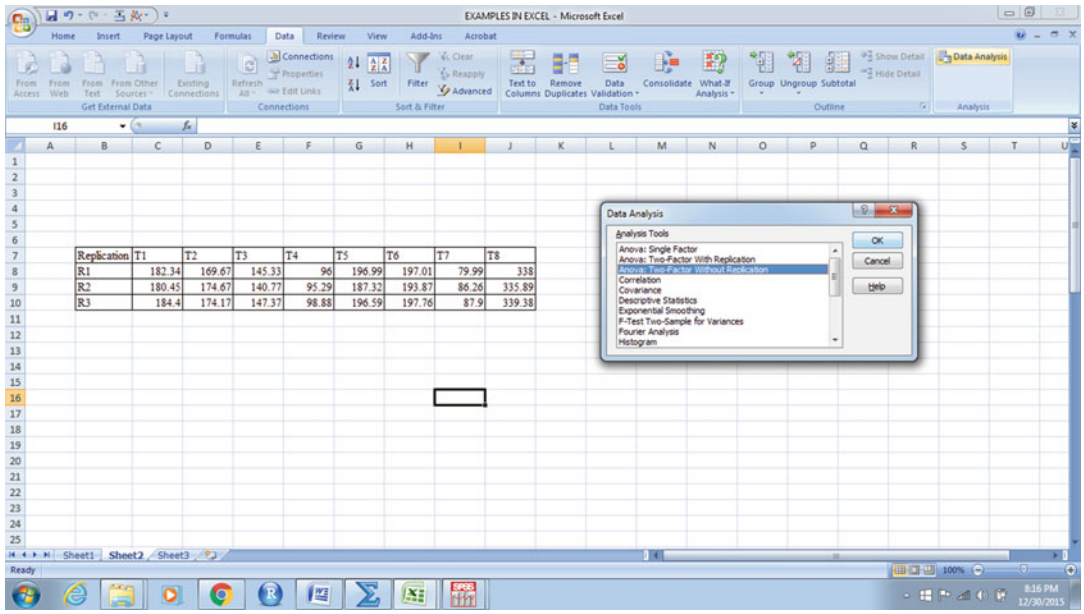
Step 1: Enter the data in the Excel sheet as below.



Step 2: Go to Data → click on the Data Analysis toolbar as below.

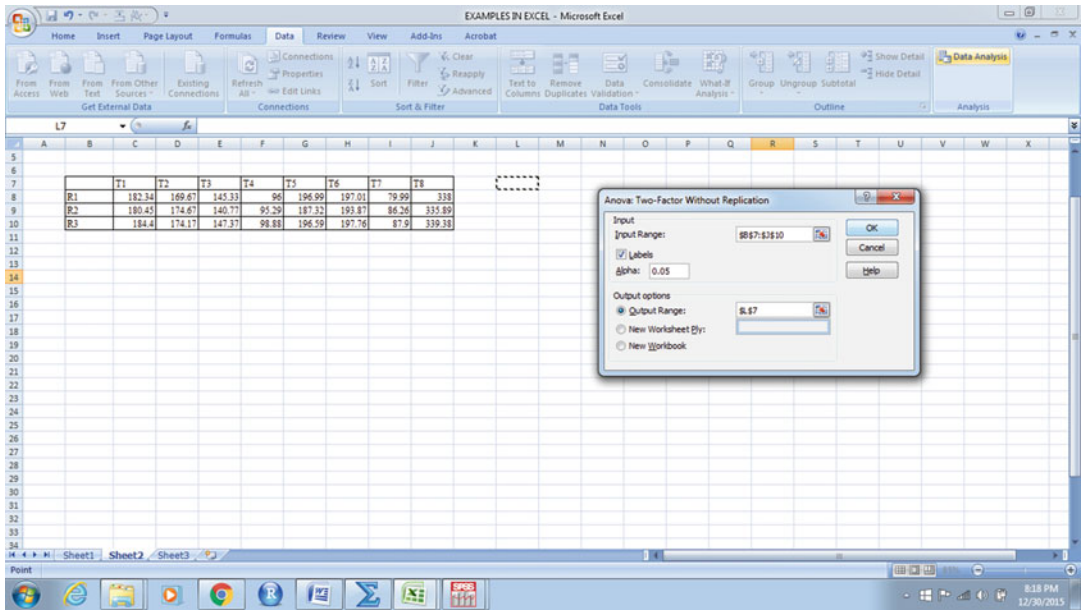


Step 3: Select the "Anova: Two Factor Without Replication" → click on OK as below.



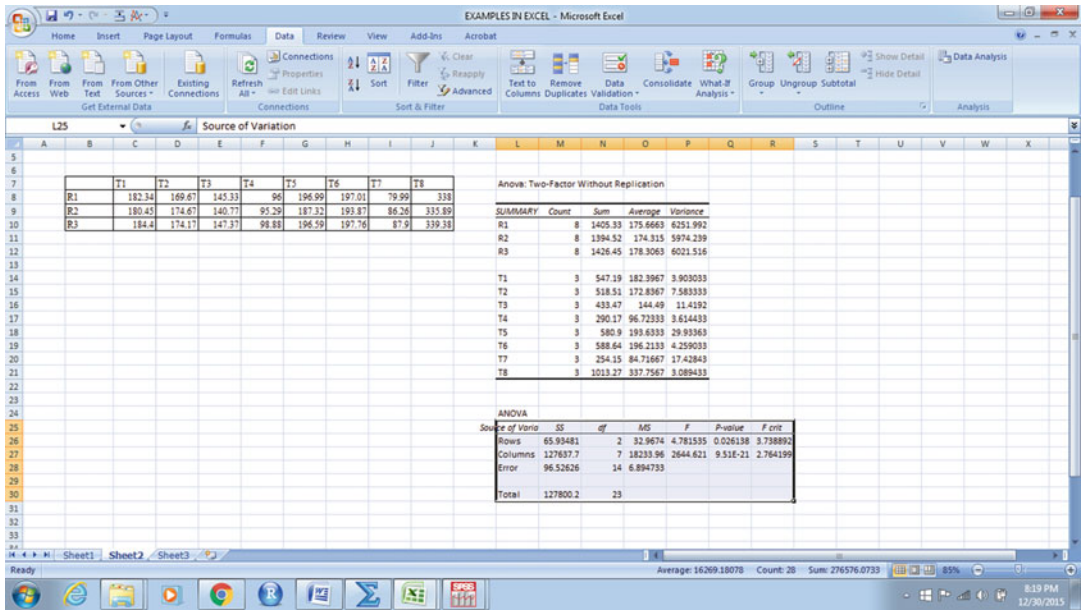
Replication	T1	T2	T3	T4	T5	T6	T7	T8
R1	182.34	169.67	145.33	96	196.99	197.01	79.99	338
R2	180.45	174.67	140.77	95.29	187.32	193.87	86.26	335.89
R3	184.4	174.17	147.37	98.88	196.59	197.76	87.9	339.38

Step 4: Select the input-output ranges, label etc., and enter the desired level of significance (we stick onto 0.05) as shown below in the figure.



	T1	T2	T3	T4	T5	T6	T7	T8
R1	182.34	169.67	145.33	96	196.99	197.01	79.99	338
R2	180.45	174.67	140.77	95.29	187.32	193.87	86.26	335.89
R3	184.4	174.17	147.37	98.88	196.59	197.76	87.9	339.38

Step 5: Click on OK to get the output as below.



EXAMPLES IN EXCEL - Microsoft Excel

Source of Variation

	T1	T2	T3	T4	T5	T6	T7	T8
R1	182.34	169.67	145.33	96	196.99	197.01	79.99	338
R2	180.45	174.67	140.77	95.29	187.32	193.87	86.26	335.89
R3	184.4	174.17	147.37	98.88	196.59	197.76	87.9	339.38

Anova: Two-Factor Without Replication

SUMMARY	Count	Sum	Average	Variance
R1	8	1405.33	175.6663	6251.992
R2	8	1394.52	174.315	5974.239
R3	8	1426.45	178.3063	6021.516
T1	3	547.19	182.3967	3.903033
T2	3	518.51	172.8367	7.583333
T3	3	433.47	144.49	11.4192
T4	3	290.17	96.72333	3.614433
T5	3	580.9	193.6333	29.93363
T6	3	588.64	196.2133	4.259033
T7	3	254.15	84.71667	17.42843
T8	3	1013.27	337.7567	3.089433

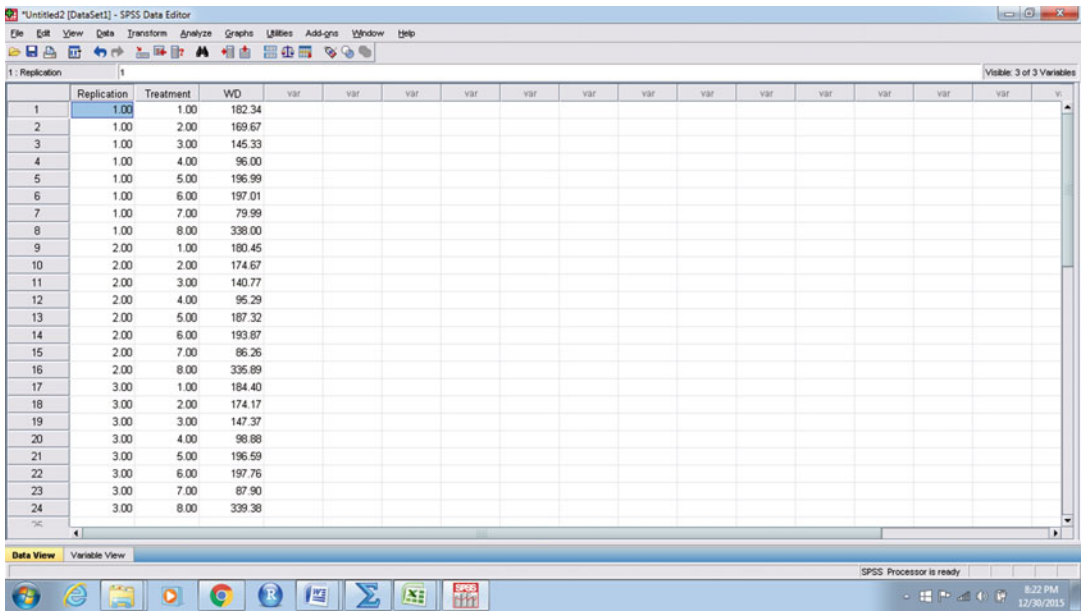
ANOVA

Source of Varia	SS	df	MS	F	P-value	F crit
Rows	65.93481	2	32.9674	4.781535	0.026138	3.738892
Columns	127637.7	7	18233.96	2644.621	9.51E-21	2.764199
Error	96.52626	14	6.894733			
Total	127800.2	23				

Here rows are the replications and columns are the herbicides. It can be seen that the results are exactly the same as what is found in manual calculation. But here the calculations of CD values are to be done manually.

Example 10.3: (Using SPSS)

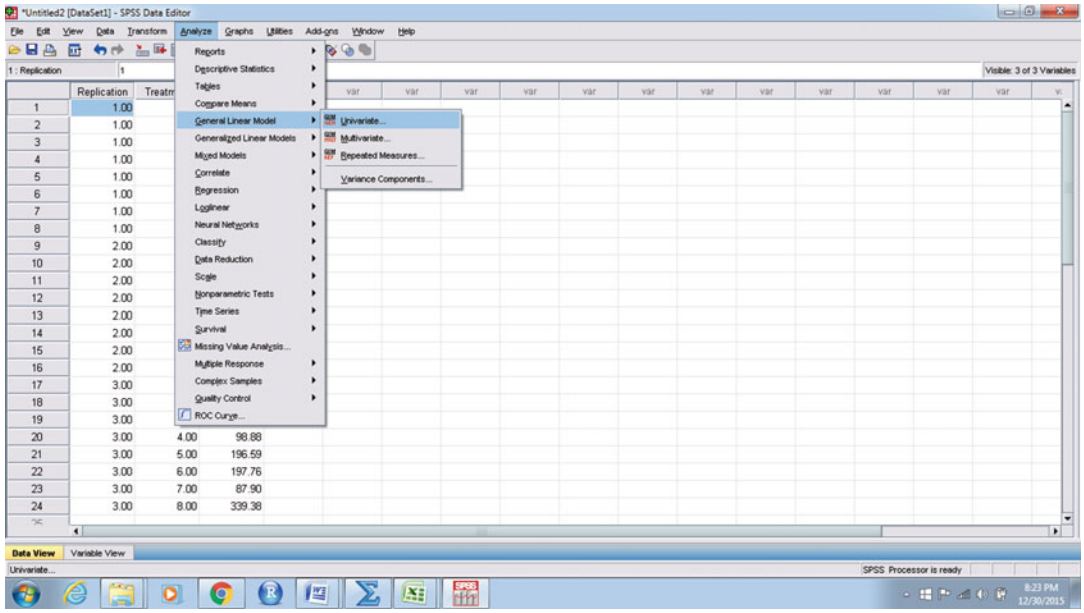
Step 1: Enter the data in SPSS data view as below; change the variable names.



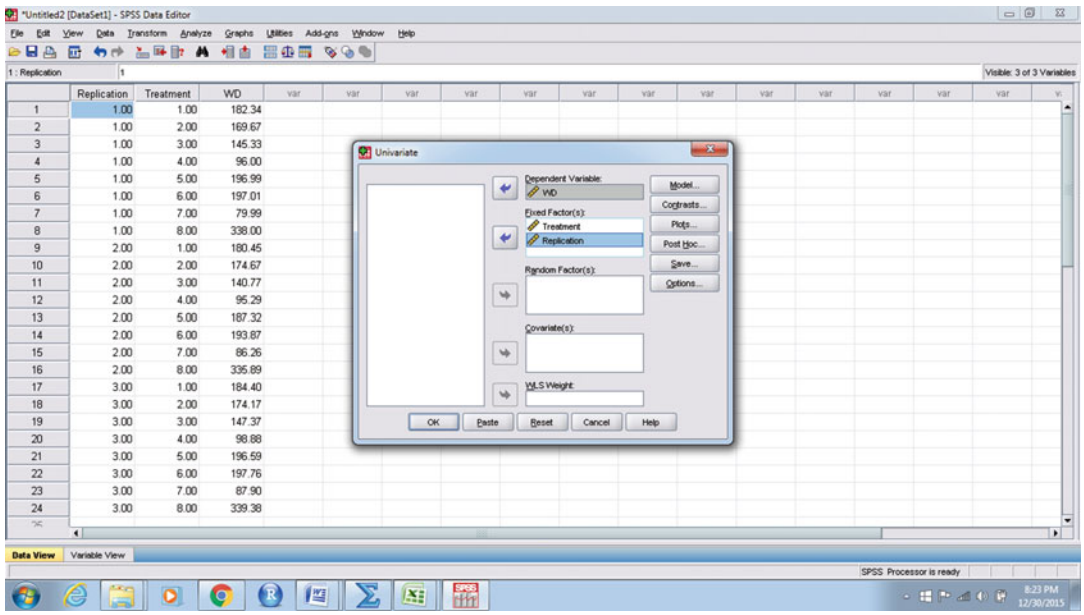
*Untitled2 [DataSet1] - SPSS Data Editor

	Replication	Treatment	WD
1	1.00	1.00	182.34
2	1.00	2.00	169.67
3	1.00	3.00	145.33
4	1.00	4.00	96.00
5	1.00	5.00	196.99
6	1.00	6.00	197.01
7	1.00	7.00	79.99
8	1.00	8.00	338.00
9	2.00	1.00	180.45
10	2.00	2.00	174.67
11	2.00	3.00	140.77
12	2.00	4.00	95.29
13	2.00	5.00	187.32
14	2.00	6.00	193.87
15	2.00	7.00	86.26
16	2.00	8.00	335.89
17	3.00	1.00	184.40
18	3.00	2.00	174.17
19	3.00	3.00	147.37
20	3.00	4.00	98.88
21	3.00	5.00	196.59
22	3.00	6.00	197.76
23	3.00	7.00	87.90
24	3.00	8.00	339.38

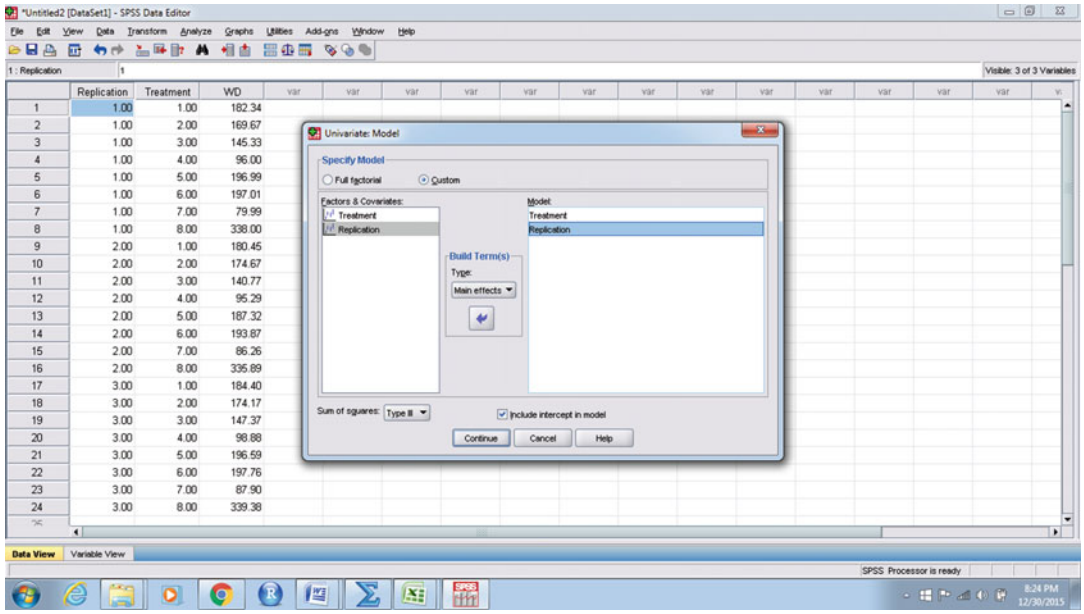
Step 2: Go to Analysis → generalize linear model → click on Univariate as below.



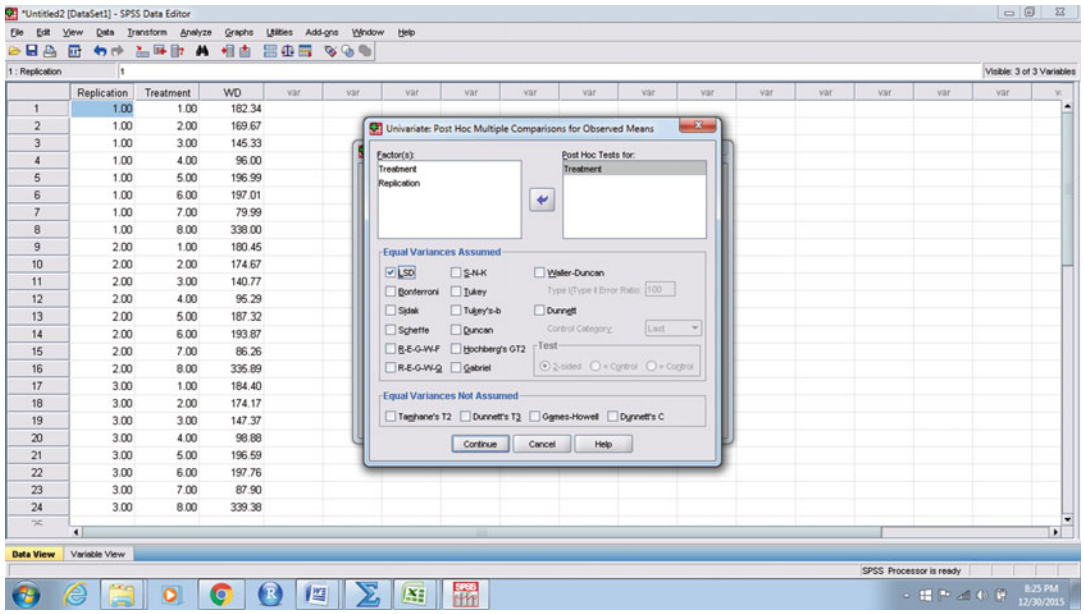
Step 3: Copy the dependent variable (in this example WD) into the Dependent variable option and fixed variables into the Fixed variable (in our case Replication and Treatment) as below.



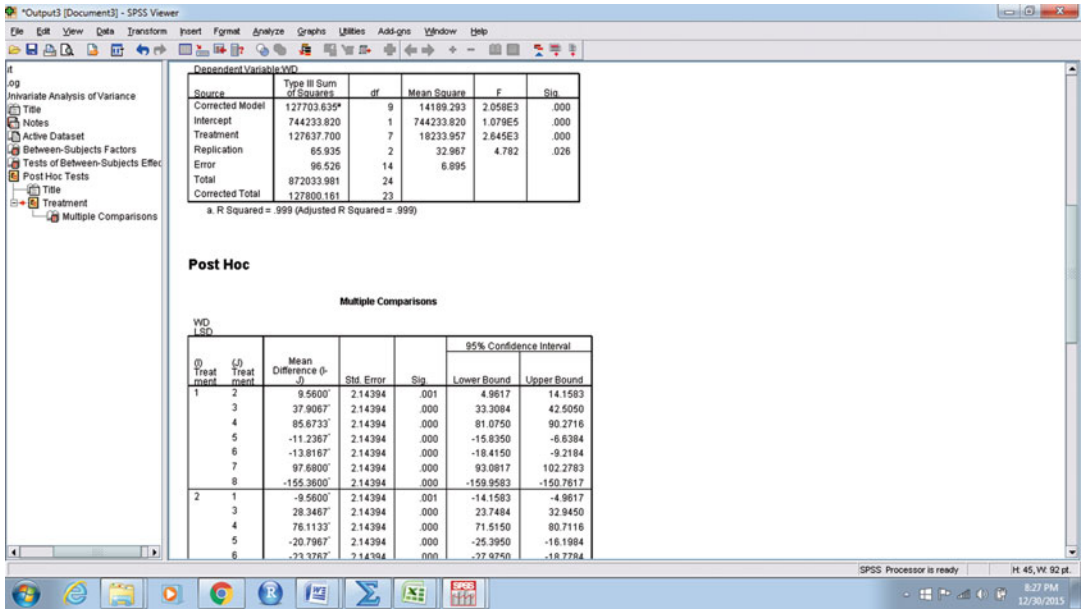
Step 4: Click on Model → change the option to custom → pass the Treatment and Replication into the Model → change the Type option to Main effect as below.



Step 5: Now click on Continue → click on Post Hoc, pass the Treatment variable into "Post Hoc test for" → select any one of the Post Hoc option to perform multiple pairwise comparison procedures as below. (We have sticked onto the LSD.)



Step 6: Click on Continue and then OK to get the output as below.



Example 10.4 The following table gives the test weight (in gram) from a yield trail of sorghum with nine treatments in a RBD. Analyze the data and find out the best treatment:

	R1	R2	R3
T1	28.00	27.30	31.70
T2	29.50	29.50	29.20
T3	30.60	29.70	30.90
T4	30.50	31.50	29.80
T5	28.40	29.10	30.80
T6	28.23	26.21	27.23
T7	32.50	29.90	30.50
T8	32.40	31.20	29.90
T9	27.50	29.50	29.00

Solution From the given information, it is clear that the appropriate statistical model will be

$$y_{ij} = \mu + \alpha_i + \beta_j + e_{ij}$$

where

$i = 1,2,\ldots, 9; j = 1,2,3.$
y_{ij} =effect due to the ith treatment in jth replication
μ =general effect
α_i =additional effect due to ith treatment
β_j =additional effect due to jth replication
e_{ij} =errors associated with ith treatment in jth replicate and are i.i.d. N(0, σ^2)

The above model is based on the assumptions that the effects are additive in nature and the error components are identically independently distributed as normal variate with mean zero and constant variance.

Let the level of significance be 0.05.

The hypotheses to be tested are

$H_{01} : \alpha_1 = \alpha_2 = \ldots = \alpha_8 = \alpha_9$ against H_{11};all α 's are not equal

$H_{02} : \beta_1 = \beta_2 = \beta_3$ against H_{12}; all β 's are not equal

First we make the following table:

	R1	R2	R3	Total	Mean
T1	28.00	27.30	31.70	*87.00*	*29.00*
T2	29.50	29.50	29.20	*88.20*	*29.40*
T3	30.60	29.70	30.90	*91.20*	*30.40*
T4	30.50	31.50	29.80	*91.80*	*30.60*
T5	28.40	29.10	30.80	*88.30*	*29.43*
T6	28.23	26.21	27.23	*81.67*	*27.22*
T7	32.50	29.90	30.50	*92.90*	*30.96*
T8	32.40	31.20	29.90	*93.50*	*31.16*
T9	27.50	29.50	29.00	*86.00*	*28.66*
Total	*267.63*	*263.91*	*269.03*	*800.57*	–

From the above table, we calculate the following quantities:

$$\text{Grand total } (GT) = 28.00 + 29.50 + \ldots\ldots\ldots\ldots + 29.90 + 29.00 = 800.57$$

$$\text{Correction factor } (CF) = \frac{GT^2}{n} = \frac{800.57^2}{27} = 23737.49$$

$$\text{Total sum of squares } (SS_{\text{Tot}}) = \sum Obs.^2 - CF$$
$$= 28.00^2 + 29.50^2 + \ldots\ldots\ldots\ldots + 29.90^2 + 29.00^2 - 23737.49 = 66.22$$

$$\text{Treatment sum of squares } (SS_{Tr}) = \frac{1}{3}\sum_{i=1}^{3} y_{i0}^2 - CF$$
$$= \frac{87.00^2 + 88.20 + \ldots\ldots\ldots\ldots + 86.00}{3} - CF$$
$$= 38.65$$

$$\text{Replication sum of squares } (SS_R) = \frac{1}{8}\sum_{j=1}^{3} y_{0j}^2 - CF$$
$$= \frac{267.63^2 + 263.91^2 + 269.03^2}{8} - 23737.49 = 1.55$$

$$\text{Error sum of squares } (SS_{Er}) = SS_{\text{Tot}}) - SS_{Tr} - SS_R$$
$$= 66.22 - 38.65 - 1.55 = 26.01$$

Construct the ANOVA table as given below

SOV	d.f.	SS	MS	F
Replication	2	1.56	0.78	0.478
Treatment	8	38.66	4.83	2.97
Error	16	26.01	1.63	–
Total	26	66.23	–	–

The table value of $F_{0.05,2,16} = 3.63$ and $F_{0.05,8,16} = 2.59$. Thus, we find that the test corresponding to the effect of different treatments is significant. So the null hypothesis of equality of treatment effect is rejected; that means there exist significant differences among the treatments. So we are to identify the treatment, which is significantly different from each other and the best treatment.

Calculate the critical difference value using the following formula:

$$CD = \sqrt{\frac{2MSE}{r}} \times t_{0.05,\text{error}.df}$$

$$CD = \sqrt{\frac{2 \times 1.63}{3}} \times 2.11 = 2.20$$

Arrange the mean of test weight in descending order, and compare the difference between any two treatment mean differences with that of the critical difference value. If the critical difference value be greater than the difference of two varietal means, then the treatments are statistically at par; there exists no significant difference among the means under comparison:

Treatment	Mean
T8	31.17
T7	30.97
T4	30.60
T3	30.40
T5	29.43
T2	29.40
T1	29.00
T9	28.67
T6	27.22

From the above one can find that treatment number 8 is the best treatment having the highest seed test weight and it is at par with treatment numbers 7, 4, 3, 5, and 2; the treatment number 6 is with the lowest test weight.

Example 10.5 The following table gives the pod yield data (q/ha) from a yield trial of pea with ten varieties in a RBD. Analyze the data and find out the best variety:

	Pod yield of pea (q/ha)			
Varieties	Block 1	Block 2	Block 3	Block 4
P1	6.2	8.0	7.2	7.1
P2	9.5	10.3	10.5	10.1
P3	8.3	8.3	8.1	8.2
P4	9.6	9.4	9.9	9.6
P5	9.0	9.6	9.8	9.5
P6	8.1	7.97	7.3	7.8
P7	8.3	8.3	8.8	8.5
P8	9	7.3	8.7	8.3
P9	7.9	8.2	7.8	7.6
P10	11.6	11.2	11.5	11.3

From the given information, it is clear that the appropriate statistical model will be

$$y_{ij} = \mu + \alpha_i + \beta_j + e_{ij},\ i = 10 \text{ and } j = 4$$

where

y_{ij} = response corresponding to jth replication of the ith variety

μ = general effect

α_i = additional effect due to ith variety and $\sum \alpha_i = 0$

β_j = additional effect due to jth replication and $\sum \beta_j = 0$

e_{ij} = error associated with jth replication of ith variety and are i.i.d. N(0, σ^2).

The above model is based on the assumptions that the effects are additive in nature.

Let the level of significance be $\alpha = 0.05$.

Hypothesis to be tested:

$H_{01} : \alpha_1 = \alpha_2 = \ldots\ldots\ldots = \alpha_{10} = 0$ against all α 's are not equal

$H_{02} : \beta_1 = \beta_2 = \beta_3 = 0$ against all β 's are not equal

First of all we make the following table:

	Pod yield (q/ha)					
Varieties	Block 1	Block 2	Block 3	Block 4	Total	Average
P1	6.2	8	7.2	7.1	28.53	7.13
P2	9.5	10.3	10.5	10.1	40.40	10.10
P3	8.3	8.3	8.1	8.2	32.93	8.23
P4	9.6	9.4	9.9	9.6	38.53	9.63
P5	9	9.6	9.8	9.5	37.87	9.47
P6	8.1	7.97	7.3	7.8	31.16	7.79
P7	8.3	8.3	8.8	8.5	33.87	8.47
P8	9	7.3	8.7	8.3	33.33	8.33
P9	7.9	8.2	7.8	7.6	31.50	7.88
P10	11.6	11.2	11.5	11.3	45.60	11.40
Total	87.5	88.57	89.6	88.05667	353.7267	

From the above table, we calculate the following quantities:

$$CF = \frac{GT^2}{n} = \frac{353.73^2}{10 \times 4} = 3128.064$$

$$SS_{\text{Tot}} = \sum \text{Obs.}^2 - CF = 6.2^2 + 9.5^2 + \ldots\ldots\ldots + 7.6^2 + 11.3^2 - 3128.064 = 64.65113$$

$$SS_{\text{R}} = \frac{1}{10}\sum_{j=1} R_j^2 - CF$$

$$= \frac{1}{10}\left[87.5^2 + 88.57^2 + 89.6^2 + 88.057^2\right] - 3128.064 = 0.239277$$

$$SS_V = \frac{1}{4}\sum_{i=1}^{10} V_i^2 - CF$$

$$= \frac{1}{4}\left[28.53^2 + 40.40^2 + \ldots\ldots + 45.60^2\right] - 3128.064 = 59.495$$

$$SS_{Er} = SS_{\text{Tot}} - SS_R - SS_V = 4.9168$$

Construct the ANOVA table as given below:

ANOVA				
SOV	d.f.	SS	MS	F
Replication	3	0.239	0.078	0.428
Variety	9	59.495	6.611	36.301
Error	27	4.917	0.182	–
Total	39	64.651	–	–

The table values corresponding to replication and variety are $F_{0.05;3,27} = 2.965$ and $F_{0.05;9,27} = 2.255$, respectively. Thus, only the test corresponding to variety is significant but the test corresponding to replication is not. So the null hypothesis of equality of replication effects cannot be rejected; that means the replication effects are statistically at par. On the other hand, the null hypothesis of equality of varietal effect is rejected; that means there exist significant differences among the varieties. So we are to identify the varieties, which are significantly different from each other and the best variety.

Calculate the critical difference value at $\alpha = 0.05$ using the following formula:

$$\begin{aligned} \mathrm{CD}_{0.05}(\text{variety}) &= \sqrt{\frac{2MSE}{r}} \times t_{0.05,\mathrm{err}.df.} \\ &= \sqrt{\frac{2 \times 0.1821}{4}} \times t_{0.05,27} \\ &= \sqrt{\frac{2 \times 0.1821}{4}} \times 2.052 \\ &= 0.619 \end{aligned}$$

Arrange the varietal mean values in descending order, and compare the difference between any two treatment mean differences with that of the critical difference value. If the critical difference value be less than the difference of two varietal means, then the treatments are statistically at par; there exists no significant difference among the means under comparison:

Variety	Average pod length
P10	11.40
P2	10.10
P4	9.63
P5	9.47
P7	8.47
P8	8.33
P3	8.23
P9	7.88
P6	7.79
P1	7.13

From the above one can find that variety 10 is the best variety having the highest yield and variety 1 the lowest pod yield producers among the varieties of pea.

10.9 Latin Square Design (LSD)

In many practical situations, it is found that the fertility gradient or soil heterogeneity varies not only in one direction but also in two perpendicular directions. Randomized complete block design takes care of soil heterogeneity in one direction. Thus, there is a need for experimental design which can take care of heterogeneity among experimental units in two perpendicular directions. Latin square design (LSD) is such a design which takes care of two perpendicular sources of variations among the experimental units. As per the principle of blocking, blocking is to be done in perpendicular direction of soil heterogeneity. Thus to take care of soil heterogeneity in two perpendicular directions, we need to frame blocks in two perpendicular directions independently. And as per characteristics of blocking, each block should contain each treatment once in each block. Thus in Latin square design, each block in perpendicular directions, i.e., each row block and column block, should contain each and every treatment once and only once. This arrangement has resulted in row and column blocks of equal size, thereby resulting in the requirement of t^2 number of experimental units to accommodate t number of treatments in a Latin square design. This type of allocation of treatments helps in estimating the variation among row blocks as well as column blocks. Subsequently the total variations among the experimental units are partitioned into different sources, viz., row, column, treatments, and errors.

Though applications of this type of designs are rare in laboratory condition, it can be conducted and is useful in field conditions or greenhouse conditions. The two major perpendicular sources of variations in greenhouse may be

the difference among the rows of the plot and their distances from the wall of the greenhouses.

10.9.1 Randomization and Layout

LSD is a design where the number of treatments equals the number of rows equals the number of columns. Because of such stringent relationship, the layout of the design is more complicated compared to the other two basic designs discussed, viz., RBD and CRD. The layout of the Latin square design starts with a standard Latin square. *A standard Latin square is an arrangement in which the treatments are arranged in natural/alphabetical order or systematically*. Then in the next step, columns are randomized, and in the last step keeping the first row intact, the rest of the rows are randomized. As such we shall get the layout of Latin square of different orders. Let us demonstrate the steps of the layout of Latin square design taking five treatments in the experiment:

Step 1: Suppose the treatments are A, B C, D, and E. So there would be $5 \times 5 = 25$ experimental units arranged in five rows and five columns. Now distribute the five treatments in alphabetical order as shown below to get the standard Latin square:

Rows	Columns				
	A	B	C	D	E
	B	C	D	E	A
	C	D	E	A	B
	D	E	A	B	C
	E	A	B	C	D

Step 2: Randomize the columns to get the following layout (for example):

B	D	A	E	C
C	E	B	A	D
D	A	C	B	E
E	B	D	C	A
A	C	E	D	B

Step 3: Keeping the first row intact, randomize the rest of the rows as follows:

B	D	A	E	C
D	A	C	B	E
E	B	D	C	A
A	C	E	D	B
C	E	B	A	D

Layout of 5 × 5 Latin square design

10.9.2 Statistical Model and Analysis

From the design and its layout, it is quite evident that the LSD is almost similar to incomplete three-way classification of data. Let there be t treatments, so there should be t rows and t columns, and we need a field of $t \times t = t^2$ experimental units. The triplet, i.e., (i, j, k), takes only t^2 of the possible t^3 values of a selected Latin square.

As such the statistical model and analysis would be as follows:

Model $= y_{ijk} = \mu + \alpha_i + \beta_j + \upsilon_k + e_{ijk}$

where

$i = 1, 2, \ldots, t; j = 1, 2, \ldots, t;$ and $k = 1, 2, \ldots, t$

μ = general effect

α_i = additional effect due to ith treatment and $\sum \alpha_i = 0$

β_j = additional effect due to jth row and $\sum r_j = 0$

υ_k = additional effect due to kth treatment and $\sum c_k = 0$

e_{ijk} = error associated with ith treatment in jth row and kth column and

$e_{ijk} \sim$ i.i.d. $N(0, \sigma^2)$.

The triplet, i.e., (i, j, k), takes only t^2 of the possible t^3 values of a selected Latin square.

Hypothesis to Be Tested

The null hypotheses to be tested are

$$H_{01}: \ \alpha_1 = \alpha_2 = ... = \alpha_i = ... = \alpha_t = 0$$
$$H_{02}: \beta_1 = \beta_2 = ... = \beta_j = ... = \beta_t = 0$$
$$H_{03}: \ \gamma_1 = \gamma_2 = ... = \gamma_k = ... = \gamma_t = 0$$

Against the alternative hypothesis,

H_{11}: all $\alpha\,'$ s are not equal
H_{12}: all $\beta\,'$ s are not equal
H_{13}: all $\gamma\,'$ s are not equal

Analysis

$SS_{\text{Tot}} = SS_{Tr} + \text{RSS} + \text{CSS} + SS_{Er}$

where $SS_{\text{Tot}} = \sum_i \sum_j \sum_k \left(y_{ijk} - \bar{y}_{...}\right)^2$

= total sum of squares

$SS_{Tr} = t\sum_i (\bar{y}_{i..} - \bar{y}_{...})^2$

= treatment sum of squares

$\text{RSS} = t\sum_j (\bar{y}_{.j.} - \bar{y}_{...})^2$ = row sum of squares

$\text{CSS} = t\sum_k (\bar{y}_{..k} - \bar{y}_{...})^2$

= column sum of squares

$$SS_{Er} = \sum_{i,\ j,\ k} \left(y_{ijk} - \bar{y}_{i..} - \bar{y}_{.j.} - \bar{y}_{..k} + 2\bar{y}_{...}\right)^2$$

Various sums of squares are calculated by using the following formulae:

$$\text{Grand total} = \sum_{(i,j,k)} y_{ijk} = G$$

$$\text{Correction factor} = \frac{(G)^2}{t^2} = \text{CF}$$

$$\text{Total sum of squares } (SS_{\text{Tot}}) = \sum_{(i,j,k)} {y_{ijk}}^2 - CF$$

Treatment sum of squares (SS_{Tr})

$$= \frac{\sum_{i=1}^{t} {y_{i..}}^2}{t} - CF = \frac{y_{1..}^2}{t} + \frac{y_{2..}^2}{t} + \frac{y_{3..}^2}{t} + ... \frac{y_{i..}^2}{t} + ... + \frac{y_{t..}^2}{t} - CF$$

ANOVA table for LSD

SOV	d.f.	*SS*	*MS*	Cal F
Treatment	$t-1$	SS_{Tr}	$MS_{Tr} = \frac{SS_{Tr}}{t-1}$	$F_{Tr} = \frac{MS_{Tr}}{MS_{Er}}$
Row	$t-1$	*RSS*	$RMS = \frac{RSS}{t-1}$	$F_R = \frac{RMS}{MS_{Er}}$
Column	$t-1$	*CSS*	$RMS = \frac{CSS}{t-1}$	$F_C = \frac{CMS}{MS_{Er}}$
Error	$(t-1)$ $(t-2)$	SS_{Er}	$MS_{Er} = \frac{SS_{Er}}{(t-1)(t-2)}$	–
Total	t^2-1	SS_{Tot}	–	–

Row sum of squares (RSS)

$$= \frac{\sum_{j=1}^{t} {y_{ojo}}^2}{t} - CF = \frac{y_{.1.}^2}{t} + \frac{y_{.2.}^2}{t} + \frac{y_{.3.}^2}{t} + ... \frac{y_{.j.}^2}{t} + ... + \frac{y_{.t.}^2}{t} - CF$$

Column sum of squares (CSS)

$$= \frac{\sum_{k=1}^{t} {y_{..k}}^2}{t} - CF = \frac{y_{..1}^2}{t} + \frac{y_{..2}^2}{t} + \frac{y_{..3}^2}{t} + ... \frac{y_{..k}^2}{t} + ... + \frac{y_{..t}^2}{t} - CF$$

Error sum of squares (by subtraction) = *T SS–TrSS–RSS–CSS*

Thus corresponding to three null hypotheses, we have three calculated values of F. If any of the value of F be greater than the corresponding table value of F at specified level of significance, then the corresponding test is to be declared as significant, and the null hypothesis is to be rejected; otherwise the null hypothesis cannot be rejected. When the test is nonsignificant, we conclude that there exist no significant differences among the treatments/rows/columns with respect to the particular characters under consideration; all treatments are statistically at par. In the event of rejection of any of the null hypotheses, LSD value is to be calculated to compare the mean differences. The formula for calculation of LSD value is same for row/column/treatment because all these degrees

of freedom are same. The critical difference for rows/columns/treatments at α level of significance is given by $\sqrt{\frac{2ErMS}{t}} \times t_{\alpha/2;(t-1)(t-2)}$, where $t_{\alpha/2;(t-1)(t-2)}$ is the table value of t at α level of significance with $(t-1)(t-2)$ degrees of freedom for both-sided test.

If the absolute value of the difference between any pair of means of row/column/treatment be more than the critical difference value, as calculated above, then the row/column/treatment means are significantly different from each other; otherwise these are statistically at par.

10.9.3 Merits and Demerits of Latin Square Design

In comparison to other two basic designs, viz., CRD and RBD, Latin square design is improved since it takes care of the heterogeneity or the variations in two perpendicular directions. In the absence of any proper idea about the soil heterogeneity among the experimental units and if sufficient time is not allowed to check the soil heterogeneity, then one can opt for LSD design. The condition for the appearance of a treatment once and only once in each row and in each column can be achieved only if the number of replications is equal to the number of treatments. While selecting a LSD design, an experimenter faces twine problems of maintaining minimum replication as well as accommodating maximum number of treatments in the experiment. This makes the LSD design applicable in limited field experimentations. The number of treatments in LSD design should generally lie in between 4 and 8. All these limitations have resulted in limited use of Latin square design, in spite of its high potentiality for controlling experimental errors. Thus in nut shell, the merits and demerits of LSD are as follows:

Merits

(i) Takes care of soil heterogeneity in two perpendicular directions.
(ii) In the absence of any knowledge about the experimental site, it is better to have LSD.
(iii) Among the three basic designs, LSD is the most efficient design, particularly toward error minimization.

Demerits

(i) The number of replications equals to the number of treatments; thereby an increased number of experimental units are required for conduction of an experiment compared to other two basic designs, viz., CRD and RBD.
(ii) The layout of the design is not so simple as was in the case of CRD or RBD.
(iii) This design requires square number plots.

Example 10.6 In a digestion trail carried out with five cows of a particular breed, each animal received of five different feeds (given in the parentheses) in five successive periods, the experimental design being a Latin square. Coefficients of digestibility of nitrogen were calculated as follows:

	Period				
Cow	1	2	3	4	5
1	60.12 (B)	67.23 (D)	63.23 (E)	54.23 (A)	62.32 (C)
2	54.23 (C)	64.27 (A)	63.23 (B)	64.23 (E)	71.23 (D)
3	65.60 (D)	63.11 (C)	60.12 (A)	65.12 (B)	63.77 (E)
4	65.23 (E)	66.26 (B)	64.15 (C)	70.32 (D)	51.98 (A)
5	66.78 (A)	64.89 (E)	73.23 (D)	52.87 (C)	60.32 (B)

Analyze the data and find out the best feed.

Solution The model for LSD is $y_{ijk} = \mu + \alpha_i + \beta_j + \gamma_k + e_{ijk}$

where

$i = 1,2,\ldots, 5$; $j = 1,2,3\ldots, 5$; $k = 1,2,\ldots,5$

y_{ijk} = effect due to the ith feed in jth row and kth column

Table of row and column

	C1	C2	C3	C4	C5	Total	Average
R1	60.12	67.23	63.23	54.23	62.32	307.13	61.43
R2	54.23	64.27	63.23	64.23	71.23	317.19	63.44
R3	65.6	63.11	60.12	65.12	63.77	317.72	63.54
R4	65.23	66.26	64.15	70.32	51.98	317.94	63.59
R5	66.78	64.89	73.23	52.87	60.32	318.09	63.62
Total	311.96	325.76	323.96	306.77	309.62	1578.07	–
Average	62.39	65.15	64.79	61.35	61.92	–	–

Table of feeds

	Feed				
	A	B	C	D	E
	66.78	60.12	54.23	65.60	65.23
	64.27	66.26	63.11	67.23	64.89
	60.12	63.23	64.15	73.23	63.23
	54.23	65.12	52.87	70.32	64.23
	51.98	60.32	62.32	71.23	63.77
Total	297.38	315.05	296.68	347.61	321.35
Average	59.48	63.01	59.34	69.52	64.27

μ =general effect

α_i =additional effect due to ith feed, $\sum_i \alpha_i = 0$

β_j =additional effect due to jth row, $\sum_j \beta_j = 0$

γ_k =additional effect due to kth coloumn, $\sum_k \gamma_k = 0$

e_{ijk} =errors associated with ith feed in jth row and kth column and are i.i.d. N(0, σ^2)

The hypotheses to be tested are

$$H_0 : \alpha_1 = \alpha_2 = \alpha_3 = \alpha_4 = \alpha_5$$
$$\beta_1 = \beta_2 = \beta_3 = \beta_4 = \beta_5$$
$$\gamma_1 = \gamma_2 = \gamma_3 = \gamma_4 = \gamma_5$$

against

$H_1 : \alpha_i$'s are not equal

β_j 's are not equal

γ_k ' s are not equal

Let the level of significance (α) be 0.05:

Step 1: Make the following two tables from the given information:

Step 2: Calculate the following quantities:

$$CF = \frac{G^2}{t \times t} = \frac{1578.07^2}{5 \times 5} = 99612.19$$

$$SS_{\text{Tot}} = \sum Obs.^2 - CF = 66.78^2 + 60.12^2 + \ldots\ldots + 63.77^2 - 99612.197 = 695.47$$

$$SS_{\text{Row}} = \frac{1}{5}\sum y_{.j.}{}^2 - CF = \frac{1}{5}[307.13^2 + 317.19^2 + 317.72^2 + 317.94^2 + 318.09^2] - 99612.197 = 18.08$$

$$SS_{\text{Col}} = \frac{1}{5}\sum y_{..k}{}^2 - CF = \frac{1}{5}[311.96^2 + 325.76^2 + 323.96^2 + 306.77^2 + 309.62^2] - 99612.197 = 60.018$$

$$SS_{\text{Feed}} = \frac{1}{5}\sum y_{i..}{}^2 - CF = \frac{1}{5}[297.38^2 + 315.05^2 + 296.68^2 + 347.61^2 + 321.35^2] - 99612.197 = 349.587$$

$$SS_{Er} = SS_{\text{Tot}} - SS_{\text{Row}} - SS_{\text{Col}} - SS_{\text{Feed}} = 695.47 - 18.08 - 60.01 - 349.58 = 267.78$$

Step 3: Construct the ANOVA table as given below:

SOV	d.f.	SS	MS	F
Row	4	18.09	4.52	0.20
Column	4	60.02	15.00	0.67
Feed	4	349.59	87.40	3.92
Error	12	267.78	22.32	–
Total	24	–	–	–

Step 4: The table value of $F_{0.05,4,12} = 3.26$ is greater than both the calculated values of F corresponding to row and column, but the table value of $F_{0.05,4,12} = 3.26$ is less than the calculated value of F for feed so the tests for effects of feeds are significant. So we are to identify the best feed.

Step 5: Calculate the CD (0.05) using the following formula:

$$CD = \sqrt{\frac{2MSE}{t}} \times t_{0.025,\text{error}.df}$$

$$CD = \sqrt{\frac{2 \times 22.32}{5}} \times 2.179 = 6.50$$

Arrange the feed mean values in descending order, and compare the difference between any two treatment mean differences with that of the critical difference value. If the critical difference value be greater than difference of two varietal means, then the treatments are statistically at par; there exists no significant difference among the means under comparison:

Feed	Mean
D	69.52
E	64.27
B	63.01
A	59.48
C	59.34

From the above one can find that the feed D is the best feed having the highest coefficients of digestibility of nitrogen which is at par with feed E. Feeds E, B, A, and C are at par with each other. Feed C is having the lowest coefficients of digestibility of nitrogen among the feed.

10.10 Missing Plot Technique

It is our common experience that in many of the field experiments, information from one or more experimental unit(s) is missing because of some reasons or otherwise. Crops of a particular experimental unit may be destroyed, animals under a particular treatment may die because of some reason, fruits/flowers from a particular experimental unit may be stolen, and errors on the part of the data recorder during recording time, etc. may result in missing data. If the information from the whole experiments is to be discarded because of one or two missing values, it will be a great loss of time, resources, and other factors. In order to avoid and overcome the situations, missing plot technique has been developed. The least square procedure can be applied to the observations recorded leaving the missing observations. The calculation has to be modified accordingly. But the simplicity, the generality, and the symmetry of the analysis of the variance are sacrificed to some extent in the process. The missing observation can however be estimated following the least square technique, and application of the analysis of variance with some modification can be used for practical purposes to provide reasonably correct result. We shall discuss the technique of estimating the missing observation(s) and modified analysis of variance thereof while discussing the specific

Treatments	Replications (Blocks)						Total
	1	2	....	j	....	r	
1	y_{11}	y_{12}	....	y_{1j}	....	y_{1r}	$y_{1.}$
2	y_{21}	y_{22}	....	y_{2j}	....	y_{2r}	$y_{2.}$
:	:	:	:	:	:	:	:
i	y_{i1}	y_{i2}	....	-	....	y_{ir}	$y'_{i.}$
:	:	:	:	:	:	:	:
t	y_{t1}	y_{t2}	....	y_{tj}	....	y_{tr}	$y_{t.}$
Total	$y_{.1}$	$y_{.2}$	....	$y'_{.j}$	....	$y_{.r}$	$y'_{..}$

experimental design in the following sections. It must be noted clearly that the missing observation is not the same as the zero observation, e.g., in an insecticidal trial, a plot may record zero pest count but that does not mean the particular observation is missing. On the other hand, if the crop record of a particular plot is not available, then it should not be substituted by zero value.

10.10.1 Missing Plot Technique in CRD

In CRD, the missing plot technique is of little use because of the fact that in CRD, the analysis of variance is possible with variable number of replications for treatments. Thus if one observation from a particular treatment is missing, then the analysis of variance is to be taken up with $(r-1)$ replication for the corresponding treatment and total $(n-1)$ number of observations for the experiments. But the effect of missing observations on the surrounding experimental units should be noted carefully.

10.10.2 Missing Plot Technique in RBD

Let us have RBD with t treatments in r replications and information on y^* that is missing:

The missing observation y^* can be estimated using the following formula: $y^* = \frac{ty'_{i0}+ry'_{0j}-y'_{00}}{(r-1)(t-1)}$

where $y_{i0}{}'$ is the total of known observations in the ith treatment

$y_{0j}{}'$ is the total of known observations in jth replication (block)

$y_{00}{}'$ is the total of all known observations

Once the estimated value for the missing observation is worked out, the usual analysis of variance is taken up with the estimated value of the missing observation. The treatment sum of square is corrected by subtracting the upward biased

$$B = \frac{\left[y'_{0j} - (t-1)y\right]^2}{t(t-1)}$$

The degrees of freedom for both total and error sum of square are reduced by 1 in each case. The treatment means are compared with the mean having the missing value and no missing value using the formula for standard error of difference as

$$SE_d = \sqrt{\frac{MS_{Er}}{r}\left[2 + \frac{t}{(r-1)(t-1)}\right]} \quad \text{and}$$

$SE_d = \sqrt{\frac{2ErMS}{r}}$, respectively.

Example 10.7 (Missing Plot in RBD)
An experiment was conducted to know the effect of five treatments on average daily weight gain of a particular breed of goat. Goats were weighed and assigned to four blocks according to initial weight. In each block there were five animals to which treatments were randomly allocated. The layout of the experiment along with daily weight gain of a goat is given below. Analyze the data and find out the best treatment:

Rep-1	Rep-2	Rep-3	Rep-4
T2 (732)	T2 (745)	T5 (749)	T2 (717)
T3 (832)	T4 (977)	T4 (985)	T1 (873)
T1	T3 (837)	T2 (713)	T5 (777)
T4 (943)	T5 (745)	T1 (856)	T3 (840)
T5 (754)	T1 (855)	T3 (848)	T4 (967)

Solution It appears from the information that the experiment has been laid out in randomized block design with five treatments in four replications and one of the values for treatment one in replication one is missing.

So the model for RBD is given by $y_{ij} = \mu + \alpha_i + \beta_j + e_{ij}$

where

$i = 1,2,\ldots, 6$; $j = 1,2,3$.

y_{ij} =effect due to the ith treatment in jth replication

μ =general effect

α_i =additional effect due to ith treatment

β_j =additional effect due to jth replication

e_{ij} =errors associated with ith treatment in jth replicate and are i.i.d. N(0, σ^2)

The hypotheses to be tested are

$$H_0 : \alpha_1 = \alpha_2 = \ldots = \alpha_5$$
$$\beta_1 = \beta_2 = \beta_3 = \beta_4$$

against

H_1 : α_i 's are not equal
: β_j 's are not equal.
Let the level of significance be 0.05.

We shall analyze the data in the following steps:

Step 1: Make the following table from the given information:

	Rep-1	Rep-2	Rep-3	Rep-4	Total
T1	X	855	856	873	2584
T2	732	745	713	717	2907
T3	832	837	848	840	3357
T4	943	977	985	967	3872
T5	754	745	749	777	3025
Total	3261	4159	4151	4174	15,745

The estimate of the missing value is given by

$$\hat{y}_{ij} = X = \frac{rR' + tT' - G'}{(r-1)(t-1)}$$

where

X = estimate of the missing value
R' = total of available goat weights of the block having the missing observation
T' = total of available goat weights of the treatment having the missing observation
G' = total of available goat weights in the whole experiment

For this problem $X = \frac{rR' + tT' - G'}{(r-1)(t-1)} = \frac{4 \times 3261 + 5 \times 2584 - 15745}{(4-1)(5-1)} = 851.58$

Now, $G = G' + X = 15{,}745 + 851.58 = 16596.58$.

Total of treatment 1 $(T_1) = 2584 + X = 3435.583$.

Total of replication 1 $(R_1) = 3261 + X = 4112.583$.

Now we proceed for the usual analysis of variance with the estimated value of the missing observation:

$$C.F. = \frac{GT^2}{n} = \frac{16596.58^2}{5 \times 4} = 13772328.92$$

$$SS_{\text{TOT}} = \sum Obs.^2 - CF = 851.58^2 + 732^2 + \ldots\ldots\ldots + 967^2 + 777^2 - 13772328.92 = 146922.25$$

$$SS_R = \frac{1}{5}\sum_{j=1}^{4} R_j^2 - CF = \frac{1}{6}\left[4112.58^2 + 4159^2 + 4151^2 + 4174^2\right] - 13772328.92 = 411.01$$

$$SS_{Tr} = \frac{1}{4}\sum_{i=1}^{5} V_i^2 - CF = \frac{1}{4}\left[3435.58^2 + 2907^2 + 3357^2 + 3872^2 + 3025^2\right] - 13772328.92 = 144256.04$$

The SS_{Tr} is an overestimate and has to be corrected by subtracting a quantity (bias) $B = \frac{[R' - (t-1)X]^2}{t(t-1)} = \frac{[3261 - (5-1)851.58]^2}{5(5-1)} = 1056.08$

Corrected $SS_{Tr} = SS_{Tr} - B = 144256.04 - 1056.08 = 143199.95$

$$SS_{Er} = SS_{\text{TOT}} - SS_R - SS_{Tr}(\text{corrected}) = 146922.3 - 411.0177 - 143199.95 = 3311.28$$

$$SE_d = \sqrt{\frac{ErMS}{r}\left[2 + \frac{t}{(r-1)(t-1)}\right]} = \sqrt{\frac{301.03}{4}\left[2 + \frac{5}{(4-1)(5-1)}\right]} = 13.01$$

where SS_{TOT}, SS_R, SS_{Tr}, and SS_{Er} are the total, replication, treatment, and error sum of squares, respectively:

SOV	d.f.	SS	MS	Cal. F	Tab F at 5 %
Replication	3	411.02	137.01	0.46	3.59
Treatment	4	144256.04	36064.01	119.80	3.36
Error (corrected)	11	3311.28	301.03		
Treatment (corrected)	4	143199.95	35799.99	118.93	3.36
Total	18	146922.26			

Note while calculating F values, we have used corrected error MS.

Thus, one can find that the treatment effect differs significantly among themselves. So we are to calculate the CD values for comparing the treatment means.

The treatment means for treatments having no missing value are compared by usual CD values given as

$$CD_{0.05} = \sqrt{\frac{2ErMS}{r}} \times t_{0.025,\text{error } df} = \sqrt{\frac{2 \times 301.03}{4}} \times 2.20 = 38.10$$

The treatment means having one missing value in one of the treatments are compared using the formula for standard error of difference as

Thus to compare the treatment having the missing value (T1) with the other treatment having no missing value is $SE_d \times t_{0.025,11} = 13.01 \times 2.20 = 28.64$:

Treatment	Average weight gained
T4	968.00
T1*	861.33
T3	839.25
T5	756.25
T2	726.75

From the table of means, it is clear that treatment 4 is the highest body weight gainer followed by T1 and T3, which are statistically at par. Again in treatment T2, we have recorded the lowest gain in body weight and which is statistically at par withT5. Thus, we have three groups of responses (i) treatment 4 the best one; (ii) treatment 1 and treatment 3, the medium group; and (iii) treatment 5 and treatment 2 the lowest group with respect to increase in body weight.

10.10.3 Missing Plot Technique in LSD

Let a missing observation in $t \times t$ Latin square be denoted by y_{ijk}, and let T', R', C', and G' be the total of available observations (excluding the missing value) of ith treatment, jth row, and kth column and of all available observations, respectively.

Let y^* be the value of the missing observation; then

$y^* = \frac{t(T'+R'+C')-2G'}{(t-1)(t-2)}$, the estimate of the missing value

Once the estimated value for the missing observation is worked out, the usual analysis of variance is taken up with the estimated value of the missing observation. The treatment sum of square is to be corrected by subtracting the upward biased

$$B = \frac{[(t-1)T' + R' + C' - G']^2}{[(t-1)(t-2)]^2}$$

The degrees of freedom for both total and error sum of square are reduced by 1 in each case. The treatment means are compared with the mean having the missing value using the formula for standard error of difference as

$$SE_d = \sqrt{\frac{MS_{Er}}{t}\left[2 + \frac{t}{(t-1)(t-2)}\right]}$$

Example 10.8 (Missing Plot in LSD)
The aim of this experiment was to test the effect of four different supplements (A, B, C, and D) on hay intake in Jersey cow. The experiment was conducted using Latin square with four animals in four periods of 20 days. The cows were housed individually. Each period consists of 10 days of adaptations and 10 days of measuring. The data in the following table are the 10 days means of

milking capacity per day. Estimate the missing value and analyze the data to find out the best hay supplement:

	Cows			
Periods	1	2	3	4
1	17 (B)	29 (D)	27 (C)	38 (A)
2	24 (C)	37 (A)	31 (D)	19 (B)
3	27 (D)	19 (B)	36 (A)	26 (C)
4	35 (A)	X (C)	21 (B)	30 (D)

Solution

The model for LSD is $y_{ijk} = \mu + \alpha_i + \beta_j + \gamma_k + e_{ijk}$ where $i = 1, 2, \ldots\ldots, 4$; $j = 1, 2, 3, 4$; and $k = 1, 2, 3, 4$

Table of information

	C1	C2	C3	C4	Total	Mean
R1	17	29	27	38	111	27.75
R2	24	37	31	19	111	27.75
R3	27	19	36	26	108	27.00
R4	35	X (C)	21	30	86	28.67
Total	103	85	115	113	416	–
Mean	25.75	28.33	28.75	28.25	–	–

Table of supplement totals

	S1	S2	S3	S4
	35	17	27	29
	37	19	24	31
	36	19	26	27
	38	21	X (C)	30
Total	146	76	77	117
Mean	36.50	19.00	25.67	29.25

y_{ijk} = effect due to the ith supplements in jth row and kth column

μ = general effect

α_i = additional effect due to ith supplements, $\sum_i \alpha_i = 0$

β_j = additional effect due to jth row $\sum_j \beta_j = 0$

γ_k = additional effect due to kth column $\sum_k \gamma_k = 0$

e_{ijk} = error associated with ith supplements in jth row and kth column and are i.i.d. N(0, σ^2).

The hypotheses to be tested are

$$H_0 : \alpha_1 = \alpha_2 = \alpha_3 = \alpha_4$$
$$\beta_1 = \beta_2 = \beta_3 = \beta_4$$
$$\gamma_1 = \gamma_2 = \gamma_3 = \gamma_4$$

against

H_1 : α_i 's are not all equal
β_j 's are not all equal
γ_k 's are not all equal

Let the level of significance be $\alpha = 0.05$.

We shall analyze the data in the following steps:

Step 1: Make the following tables from the given information:

Let us first estimate the missing value using the following formula:

$$\hat{y} = X = \frac{t(R' + C' + T') - 2G'}{(t-1)(t-2)}$$
$$= \frac{4(86 + 85 + 77) - 2 \times 416}{(4-1)(4-2)} = 26.66$$

where

X = estimate of the missing value
R' = total of available supplements of the row having the missing observation
T' = total of available supplements of the supplement C having the missing observation
C' = total of available supplements of the column having the missing observation
G' = total of available supplements in the whole experiment

Now, $G = G' + X = 311 + 26.66 = 442.66$.

Total of supplement $C = 77 + X = 103.66$.
Total of row 4 having supplement $C = 86 + X = 112.66$.
Total of column 2 having supplement $C = 85 + X = 111.66$.

Now we proceed for the usual analysis of variance that is with the estimated value of the missing observation.

Step 2: Calculate the following quantities:

$$CF = \frac{G^2}{t \times \mathrm{t}} = \frac{442.66^2}{4 \times 4} = 12247.11$$

$$SS_{\mathrm{Tot}} = \sum Obs.^2 - CF$$
$$= 17^2 + 24^2 + \ldots\ldots + 26^2 + 30^2 - 12247.11$$
$$= 662$$

$$SS_R = \frac{1}{4}\sum_{j=1}^{4} y_{.j.}^2 - CF = \frac{1}{5}[103^2 + 111.66^2 + 115^2 + 113^2] - 12247.11 = 21$$

$$SS_C = \frac{1}{4}\sum_{k=1}^{4} y_{..k}^2 - CF = \frac{1}{5}[111^2 + 111^2 + 108^2 + 112.66^2] - 12247.11 = 2.83$$

$$SS_{\mathrm{SUP}} = \frac{1}{4}\sum_{i=1}^{4} y_{i..}^2 - CF = \frac{1}{4}[146^2 + 76^2 + 103.66^2 + 117^2] - 12247.11 = 634.83$$

$$SS_{Er} = SS - RSS - CSS - VSS = 662 - 21 - 2.83 - 634.83 = 3.33$$

where, SS_{Tot}, SS_R, SS_C, SS_{SUP}, and SS_{Er} are the total, row, column, supplement, and error sum of squares, respectively.

The upward bias is calculated as follows:

$$B = \frac{(G' - R' - C' - (t-1)T')^2}{[(t-1)(t-2)]^2} = \frac{(416 - 86 - 85 - (4-1)77)^2}{[(4-1)(4-2)]^2} = 5.44$$

Step 3: Construct the ANOVA table as given below:

ANOVA				
SOV	d.f.	SS	MS	F
Row	3	21	7.00	3.99
Column	3	2.83	0.94	0.54
Supplements	3	634.83	–	–
Error	5	3.33	–	–
Total	14	662	–	–
Supplements (corrected)	–	629.38	209.79	119.61
Error (corrected)	–	8.77	1.75	–

Step 4: The table value of $F_{0.05;3,5} = 5.04$. Thus we find that the calculated values of F are less than the corresponding table value, excepting for supplements. So the tests for row and columns are nonsignificant. We conclude that neither the row effects nor the column effects are significant. But the effects of hay supplements are significant. So we are to identify the best hay supplement.

Step 5: To compare the supplement means involving no missing value, the CD (0.05) is calculated using the following formula:

$$\mathrm{CD}_{0.05}(\text{supplement}) = \sqrt{\frac{2 \times \mathrm{MSE}}{t}} \times t_{0.025,\mathrm{err}.df.}$$
$$= \sqrt{\frac{2 \times MSE}{4}} \times t_{0.025,5}$$
$$= \sqrt{\frac{2 \times 1.75}{4}} \times 2.57$$
$$= 2.40$$

and to compare the hay supplement means with supplement C, having the missing value, the CD (0.05) is calculated using the following formula:

$$\mathrm{CD}_{0.05}(\text{variety}) = \sqrt{\frac{\mathrm{MSE}}{t}\left(2 + \frac{t}{(t-1)(t-2)}\right)} \times t_{0.025,\mathrm{err}.df.}$$
$$= \sqrt{\frac{\mathrm{MSE}}{t}\left(2 + \frac{t}{(t-1)(t-2)}\right)} \times t_{0.025,5}$$
$$= \sqrt{\frac{1.75}{4}\left(2 + \frac{4}{3 \times 2}\right)} \times 2.57$$
$$= 2.77$$

Supplements	Mean milk yield
A	36.50
D	29.25
C	25.91
B	19.00

Comparing the supplement differences with appropriate CD values, it can be inferred that all the supplements are significantly different from each other. Supplement A is the best milk yielder, while supplement B is the lowest yielder.

Factorial Experiment 11

11.1 Introduction

Basic experimental designs, what we have discussed in the previous chapter take care of one type/group of treatments at a time. If an experimenter wants to test more than one type/group of treatments, then more than one set of experiments are required to be set, thereby requiring a huge amount of resources (land, money, other inputs) and time. Even with ample resources and time, desirable information may not be obtained from simple experiments. Suppose an experimenter wants to know not only the best treatment from each of the two sets of treatments but also wants to know the interaction effects of the two sets of treatments. This information cannot be obtained by conducting two separate sets of simple experiments with two groups/types of treatments. Let us suppose an experimenter wants to know (i) the best varieties among five newly developed varieties of a crop, (ii) the best dose of nitrogenous fertilizer for the best yield of the same crop and (iii) also wants to know which variety among the five varieties under which dose of nitrogen provides the best yield (i.e., variety and dose interaction effect). The first two objectives (i.e., the best variety and best dose of nitrogen) can be accomplished by framing two separate simple experiments (one with five varieties and the other one with different doses of nitrogen with a single variety), but the third objective, i.e., interaction of varieties with different doses of nitrogen, cannot be obtained from these two experiments. For this purpose we are to think for an experiment which can accommodate both the groups of treatments together. Thus, in agriculture and other experiments, the response of different doses/levels of one group of treatments (factor) is supposed to vary over the different doses or levels of other set(s) of treatments (factor(s)). In our daily life, we have the experience that a particular poultry bird is responding differentially under different diets and diet schedule. That means diet and diet schedule have got different interaction effects. Factorial experiments are such a mechanism in which more than one group (factor) of treatments can be accommodated in one experiment, and from the experiment, not only the best treatment in each group of treatments could be identified but also the interaction effects among the treatments in different groups could also be estimated. *It may be noted in this context that the factorial concept is nothing but a technique of combining two or more groups of treatments in one experiment so that group-wise treatments and the combination of intergroup treatment effects could be estimated and compared. But the experimental design to be followed remains one of the basic designs, i.e., completely randomized design, randomized block design, and Latin square design. Thus, a factorial experiment is known as factorial CRD/factorial RBD/factorial LSD depending upon the basic*

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design adopted during experimentation with factorial combinations of treatments. Before discussing the different factorial experiments in details, let us define the related terminologies associated with the factorial experiments.

11.1.1 Factor and Its Levels

In its simplest form, a factor in factorial experiments, is a concept used to denote a group of treatments. For example, different breeds of cattle, different diets, different varieties, different doses of nitrogen, different methods of irrigation, etc. may form different factors in factorial experiments. In factorial experiment, conducted with different breeds of cattle and different types of feed, two factors (viz. breed and feed) are constituted in the factorial experiment. If five varieties of wheat are tested with four doses of nitrogen, then the varieties and the doses of nitrogen are the two factors considered in the experiment. Different breeds of cattle and different types of feed are known as the *levels of the factors* breed and diet, respectively. Similarly five varieties of wheat and four doses of nitrogen constitute the levels of the factors variety and dose of nitrogen, respectively. Different components of a factor are known as the levels of the factor. Both the factors and their levels may be quantitative (doses of nitrogen) as well as qualitative (different breeds, different diets, different varieties) in nature.

11.1.2 Type of Factorial Experiment

Factorial experiments are of different types. (a) - Depending upon the number of factors included in the experiment, a factorial experiment is a *two-factor factorial experiment* (when two sets of treatments, i.e., two factors), *three-factor factorial experiment* (when three sets of treatments, i.e., three factors)……., or *p-factor factorial experiment* (when "*p*" sets of treatments, i.e., *p* number of factors). (b) Whether all the factors included in the experiment are having the same levels or different levels, a factorial experiment is either *symmetrical* (the same levels for all the factor) or *asymmetrical* (different levels for different factors), respectively. A factorial experiment is symmetrical, if the numbers of levels for all the factors are the same, e.g., a two-factor factorial experiment with five breeds and five different diets is a symmetrical factorial experiment. On the other hand, a two-factor factorial experiment with five varieties and other than five doses of nitrogen (doses of nitrogen not equal to 5) is an asymmetrical factorial experiment.

Generally *a symmetrical factorial experiment with "n" factors each at "m" levels is denoted as* m^n *factorial experiment*. Thus, a 2^3 factorial experiment is a symmetrical factorial experiment with three factors each at two levels. An asymmetrical *two-factorial experiment with p levels for the first factor and q levels for the second factor is denoted as* $p \times q$ *factorial experiment*. Thus a 2×3 asymmetrical factorial experiment means there are two factors in the experiment with the first factor having two levels and the second factor having three levels. So asymmetrical factorial experiments cannot be presented in the form of m^n; rather these can be presented in the form of $m \times n \times p \times q \times .....$, where the levels of the first, second, third, fourth, . . . factors are m, n, p, q, . . ., respectively.

11.1.3 Effects and Notations in Factorial Experiment

Main effects and *interaction effects* are the two types of effects found in factorial experiments. *The main effect of a factor is the effect of the factor concerned irrespective of the levels of other factors*, while *the interaction effects are the effects of one factor with the change in levels of the other factor and vice versa*. When the factors are independent of one another, one would expect the *same effect* of one factor at various levels of the other factors resulting in the zero interaction effect. Thus interaction effects come into picture when the factors are not independent and the effects of different factors will not be the same in magnitude and order over the different levels of other factors.

Depending upon the number of factors involved in the factorial experiment, the interaction effects would be the first-order interaction, second-order interaction, third-order interaction, and so on when the number of factors in the experiment is 2, 3, 4, and so on.

When two factors are involved in a factorial experiment, then we are concerned about the interaction effects of two factors, known as the first-order interaction. But when more than two factors are involved, then the interaction will be pairwise as well as overall. That means for a three factor factorial experiment we shall have two-factor interaction, i.e., first-order interaction, as well as the three-factor interaction, i.e., second-order interaction. Therefore, as we go on increasing the number of factors in any factorial experiment, then the type of interaction increases.

In factorial experiments general levels of qualitative factors are denoted by the numbers 1, 2, 3, etc. suffixed to the symbol of a particular factor, e.g., if four varieties are there in a factorial experiment, then these are denoted as V_1, V_2, V_3, and V_4. On the other hand, general levels of quantitative factors are denoted by the numbers 0, 1, 2, 3, etc. suffixed to the symbol of a particular factor, e.g., if nitrogen be a factor having four levels, then these are denoted by n_0, n_1, n_2, and n_3 where n_0 is the lowest level of nitrogen generally denoted for no nitrogen or zero nitrogen level and n_3 is the highest level of nitrogen.

11.1.4 Merits of Factorial Experiment

(i) Factorial experiments can accommodate more than one set of treatments (factors) in one experiment.
(ii) Interaction effect could be worked out from factorial experiments.
(iii) Factorial experiments are resource and time saving.
(iv) The required minimum degrees of freedom for error components in the analysis of variance can easily be achieved in factorial experiments compared to single factorial experiments.

11.1.5 Demerits of Factorial Experiment

(i) With the increase in number of factors or the levels of the factors or both the number and levels of factors are more, the number of treatment combinations will be more, resulting in the requirement of bigger experimental area and bigger block size. As the block size increases, it is very difficult under field condition to maintain homogeneity among the plots within the block. Thus, there is a possibility of increasing the experimental error vis-à-vis decrease in the precision of experiment.
(ii) The layout of the factorial experiment is comparatively difficult than simple experiments.
(iii) Statistical procedure and calculation of factorial experiments are more complicated than the single factor experiments.
(iv) With the increase in the number of factors or the levels of the factor or both, the number of effects, including the interaction effects, also increases. Sometimes it becomes very difficult to explain the information from interactions, particularly the higher-order interaction effects.
(v) The risk is high. Failure in one experiment may result in greater loss of information compared to single-factor simple experiments.

In spite of all these demerits, factorial experiments, if planned properly and executed meticulously, are more informative and useful than single factor experiments.

11.2 Two-Factor Factorial Experiments

11.2.1 2^2 Factorial Experiment

The most initial factorial experiment is comprised of two factors each at two levels, i.e., 2^2 factorial experiment. In a 2^2 factorial experiment with two factors A and B and each having two levels, viz., A_1, A_2 and B_1, B_2,

respectively, the total number of treatment combinations will be 4, i.e., A_1B_1, A_1B_2, A_2B_1, and A_2B_2.

	B_1	B_2
A_1	A_1B_1	A_1B_2
A_2	A_2B_1	A_2B_2

Each of the treatment combinations would be repeated k number of times. Again these four treatment combinations can be put under experimentation in basic CRD/RBD/LSD design depending upon the situation and requirement of the experimentation. As usual when blocking is not required or possible in that case, factorial CRD is to be conducted. If filed experiment is conducted and blocking is essential, then either factorial RBD or factorial LSD with four treatment combinations is to be conducted. The layout will follow the identical procedure as discussed for the layout of basic CRD/RBD/LSD in Chap. 10 with these four treatment combinations. However, during analysis partitioning of the total variance is to be taken up as per the statistical model concerned.

The data set for 2^2 factorial experiment with n observations per treatment would be as follows:

A_1		A_2	
B_1	B_2	B_1	B_2
y_{111}	y_{121}	y_{211}	y_{221}
y_{112}	y_{122}	y_{212}	y_{222}
y_{113}	y_{123}	y_{213}	y_{223}
:	:	:	:
:	:	:	:
y_{11r}	y_{12r}	y_{21r}	y_{21r}

The statistical model and analyses of the variance for the above 2^2 factorial experiment in CRD and RBD are discussed separately in the following sections.

11.2.1.1 Model and Analysis of 2^2 Factorial CRD Experiment

Let us suppose we have a 2^2 factorial CRD experiment conducted for two factors A and B each having two levels and repeated r number of times. Then the appropriate statistical model would be

$y_{ijk} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + e_{ijk}$ where $i = 1, 2$; $j = 1, 2$; and $k = 1, 2, \ldots, r$

y_{ijk} = response for observation due to kth repetition of ith level of the first fact or A and jth level of the second factor B

μ = general effect

α_i = additional effect due to ith level of the first factor A, $\sum \alpha_i = 0$

β_j = additional effect due to jth level of the second factor B, $\sum \beta_j = 0$

$(\alpha\beta)_{ij}$ = interaction effect of the ith level of the first factor A and jth level of the second factor, B with $\sum_i (\alpha\beta)_{ij} = \sum_j (\alpha\beta)_{ij} = 0$

e_{ijk} = error component associated with ith level of the first factor A, jth level of the second factor B in kth repetition, and $e_{ijk} \sim$ i.i.d. $N(0, \sigma^2)$

Hypotheses to be tested are

$H_{01} : \alpha_1 = \alpha_2 = 0$ against the alternative hypothesis $H_{11} : \alpha_1 \neq \alpha_2$
$H_{02} : \beta_1 = \beta_2 = 0$ against the alternative hypothesis $H_{12} : \beta_1 \neq \beta_2$
$H_{03} : \alpha_1\beta_1 = \alpha_1\beta_2 = \alpha_2\beta_1 = \alpha_2\beta_2 = 0$ against the alternative hypothesis
H_{13} : all interaction effects are not equal

Let the level of significance be α.

Analysis All together there would be $4r$ number of observations. The total sum of squares is partitioned into the sum of squares due to factor A and due to factor B and sum of squares due to interaction of factors A and B and due to residuals, i.e.,

$SS_{\text{Tot}} = SS_A + SS_B + SS_{AB} + SS_{Er}$, and the corresponding degrees of freedom would be

$$4r - 1 = 2 - 1\,2 - 1\,1 \times 1\,(4r - 1 - 1 - 1)$$

For practical purposes, different sums of squares are calculated by using the following formulae:

$$\text{Step 1: Grand total} = G = \sum_{i}^{2}\sum_{j}^{2}\sum_{k}^{r} y_{ijk}$$

$$\text{Step 2: Correction factor} = CF = \frac{G^2}{4r}$$

$$\text{Step 3: Treatment sum of squares} = SS_{Tr}$$

$$= \sum_{i}^{2}\sum_{j}^{2}\sum_{k}^{\text{r}} (y_{ijk} - \overline{y}_{...})^2$$

$$= \sum_{i}^{2}\sum_{j}^{2}\sum_{k}^{\text{r}} (y_{ijk})^2 - CF$$

$$\text{Step 4: Sum of squares due to A} = SS_A$$

$$= 2 \times 2\sum_{i} (\overline{y}_{i..} - \overline{y}_{...})^2$$

$$= 2 \times 2\left[\sum_{i} \overline{y}_{i..}^2 - 2\overline{y}_{...}{}^2\right]$$

$$= 2 \times 2\sum_{i}\left(\frac{\sum_{j}\sum_{k} y_{ijk}}{2 \times 2}\right)^2 - CF$$

$$= \frac{1}{2 \times r}\sum_{i} y_{i..}^2 - CF$$

$$\text{Step 5: Sum of squares due to B} = SS_B$$

$$= 2 \times r\sum_{j}\left(\overline{y}_{.j.} - \overline{y}_{...}\right)^2$$

$$= \frac{1}{2 \times r}\sum_{i} y_{.j.}^2 - CF$$

$$\text{Step 6: Sum of squares due to AB}$$

$$= r\sum_{i}\sum_{j} (\overline{y}_{ij.} - \overline{y}_{i..} - \overline{y}_{.j.} + \overline{y}_{...})^2$$

$$= r\sum_{i}\sum_{j} (\overline{y}_{ij.} - \overline{y}_{...} - (\overline{y}_{i..} - \overline{y}_{...}) - (\overline{y}_{.j.} - \overline{y}_{...})]^2$$

$$= r\Bigg[\sum_{i}\sum_{j} (\overline{y}_{ij.} - \overline{y}_{...})^2 - 2\sum_{i} (\overline{y}_{i..} - \overline{y}_{...})^2 - 2\sum_{j} (\overline{y}_{.j.} - \overline{y}_{...})^2$$

$$= r\sum_{i}\sum_{j} (\overline{y}_{ij.} - \overline{y}_{...})^2 - SS_A - SS_B$$

$$= r\left[\sum_{i}^{m}\sum_{j}^{n} y_{ij.}^2 - 2 \times 2y_{...}^2\right] - SS_A - SS_B$$

$$= \sum \overline{i}^{m}\sum_{j}^{n} \frac{y_{ij.}^2}{r} - CF - SS_A - SS_B$$

$$= SS_{Tr} - SS_A - SS_B$$

$$\therefore ErSS = SS_{\text{Tot}} - SS_{Tr}$$
$$= SS_{\text{Tot}} - (SS_A + SS_B + SS_{AB})$$
$$= SS_{\text{Tot}} - SS_A - SS_B - SS_{AB}$$

The ANOVA table is given by

Sources of variation	d.f.	SS	MS	F ratio
A	1	SS_A	$MS_A = \frac{SS_A}{1}$	$F_A = \frac{MS_A}{MS_{Er}}$
B	1	SS_B	$MS_B = \frac{SS_B}{1}$	$F_B = \frac{MS_B}{MS_{Er}}$
AB	1	SS_{AB}	$MS_{AB} = \frac{SS_{AB}}{1}$	$F_{AB} = \frac{MS_{AB}}{MS_{Er}}$
Error	$3(r-1)$	SS_{Er}	$MS_{Er} = \frac{SS_{Er}}{3(r-1)}$	
Total	$4r-1$	SS_{Tot}		

There are different methods for the calculation of these sums of squares like Yates method and tabular method. But for its relative simplicity and wider use, we should adopt the latter one, i.e., the tabular method.

The hypothesis of the absence of a main factorial effect due to either A or B is rejected at the α level if the corresponding Cal $F > F_{\alpha;1,3(r-1)}$; otherwise, it cannot be rejected. As there are only

two levels for each of the factors A and B, in the event of rejection of null hypotheses corresponding to main effects of these two factors, the best treatment would be the level of each factor having high or low value, depending upon the parameter under study.

If the Cal $F > F_{\alpha;1,3(r-1)}$, corresponding to interaction effect, then we need to find out the *LSD* or *CD* value at specified level of significance and error degrees of freedom using the following formula: $LSD/CD(\alpha) = \sqrt{\frac{2MS_{Er}}{r}}\, t_{\alpha/2,\text{error d.f.}}$

Example 11.1 (2^2 CRD)
To know the effect of two dietary protein levels (15 and 20) and two energy contents (3000 and 3200 ME kcal/kg) on broiler chicken, an experiment with 5 replications was conducted. From the following information, find out (i) which of the two dietary protein levels, (ii) which of the two energy contents, and (iii) the combination of two dietary protein levels and two energy contents having maximum food conversion ratio (FCR):

	FCR									
	R1		R2		R3		R4		R5	
	15 % CP (b_0)	20% CP (b_1)	15 % CP (b_0)	20 % CP (b_1)	15 % CP (b_0)	20 % CP (b_1)	15 % CP (b_0)	20 % CP (b_1)	15 % CP (b_0)	20 % CP (b_1)
3000 ME Kcal/Kg(a_0)	4.04	3.32	4.16	3.414	4.21	3.32	4.07	3.34	4.18	3.33
3200 ME Kcal/Kg (a_1)	4.01	3.26	4.19	3.43	4.07	3.37	3.97	3.27	4.04	3.27

Solution As the experiment has been conducted under controlled condition, so we can assume that all the experimental units were homogeneous in nature except for the treatment condition; hence CRD should be the appropriate basic design for the analysis. Thus from the given conditions, it is clear that the information can be analyzed in a two-factor factorial CRD, where both the factors have the same levels, i.e., 2.

So the appropriate statistical model for the analysis will be

$y_{ijk} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + e_{ijk}$ where $i = 1, 2$; $j = 1, 2$; and $k = 1, 2, \ldots, 5$

y_{ijk} = response in kth observation due to ith level of the first factor (i.e., dietary protein) and jth level of the second factor (i.e., energy content)

μ = general effect

α_i = additional effect due to ith level of the first factor (i.e., dietary protein), $\sum \alpha_i = 0$

β_j = additional effect due to jth level of the second factor (i.e., energy content), $\sum \beta_j = 0$

$(\alpha\beta)_{ij}$ = interaction effect of the ith level of dietary protein and jth level energy content, $\sum_i (\alpha\beta)_{ij} = \sum_j (\alpha\beta)_{ij} = 0$

e_{ijk} = error component associated with ith level of dietary protein, jth level of energy content, and kth replicates and $e_{ijk} \sim$ i.i.d. $N(0, \sigma^2)$

Hypothesis to be tested:

$H_{01} : \alpha_1 = \alpha_2 = 0$
$H_{02} : \beta_1 = \beta_2 = 0$
H_{03}: all interaction effects are equal and equal to zero against
H_{11} : all α's are not equal to zero
H_{12} : All β's are not equal to zero
H_{13} : all interaction effects are not equal to zero

Let the level of significance be $\alpha = 0.05$.

From the given information, first let us form the following table:

Replication	$a_0b_0 = (1)$	$a_1b_0 = (a)$	$a_0b_1 = b$	$a_1b_1 = ab$
R1	4.04	4.01	3.32	3.26
R2	4.16	4.19	3.414	3.43
R3	4.21	4.07	3.32	3.37
R4	4.07	3.97	3.34	3.27
R5	4.18	4.04	3.33	3.27
Total	20.66	20.28	16.724	16.6

Thus we have grand total $= G = 74.264$.

Correction factor $= CF = \dfrac{GT^2}{n} = \dfrac{74.264^2}{20} = 275.757$

$$SS_{\text{Tot}} = 4.04^2 + 4.16^2 + \ldots\ldots + 3.34^2 + 3.27^2 - CF = 2.995$$

$$SS_{Tr} = \frac{20.66^2 + 20.28^2 + 16.72^2 + 16.60^2}{5} - CF = 2.916$$

$$SS_{Er} = SS_{\text{Tot}} - SS_{Tr} = 2.995 - 2.916 = 0.079$$

Now the calculations for different sums of squares (i.e., SS_A, SS_B, and SS_{AB}) can be made with the help of the following table for totals:

Energy contents	Dietary protein		Total	Average
	15 % CP (b_0)	20 % CP (b_1)		
3000 ME Kcal/Kg (a_0)	20.660	16.724	37.384	3.738
3200 ME Kcal/Kg (a_1)	20.280	16.600	36.880	3.688
Total	40.940	33.324		
Average	4.094	3.332		

From the above table, let us calculate the following quantities:

$$SS_{EC} = \frac{1}{2 \times 10}\sum_{i=1}^{2} y_{i..}^2 - CF = \frac{37.384^2 + 36.880^2}{2 \times 10} - 275.757 = 0.0127$$

$$SS_{DP} = \frac{1}{2 \times 10}\sum_{i=1}^{2} y_{.j.}^2 - CF = \frac{40.940^2 + 33.324^2}{2 \times 10} - 275.757 = 2.900$$

$$SS_{EC \times DP} = \frac{1}{5}\sum_{i=1}^{2}\sum_{j=1}^{2} y_{ij.}^2 - CF - SS(EC) - SS(DP) = 2.916 - 0.0127 - 2.900 = 0.003$$

Now we make the following analysis of variance table with the help of the above quantities:

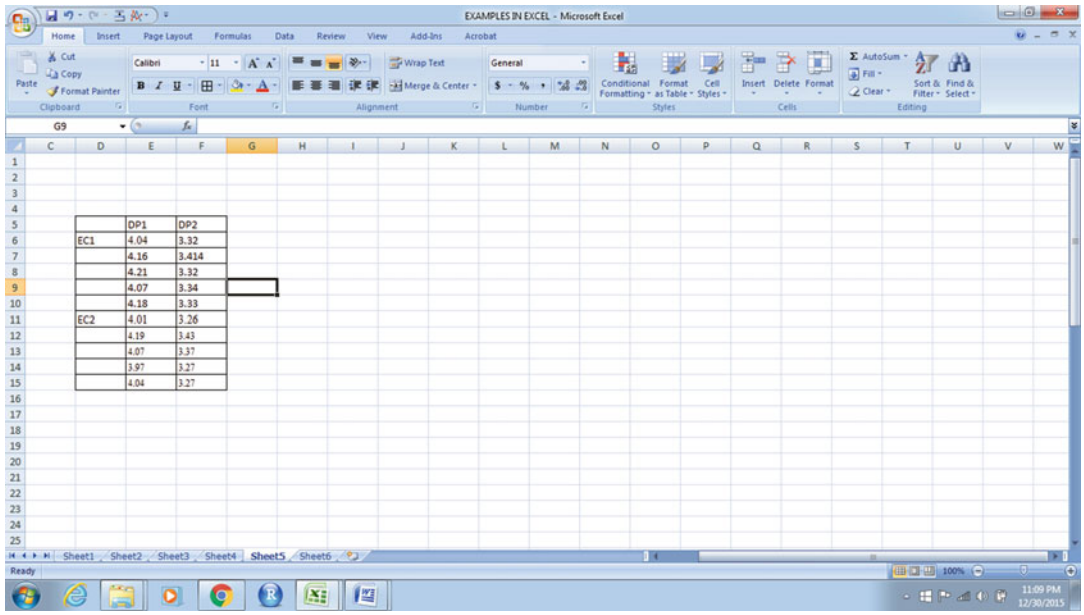
ANOVA					
SOV	d.f.	*SS*	*MS*	Cal F	Tab F
Treatment	$4-1=3$	2.916	0.972	197.218	5.29
Energy content (A)	$2-1=1$	0.013	0.004	0.859	8.53
Dietary protein levels (B)	$2-1=1$	2.900	0.967	196.138	8.53
AB	$1\times 1=1$	0.003	0.001	0.222	8.53
Error	$19-3=16$	0.079	0.005		
Total	$20-1=19$	2.995			

It is clear from the above table that only dietary protein level is significant at 5 % level of significance, while energy content levels and combination are statistically at par with each other.

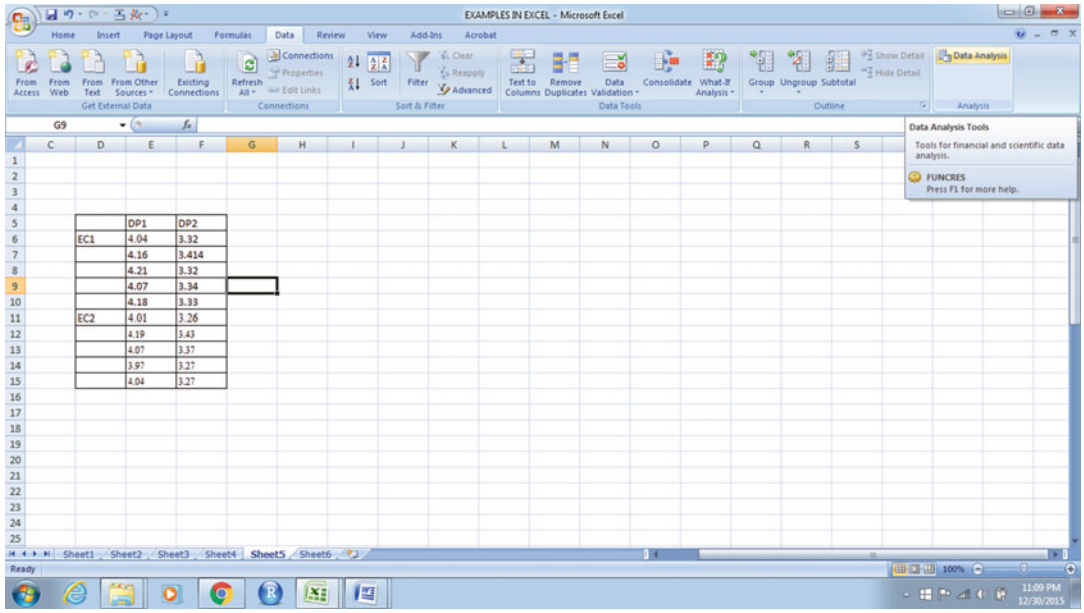
As the mean for dietary protein at 15 % CP is more than 20 % CP, 15 % CP is the best level compared to 20 % CP.

Example 11.1 (2^2 CRD) Using MS Excel

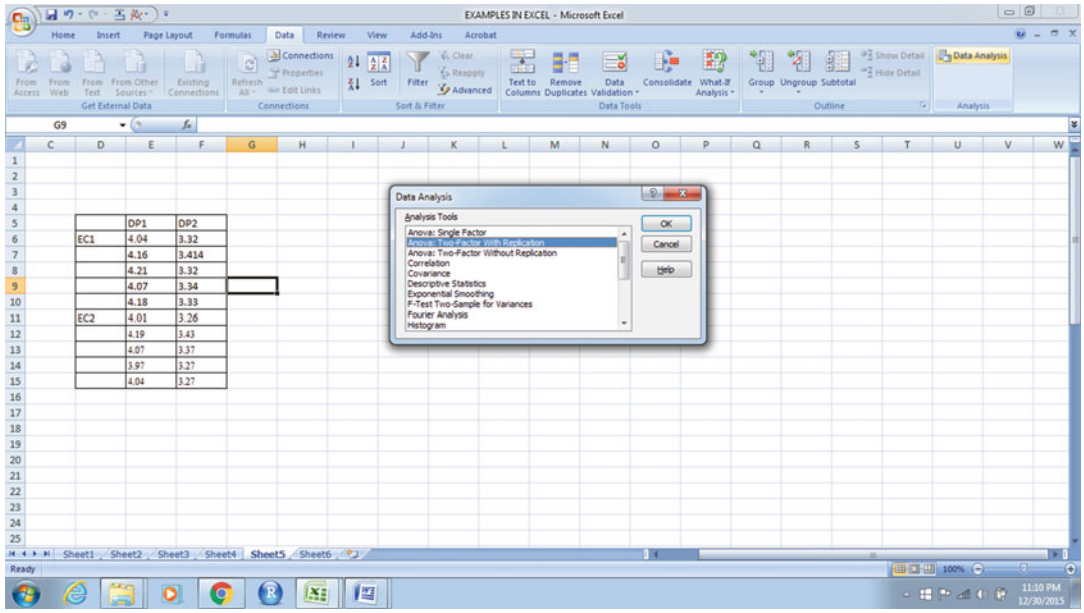
Step 1: Enter the data in the Excel as below.



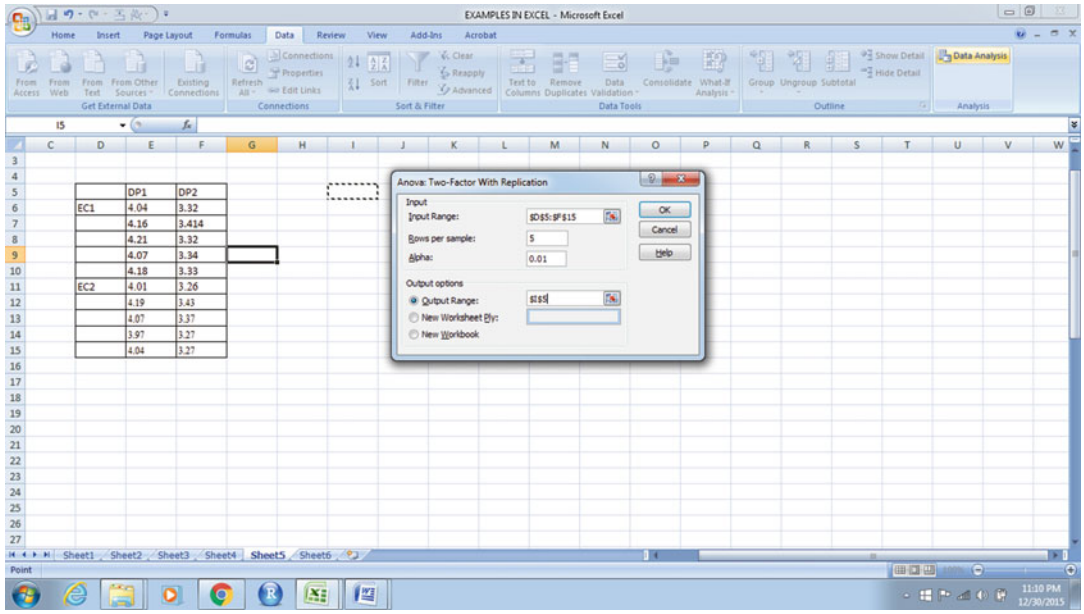
Step 2: Go to Data → Click on the Data Analysis toolbar.



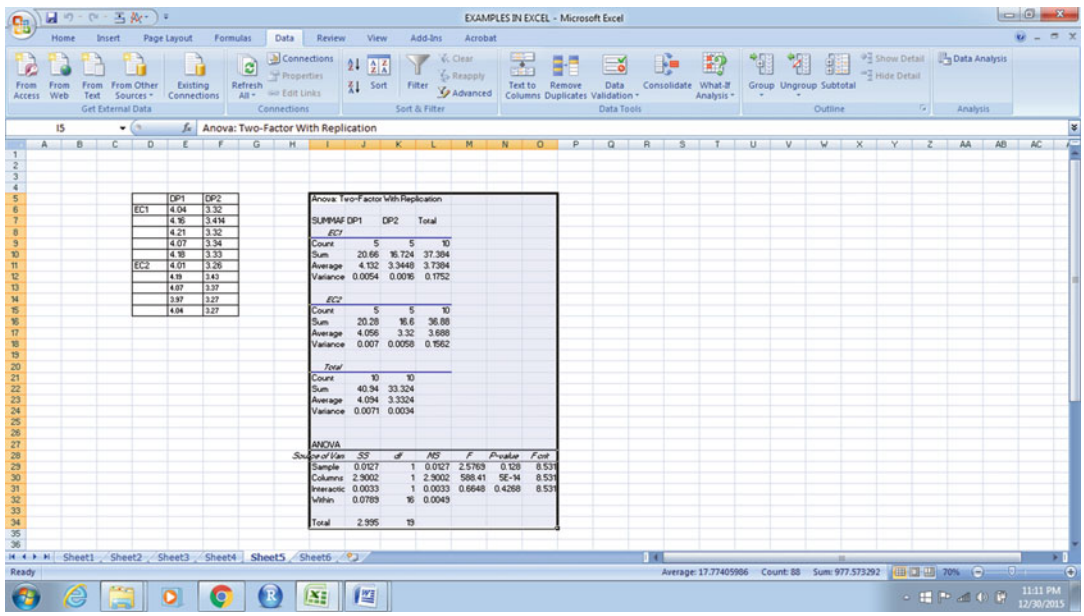
Step 3: Search for the option "Anova: Two Factor With Replication" → Click on OK.



Step 4: Select the input-output ranges, label etc., and select group by rows as shown below in the figure.

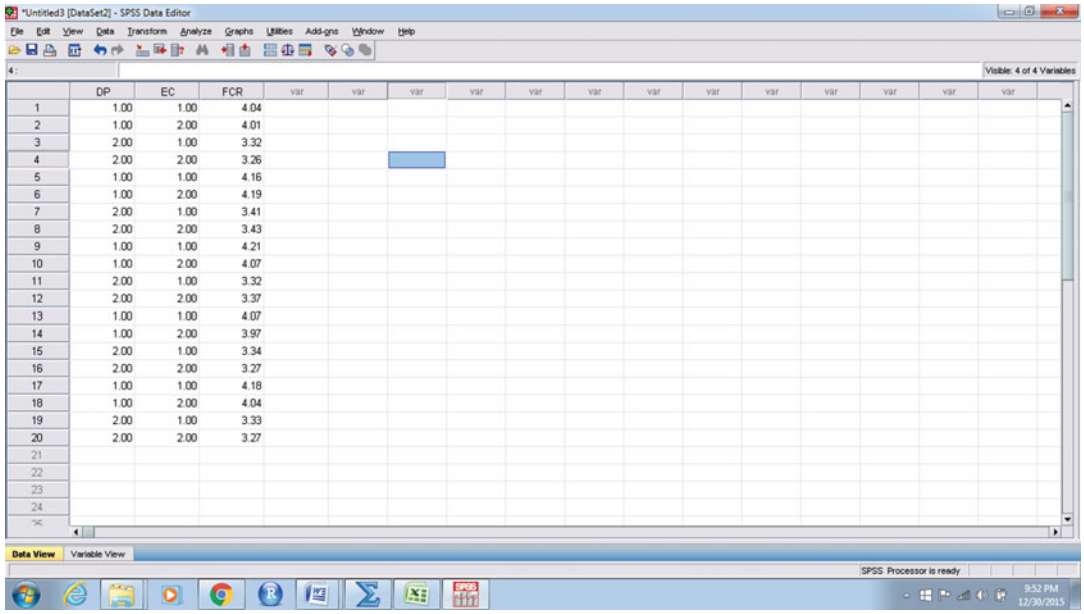


Step 5: Click on OK; then results will appear as shown below.

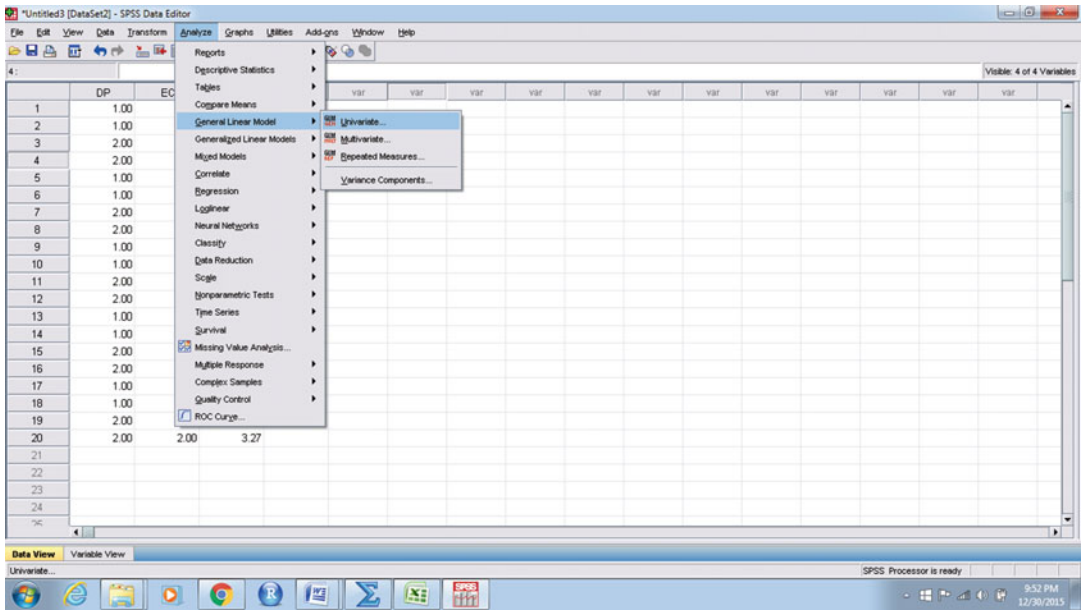


Example 11.1 (2^2 CRD) Using SPSS

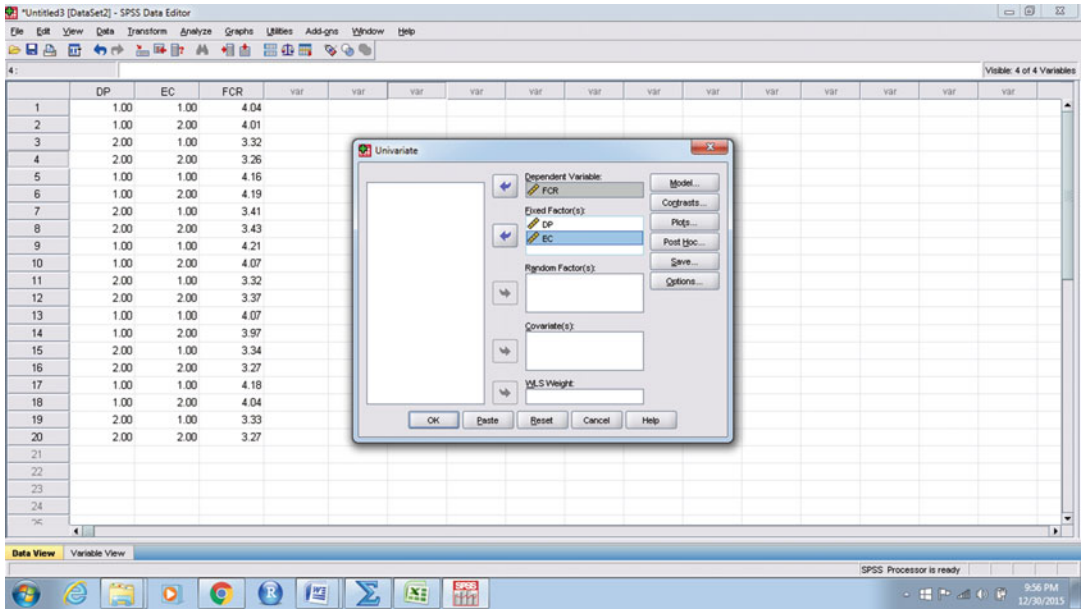
Step 1: Enter the data in SPSS data view as below; change the variable names.



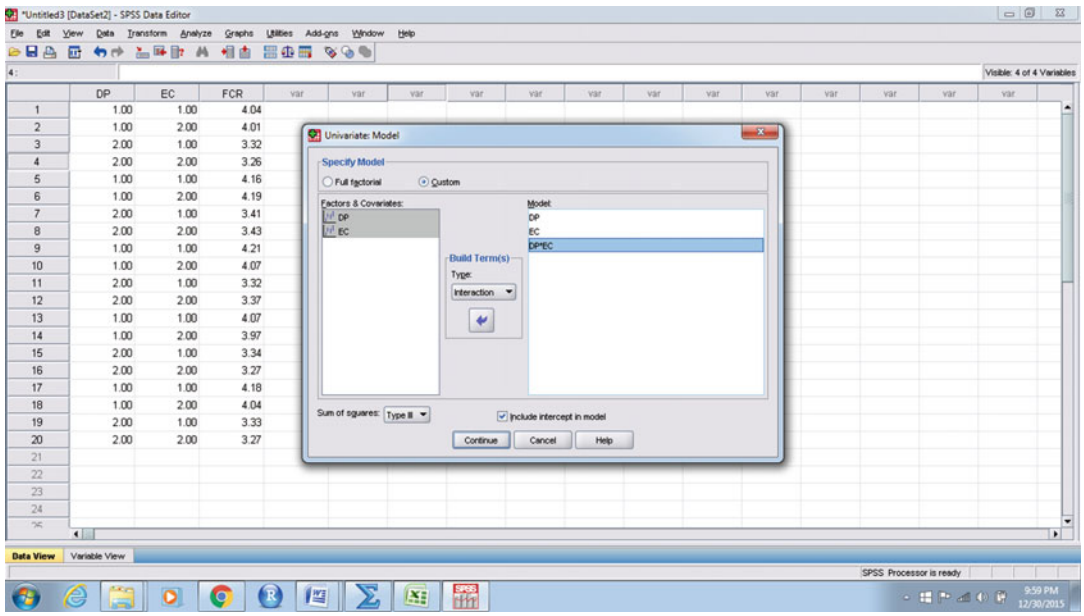
Step 2: Go to Analysis → Generalized linear model → Click on Univariate as below.



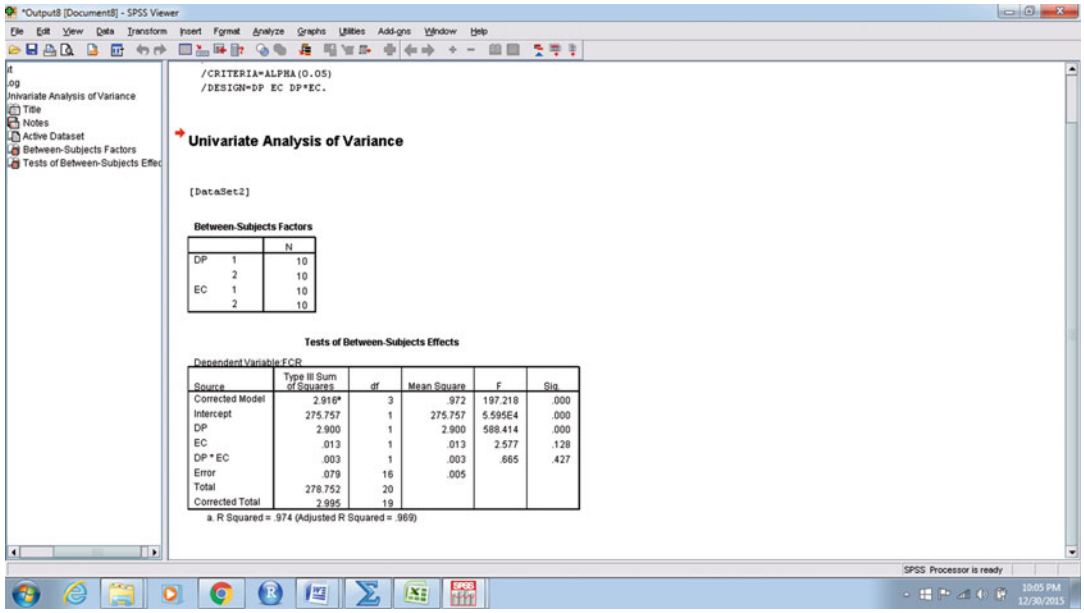
Step 3: Pass the dependent variable (in our case FCR) to Dependent variable option and fixed variables into the Fixed variable (in our case DP and EC) as below.



Step 4: Click on Model → Change the option to custom → Pass the DP, EC, and DP*EC (by selecting DP and EC with shift) into the Model as below.



Step 5: Click on Continue and then OK to get the output as below.



11.2.1.2 Model and Analysis of 2^2 Factorial RBD Experiment

Let us suppose we have a 2^2 factorial RBD experiment conducted for two factors A and B each having two levels and replicated r number of times. Then the appropriate statistical model would be

$$y_{ijk} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + \gamma_k + e_{ijk}$$

where $i = 1, 2$; $j = 1, 2$; and $k = 1, 2, \ldots, r$

y_{ijk} = response for observation due to kth replication of ith level of the first factor A and jth level of the second factor B

μ = general effect

α_i = additional effect due to ith level of the first factor A, $\sum \alpha_i = 0$

β_j = additional effect due to jth level of the second factor B, $\sum \beta_j = 0$

γ_k = additional effect due to kth replication, $\sum \gamma_k = 0$

$(\alpha\beta)_{ij}$ = interaction effect of the ith level of the first factor A and jth level of the second factor B with $\sum_i (\alpha\beta)_{ij} = \sum_j (\alpha\beta)_{ij} = 0$

e_{ijk} = error component associated with ith level of the first factor A, jth level of the second factor B in kth replication, and $e_{ijk} \sim$ i.i.d. $N(0, \sigma^2)$

Hypotheses to be tested are

$H_{01} : \alpha_1 = \alpha_2 = 0$ against the alternative hypothesis $H_{11} : \alpha_1 \neq \alpha_2$

$H_{02} : \beta_1 = \beta_2 = 0$ against the alternative hypothesis $H_{12} : \beta_1 \neq \beta_2$

$H_{02} : \gamma_1 = \gamma_2 = \ldots\ldots = \gamma_k = 0$ against the alternative hypothesis

$H_{12} : \gamma_1 \neq \gamma_2 \doteq \ldots\ldots \neq \gamma_k$

$H_{03} : \alpha_1\beta_1 = \alpha_1\beta_2 = \alpha_2\beta_1 = \alpha_2\beta_2 = 0$ against the alternative hypothesis

H_{13} : all interaction effects are not equal

Let the level of significance be α.

Analysis All together there would be $4r$ number observations. The total sum of squares is partitioned into the sum of squares due to factor A and due to factor B and sum of squares due to interaction of factors A and B and due to residuals, i.e.,

$SS_{\text{Tot}} = SS_A + SS_B + SS_{AB} + SS_R + SS_{Er}$, and the corresponding degrees of freedom would be

$$4r-1 = 2-1\,2-1\,1 \times 1\,r-1$$
$$(4r-1-1-1-r+1)$$

For practical purposes, different sums of squares are calculated by using the following formulae:

$$\text{Step 1 : Grand total} = \text{G} = \sum_i^2 \sum_j^2 \sum_k^r y_{ijk}$$

$$\text{Step 2 : Correction factor} = CF = \frac{\text{G}^2}{4r}$$

$$\text{Step 3 : Treatment sum of squares} = SS_{Tr}$$

$$= \sum_i^2 \sum_j^2 \sum_k^{\text{r}} \left(y_{ijk} - \overline{y}_{...}\right)^2$$

$$= \sum_i^2 \sum_j^2 \sum_k^{\text{r}} \left(y_{ijk}\right)^2 - CF$$

$$\text{Step 4 : Sum of squares due to A} = SS_A$$

$$= 2 \times 2 \sum_i (\overline{y}_{i..} - \overline{y}_{...})^2$$

$$= 2 \times 2 \left[\sum_i \overline{y}_{i..}^2 - 2\overline{y}_{...}{}^2\right]$$

$$= 2 \times 2 \sum_i \left(\frac{\sum_j \sum_k y_{ijk}}{2 \times 2}\right)^2 - CF$$

$$= \frac{1}{2 \times r} \sum_i y_{i..}^2 - CF$$

$$\text{Step 5 : Sum of squares due to B} = SS_B$$

$$= 2 \times r \sum_j \left(\overline{y}_{.j.} - \overline{y}_{...}\right)^2 = \frac{1}{2 \times r} \sum_i y_{.j.}^2 - CF$$

$$\text{Step 6 : Sum of squares due to AB}$$

$$= r \sum_i \sum_j \left(\overline{y}_{ij.} - \overline{y}_{i..} - \overline{y}_{.j.} + \overline{y}_{...}\right)^2$$

$$= r \sum_i \sum_j \left(\overline{y}_{ij.} - \overline{y}_{...} - (\overline{y}_{i..} - \overline{y}_{...}) - \left(\overline{y}_{.j.} - \overline{y}_{...}\right)\right]^2$$

$$= r \Big[\sum_i \sum_j \left(\overline{y}_{ij.} - \overline{y}_{...}\right)^2$$

$$- 2 \sum_i (\overline{y}_{i..} - \overline{y}_{...})^2 - 2 \sum_j \left(\overline{y}_{.j.} - \overline{y}_{...}\right)^2$$

$$= r \sum_i \sum_j \left(\overline{y}_{ij.} - \overline{y}_{...}\right)^2 - SS_A - SS_B$$

$$= r \left[\sum_i^m \sum_j^n y_{ij.}^2 - 2 \times 2 y_{...}^2\right] - SS_A - SS_B$$

$$= \sum_i^m \sum_j^n \frac{\text{y}_{ij.}^2}{r} - CF - SS_A - SS_B$$

$$= SS_{Tr} - SS_A - SS_B$$

$$SS_R = \frac{1}{2 \times 2} \sum_k y_{..k}^2 - CF$$

$$\therefore ErSS = SS_{\text{Tot}} - SS_{Tr}$$
$$= SS_{\text{Tot}} - (SS_A + SS_B + SS_{AB})$$
$$= SS_{\text{Tot}} - SS_A - SS_B - SS_{AB}$$

The ANOVA table is given by

Sources of variation	d.f.	SS	MS	F ratio
Replication	$r-1$	SS_R	$MS_R = \frac{SS_R}{r-1}$	$F_R = \frac{MS_R}{MS_{Er}}$
A	1	SS_A	$MS_A = \frac{SS_A}{1}$	$F_A = \frac{MS_A}{MS_{Er}}$
B	1	SS_B	$MS_B = \frac{SS_B}{1}$	$F_B = \frac{MS_B}{MS_{Er}}$
AB	1	SS_{AB}	$MS_{AB} = \frac{SS_{AB}}{1}$	$F_{AB} = \frac{MS_{AB}}{MS_{Er}}$
Error	$3(r-1)$	SS_{Er}	$MS_{Er} = \frac{SS_{Er}}{3(r-1)}$	
Total	$4r-1$	SS_{Tot}		

If the calculated value of F be greater than the table value of F at α level of significance and at $(r-1),3(r-1)$ d.f., then the null hypothesis of equality of replications is rejected, and we need to find out the replication which differs significantly from others using the following: $LSD/CD(\alpha) = \sqrt{\frac{2MS_{Er}}{2\times 2}}\, t_{\alpha/2,\text{error d.f.}}$

The hypothesis of the absence of a main factorial effect due to either A or B is rejected at the α level if the corresponding Cal $F > F_{\alpha;1,3(r-1)}$; otherwise, it cannot be rejected. As there are

only two levels for each of the factors A and B, in the event of rejection of null hypotheses corresponding to main effects of these two factors, the best treatment would be the level of each factor having high or low value, depending upon the parameter under study.

If the Cal $F > F_{\alpha;1,3(r-1)}$, corresponding to interaction effect, then we need to find out the *LSD* or *CD* value at specified level of significance and error degrees of freedom using the following formula: $LSD/CD(\alpha) = \sqrt{\frac{2MS_{Er}}{r}}\, t_{\alpha/2,\text{error d.f.}}$

Example 11.2 (2^2 RBD)
To know the effect of different levels of sulfur and nitrogen on garlic yield, an experiment with two levels of sulfur (20 and 40 kg ha^{-1}) and two levels of nitrogen (50 and 100 kg ha^{-1}) was laid out in RBD design with five replications. The following table gives the plot yield in kg per 3 sq. m of garlic. Analyze the data to find out (i) the best dose of sulfur, (ii) the best dose of nitrogen, and (iii) the combination of sulfur and nitrogen dose for the best yield of garlic:

	Yield (kg/3 m^2)									
	R1		R2		R3		R4		R5	
Sulfur dose	N1	N2	N1	N2	N1	N2	N1	N2	N1	N2
S1 (20 kg/ha)	1.81	1.97	1.78	1.95	1.83	1.99	1.87	1.96	1.77	1.93
S2 (40 kg/ha)	2.17	2.42	2.19	2.37	2.22	2.4	2.07	2.47	2.15	2.41

N1 (50 kg/ha) and N2 (100 kg/ha) and S1 (20 kg/ha) and S2 (40 kg/ha)

Solution From the given information, it is clear that it is a case of a two-factorial RBD, where both the factors have the same levels, i.e., 2. So the appropriate statistical model for the analysis will be

$$y_{ijk} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + \gamma_k + e_{ijk}$$

where $i = 1, 2$; $j = 1, 2$; and $k = 1, 2, \ldots, 5$

y_{ijk} = response in kth replicate due to ith level of the first factor (sulfur) and jth level of the second factor (nitrogen)

μ = general effect

α_i = additional effect due to ith level of the first factor (sulfur), $\sum \alpha_i = 0$

β_j = additional effect due to jth level of the second factor (nitrogen), $\sum \beta_j = 0$

$(\alpha\beta)_{ij}$ = interaction effect of the ith level of the first factor (sulfur) and jth level of the second factor (nitrogen), $\sum_i (\alpha\beta)_{ij} = \sum_j (\alpha\beta)_{ij} = 0$

γ_k = additional effect due to kth replicate, $\sum \gamma_k = 0$

e_{ijk} = error component associated with ith level of the first factor (sulfur), jth level of the second factor (nitrogen), and kth replicates and $e_{ijk} \sim i.i.d.\ \mathrm{N}(0, \sigma^2)$

Hypothesis to be tested:

$$H_0 : \alpha_1 = \alpha_2 = 0$$
$$\beta_1 = \beta_2 = 0$$
$$\gamma_1 = \gamma_2 = \gamma_3 = \gamma_4 = \gamma_5 = 0$$
$$\mathrm{All}(\alpha\beta)_{ij} = 0$$

against

$$H_1 : \text{All } \alpha's \text{ are not equal}$$
$$\text{All } \beta's \text{ are not equal}$$
$$\text{All } \gamma's \text{ are not equal}$$
$$All(\alpha\beta)_{ij} \text{are not equal}$$

Let the level of significance be 0.01.

From the given information, first let us form the following table and from the table get the following quantities.

Table of arranged field data:

	R1	R2	R3	R4	R5	R1	R2	R3	R4	R5
	N1 (b0)	N1 (b0)	N1 (b0)	N1 (b0)	N1 (b0)	N2 (b1)	N2 (b1)	N2 (b1)	N2 (b1)	N2 (b1)
S1 (a0)	1.81	1.78	1.83	1.87	1.77	1.97	1.95	1.99	1.96	1.93
S2 (a1)	2.17	2.19	2.22	2.07	2.15	2.42	2.37	2.4	2.47	2.41

$$\text{Grand total} = \sum_{i=1}^{2}\sum_{j=1}^{2}\sum_{k=1}^{5} y_{ijk} = 41.730$$

$$\text{Correction factor} = \frac{GT^2}{2 \times 2 \times 5} = \frac{41.730^2}{20} = 87.069$$

$$SS_{\text{TOT}} = \sum_{i=1}^{2}\sum_{j=1}^{2}\sum_{k=1}^{5} y_{ijk}^2 - CF = 88.116 - 87.069 = 1.046$$

$$SS_R = \frac{1}{ij}\sum_{k=1}^{5} y_{00k}^2 - \text{CF} = \frac{8.37^2 + 8.29^2 + 8.44^2 + 8.37^2 + 8.26^2}{2 \times 2} - 87.069 = 0.005$$

From the data table, let us calculate the table of totals:

	N1	N2	Total	Average
S1	9.06	9.8	18.86	1.886
S2	10.8	12.07	22.87	2.286
Total	19.86	21.87	41.73	
Average	1.986	2.187	2.085	

From the above table of totals, we have

$$SS_{(\text{Tab/Treat.})} = \frac{1}{r}\sum_{i=1}^{2}\sum_{j=1}^{2} y_{ijo}^2 - CF = \frac{9.06^2 + 9.80^2 + 10.80^2 + 12.07^2}{5} - 87.069 = 1.02$$

$$SS(\text{sulfur}) = \frac{1}{2 \times 5}\sum_{i=1}^{2} y_{i..}^2 - CF = \frac{18.86^2 + 22.87^2}{10} - 87.069 = 0.804.$$

$$SS(\text{nitrogen}) = \frac{1}{2 \times 5}\sum_{j=1}^{2} y_{.j.}^2 - CF = \frac{19.86^2 + 21.87^2}{10} - 87.069 = 0.202$$

$$SS(S \times N) = SS(Tab./\text{Treat.}) - SS_R - SS_{(\text{Sulfur})} - SS_{(\text{Nitrogen})} = 0.014$$

$$SS_{Er} = SS_{\text{TOT}} - SS_{Tr} - SS_R = 1.046 - 1.02 - 0.005 = 0.021$$

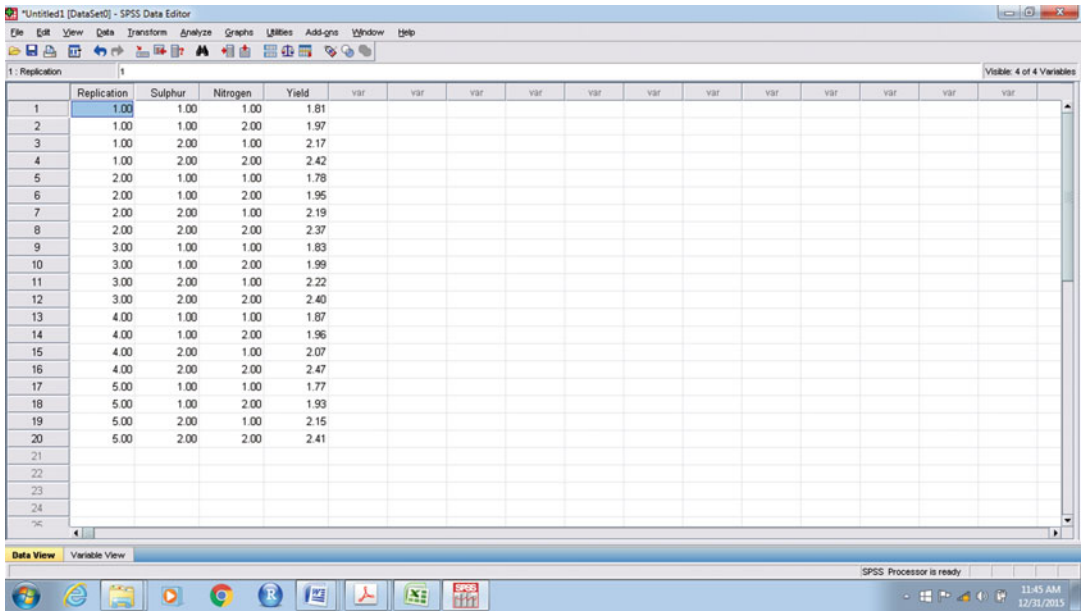
Now the analysis of variance table is made according with the help of the above quantities:

SOV	d.f.	*SS*	*MS*	Cal F	Tab F
Replication	4	0.005	0.001	0.717	5.412
Sulfur	1	0.804	0.804	449.374	9.330
Nitrogen	1	0.202	0.202	112.905	9.330
Sulfur × nitrogen	1	0.014	0.014	7.850	9.330
Error	12	0.021	0.002		
Total	19				

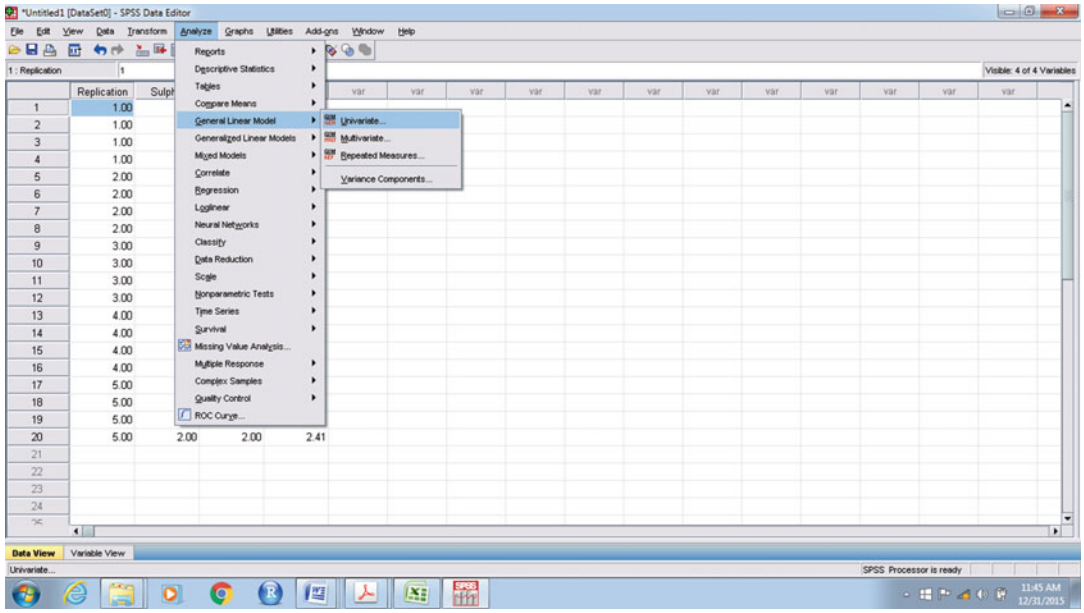
It is clear from the above table that all the effects are significant at 1 % level of significance except the replication and interaction effects, which are nonsignificant at 1 % level of significance. From the average values, we have that S2 and N2 are the best dose of sulfur and nitrogen, respectively. As interaction effects are not significant, so we cannot fix any combination as better over the other combination of sulfur and nitrogen.

Example 11.2 (2^2 RBD) Using SPSS

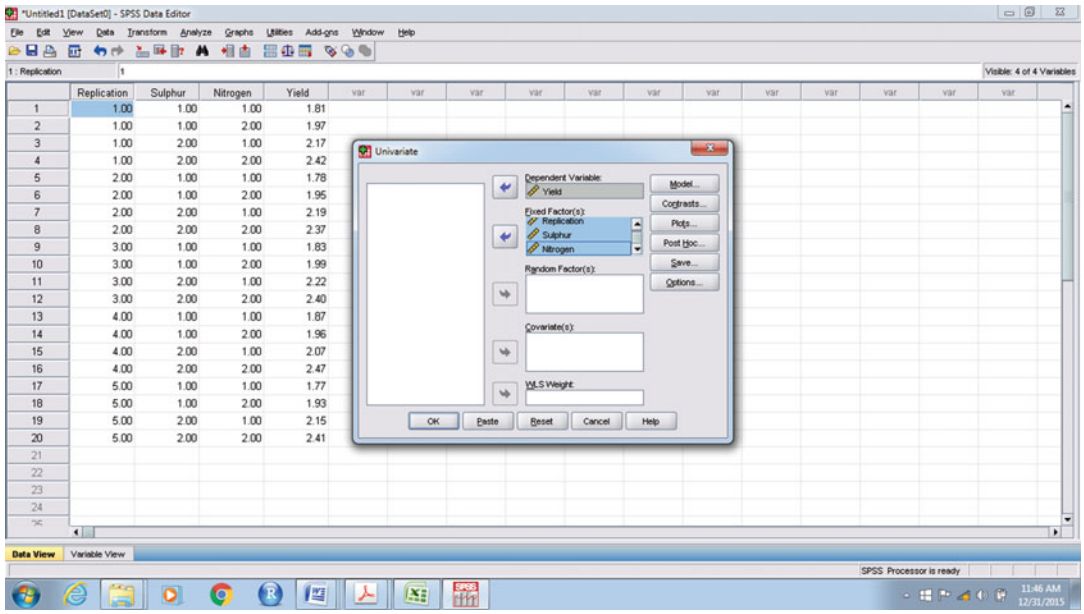
Step 1: Enter the data in SPSS data view as below; change the variable names.



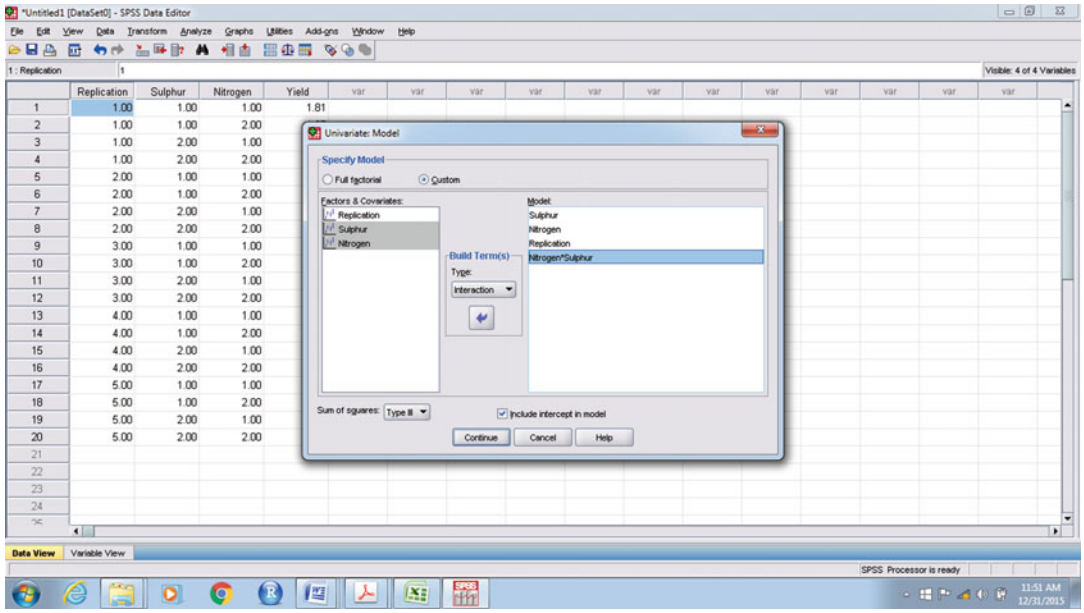
Step 2: Go to Analysis → Generalized linear model → Click on Univariate as below.



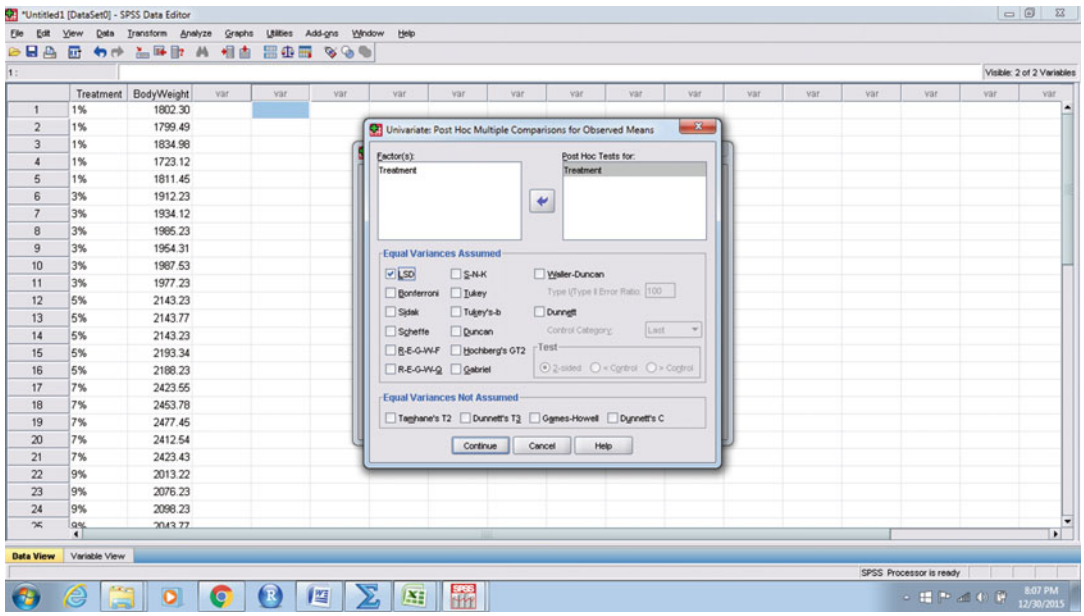
Step 3: Pass the dependent variable (in our case Yield) into the Dependent variable option and fixed variable into the Fixed variable (in our case Replication, Sulfur, and Nitrogen) as below.



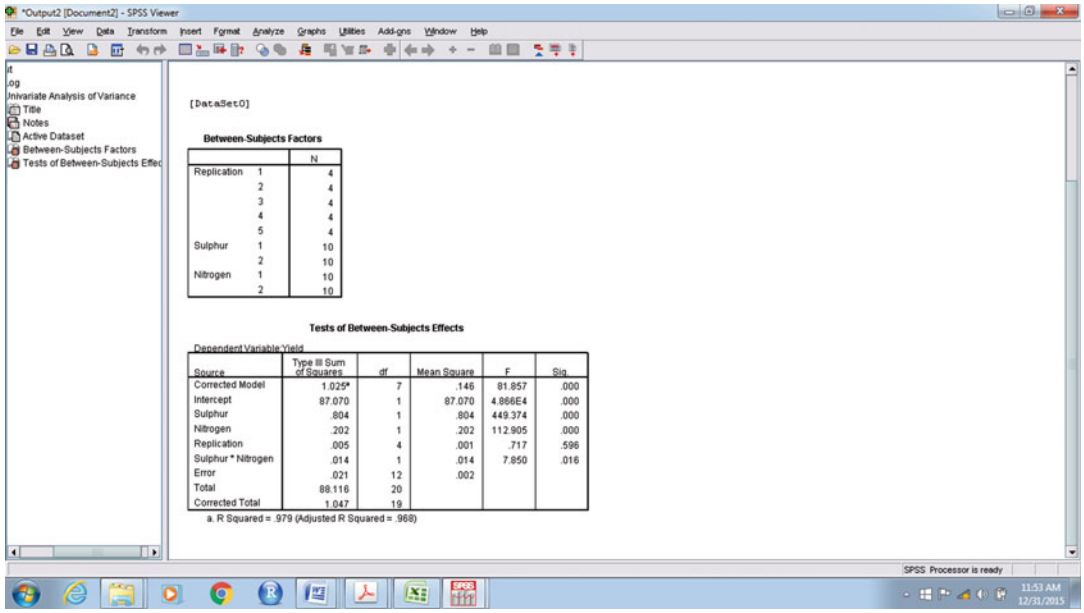
Step 4: Click on Model → Change the option to custom → Pass the Sulfur, Nitrogen, Replication, and Nitrogen*Sulfur (by selecting Nitrogen and Sulfur with shift) into the Model as below.



Step 5: Click on Continue and then OK to get the output as below.



Step 6: Click on Continue and then OK to get the output as below.



Example 11.3 (3^2 Factorial CRD Experiment) An experiment was conducted to determine the effect of adding a vitamin (A) in three different types of feed on average daily weight gain of swine. Three levels of vitamin A (0, 3, and 6 mg) and three levels of feeds, viz., F1, F2, and F3, were used. The total sample size was 27 pigs, on which the nine combinations of vitamin A and feeds were randomly assigned. The following daily gains were measured:

	Vitamin		
Feed	A1	A2	A3
F1	0.585	0.567	0.473
	0.613	0.557	0.477
	0.623	0.553	0.482
F2	0.536	0.545	0.450
	0.538	0.548	0.457
	0.537	0.550	0.540
F3	0.458	0.589	0.869
	0.459	0.597	0.913
	0.477	0.597	0.937

Find out the best level of vitamin A, feed, and combination of vitamin A and feed.

Solution As the experiment has been conducted under controlled condition, so we can assume that all the experimental units were homogeneous in nature except for the treatment condition; hence, CRD should be the appropriate basic design for the analysis.

Thus from the given conditions, it is clear that the information can be analyzed in a two-factor factorial CRD, where both the factors have the same levels, i.e., 3. So the appropriate statistical model for the analysis will be

$$y_{ijk} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + e_{ijk}$$

where $i = 1, 2,3$; $j = 1, 2,3$; and $k = 1, 2, 3$

y_{ijk} = response in kth observation due to ith level of the first factor (vitamin A) and jth level of the second factor (feed)

μ = general effect

α_i = additional effect due to ith level of the first factor (vitamin A), $\sum \alpha_i = 0$

β_j = additional effect due to jth level of the second factor (feed), $\sum \beta_j = 0$

$(\alpha\beta)_{ij}$ = interaction effect of the ith level of the first factor (vitamin A) and jth level of the second factor (feed) and $\sum_i (\alpha\beta)_{ij} = 0,\ \sum_j (\alpha\beta)_{ij} = 0$

e_{ijk} = error component associated with ith level of the first factor (vitamin A), jth level of the second factor (feed), and kth replicates and $e_{ijk} \sim N(0, \sigma^2)$

Hypothesis to be tested:

$H_0 : \alpha_1 = \alpha_2 = \alpha_3 = 0$

$\beta_1 = \beta_2 = \beta_3 = 0$

$\text{All}(\alpha\beta)_{ij}{}'s = 0$

against

H_1: $\alpha_i{}'$s are not all equal

$\beta_j{}'$s are not all equal

$(\alpha\beta)_{ij}{}'$s are not all equal

Let the level of significance be 0.01.

From the given data, first let us form the following table and from the table get the following quantities:

	Vitamin A				
Feed	A1	A2	A3	Total	Mean
F1	1.821	1.677	1.432	4.930	1.643
F2	1.611	1.643	1.447	4.701	1.567
F3	1.394	1.783	2.719	5.896	1.965
Total	4.826	5.103	5.598	15.527	
Mean	1.609	1.701	1.866		

$$\text{Grand total } (GT) = \sum_{i=1}^{3}\sum_{j=1}^{3}\sum_{k=1}^{3} y_{ijk} = 15.527$$

$$\text{Correction factor } (CF) = \frac{GT^2}{3 \times 3 \times 3} = \frac{15.527^2}{27} = 8.929$$

$$SS_{\text{Tot}} = \sum_{i=1}^{3}\sum_{j=1}^{3}\sum_{k=1}^{3} y_{ijk}^2 - CF = 9.369 - 8.929 = 0.4403$$

$$SS_{Tr} = \frac{1}{3}\sum_{i=1}^{3}\sum_{j=1}^{3} y_{ij.}^2 - CF = \frac{1.821^2 + 1.611^2 + 1.394^2 + \ldots\ldots\ldots + 1.447^2 + 2.719^2}{3} - 8.929 = 0.431$$

$$ErSS = TSS - TrSS = 0.440 - 0.431 = 0.009$$

$$SS_A = \frac{1}{3 \times 3}\sum_{i=1}^{3} y_{i..}^2 - CF = \frac{4.826^2 + 5.103^2 + 5.598}{9} - 8.929 = 0.033.$$

$$SS_F = \frac{1}{3 \times 3}\sum_{j=1}^{3} y_{.j.}^2 - CF = \frac{4.930^2 + 4.701^2 + 5.896^2}{9} - 8.929 = 0.089$$

$$SS_{(A \times F)} = \frac{1}{3}\sum_{i=1}^{3}\sum_{j=1}^{3} y_{ij.}^2 - CF - SS_A - SS_B = 0.431 - 0.033 - 0.089 = 0.308$$

The main effects will be based on 2 d.f. which can further be split in to two components, viz., linear contrast and quadratic contrast.

Now we make the following analysis of variance table with the help of the above quantities:

ANOVA					
SOV	d.f.	*SS*	*MS*	Cal F	Tab F at 1 %
Vitamin A	2	0.0340	0.0170	35.5795	6.0129
Feed	2	0.0894	0.0447	93.5730	6.0129
Vit. × feed	4	0.3084	0.0771	161.4066	4.5790
Error	18	0.0086	0.0005		
Total	26	0.4404			

It is clear from the above table that all the effects are significant at 1 % level of significance.

Now the question is which level of vitamin A, feed, and combination of vitamin A and feed has maximum weight gain. To answer these we are to calculate the critical difference values for vitamin A and feed and interaction effects separately using the following formulae:

$$CD_{0.01}(\text{vitamin A}) = \sqrt{\frac{2ErMS}{r.f}} t_{0.005,\text{err}.d.f}$$
$$= \sqrt{\frac{2 \times 0.0005}{3 \times 3}} \times 2.878$$
$$= 0.029$$

$$CD_{0.01}(\text{feed}) = \sqrt{\frac{2ErMS}{r.a}} t_{0.005,\text{err}.d.f}$$
$$= \sqrt{\frac{2 \times 0.0005}{3 \times 3}} \times 2.878 = 0.029$$

$$CD_{0.01}(\text{vitamin A} \times \text{feed})$$
$$= \sqrt{\frac{2ErMS}{r}} t_{0.005,\text{err}.d.f}$$
$$= \sqrt{\frac{2 \times 0.0005}{3}} \times 2.878 = 0.051$$

Vitamin A	Gain in weight	Feed	Gain in weight
A3	0.622	B3	0.655
A2	0.567	B1	0.547
A1	0.536	B2	0.522

A × F	Gain in weight
A3F3	0.906
A1F1	0.607
A2F3	0.594
A2F1	0.559
A2F2	0.548
A1F2	0.537
A3F2	0.482
A3F1	0.477
A1F3	0.465

It is clear from the above tables that all the levels of vitamin A are significantly different from each other and vitamin A at level 3 has recorded significantly the highest gain in weight compared to other levels of vitamin A. On the other hand, feed 3 is the best for getting maximum weight gain in swine. So far as the interaction effect of vitamin A and feed is concerned, A3F3 followed by A1F1 is the best combination.

Example 11.4 (3^2 Factorial RBD Experiment) An experiment was conducted to assess the best nitrogen and potash fertilizer in chickpea to get maximum yield in a randomized block design. The following data gives the yield in quintal per hectare in response to different doses of N and K. Analyze the data to estimate the best dose of both nitrogen and potash along with the best combination of N and K dose to provide maximum yield:

K1								
N1			N2			N3		
R1	R2	R3	R1	R2	R3	R1	R2	R3
12.43	12.45	12.54	12.84	12.88	12.92	12.67	12.73	12.77
K2								
N1			N2			N3		
R1	R2	R3	R1	R2	R3	R1	R2	R3
14.71	14.86	14.84	14.87	14.96	14.91	14.98	15.06	15.05
K3								
N1			N2			N3		
R1	R2	R3	R1	R2	R3	R1	R2	R3
16.93	16.99	16.87	17.24	17.33	17.45	17.34	17.37	17.45

Solution From the given information, it is clear that the information is to be analyzed in a two-factor factorial RBD, where both the factors have the same levels, i.e., 3. So the appropriate statistical model for the analysis will be

$$y_{ijk} = \mu + \alpha_i + \beta_j + \gamma_k + (\alpha\beta)_{ij} + e_{ijk}$$

where $i = 1, 2, 3$; $j = 1, 2,3$; and $k = 1, 2, 3$

y_{ijk} = response in kth replicate due to the ith level of the first factor (doses of nitrogen) and jth level of the second factor (doses of potash)

μ = general effect

α_i = additional effect due to the ith level of the first factor (doses of nitrogen), $\sum \alpha_i = 0$

β_j = additional effect due to the jth level of the second factor (doses of potash), $\sum \beta_j = 0$

γ_k = additional effect due to kth replicate, $\sum \gamma_k = 0$

$(\alpha\beta)_{ij}$ = interaction effect of the ith level of the first factor (doses of nitrogen) and jth level of the second factor (doses of potash)

e_{ijk} = error component associated with the ith level of the first factor (doses of nitrogen), the jth level of the second factor (doses of potash), and kth replicates and $e_{ijk} \sim$ i.i.d. $N(0, \sigma^2)$

Hypothesis to be tested:

$H_{01} : \alpha_1 = \alpha_2 = \alpha_3 = 0$

$H_{02} : \beta_1 = \beta_2 = \beta_3 = 0$

$H_{03} : \gamma_1 = \gamma_2 = \gamma_3 = 0$

H_{04} : all$(\alpha\beta)_{ij}{}'$s are equal

against

$H_{11} : \alpha_i'$s are not all equal

$H_{12} : \beta_j{}'$s are not all equal

$H_{13} : \gamma'$s are not all equal

H_{14} : all$(\alpha\beta)_{ij}{}'s$ are not equal

Let the level of significance be 0.05.

From the given data table, let us calculate the following quantities:

$$\begin{aligned}\text{Grand total } (GT) &= \sum_{i=1}^{3}\sum_{j=1}^{3}\sum_{k=1}^{3} y_{ijk} \\ &= 12.43 + 12.45 + ... \\ &\quad + 17.37 + 17.45 \\ &= 403.36\end{aligned}$$

$$\begin{aligned}\text{Correction factor } (CF) &= \frac{\text{GT}^2}{3 \times 3 \times 3} \\ &= \frac{403.36^2}{27} = 6025.8\end{aligned}$$

$$\begin{aligned}SS_{\text{TOT}} &= \sum_{i=1}^{3}\sum_{j=1}^{3}\sum_{k=1}^{3} y_{ijk}^2 - \text{CF} \\ &= 12.43^2 + 12.45^2 + ... + 17.37^2 \\ &\quad + 17.45^2 - 6025.89 \\ &= 93.35\end{aligned}$$

$$SS_R = \frac{1}{mn}\sum_{i=1}^{3} y_{..k}^2 - CF = \frac{134.01^2 + 122.18^2 + 134.8^2}{9} - 6025.89 = 0.033$$

From the above raw data table, let us form the following table and from the table get the following quantities:

	N1	N2	N3	Total	Mean
K1	37.47	38.64	38.17	114.15	38.05
K2	44.41	44.74	45.09	134.24	44.75
K3	50.79	52.02	52.16	154.97	51.66
Total	132.62	135.40	135.42	390.99	
Mean	44.26	45.13	45.14		

$$SS_{Tr} = \frac{1}{3}\sum_{i=1}^{3}\sum_{j=1}^{3} y_{ij.}^2 - CF = \frac{24.97^2 + 38.64^2 + \ldots\ldots\ldots + 135.40 + {}^2135.42^2}{3} - 6025.89 = 93.28$$

$$SS_{Er} = SS_{\text{TOT}} - SS_{Tr} - SS_R = 93.35 - 93.28 - 0.03 = 0.03$$

$$SS_N = \frac{1}{3 \times 3}\sum_{i=1}^{3} y_{i..}^2 - CF = \frac{132.62^2 + 135.40^2 + 135.42^2}{9} - 6025.89 = 0.56.$$

$$SS_K = \frac{1}{3 \times 3}\sum_{j=1}^{3} y_{.j.}^2 - CF = \frac{114.15^2 + 134.24^2 + 154.97^2}{9} - 6025.89 = 92.57$$

$$SS_{(N\times P)} = SS_{Tr} - SS_{(N)} - SS_{(K)} = 93.28 - 0.56 - 92.57 = 0.14$$

Now we make the following analysis of variance table with the help of the above quantities:

ANOVA table					
SOV	d.f.	SS	MS	Cal F	Tab F at 5 %
Replication	2	0.03	0.02	7.44	3.63
N	2	0.56	0.28	125.49	3.63
K	2	92.58	46.29	20730.78	3.63
$N \times K$	4	0.14	0.04	16.17	3.01
Error	16	0.04	0.002		
Total	26	93.35			

From the above table, it is clear that all the null hypotheses are rejected at the desired 5 % level of significance. So we are to find out the best dose of nitrogen and potash separately with the help of critical difference values. Significant interaction between levels of nitrogen and potash shows that a given dose of nitrogen has different effects over different doses of potash, and similarly a given dose of potash has different effects over different doses of nitrogen. Main effects due to nitrogen as well as potash are not equal to zero.

Now our task is to find out the best dose of *N* and *K* as well as their combination:

$$CD_{0.05\ (\text{Nitrogen})} = \sqrt{\frac{2ErMS}{r.k}}t_{0.025,\text{err}.d.f} = \sqrt{\frac{2 \times 0.002}{3 \times 3}} \times 2.12 = 0.05$$

$$CD_{0.05\ (\text{Potash})} = \sqrt{\frac{2ErMS}{r.n}}t_{0.025,\text{err}.d.f} = \sqrt{\frac{2 \times 0.002}{3 \times 3}} \times 2.12 = 0.05$$

$$CD_{0.05,(N\times K)} = \sqrt{\frac{2ErMS}{r}}t_{0.025,\text{err}.d.f} = \sqrt{\frac{2 \times 0.002}{3}} \times 2.12 = 0.08$$

Table of averages:

Nitrogen level	Mean yield
N2	45.13
N3	45.11
N1	44.21
Potash level	Mean yield
K3	51.66
K2	44.75
K1	38.05
Interaction effect	Mean yield
N3K3	17.39
N2K3	17.34
N1K3	16.93
N3K2	15.03
N2K2	14.91
N1K2	14.80
N2K1	12.88
N3K1	12.70
N1K1	12.47

It is clear from the above tables that N_2 dose of nitrogen has recorded significantly the highest

yield compared to other doses. On the other hand, K_3 is the best dose of potash for getting maximum yield. So far as the interaction effect of nitrogen and potash is concerned, N_3K_3 combination is found to be the best nitrogen potash dose followed by N_2K_3 and so on.

11.2.2 Two-Factor Asymmetrical ($m \times n$, $m \neq n$) Factorial Experiment

As has already been mentioned that in a factorial experiment, if the levels of the factors are different, it is known as asymmetrical factorial experiment, in this section we shall discuss about two-factor asymmetrical factorial experiment. As the name suggests, this type of experiment is having two factors, each having different levels.

11.2.2.1 Two-Factor Asymmetrical ($m \times n$, $m \neq n$) Factorial CRD Experiment

Let us consider an $m \times n$ factorial experiment; that means an experiment with two factors A and B (say) having m and n levels, respectively, is conducted with r repetitions for each treatment combination. It is not necessary that each treatment combination is to be repeated an equal number of times, but for the sake of simplicity and easy explanation and understanding, let us have an equal number of repetitions for all the treatment combinations. So there would be $m \times n$ treatment combinations. Thus the model for the design can be presented as follows:

$$y_{ijk} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + e_{ijk}$$

where $i = 1, 2, \ldots, m$; $j = 1, 2, \ldots, n$; and $k = 1, 2, \ldots..., r$

y_{ijk} = response in kth observation due to ith level of the first factor A and jth level of the second factor B

μ = general effect

α_i = additional effect due to ith level of the first factor A, $\sum \alpha_i = 0$

β_j = additional effect due to jth level of the second factor B, $\sum \beta_j = 0$

$(\alpha\beta)_{ij}$ = interaction effect of the ith level of the first factor A and jth level of the second factor B, $\sum_i (\alpha\beta)_{ij} = \sum_j (\alpha\beta)_{ij} = 0$

e_{ijk} = error component associated with the ith level of the first factor, the jth level of the second factor in kth replicate, and $e_{ijk} \sim$ i.i.d. $N(0, \sigma^2)$

Randomization and Layout

In total there will be $m \times n$ number of treatments each being repeated r times. That means we require to have $m \times n \times r$ number of experimental units in the whole experiment. $m \times n$ number of treatments are to be allotted randomly among mnr experimental units as per the procedure discussed during the layout of CRD design in Chap. 10.7.1.

Hypothesis to be tested in $m \times n$ factorial RBD experiment:

$$H_{01} : \alpha_1 = \alpha_2 = \cdots = \alpha_i = \cdots = \alpha_m = 0$$
$$H_{02} : \beta_1 = \beta_2 = \cdots = \beta_j = \cdots = \beta_n = 0$$
$$H_{03} : \text{ all } (\alpha\beta)_{ij}\text{s are equal}$$

against the alternative hypotheses

H_{11} : all α's are not equal

H_{12} : all β's are not equal

H_{13} : all $(\alpha\beta)'$s are not equal

Let the level of significance be α.

Analysis The following table gives the plot-wise information recorded on response variable y_{ijk} s:

	B_1	B_2	$\ldots B_j \ldots$	B_n
A_1	y_{111} y_{112} : y_{11r}	y_{121} y_{122} : y_{12r}	$\ldots\ldots\ldots y_{1j1}\ldots\ldots$ $\ldots\ldots\ldots y_{1j2}\ldots\ldots$: $\ldots\ldots\ldots y_{1jr}\ldots\ldots$	y_{1n1} y_{1n2} : y_{1nr}
A_2	y_{211} y_{212} : y_{21r}	y_{221} y_{222} : y_{22r}	$\ldots\ldots\ldots y_{2j1}\ldots\ldots$ $\ldots\ldots\ldots y_{2j2}\ldots\ldots$: $\ldots\ldots\ldots y_{2jr}\ldots\ldots$	y_{2n1} y_{2n2} : y_{2nr}
. : : :	. : : :	. : : :	$\ldots\ldots\ldots\ldots$ $\ldots\ldots\ldots\ldots$ $\ldots\ldots\ldots\ldots$	. : : :
A_i	y_{i11} y_{i12} : y_{i1r}	y_{i21} y_{i22} : y_{i2r}	$\ldots\ldots\ldots y_{ij1}\ldots\ldots$ $\ldots\ldots\ldots y_{ij2}\ldots\ldots$: $\ldots\ldots\ldots y_{ijr}\ldots\ldots$	y_{in1} y_{in2} : y_{inr}
. : : :	. : : :	. :	$\ldots\ldots\ldots\ldots$ $\ldots\ldots\ldots\ldots$ $\ldots\ldots\ldots\ldots$	. : : :
A_m	y_{m11} y_{m12} : y_{m1r}	y_{m21} y_{m22} : y_{m2r}	$\ldots\ldots\ldots y_{mj1}\ldots\ldots$ $\ldots\ldots\ldots y_{mj2}\ldots\ldots$: $\ldots\ldots\ldots y_{mjr}\ldots\ldots$	y_{mn1} y_{mn2} : y_{mnr}

We calculate the following quantities from the table:

$$\text{Grand total } (G) = \sum_{i=1}^{m}\sum_{j=1}^{n}\sum_{k=1}^{r} y_{ijk}.$$

$$\text{Correction factor } (CF) = \frac{G^2}{mnr}.$$

$$SS_{\text{Tot}} = \sum_{i=1}^{m}\sum_{j=1}^{n}\sum_{k=1}^{r} y_{ijk}^2 - CF.$$

Let us make the following table for calculating other sums of squares.

Table of treatment totals:

	B_1	B_2	. . . . . .B_j.	B_n	Total
A_1	$\sum_{k=1}^{r} y_{11k}$	$\sum_{k=1}^{r} y_{12k}$	$\sum_{k=1}^{r} y_{1jk}$	$\sum_{k=1}^{r} y_{1nk}$	$y_{1..}$
A_2	$\sum_{k=1}^{r} y_{21k}$	$\sum_{k=1}^{r} y_{22k}$	$\sum_{k=1}^{r} y_{2jk}$	$\sum_{k=1}^{r} y_{2nk}$	$y_{2..}$
.....	.....	.....	.....	.....	.....
.....	.....	.....	.....	.....	.....
A_i	$\sum_{k=1}^{r} y_{i1k}$	$\sum_{k=1}^{r} y_{i2k}$	$\sum_{k=1}^{r} y_{2jk}$	$\sum_{k=1}^{r} y_{2nk}$	$y_{i..}$
.....	.....	.....	.....	.....	.....
.....	.....	.....	.....	.....	.....
A_m	$\sum_{k=1}^{r} y_{m1k}$	$\sum_{k=1}^{r} y_{m2k}$	$\sum_{k=1}^{r} y_{mjk}$	$\sum_{k=1}^{r} y_{mnk}$	$y_{m..}$
Total	$y_{.1.}$	$y_{.2.}$	$y_{.j.}$	$y_{.n.}$	$y_{...}$

$$SS_{Tr} = \frac{1}{r}\sum_{i=1}^{m}\sum_{j=1}^{n} y_{ij.}^2 - CF, \text{ where } y_{ij.} = \sum_{k=1}^{r} y_{ijk}$$

$$SS_{Er} = TSS - TrSS.$$

$$SS_{(A)} = \frac{1}{nr}\sum_{i=1}^{m} y_{i..}^2 - CF.$$

$$SS_{(B)} = \frac{1}{mr}\sum_{j=1}^{n} y_{.j.}^2 - CF.$$

$$SS_{(AB)} = SS_{Tr} - SS_{(A)} - SS_{(B)}.$$

Analysis of Variance The structure of analysis of variance table is as follows:

SOV	*d.f.*	*SS*	*MS*	*F*
Factor A	$m-1$	$SS_{(A)}$	$MS_{(A)} = SS_{(A)}/(m-1)$	$MS_{(A)}/MS_{Er}$
Factor B	$n-1$	$SS_{(B)}$	$MS_{(B)} = SS_{(B)}/(n-1)$	$MS_{(B)}/MS_{Er}$
Interaction (A × B)	$(m-1)(n-1)$	$SS_{(AB)}$	$MS_{(AB)} = SS_{(AB)}/(m-1)(n-1)$	$MS_{(AB)}/MS_{Er}$
Error	$mnr-m-n+1$	SS_{Er}	$MS_{Er} = SS_{Er}/(mnr-m-n+1)$	
Total	$mnr-1$	SS_{Tot}		

The hypothesis with respect to the main effect of A, main effect of B, and interaction effect ofA and B will be rejected at the α level of significance if the Cal F $>$ $F_{\alpha;(m-1),(mnr-m-n+1)}$, Cal F $>$ $F_{\alpha;(n-1),(mnr-m-n+1)}$, Cal F $>$ $F_{\alpha;(m-1)(n-1),(mnr-m-n+1)}$, respectively, otherwise the corresponding null hypothesis cannot be rejected. In the event of rejection of the null hypothesis, the best level corresponding to the main or interaction effect is to be worked out using the respective LSD/CD formula as given below:

$$LSD/CD(\alpha)_A = \sqrt{\frac{2MS_{Er}}{nr}}\, t_{\alpha/2,\text{error d.f.}} \text{ for factor A}$$

$$LSD/CD(\alpha)_B = \sqrt{\frac{2MS_{Er}}{mr}}\, t_{\alpha/2,\text{error d.f.}} \text{ for factor B}$$

$$LSD/CD(\alpha)_{AB} = \sqrt{\frac{2MS_{Er}}{r}}\, t_{\alpha/2,\text{error d.f.}} \text{ for interaction of factors A and B}$$

The best levels of the main effect or interaction effect are worked out by comparing the treatment mean difference with respective *LSD*/*CD* values. If the difference between any pair of level/interaction means is more than corresponding *LSD*/*CD* values, then these two levels/interactions under comparison are declared significantly different, and the best level/interaction is selected on the basis of the mean of the levels/interaction under comparison. On the other hand, if the difference between any pair of level/interaction means is equal to or less than the corresponding *LSD*/*CD* value, then these two levels/interactions under comparison are declared statistically at par.

Example 11.5 (3 × 4 Two-Factor Asymmetrical Factorial CRD)
A laboratory experiment was conducted to find out the role of four different media (soil, compost, coco peat, and river sand) and three bio-regulators (GA_3, borax, and thiourea) on seed germination of papaya in three replications. Analyze the data to find out the best media and the best bio-regulator and the best interaction effects among the factors to have good seed germination percentage:

Bio-regulator	B1				B2				B3			
Media	M1	M2	M3	M4	M1	M2	M3	M4	M1	M2	M3	M4
R1	83.33	76.67	79.33	75.65	77.23	73.33	77.67	71.223	77.67	76.45	78.67	74.23
R2	83.63	76.17	78.53	74.95	76.43	72.43	77.57	70.623	77.57	75.75	77.67	74.13
R3	83.53	76.87	80.23	76.55	78.03	73.83	77.97	72.023	78.37	76.85	79.17	74.73

Solution From the given information, it is clear that the experiment was an asymmetrical (3 × 4) factorial CRD experiment; so the appropriate statistical model will be

$$y_{ijk} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + e_{ijk}$$

where $i = 1, 2$; $j = 1, 2$; and $k = 1, 2, \ldots..., 5$

y_{ijk} = response in kth observation due to the ith level of the first factor (i.e., bio-regulator) and the jth level of the second factor (i.e., media)

μ = general effect

α_i = additional effect due to ith level of the first factor (i.e., bio-regulator), $\sum \alpha_i = 0$

β_j = additional effect due to jth level of the second factor (i.e., media), $\sum \beta_j = 0$

$(\alpha\beta)_{ij}$ = interaction effect of the ith level of bio-regulator and jth level of media, $\sum_i (\alpha\beta)_{ij} = \sum_j (\alpha\beta)_{ij} = 0$

e_{ijk} = error component associated with the ith level of bio-regulator, the jth level of media, and the kth replication and $e_{ijk} \sim$ i.i.d. $N(0, \sigma^2)$

Hypothesis to be tested:

$H_{01} : \alpha_1 = \alpha_2 = \alpha_3 = 0$
$H_{02} : \beta_1 = \beta_2 = \beta_3 = \beta_4 = 0$
H_{03} : all interaction effects are equal to zero

against

H_{11} : all α's are not equal to zero
H_{12} : all β's are not equal to zero
H_{13} : all interaction effects are not equal to zero

Let the level of significance be $\alpha = 0.01$.

$$\text{Grand total } (GT) = 83.33 + 83.63 + \ldots\ldots\ldots + 74.13 + 74.73 = 2765.059$$

$$\text{Correction factor } (CF) = \frac{GT^2}{mnr} = \frac{2765.059^2}{3 \times 4 \times 3} = 212376.424$$

$$\text{Total sum of square } (SS_{\text{Tot}}) = 83.33^2 + 83.63^2 + \ldots\ldots\ldots + 74.13^2 + 74.73^2 - 212376.424 = 330.487$$

$$\text{Treatment sum of square } (SS_{\text{T}}) = \frac{250.49^2 + 229.71^2 + 238.09^2 + \ldots\ldots + 235.51^2 + 223.09^2}{3} - 212376.424 = 321.714$$

$$\text{Error sum of square } (SS_{Er.}) = SS_{\text{TOT}} - SS_T = 330.487 - 321.714 = 8.773$$

From the given information, let us construct the following table totals:

Medium	Bio-regulator			Total	Mean
	B1	B2	B3		
M1	250.49	231.69	233.61	715.79	79.53
M2	229.71	219.59	229.05	678.35	75.37
M3	238.09	233.21	235.51	706.81	78.53
M4	227.15	213.87	223.09	664.11	73.79
Total	945.44	898.36	921.26	2765.06	
Mean	78.79	74.86	76.77		

$$SS_{(\text{Bio})} = \frac{1}{3\times 4}\sum_{i=1}^{3} y_{i..}^2 - CF = \frac{945.44^2 + 898.36^2 + 921.26^2}{12} - 212376.424 = 92.38$$

$$SS_{(\text{Med})} = \frac{1}{3\times 3}\sum_{j=1}^{4} y_{.j.}^2 - CF = \frac{715.79^2 + 678.35^2 + 706.81^2 + 664.11^2}{9} - 212376.42 = 194.152$$

$$SS_{(BioxMed)} = \frac{1}{3}\sum_{i=1}^{3}\sum_{j=1}^{4} y_{ij.}^2 - CF - SS_{(Bio)} - SS_{(Med)} = 321.714 - 92.381 - 194.152 = 35.180$$

Now we make the following analysis of variance table with the help of the above quantities:

ANOVA					Table value of F
SOV	d.f.	SS	MS	Cal F	
Treatment	11	321.714	29.247	80.006	3.094
Bio-regulator	2	92.382	46.191	17.251	5.614
Media	3	194.152	64.717	185.128	4.718
Bio-regulator × media	6	35.180	5.863	4.615	3.667
Error	24	8.773	0.366		
Total	35	330.487			

As all the calculated values of F are greater than the corresponding table values of F, so it is clear from the above table that all the effects are significant at 1 % level of significance. Now the question is which bio-regulator, which media, and which combination of bio-regulator and media will result in maximum germination. To answer these we are to calculate the critical difference values for bio-regulator and media and their interaction effects separately using the following formulae:

$$CD_{0.01}\ (\text{bio-regulator}) = \sqrt{\frac{2MS_{Er}}{r.n}}\, t_{0.005,\,\text{err}.d.f} = \sqrt{\frac{2\times 0.366}{3\times 4}}\, 2.796 = 0.690$$

$$CD_{0.01}\ (\text{media}) = \sqrt{\frac{2MS_{Er}}{r.m}}\, t_{0.005,\,\text{err}.d.f} = \sqrt{\frac{2\times 0.366}{3\times 3}}\, 2.796 = 0.797$$

$$CD_{0.01}\ (\text{bio-regulator} \times \text{media}) = \sqrt{\frac{2MS_{Er}}{r}}\, t_{0.005,\,\text{err}.d.f} = \sqrt{\frac{2\times 0.366}{3}}\, 2.796 = 1.380$$

Our next task is to calculate the mean of all the effect to compare their difference with the calculated CD.

Bio Regulator	Mean	CD	
B1	78.787	**0.690**	
B3	76.772		
B2	74.863		
Media	**Mean**	**CD**	
M1	79.532	**0.797**	
M3	78.534		
M2	75.372		
M4	73.790		
Interaction	**Mean**	**CD**	
B1M1	83.497	**1.380**	
B1M3	79.363		
B3M3	78.503		
B3M1	77.870		
B2M3	77.737		
B2M1	77.230		
B1M2	76.570		
B3M2	76.350		
B1M4	75.717		
B3M4	74.363		
B2M2	73.197		
B2M4	71.290		*

* line joining the treatment means are statistically at par

Thus, from the above mean comparisons, it can be inferred that (i) among the three bio-regulators, B1, i.e., GA_3, is the best followed by thiourea and borax; (ii) among the four media, M1, i.e., soil, is significantly better than the other three media, followed by coco peat; and (iii) among the 12 bio-regulator and media combinations, the best germination could be with soil–GA_3 combination.

11.2.2.2 Two-Factor Asymmetrical ($m \times n$, $m \neq n$) Factorial RBD Experiment

Let us consider an $m \times n$ factorial experiment; that means an experiment with two factors A and B (say) having m and n levels, respectively, is conducted with r replications. So there would be $m \times n$ treatment combinations in each replication. Thus the model for the design can be presented as

$$y_{ijk} = \mu + \gamma_k + \alpha_i + \beta_j + (\alpha\beta)_{ij} + e_{ijk}$$

where $i = 1, 2, \ldots, m$; $j = 1, 2, \ldots, n$; and $k = 1, 2, \ldots, r$

y_{ijk} = response in kth observation due to ith level of the first factor A and jth level of the second factor B

μ = general effect

γ_k = additional effect due to kth replicate, $\sum \gamma_k = 0$

α_i = additional effect due to the ith level of the first factor A, $\sum \alpha_i = 0$

β_j = additional effect due to the jth level of the second factor B, $\sum \beta_j = 0$

$(\alpha\beta)_{ij}$ = interaction effect of the ith level of the first factor A and jth level of the second factor B, $\sum_i (\alpha\beta)_{ij} = \sum_j (\alpha\beta)_{ij} = 0$

e_{ijk} = error component associated with the ith level of the first factor, the jth level of the second factor in kth replicate, and $e_{ijk} \sim$ i.i.d. $N(0, \sigma^2)$

Randomization and Layout In total there will be an $m \times n$ number of treatments in each and every replication. That means we require to have an $m \times n$ number of experimental units per replication. The $m \times n$ numbers of treatments are to be allotted randomly as per the procedure discussed during the layout of RBD design in Chap. 10.8.1.

Hypothesis to be tested in $m \times n$ factorial RBD experiment:

$H_{01} : \alpha_1 = \alpha_2 = \ldots = \alpha_i = \ldots = \alpha_m = 0$

$H_{02} : \beta_1 = \beta_2 = \ldots = \beta_j = \ldots = \beta_n = 0$

$H_{03} : \gamma_1 = \gamma_2 = \ldots = \gamma_k = \ldots = \gamma_r = 0$

H_{04} : all $(\alpha\beta)_{ij}$s are equal

against the alternative hypotheses

H_{11} : all α's are not equal

H_{12} : all β's are not equal

H_{13} : all γ's are not equal

H_{14} : all $(\alpha\beta)'$s are not equal

Let the level of significance be 0.05.

Analysis The following table gives the plot-wise information recorded on response variable y_{ijk} s:

B / A	R1				R2				.....	Rr			
	B_1	B_2	…B_j …	B_n	B_1	B_2	…B_j…	B_n		B_1	B_2	…B_j…	B_n
A_1	y_{111}	y_{121}	y_{1j1}	y_{1n1}	y_{112}	y_{122}	y_{1j2}	y_{1n2}		y_{11r}	y_{12r}	y_{1jr}	y_{1nr}
A_2	y_{211}	y_{221}	y_{2j1}	y_{2n1}	y_{212}	y_{222}	y_{2j2}	y_{2n2}		y_{21r}	y_{22r}	y_{2jr}	y_{2nr}
. . .	. . .	. . .	....						.....				
A_i	y_{i11}	y_{i21}	y_{ij1}	y_{in1}	y_{i12}	y_{i22}	y_{ij2}	y_{in2}		y_{i1r}	y_{i2r}	y_{ijr}	y_{inr}
:	:	:	:										
:	:	:	:						.....				
A_m	y_{m11}	y_{m21}	y_{mj1}	y_{mn1}	y_{m12}	y_{m22}	y_{mj2}	y_{mn2}		y_{m1r}	y_{m2r}	y_{mjr}	y_{mnr}

We calculate the following quantities from the table:

$$\text{Grand total } (G) = \sum_{i=1}^{m}\sum_{j=1}^{n}\sum_{k=1}^{r} y_{ijk}$$

$$\text{Correction factor } (CF) = \frac{G^2}{mnr}.$$

$$SS_{\text{Tot}} = \sum_{i=1}^{m}\sum_{j=1}^{n}\sum_{k=1}^{r} y_{ijk}^2 - CF.$$

$$SS_R = \frac{1}{mn}\sum_{k=1}^{r} y_{..k}^2 - CF \text{ where, } y_{..k} = \sum_{i}^{m}\sum_{j}^{n} y_{ijk}$$

$= k$th replication total.

Let us make the following table for calculating other sums of squares.

Table of treatment totals:

	B_1	B_2	….. ….. B_j. ….. …..	B_n	Total
A_1	$\sum_{k=1}^{r} y_{11k}$	$\sum_{k=1}^{r} y_{12k}$	$\sum_{k=1}^{r} y_{1jk}$	$\sum_{k=1}^{r} y_{1nk}$	$y_{1..}$
A_2	$\sum_{k=1}^{r} y_{21k}$	$\sum_{k=1}^{r} y_{22k}$	$\sum_{k=1}^{r} y_{2jk}$	$\sum_{k=1}^{r} y_{2nk}$	$y_{2..}$
....	....	....	....	....	....
A_i	$\sum_{k=1}^{r} y_{i1k}$	$\sum_{k=1}^{r} y_{i2k}$	$\sum_{k=1}^{r} y_{2jk}$	$\sum_{k=1}^{r} y_{2nk}$	$y_{i..}$
....	....	....	....	....	....
A_m	$\sum_{k=1}^{r} y_{m1k}$	$\sum_{k=1}^{r} y_{m2k}$	$\sum_{k=1}^{r} y_{mjk}$	$\sum_{k=1}^{r} y_{mnk}$	$y_{m..}$
Total	$y_{.1.}$	$y_{.2.}$	$y_{.j.}$	$y_{.n.}$	$y_{...}$

$$SS_{Tr} = \frac{1}{r}\sum_{i=1}^{m}\sum_{j=1}^{n} y_{ij.}^2 - CF, \text{ where } y_{ij.} = \sum_{k=1}^{r} y_{ijk}.$$

$$SS_{Er} = TSS - RSS - TrSS.$$

$$SS_{(A)} = \frac{1}{nr}\sum_{i=1}^{m} y_{i..}^2 - CF.$$

$$SS_{(B)} = \frac{1}{mr}\sum_{j=1}^{n} y_{j.}^2 - CF.$$

$$SS_{(AB)} = SS_{Tr} - SS_{(A)} - SS_{(B)}.$$

Analysis of Variance The structure of analysis of variance table is as follows:

SOV	d.f.	*SS*	*MS*	*F*
Replication	$r-1$	SS_R	$MS_R = SS_R/(r-1)$	MS_R/MS_{Er}
Factor A	$m-1$	$SS_{(A)}$	$MS_{(A)} = SS_{(A)}/(m-1)$	$MS_{(A)}/MS_{Er}$
Factor B	$n-1$	$SS_{(B)}$	$MS_{(B)} = SS_{(B)}/(n-1)$	$MS_{(B)}/MS_{Er}$
Interaction (A × B)	$(m-1)(n-1)$	$SS_{(AB)}$	$MS_{(AB)} = SS_{(AB)}/(m-1)(n-1)$	$MS_{(AB)}/MS_{Er}$
Error	$(r-1)(mn-1)$	SS_{Er}	$MS_{Er} = SS_{Er}/(r-1)(mn-1)$	
Total	$mnr-1$	SS_{Tot}		

The hypothesis with respect to the replication, main effect of A, main effect of B, and interaction effect of A and B will be rejected at the α level of significance if the $\text{Cal F} > \text{F}_{\alpha;(r-1),(r-1)(mn-1)}$, $\text{Cal } F > F_{\alpha;(m-1),(r-1)(mn-1)}$, $\text{Cal } F > F_{\alpha;(n-1),(r-1)(mn-1)}$, $\text{Cal } F > F_{\alpha;(m-1)(n-1),(r-1)(mn-1)}$, respectively; otherwise, the corresponding null hypothesis cannot be rejected. In the event of rejection of the null hypothesis, the best level corresponding to the main or interaction effect is to be worked out using the respective LSD/CD formula as given below:

$$LSD/CD(\alpha)_R = \sqrt{\frac{2MS_{Er}}{mn}}\, t_{\alpha/2,\text{error d.f.}} \text{ for replication}$$

$$LSD/CD(\alpha)_A = \sqrt{\frac{2MS_{Er}}{nr}}\, t_{\alpha/2,\text{error d.f.}} \text{ for factor A}$$

$$LSD/CD(\alpha)_B = \sqrt{\frac{2MS_{Er}}{mr}}\, t_{\alpha/2,\text{error d.f.}} \text{ for factor B}$$

$$LSD/CD(\alpha)_{AB} = \sqrt{\frac{2MS_{Er}}{r}}\, t_{\alpha/2,\text{error d.f.}} \text{ for interaction of factors A and B}$$

The best levels of the main effect or interaction effect are worked out by comparing the treatment mean difference with respective LSD/CD values. If the difference between any pair of level means is more than corresponding LSD/CD values, then these two levels under comparison are declared significantly different, and the best level is selected on the basis of the mean of the levels under comparison. On the other hand, if the difference between any pair of level means is equal to or less than the corresponding LSD/CD value, then these two levels under comparison are declared statistically at par.

Example 11.6 (Two-Factor Asymmetrical Factorial RBD)
An experiment was conducted in order to investigate four feeds (F) and a vitamin (V) supplement at three levels on milk yield. The following table gives the information conducted in three replications in a randomized block design. Analyze the data and draw your conclusion:

	R1			R2			R3		
Feed	V1	V2	V3	V1	V2	V3	V1	V2	V3
F1	25	26	28	24	27	27	25	28	29
F2	22	23	25	22	24	26	23	23	26
F3	25	26	27	26	27	29	25	26	28
F4	28	30	31	27	29	30	28	30	31

Solution From the given information, it is clear that the experiment is an asymmetrical (4 × 3) factorial experiment conducted in randomized block design, so the appropriate statistical model for the analysis will be

$$y_{ijk} = \mu + \alpha_i + \beta_j + \gamma_k + (\alpha\beta)_{ij} + e_{ijk}$$

where $i = 1, 2, 3,4$; $j = 1, 2,3$; and $k = 1, 2, 3$

y_{ijk} = response in kth replicate due to ith level of the first factor (feed) and jth level of the second factor (vitamin)

μ = general effect

α_i = additional effect due to the ith level of the first factor (feed), $\sum \alpha_i = 0$

β_j = additional effect due to the jth level of the second factor (vitamin), $\sum \beta_j = 0$

γ_k = additional effect due to kth replicate, $\sum \gamma_k = 0$

$(\alpha\beta)_{ij}$ = interaction effect of the ith level of the first factor (feed) and jth level of the second factor (vitamin), $\sum_i (\alpha\beta)_{ij} = \sum_j (\alpha\beta)_{ij} = 0$

e_{ijk} = error component associated with the ith level of the first factor (feed), the jth level of the second factor (vitamin), and kth replicates and $e_{ijk} \sim N(0, \sigma^2)$

Hypothesis to be tested:

$H_0 : \alpha_1 = \alpha_2 = \alpha_3 = \alpha_4 = 0$
$\beta_1 = \beta_2 = \beta_3 = 0$
$\gamma_1 = \gamma_2 = \gamma_3 = 0$
$All (\alpha\beta)_{ij}{}'s$ are equal

against

α's are not all equal
β_j's are not all equal
γ's are not all equal
$All (\alpha\beta)_{ij}{}'s$ are not equal

Let the level of significance be 0.05.

From the given data table, let us calculate the following quantities:

$$GT = \sum_{i=1}^{4}\sum_{j=1}^{3}\sum_{k=1}^{3} y_{ijk} = 956$$

$$\text{Correction factor } (CF) = \frac{GT^2}{4 \times 3 \times 3} = \frac{956^2}{36} = 25387.111$$

$$SS_{\text{TOT}} = \sum_{i=1}^{4}\sum_{j=1}^{3}\sum_{k=1}^{3} y_{ijk}^2 - CF = 25598 - 25387.111 = 210.888$$

$$SS_R = \frac{1}{f \times v}\sum_{k=1}^{3} y_{ijk}^2 - CF = \frac{316^2 + 318^2 + 322^2}{12} - 25387.111 = 1.555$$

Table of totals:

	Vitamin supplements				
Feed	V1	V2	V3	Total	Average
F1	74	81	84	239	79.67
F2	67	70	77	214	71.33
F3	76	79	84	239	79.67
F4	83	89	92	264	88.00
Total	300	319	337		
Average	75.00	79.75	84.25		

From the above table, first let us form the following table and from the table get the following quantities:

$$SS_{Tr} = \frac{1}{3}\sum_{i=1}^{4}\sum_{j=1}^{3} y_{ijo}^2 - CF = \frac{74^2 + 67^2 + 76^2 + \ldots\ldots\ldots + 84^2 + 92^2}{3} - 25387.111 = 198.888$$

$$SS_{Er} = SS_{\text{TOT}} - SS_{Tr} - SS_R = 210.888 - 198.888 - 1.555 = 10.444$$

$$\text{SS}_{\text{Feed}} = \frac{1}{3 \times 3}\sum_{i=1}^{4} y_{ioo}^2 - CF = \frac{239^2 + 214^2 + 239^2 + 264^2}{9} - 25387.1111 = 138.888$$

$$SS_{\text{Vit}} = \frac{1}{4 \times 3}\sum_{j=1}^{3} y_{ojo}^2 - CF = \frac{300^2 + 319^2 + 337^2}{12} - 25387.111 = 57.055$$

$$SS_{(FV)} = SS_{Tr} - SS_{(Feed)} - SS_{(Vit)} = 198.888 - 138.888 - 57.055 = 2.944$$

Now we make the following analysis of variance table with the help of the above quantities:

ANOVA SOV	d.f.	*MS*	*MS*	F ratio	Table value of F	
Replication	3−1 = 2	1.556	0.778	1.638	$F_{0.05;2,22}$ =3.44	$F_{0.01;2,22} = 5.72$
Treatment	12−1 = 11	198.889	18.081	38.085	$F_{0.05;11,22} = 2.27$	$F_{0.01;11,22} = 3.19$
Feed (F)	4−1 = 3	138.889	46.296	97.518	$F_{0.05;3,22} = 3.05$	$F_{0.01;3,22} = 4.82$
Vitamin (V)	3−1 = 2	57.056	28.528	60.090	$F_{0.05;2,22} = 3.44$	$F_{0.01;2,22} = 5.72$
F×V	3 × 2 = 6	2.944	0.491	1.034	$F_{0.05;6,22} = 2.55$	$F_{0.01;6,22} = 3.76$
Error	35−2−11 = 22	10.444	0.475			
Total	36−1 = 35	210.889				

It is clear from the above table that all the effects of feed as well as the vitamin are significant at 1 % level of significance. But the interaction effects of feed and vitamin are not significant even at 5 % (desired level of significance) level of significance.

Now the question is which feed and which level of vitamin have maximum milking potentiality. To answer these we are to calculate the critical difference values for feed and vitamin effects separately using the following formulae:

$$\mathrm{CD}_{0.01\ (\mathrm{Feed})} = \sqrt{\frac{2ErMS}{\mathrm{r} \times \mathrm{v}}} t_{0.005,\mathrm{err}.d.f}$$

$$= \sqrt{\frac{2 \times 0.475}{3 \times 3}} 2.819 = 0.915$$

$$\mathrm{CD}_{0.01\ (\mathrm{Vitamin})} = \sqrt{\frac{2ErMS}{\mathrm{r} \times \mathrm{f}}} t_{0.005,\mathrm{err}.d.f}$$

$$= \sqrt{\frac{2 \times 0.475}{3 \times 4}} \times 2.819 = 0.792$$

Feed	Average Milk (liter)
F4	88.00
F1	79.67
F3	79.67
F2	71.33
Vitamin	Average milk yield(*l*)
V3	84.25
V2	79.75
V1	75.00

It is clear from the above table that feed at level F4 has recorded significantly the highest milking capacity compared to other feeds. The difference of means between F1 and F3 is zero, i.e., not greater than the critical difference value; they are statistically at par. On the other hand, the vitamin at level V3 is the best for getting maximum milk followed by V2 and V1. So far as the interaction effect of feed and vitamin is concerned, no significant difference is recorded among the different treatment combinations.

11.3 Three-Factor Factorial Experiments

11.3.1 2^3 Factorial Experiment

As the name suggests, three-factor factorial experiments are having three factors, each having different or the same levels. The most initial three-factor factorial experiment is comprised of three factors each of two levels, i.e., 2^3 factorial experiment. In a 2^3 factorial experiment with three factors A, B, and C each having two levels, viz., A_1, A_2; B_1, B_2; and C_1, C_2, respectively, the total number of treatment combinations will be 8, i.e., $A_1B_1C_1$, $A_1B_1C_2$, $A_1B_2C_1$, $A_1B_2C_2$, $A_2B_1C_1$, $A_2B_2C_1$, $A_2B_1C_2$, and $A_2B_2C_2$:

	C_1		C_2	
	B_1	B_2	B_1	B_2
A_1	$A_1B_1C_1$	$A_1B_2C_1$	$A_1B_1C_2$	$A_1B_2C_2$
A_2	$A_2B_1C_1$	$A_2B_2C_1$	$A_2B_1C_2$	$A_2B_2C_2$

Each of treatment combinations would be repeated k number of times. Again these eight treatment combinations can be put under

experimentation in basic CRD/RBD/LSD design depending upon the situation and requirement of the experimentation. As usual when blocking is not required or possible in that case, factorial CRD is to be conducted. If filed experiment is conducted and blocking is essential, then either factorial RBD or factorial LSD with eight treatment combinations is to be conducted. The layout will follow the identical procedure as discussed for the layout of basic CRD/RBD/LSD in Chap. 10 with these eight treatment combinations. However, during analysis partitioning of the total variance is to be taken up as per the statistical model concerned.

11.3.1.1 2^3 Factorial CRD Experiment

The data set for 2^3 factorial CRD experiment with n observations per treatment would be as follows:

C_1				C_2			
B_1		B_2		B_1		B_2	
A_1	A_2	A_1	A_2	A_1	A_2	A_1	A_2
y_{1111}	y_{2111}	y_{1211}	y_{2211}	y_{1121}	y_{2121}	y_{1221}	y_{2221}
y_{1112}	y_{2112}	y_{1212}	y_{2212}	y_{1122}	y_{2122}	y_{1222}	y_{2222}
y_{1113}	y_{2113}	y_{1213}	y_{2213}	y_{1123}	y_{2123}	y_{1223}	y_{2223}
:	:	:	:	:	:	:	:
:	:	:	:	:	:	:	:
y_{111n}	y_{211n}	y_{121n}	y_{221n}	y_{112n}	y_{212n}	y_{122n}	y_{222n}

The statistical model and analyses of the variance for the above 2^3 factorial experiment in CRD are discussed in the following section.

Model for 2^3 Factorial CRD Experiment

$$y_{ijkl} = \mu + \alpha_i + \beta_j + \gamma_k + (\alpha\beta)_{ij} + (\alpha\gamma)_{ik} + (\beta\gamma)_{jk} + (\alpha\beta\gamma)_{ijk} + \delta_l + e_{ijkl}$$

where $i = 1, 2$; $j = 1, 2$; and $k = 1, 2$; $l = 1, 2, 3, \ldots, n$

y_{ijkl} = response in lth observation due to the ith level of the first factor A and the jth level of the second factor B and kth level of the third factor C

μ = general effect

α_i = additional effect due to the ith level of the first factor A, $\sum \alpha_i = 0$

β_j = additional effect due to the jth level of second factor B, $\sum \beta_j = 0$.

γ_k = additional effect due to the kth level of the third factor C, $\sum \gamma_k = 0$

$(\alpha\beta)_{ij}$ = interaction effect of the ith level of the first factor A and jth level of the second factor B, $\sum_i (\alpha\beta)_{ij} = \sum_j (\alpha\beta)_{ij} = 0$

$(\alpha\gamma)_{ik}$ = interaction effect of the ith level of the first factor A and kth level of the third factor C, $\sum_i (\alpha\gamma)_{ik} = \sum_k (\alpha\gamma)_{ik} = 0$

$(\beta\gamma)_{jk}$ = interaction effect of the jth level of the second factor B and kth level of the third factor C, $\sum_j (\beta\gamma)_{jk} = \sum_k (\beta\gamma)_{jk} = 0$

$(\alpha\beta\gamma)_{ijk}$ = interaction effect of the ith level of the first factor A, jth level of the second factor B, and kth level of the third factor C, $\sum_i (\alpha\beta\gamma)_{ijk} = \sum_j (\alpha\beta\gamma)_{ijk} = \sum_k (\alpha\beta\gamma)_{ijk} = 0$

e_{ijkl} = error component associated with lth observation due to ith level of the first factor A and jth level of the second factor B and kth level of the third factor C and $e_{ijkl} \sim$ i.i.d. $N(0, \sigma^2)$

Hypothesis to be tested:

H_{01} : $\alpha_1 = \alpha_2$ against H_{11} : $\alpha_1 \neq \alpha_2$

H_{02} : $\beta_1 = \beta_2$ against H_{12} : $\beta_1 \neq \beta_2$

H_{03} : $\gamma_1 = \gamma_2$ against H_{13} : $\gamma_1 \neq \gamma_2$

H_{04} : $\alpha_1\beta_1 = \alpha_1\beta_2 = \alpha_2\beta_1 = \alpha_2\beta_2$ against H_{14}; all $(\alpha\beta)_{ij}$'s are not equal

H_{05} : $\alpha_1\gamma_1 = \alpha_1\gamma_2 = \alpha_2\gamma_1 = \alpha_2\gamma_2$ against H_{15}; all $(\alpha\gamma)_{ik}$'s are not equal

H_{06} : $\beta_1\gamma_1 = \beta_1\gamma_2 = \beta_2\gamma_1 = \beta_2\gamma_2$ against H_{16}; all $(\beta\gamma)_{jk}$'s are not equal

H_{07} : all $(\alpha\beta\gamma)_{ijk}$'s are equal against H_{17}; all $(\alpha\beta\gamma)_{ijk}$'s are not equal

Let the level of significance be α.

Now we calculate the following quantities:

$$G = \sum_{i,j,k,l} y_{ijkl} \text{ and } CF = \frac{G^2}{2^3 n}$$

$$SS_{\text{Tot}} = \sum_{i,j,k,l} y_{ijkl}^2 - CF$$

$$SS_{Er} = SS_{\text{Tot}} - SS_{(A)} - SS_{(B)} - SS_{(AB)} - SS_{(C)} - SS_{(AC)} - SS_{(BC)} - SS_{(ABC)}$$

The first-order interaction sum of squares is worked out from the two-way table of totals of the factors involved, and the third-way interaction effects are worked out by framing three-way table of all the eight treatment combinations totaled over n observations.

Table of two-way interaction totals A and B:

	B1	B2	Total (T_{Ai})
A1	A1B1	A1B2	$\sum_{j,k,l} A_{1...}$
A2	A2B1	A2B2	$\sum_{j,k,l} A_{1...}$
Total (T_{Bj})	$\sum_{i,k,l} B_{.1..}$	$\sum_{i,k,l} B_{.2..}$	

AiBjs are totals of 2n observations in which AiBj has occurred:

$$SS_{(A)} = \frac{\sum_{i} (T_{Ai})^2}{2 \times 2 \times n} - CF,$$

$$SS_{(B)} = \frac{\sum_{j} (T_{Bj})^2}{2 \times 2 \times n} - CF, \text{ and}$$

$$SS_{(AB)} = \frac{\sum_{\text{i}} \sum_{j} (A_i B_j)^2}{2n} - CF$$

Table of two-way interaction totals A and C:

	C1	C2	Total (T_{Ai})
A1	A1C1	A1C2	$\sum_{j,k,l} A_{1...}$
A2	A2C1	A2C2	$\sum_{j,k,l} A_{2...}$
Total (T_{Ck})	$\sum_{i,j,l} C_{..1.}$	$\sum_{i,j,l} C_{..2.}$	

AiCk's are totals of 2n observations in which AiCk has occurred:

$$SS_{(C)} = \frac{\sum_{k} (T_{Ck})^2}{2 \times 2 \times n} - CF \text{ and}$$

$$SS_{(AC)} = \frac{\sum_{\text{i}} \sum_{j} (A_i C_k)^2}{2n} - CF$$

Table of two-way interaction totals B and C:

	B1	B2	Total (T_{Ck})
C1	C1B1	C1B2	$\sum_{i,j,l} C_{..1.}$
C2	C2B1	C2B2	$\sum_{i,j,l} C_{..2.}$
Total (T_{Bj})	$\sum_{i,k,l} B_{.1..}$	$\sum_{i,k,l} B_{.2..}$	

BjCk's are totals of 2n observations in which BjCk has occurred:

$$SS_{(BC)} = \frac{\sum_{\text{i}} \sum_{j} (B_j C_k)^2}{2n} - CF$$

Table of three-way interaction totals:

Treatment combinations	R1	R2.....	Rn	Treatment total (T_m; $m = 1, 2, \ldots, 8$)
$A_1B_1C_1$	$A_1B_1C_1R1$	$A_1B_1C_1R2$.....	$A_1B_1C_1Rk$	$\sum_{l=1}^{n} (A_1B_1C_1)_l$
$A_1B_1C_2$	$A_1B_1C_2R1$	$A_1B_1C_2R2$.....	$A_1B_1C_2Rk$	$\sum_{l=1}^{n} (A_1B_1C_2)_l$
$A_1B_2C_1$	$A_1B_2C_1R1$	$A_1B_2C_1R2$.....	$A_1B_2C_1Rk$	$\sum_{l=1}^{n} (A_1B_2C_1)_l$
$A_1B_2C_2$	$A_1B_2C_2R1$	$A_1B_2C_2R2$.....	$A_1B_2C_2Rk$	$\sum_{l=1}^{n} (A_1B_2C_2)_l$
$A_2B_1C_1$	$A_2B_1C_1R1$	$A_2B_1C_1R2$.....	$A_2B_1C_1Rk$	$\sum_{l=1}^{n} (A_2B_1C_1)_l$
$A_2B_1C_2$	$A_2B_1C_2R1$	$A_2B_1C_2R2$.....	$A_2B_1C_2Rk$	$\sum_{l=1}^{n} (A_2B_1C_2)_l$
$A_2B_2C_1$	$A_2B_2C_1R1$	$A_2B_2C_1R2$.....	$A_2B_2C_1Rk$	$\sum_{l=1}^{n} (A_2B_2C_1)_l$
$A_2B_2C_2$	$A_2B_2C_2R1$	$A_2B_2C_2R2$.....	$A_2B_2C_2Rk$	$\sum_{l=1}^{n} (A_2B_2C_2)_l$

$$SS_{(ABC)} = \frac{\sum_{m=1}^{8} T_m^2}{n} - CF$$

The structure of the analysis of variance for 2^3 factorial experiment in a randomized complete design is given as follows:

SOV	d.f.	SS	MS	Cal F
A	1	$SS_{(A)}$	$MS_{(A)} = SS_{(A)}/1$	$MS_{(A)}/MS_{Er}$
B	1	$SS_{(B)}$	$MS_{(B)} = SS_{(B)}/1$	$MS_{(B)}/MS_{Er}$
AB	1	$SS_{(AB)}$	$MS_{(AB)} = SS_{(AB)}/1$	$MS_{(AB)}/MS_{Er}$
C	1	$SS_{(C)}$	$MS_{(C)} = SS_{(C)}/1$	$MS_{(C)}/MS_{Er}$
AC	1	$SS_{(AC)}$	$MS_{(AC)} = SS_{(AC)}/1$	$MS_{(AC)}/MS_{Er}$
BC	1	$SS_{(BC)}$	$MS_{(BC)} = SS_{(BC)}/1$	$MS_{(BC)}/MS_{Er}$
ABC	1	$SS_{(ABC)}$	$MS_{(ABC)} = SS_{(ABC)}/1$	$MS_{(ABC)}/MS_{Er}$
Error	$(n-1)(2^3-1)$	SS_{Er}	$MS_{Er} = SS_{Er}/(n-1)(2^3-1)$	
Total	$2^3.n-1$	SS_{Tot}		

If calculated value of F for any effect be greater than the corresponding tabulated value of F at α level of significance and specific degrees of freedom, then the corresponding factorial effect is significant, and the respective null hypothesis of equality is rejected; otherwise the test is nonsignificant and the respective null hypothesis cannot be rejected. In the event of significance of any one of the seven F tests, we are to follow as given below:

1. If any one of the three F tests corresponds to main effects of three factors, the higher mean value corresponding to the level of the factor is declared the best level for that particular factor.
2. For first-order interactions (i.e., $(\alpha\beta)_{ij}$ or $(\alpha\gamma)_{ik}$or$(\beta\gamma)_{jk}$), we are to calculate the LSD/CD value as follows:

$$LSD/CD(\alpha) \text{ for A/B/C} = \sqrt{\frac{2\text{MSE}}{2 \times \text{n}}} t_{\alpha/2;\text{err } d.f.}$$

   If the difference between means of any pair of treatment combination be greater than the corresponding CD value, then these two means under comparison are declared significantly different from each other, and the treatment combination having better value is treated as the better one.
3. If the F test corresponding to second-order interactions (i.e., $(\alpha\beta\gamma)_{ijk}$) be significant, we are to calculate the LSD/CD value as follows:

$$LSD/CD(\alpha) = \sqrt{\frac{2\text{MSE}}{\text{n}}} t_{\alpha/2;\text{err } d.f.}$$

   If the difference between means of any pair of treatment combination be greater than the corresponding CD value, then these two means under comparison are declared significantly different from each other, and the treatment combination having better value is treated as the better one.

Example 11.7 (2^3 Three-Factor Symmetrical Factorial CRD)

A laboratory experiment was conducted to find out the change in reducing sugar (RS) content of guava jelly bar made from two varieties kept in two different packing materials under two different temperatures for 45 days. The following table gives the RS under different treatment combinations. Analyze the data to find out the best variety, best packing material, best temperature, and best interaction effects among the factors to maintain the RS content in guava:

Variety	V1				V2			
Packing material	P1		P2		P1		P2	
Temperature	T1	T2	T1	T2	T1	T2	T1	T2
	26.35	27.29	26.82	27.87	27.43	27.82	28.32	29.21
	26.43	27.41	26.92	27.91	27.53	27.88	28.36	29.29
	26.49	27.41	26.88	27.99	27.57	27.94	28.46	29.35

Solution From the given information, it is clear that the experiment is a three-factorial (2^3) CRD experiment each factor with two levels and three repetitions, so the appropriate statistical model for the analysis will be

$$y_{ijkl} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + \gamma_k + (\alpha\gamma)_{ik} + (\beta\gamma)_{jk} + (\alpha\beta\gamma)_{ijk} + e_{ijkl}$$

where $i = 1, 2$; $j = 1, 2$; $k = 1, 2$; and $l = 1,2,3$

y_{ijkl} = response in lth observation due to the ith level of the first factor (i.e., variety), jth level of the second factor (i.e., packing material), and kth level of the third factor (i.e., temperature)

μ = general effect

α_i = additional effect due to ith level of the first factor (i.e., variety), $\sum \alpha_i = 0$

β_j = additional effect due to jth level of the second factor (i.e., packing material), $\sum \beta_j = 0$

γ_k = additional effect due to kth level of the third factor (i.e., temperature) $\sum \gamma_k = 0$

$(\alpha\beta)_{ij}$ = interaction effect of the ith variety and jth packing material, $\sum_i (\alpha\beta)_{ij} = \sum_j (\alpha\beta)_{ij} = 0$

$(\alpha\gamma)_{ik}$ = interaction effect of the ith variety and kth temperature, $\sum_i (\alpha\gamma)_{ik} = \sum_k (\alpha\gamma)_{ik} = 0$

$(\beta\gamma)_{jk}$ = interaction effect of the jth packing material and kth level of temperature, $\sum_j (\beta\gamma)_{jk} = \sum_k (\beta\gamma)_{jk} = 0$

$(\alpha\beta\gamma)_{ijk}$ = interaction effect of the ith variety, jth packing material, and kth temperature, $\sum_i (\alpha\beta\gamma)_{ijk} = \sum_j (\alpha\beta\gamma)_{ijk} = \sum_k (\alpha\beta\gamma)_{ijk} = 0$

e_{ijkl} = error component associated with lth observation of ith variety, jth packing material, and kth temperature and $e_{ijkl} \sim$ i.i.d. N(0, σ^2)

Hypothesis to be tested:

$H_{01} : \alpha_1 = \alpha_2 = 0$
$H_{02} : \beta_1 = \beta_2 = 0$
$H_{03} : \gamma_1 = \gamma_2 = 0$
H_{04} : all $(\alpha\beta)_{ij}$ are equal to zero
H_{05} : all $(\alpha\gamma)_{ik}$ are equal to zero
H_{06} : all $(\beta\gamma)_{jk}$ are equal to zero
H_{06} : all $(\alpha\beta\gamma)_{ijk}$ are equal to zero

against

H_{11} : all α's are not equal to zero
H_{12} : all β's are not equal to zero
H_{13} : all γ's are not equal to zero
H_{14} : all $(\alpha\beta)_{ij}$ are not equal to zero
H_{15} : all $(\alpha\gamma)_{ik}$ are not equal to zero
H_{16} : all $(\beta\gamma)_{jk}$ are not equal to zero
H_{17} : all $(\alpha\beta\gamma)_{ijk}$ are not equal to zero

Let the level of significance be $\alpha = 0.01$.

From the given table, let us calculate the following quantities:

$$\text{Grand total } (GT) = 26.35 + 26.43 + \ldots\ldots\ldots + 29.29 + 29.35 = 664.93$$

$$\text{Correction factor } (CF) = \frac{GT^2}{mnpr} = \frac{664.93^2}{2 \times 2 \times 2 \times 3} = 18422.162$$

$$\text{Total sum of squares } (SS_{\text{Tot}}) = 26.35^2 + 26.43^2 + \ldots\ldots\ldots + 29.29^2 + 29.35^2 - 18422.162 = 16.598$$

$$\text{Treatment sum of squares } (SS_{\text{T}}) = \frac{79.27^2 + 82.11^2 + \ldots\ldots\ldots\ldots + 85.14^2 + 87.85^2}{3} - 18422.1627 = 16.528$$

$$\text{Error sum of squares } (SS_{Er.}) = SS_{\text{Tot}} - SS_{\text{T}} = 16.598 - 16.528 = 0.070$$

From the given data, let us construct the following tables of totals and from the tables get the following quantities:

Packing material	Variety		Total	Mean
	V1	V2		
P1	161.38	166.17	327.55	27.30
P2	164.39	172.99	337.38	28.12
Total	325.77	339.16		
Mean	27.15	28.26		

$$SS_{(\text{Var})} = \frac{1}{npr}\sum_{i=1}^{2} y_{i...}^2 - CF = \frac{325.77^2 + 339.16^2}{12} - 18422.1627 = 7.470$$

$$SS_{(\text{PM})} = \frac{1}{mpr}\sum_{j=1}^{2} y_{.j..}^2 - CF = \frac{327.55^2 + 337.38^2}{12} - 18422.1627 = 4.026$$

$$SS_{(\text{Var} \times \text{PM})} = \frac{1}{pr}\sum_{i=1}^{2}\sum_{j=1}^{2} y_{ij..}^2 - CF - SS_{\text{Var}} - SS_{\text{PM}} = \frac{161.38^2 + 164.39^2 + 166.17^2 + 172.99^2}{6} - 18422.162 - 7.470 - 4.026 = 0.604$$

	Packing material			
Temperature	P1	P2	Total	Mean
T1	161.8	165.76	327.56	27.30
T2	165.75	171.62	337.37	28.11
Total	327.55	337.38		
Mean	27.30	28.12		

$$SS_{(\text{Temp})} = \frac{1}{mnr}\sum_{j=1}^{2} y_{..k.}^2 - CF = \frac{327.56^2 + 337.37^2}{12} - 18422.162 = 4.009$$

$$SS_{(PM \times \text{Temp})} = \frac{1}{mr}\sum_{i=1}^{2}\sum_{k=1}^{2} y_{i.k.}^2 - CF - SS_{\text{PM}} - SS_{\text{Temp}} = \frac{161.8^2 + 165.76^2 + 165.75^2 + 171.62^2}{6} - 18422.162 - 7.470 - 4.009 = 0.1520$$

	Variety			
Temperature	V1	V2	Total	Mean
T1	159.89	167.67	327.56	27.30
T2	165.88	171.49	337.37	28.11
Total	325.77	339.16		
Mean	27.15	28.26		

$$SS_{(\text{Var}\times\text{Temp})} = \frac{1}{nr}\sum_{j=1}^{2}\sum_{\text{k}=1}^{2} y_{.jk.}^2 - CF - SS_{\text{Var}} - SS_{\text{Temp}} = \frac{159.89^2 + 165.88^2 + 167.67^2 + 171.49^2}{6} - 18422.162 - 7.470 - 4.009 = 0.1962$$

	V1		V2			
	P1	P2	P1	P2	Total	Mean
T1	79.27	80.62	82.53	85.14	327.56	27.30
T2	82.11	83.77	83.64	87.85	337.37	28.11
Total	161.38	164.39	166.17	172.99		
Mean	26.90	27.40	27.70	28.83		

$$SS_{(\text{Var}\times\text{PM}\times\text{Temp})} = \frac{1}{r}\sum_{i=1}^{2}\sum_{j=1}^{2}\sum_{k=1}^{2} y_{ijk.}^2 - CF - SS_{\text{Var}} - SS_{PM} - SS_{\text{Temp}} - SS_{\text{Var}\times\text{PM}} - SS_{\text{Var}\times\text{Temp}} - SS_{\text{PM}\times\text{Temp}} = \frac{79.27^2 + 82.11^2 + \ldots\ldots + 85.14^2 + 87.85^2}{3} - 18422.162 - 7.470 - 4.026 - 4.009 - 0.604 - 0.196 - 0.152 = 0.0693$$

ANOVA table					
SOV	d.f.	*SS*	*MS*	Cal F	Tab F at 1 %
Treatment	7	16.529	2.361	540.750	4.026
Variety	1	7.471	7.471	1710.802	8.531
Packing material	1	0.605	0.605	138.512	8.531
Var × PM	1	0.605	0.605	138.512	8.531
Temperature	1	4.010	4.010	918.283	8.531
Var × temp	1	0.196	0.196	44.932	8.531
PM × temp	1	0.152	0.152	34.810	8.531
Var × PM × temp	1	0.069	0.069	15.879	8.531
Error	16	0.070	0.004		
Total	23	16.599			

As all the calculated values of F are greater than the corresponding table values of F, so it is clear from the above table that all the effects are significant at 1 % level of significance. So our next task is to find out the best level of these effects. For the purpose we are to calculate the critical difference values for variety, packing

material, temperature, and interaction effects of different factors using the following formulae:

$$CD_{0.01}\ (\text{variety}) = \sqrt{\frac{2MS_{Er}}{r.np}}t_{0.005,\text{err}.d.f}$$
$$= \sqrt{\frac{2 \times 0.004}{3 \times 2 \times 2}}2.920 = 0.078$$

$$CD_{0.01}\ (\text{PM}) = \sqrt{\frac{2MS_{Er}}{r.mp}}t_{0.005,\text{err}.d.f}$$
$$= \sqrt{\frac{2 \times 0.004}{3 \times 2 \times 2}}2.920 = 0.078$$

$$CD_{0.01}\ (\text{var} \times \text{PM}) = \sqrt{\frac{2MS_{Er}}{rp}}t_{0.005,\text{err}.d.f}$$
$$= \sqrt{\frac{2 \times 0.004}{6}}2.920$$
$$= 0.111$$

$$CD_{0.01}\ (\text{temp}) = \sqrt{\frac{2MS_{Er}}{r.mn}}t_{0.005,\text{err}.d.f}$$
$$= \sqrt{\frac{2 \times 0.004}{3 \times 2 \times 2}}2.920 = 0.078$$

$$CD_{0.01}\ (\text{var} \times \text{temp}) = \sqrt{\frac{2MS_{Er}}{rn}}t_{0.005,\text{err}.d.f}$$
$$= \sqrt{\frac{2 \times 0.004}{6}}2.920$$
$$= 0.111$$

$$CD_{0.01}\ (\text{PM} \times \text{temp}) = \sqrt{\frac{2MS_{Er}}{rm}}t_{0.005,\text{err}.d.f}$$
$$= \sqrt{\frac{2 \times 0.004}{6}}2.920$$
$$= 0.111$$

$$CD_{0.01}\ (\text{var} \times \text{PM} \times \text{temp})$$
$$= \sqrt{\frac{2MS_{Er}}{r}}t_{0.005,\text{err}.d.f} = \sqrt{\frac{2 \times 0.004}{3}}2.920$$
$$= 0.157$$

Now let us make the mean tables for comparison.

Variety	Mean	CD	
V2	28.263	0.078	
V1	27.148		
Packing Material			
P2	28.115	0.078	
P1	27.296		
Var X PM			
V2P2	28.832	0.078	
V2P1	27.695		
V1P2	27.398		
V1P1	26.897		
Temperature			
T2	28.114	0.111	
T1	27.297		
PM X Temp			
P2T2	28.603	0.111	
P2T1	27.627		
P1T2	27.625		
P1T1	26.967		
Var X Temp			
V2T2	28.582	0.111	
V2T1	27.945		
V1T2	27.647		
V1T1	26.648		
Var X PM X Temp			
V2P2T2	29.283	0.157	
V2P2T1	28.380		
V1P2T2	27.923		
V2P1T2	27.880		
V2P1T1	27.510		
V1P1T2	27.370		
V1P2T1	26.873		
V1P1T1	26.423		

From the above tables after comparison of pairwise differences of means with corresponding CD values, one can conclude that (i) variety V2 is the best between the two varieties, (ii) packaging material 2 is the best in between the packaging materials, (iii)

temperature T2 is the best temperature in maintaining the reducing sugar in papaya bar, (iv) combinations of variety 2 and packaging material 2 are the best among four combinations, (v) similarly the combination of P2T2 and V2T2 is the best in maintaining reducing sugar, and (vi) combinations of variety 2, packaging material 2, and temperature 2 are the best combination to maintain reducing sugar in papaya jelly bar after 45 days of storing.

11.3.1.2 Model for 2^3 Factorial RBD Experiment

Let us suppose a 2^3 factorial experiment is conducted in an RBD with r blocks with three factors A, B, and C each at two levels. Then there would be eight treatment combinations $A_1B_1C_1$, $A_1B_1C_2$, $A_1B_2C_1$, $A_1B_2C_2$, $A_2B_1C_1$, $A_2B_2C_1$, $A_2B_1C_2$, and $A_2B_2C_2$, and the data structure for the same experiment would be as follows:

	C_1				C_2			
	B_1		B_2		B_1		B_2	
Replication	A_1	A_2	A_1	A_2	A_1	A_2	A_1	A_2
R1	y_{1111}	y_{2111}	y_{1211}	y_{2211}	y_{1121}	y_{2121}	y_{1221}	y_{2221}
R2	y_{1112}	y_{2112}	y_{1212}	y_{2212}	y_{1122}	y_{2122}	y_{1222}	y_{2222}
:	:	:	:	:	:	:	:	:
:	:	:	:	:	:	:	:	:
Rr	y_{111n}	y_{211n}	y_{121n}	y_{221n}	y_{112n}	y_{212n}	y_{122n}	y_{222n}

Corresponding model is given as follows:

$$y_{ijkl} = \mu + \alpha_i + \beta_j + \gamma_k + (\alpha\beta)_{ij} + (\alpha\gamma)_{ik} + (\beta\gamma)_{jk} + (\alpha\beta\gamma)_{ijk} + \delta_l + e_{ijkl}$$

where $i = 1, 2$; $j = 1, 2$; $k = 1, 2$; and $l = 1, 2, 3, \ldots, r$

y_{ijkl} = response in lth replicate due to ith level of the first factor A and jth level of the second factor B and kth level of the third factor C

μ = general effect

α_i = additional effect due to ith level of the first factor A, $\sum \alpha_i = 0$

β_j = additional effect due to jth level of the second factor B, $\sum \beta_j = 0$

γ_k = additional effect due to kth level of the third factor C, $\sum \gamma_k = 0$

$(\alpha\beta)_{ij}$ = interaction effect of the ith level of the first factor A and jth level of the second factor B, $\sum_i (\alpha\beta)_{ij} = \sum_j (\alpha\beta)_{ij} = 0$

$(\alpha\gamma)_{ik}$ = interaction effect of the ith level of the first factor A and kth level of the third factor C, $\sum_i (\alpha\gamma)_{ik} = \sum_k (\alpha\gamma)_{ik} = 0$

$(\beta\gamma)_{jk}$ = interaction effect of the jth level of the second factor B and kth level of the third factor C, $\sum_j (\beta\gamma)_{jk} = \sum_k (\beta\gamma)_{jk} = 0$

$(\alpha\beta\gamma)_{ijk}$ = interaction effect of the ith level of the first factor A, jth level of the second factor B, and kth level of the third factor C, $\sum_i (\alpha\beta\gamma)_{ijk} = \sum_j (\alpha\beta\gamma)_{ijk} = \sum_k (\alpha\beta\gamma)_{ijk} = 0$

δ_l = additional effect due to lth replication $\sum_l \delta_l = 0$

e_{ijkl} = error component associated with lth replicate due to ith level of the first factor A and jth level of the second factor B and kth level of the third factor C and $e_{ijkl} \sim$ i.i.d. $N(0, \sigma^2)$

Hypothesis to be tested:

H_{01} : $\delta_1 = \delta_2 = \ldots\ldots = \delta_l$ against $H_{11} : \delta_1 \neq \delta_2 \neq \ldots\ldots \neq \delta_l$

H_{02} : $\alpha_1 = \alpha_2$ against $H_{12} : \alpha_1 \neq \alpha_2$

H_{03} : $\beta_1 = \beta_2$ against $H_{13} : \beta_1 \neq \beta_2$

H_{04} : $\gamma_1 = \gamma_2$ against $H_{14} : \gamma_1 \neq \gamma_2$

H_{05} : $\alpha_1\beta_1 = \alpha_1\beta_2 = \alpha_2\beta_1 = \alpha_2\beta_2$ against H_{15}; all $(\alpha\beta)_{ij}{}'$s are not equal

H_{06} : $\alpha_1\gamma_1 = \alpha_1\gamma_2 = \alpha_2\gamma_1 = \alpha_2\gamma_2$ against H_{16}; all $(\alpha\gamma)_{ik}{}'$s are not equal

H_{07} : $\beta_1\gamma_1 = \beta_1\gamma_2 = \beta_2\gamma_1 = \beta_2\gamma_2$ against H_{17}; all $(\beta\gamma)_{jk}{}'$s are not equal

H_{08} : All $(\alpha\beta\gamma)_{ijk}{}'$s are equal against H_{18}; all $(\alpha\beta\gamma)_{ijk}{}'$s are not equal

Let the level of significance be α.

Now we calculate the following quantities:

$$G = \sum_{i,j,k,l} y_{ijkl} \text{ and } CF = \frac{G^2}{2^3 r}.$$

$$SS_{\text{Tot}} = \sum_{i,j,k,l} y_{ijkl}^2 - CF.$$

$SS_R = \sum_{l=1}^{r} \frac{R_l^2}{2^3} - CF$ where R_l is the total of all the observations in the lth block.

$SS_{Er} = SS_{\text{Tot}} - SS_{\text{R}} - SS_{(A)} - SS_{(B)} - SS_{(AB)} - SS_{(C)} - SS_{(AC)} - SS_{(BC)} - SS_{(ABC)}$.

The first-order interaction sums of squares are worked out from the two-way table of totals of the factors involved, and the third-way interaction effects are worked out by framing three-way table of all the eight treatment combinations totaled over r replications.

Table of two-way interaction totals (A and B):

	B_1	B_2	Total (T_{Ai})
A1	A1B1	A1B2	$\sum_{j,k,l} A_{1\ldots}$
A2	A2B1	A2B2	$\sum_{j,k,l} A_{2\ldots}$
Total (T_{Bj})	$\sum_{i,k,l} B_{.1..}$	$\sum_{i,k,l} B_{.2..}$	

AiBjs are totals of 2r observations in which AiBj has occurred:

$$SS_{(A)} = \frac{\sum_{i} (T_{Ai})^2}{2 \times 2 \times r} - CF,$$

$$SS_{(B)} = \frac{\sum_{j} (T_{Bj})^2}{2 \times 2 \times r} - CF, \text{ and}$$

$$SS_{(AB)} = \frac{\sum_{i} \sum_{j} (A_i B_j)^2}{2r} - CF$$

Table of two-way interaction totals (A and C):

	C_1	C_2	Total (T_{Ai})
A1	A1C1	A1C2	$\sum_{j,k,l} A_{1\ldots}$
A2	A2C1	A2C2	$\sum_{j,k,l} A_{2\ldots}$
Total (T_{Ck})	$\sum_{i,j,l} C_{..1.}$	$\sum_{i,j,l} C_{..2.}$	

AiCk's are totals of 2r observations in which AiCk has occurred:

$$SS_{(C)} = \frac{\sum_{k} (T_{Ck})^2}{2 \times 2 \times r} - CF \text{ and}$$

$$SS_{(AC)} = \frac{\sum_{\text{i}} \sum_{j} (A_i C_k)^2}{2r} - CF$$

Table of two-way interaction totals (B and C):

	B_1	B_2	Total (T_{Ck})
C1	C1B1	C1B2	$\sum_{i,j,l} C_{..1.}$
C2	C2B1	C2B2	$\sum_{i,j,l} C_{..2.}$
Total (T_{Bj})	$\sum_{i,k,l} B_{.1..}$	$\sum_{i,k,l} B_{.2..}$	

BjCk's are totals of 2r observations in which BjCk has occurred:

$$SS_{(BC)} = \frac{\sum_{i} \sum_{j} (B_j C_k)^2}{2r} - CF$$

Table of three-way interaction totals (A, B and C):

Treatment combinations	R1	R2.....	Rk	Treatment total (T_m; $m = 1, 2, \ldots, 8$)
$A_1B_1C_1$	$A_1B_1C_1R1$	$A_1B_1C_1R2$.....	$A_1B_1C_1Rk$	$\sum_{l=1}^{r} (\text{A1B1 C1})_l$
$A_1B_1C_2$	$A_1B_1C_2R1$	$A_1B_1C_2R2$.....	$A_1B_1C_2Rk$	$\sum_{l=1}^{r} (\text{A1B1C2})_l$
$A_1B_2C_1$	$A_1B_2C_1R1$	$A_1B_2C_1R2$.....	$A_1B_2C_1Rk$	$\sum_{l=1}^{r} (\text{A1B2 C1})_l$
$A_1B_2C_2$	$A_1B_2C_2R1$	$A_1B_2C_2R2$.....	$A_1B_2C_2Rk$	$\sum_{l=1}^{r} (\text{A1B2C2})_l$
$A_2B_1C_1$	$A_2B_1C_1R1$	$A_2B_1C_1R2$.....	$A_2B_1C_1Rk$	$\sum_{l=1}^{r} (\text{A2B1 C1})_l$
$A_2B_1C_2$	$A_2B_1C_2R1$	$A_2B_1C_2R2$.....	$A_2B_1C_2Rk$	$\sum_{l=1}^{r} (\text{A2B1 C2})_l$
$A_2B_2C_1$	$A_2B_2C_1R1$	$A_2B_2C_1R2$.....	$A_2B_2C_1Rk$	$\sum_{l=1}^{r} (\text{A2B2 C1})_l$
$A_2B_2C_2$	$A_2B_2C_2R1$	$A_2B_2C_2R2$.....	$A_2B_2C_2Rk$	$\sum_{l=1}^{r} (\text{A2B2 C2})_l$

$$SS_{(ABC)} = \frac{\sum_{m=1}^{8} T_m^2}{r} - CF$$

The structure of the analysis of variance for 2^3 factorial experiment in a randomized complete block design is given as follows:

SOV	d.f.	SS	MS	F
Replication	$r-1$	$SS_{(R)}$	$MS_R = SS_{(R)}/(r-1)$	MS_R/MS_{Er}
A	1	$SS_{(A)}$	$MS_{(A)} = SS_{(A)}/1$	$MS_{(A)}/MS_{Er}$
B	1	$SS_{(B)}$	$MS_{(B)} = SS_{(B)}/1$	$MS_{(B)}/MS_{Er}$
AB	1	$SS_{(AB)}$	$MS_{(AB)} = SS_{(AB)}/1$	$MS_{(AB)}/MS_{Er}$
C	1	$SS_{(C)}$	$MS_{(C)} = SS_{(C)}/1$	$MS_{(C)}/MS_{Er}$
AC	1	$SS_{(AC)}$	$MS_{(AC)} = SS_{(AC)}/1$	$MS_{(AC)}/MS_{Er}$
BC	1	$SS_{(BC)}$	$MS_{(BC)} = SS_{(BC)}/1$	$MS_{(BC)}/MS_{Er}$
ABC	1	$SS_{(ABC)}$	$MS_{(ABC)} = SS_{(ABC)}/1$	$MS_{(ABC)}/MS_{Er}$
Error	$(r-1)(2^3-1)$	SS_{Er}	$MS_{Er} = SS_{Er}/(r-1)(2^3-1)$	
Total	$2^3.r-1$	$SS_{\text{Tot.}}$		

If the calculated value of F for any effect be greater than the corresponding tabulated value of F at α level of significance and specific degrees of freedom, then the corresponding factorial effect is significant, and the respective null hypothesis of equality is rejected; otherwise, the test is nonsignificant and the respective null hypothesis cannot be rejected. In the event of significance of any one of the seven F tests, we are to follow as given below:

1. If the F test corresponding to the replication be significant, then we are to calculate the *LSD*/*CD* value for identifying which are the replications significantly different from each other using the following formula: $LSD/CD\ (\alpha) \text{ for replication} = \sqrt{\frac{2\text{MSE}}{2\times 2\times 2}} t_{\alpha/2;\text{err } d.f.}$
2. If any one of the three F tests corresponding to main effects of three factors be significant at specified level of significance, the higher mean value corresponding to the level of the factor is declared the best level for that particular factor.
3. For first-order interactions (i.e., $(\alpha\beta)_{ij}$ or $(\alpha\gamma)_{ik}$or$(\beta\gamma)_{jk}$), we are to calculate the *LSD*/*CD* value as follows:

$$LSD/CD(\alpha) \text{ for A/B/C} = \sqrt{\frac{2\text{MSE}}{2\times r}} t_{\alpha/2;\text{err } d.f.}$$

If the difference between means of any pair of treatment combination be greater than the corresponding *CD* value, then these two means under comparison are declared significantly different from each other, and the treatment combination having better value is treated as the better one.

4. If the F test corresponding to second-order interactions (i.e., $(\alpha\beta\gamma)_{ijk}$) be significant, we are to calculate the LSD/CD value as follows:

$$LSD/CD(\alpha) = \sqrt{\frac{2MSE}{r}} t_{\alpha/2;\text{err } d.f.}$$

If the difference between means of any pair of treatment combination be greater than the corresponding *CD* value, then these two means under comparison are declared significantly different from each other, and the treatment combination having better value is treated as the better one.

Example 11.8 (Three-Factor Symmetrical 2^3 Factorial RBD)

In a field trial of lentil with two varieties (PL639 and B77), two sowing times and two doses of potash were assessed to find out the best variety under the best sowing time and best dose of potash. The experiment was conducted in a randomized block design with three replications. The following table gives the ten seed weights (g) in response to different

Variety	PL639				B77			
Sowing time	S1		S2		S1		S2	
Potash	K1	K2	K1	K2	K1	K2	K1	K2
Ten seed weights (g)								
Rep-1	1.95	2.07	2.07	1.88	1.73	1.65	2.47	2.11
Rep-2	1.97	2.09	2.1	1.9	1.75	1.67	2.5	2.15
Rep-3	1.92	2.07	2.14	1.93	1.77	1.69	2.45	2.17

treatments. Analyze the information and draw your conclusion:

Solution From the given information, it appears that the experiment was conducted with three treatments variety, sowing time, and potassium fertilizer, each at two levels; hence it can be treated as a 2^3 factorial experiment conducted in a randomized block design with three replications.

So the appropriate model will be

$$y_{ijkl} = \mu + \alpha_i + \beta_j + \gamma_k + (\alpha\beta)_{ij} + (\alpha\gamma)_{ik} + (\beta\gamma)_{jk} + (\alpha\beta\gamma)_{ijk} + \delta_l + e_{ijkl}$$

where $i = 1, 2; j = 1, 2; k = 1, 2;$ and $l = 1, 2, 3$

y_{ijkl} = response in lth replicate due to ith variety and jth sowing time and kth dose of potash

μ = general effect

α_i = additional effect due to ith variety, $\sum \alpha_i = 0$

β_j = additional effect due to jth sowing time, $\sum \beta_j = 0$

γ_k = additional effect due to kth dose of potash, $\sum \gamma_k = 0$

$(\alpha\beta)_{ij}$ = interaction effect due to ith variety and jth sowing time, $\sum_i (\alpha\beta)_{ij} = \sum_j (\alpha\beta)_{ij} = 0$

$(\alpha\gamma)_{ik}$ = interaction effect due to ith variety and kth potash, $\sum_i (\alpha\gamma)_{ik} = \sum_k (\alpha\gamma)_{ik} = 0$

$(\beta\gamma)_{jk}$ = interaction effect of the jth sowing time and lth dose of potash, $\sum_j (\beta\gamma)_{jk} = \sum_k (\beta\gamma)_{jk} = 0$

$(\alpha\beta\gamma)_{ijk}$ = interaction effect due ith variety, jth sowing time, and kth dose of potash, $\sum_i (\alpha\beta\gamma)_{ijk} = \sum_j (\alpha\beta\gamma)_{ijk} = \sum_k (\alpha\beta\gamma)_{ijk} = 0$

δ_l = additional effect due to lth replication, $\sum_l \delta_l = 0$

e_{ijkl} = error component associated with lth replicate due to ith variety and jth sowing time and kth dose potash and $e_{ijkl} \sim$ i.i.d. N(0, σ^2)

Hypothesis to be tested:

H_{01} : $\delta_1 = \delta_2 = \delta_3$ against H_{11} : $\delta_1 \neq \delta_2 \neq \delta_3$

H_{02} : $\alpha_1 = \alpha_2$ against H_{12} : $\alpha_1 \neq \alpha_2$

H_{03} : $\beta_1 = \beta_2$ against H_{13} : $\beta_1 \neq \beta_2$

H_{04} : $\gamma_1 = \gamma_2$ against H_{14} : $\gamma_1 \neq \gamma_2$

H_{05} : $\alpha_1\beta_1 = \alpha_1\beta_2 = \alpha_2\beta_1 = \alpha_2\beta_2$ against H_{15} : all $(\alpha\beta)_{ij}$'s are not equal

H_{06} : $\alpha_1\gamma_1 = \alpha_1\gamma_2 = \alpha_2\gamma_1 = \alpha_2\gamma_2$ against H_{16} : all $(\alpha\gamma)_{ik}$'s are not equal

H_{07} : $\beta_1\gamma_1 = \beta_1\gamma_2 = \beta_2\gamma_1 = \beta_2\gamma_2$ against H_{17} : all $(\beta\gamma)_{jk}$'s are not equal

H_{08} : all $(\alpha\beta\gamma)_{ijk}$'s are equal against H_{18} : all $(\alpha\beta\gamma)_{ijk}$'s are not equal

Let the level of significance be $\alpha = 0.05$.

Now we calculate the following quantities:

$$G = \sum_{i,j,k,l} y_{ijkl} = 1.95 + 2.07 + 2.07 + ... + 1.69 + 2.45 + 2.17 = 48.2$$

and

$$CF = \frac{G^2}{2^3 r} = \frac{48.2^2}{2^3.3} = 96.80$$

$$SS_{TOT} = \sum_{i,j,k,l} y_{ijkl}^2 - CF = 1.95^2 + 2.07^2 + 2.07^2 + ... + 1.69^2 + 2.45^2 + 2.17^2 - 96.80 = 1.342$$

$$SS_R = \sum_{l=1}^{r} \frac{R_l^2}{2^3} - CF = \sum_{l=1}^{3} \frac{R_l^2}{2^3} - CF$$
$$= \frac{15.93^2 + 16.13^2 + 16.14^2}{8} - 96.80$$
$$= 0.003$$

R_l is the total of all the observations in the lth block.

From the above table, first let us form the following tables of totals and from the tables get the following quantities:

Table of totals for variety × sowing time:

	Variety			
Sowing time	V1	V2	Total	Mean
S1	12.070	10.260	22.330	1.396
S2	12.020	13.850	25.870	1.617
Total	24.090	24.110		
Mean	1.506	1.507		

$$SS_{(\text{Var})} = \frac{1}{m \times \text{p} \times r} \sum_{j=1}^{2} y_{j..}^2 - CF$$
$$= \frac{24.090^2 + 24.110^2}{2 \times 2 \times 3} - 96.80$$
$$= 0.00002$$

$$SS_{(ST)} = \frac{1}{n \times p \times r} \sum_{i=1}^{2} y_{i...}^2 - CF$$
$$= \frac{22.330^2 + 25.870^2}{2 \times 2 \times 3} - 96.80$$
$$= 0.52215$$

$$SS_{(\text{Var} \times \text{ST})} = \frac{1}{n \times r} \sum\sum y_{ij..}^2 - CF - SS_{(\text{Var})} - SS_{(ST)}$$
$$= \frac{12.070^2 + 12.020^2 + 10.260^2 + 13.850^2}{2 \times 3}$$
$$-90.80 - 0.00002 - 0.52215 = 0.55206$$

Table of totals for sowing time × potassium:

	Sowing time			
Potassium	S1	S2	Total	Mean
K1	11.09	13.73	24.820	1.551
K2	11.24	12.14	23.380	1.461
Total	22.330	25.870		
Mean	1.396	1.617		

$$SS_{(\text{Pot})} = \frac{1}{m \times \text{n} \times r} \sum_{k=1}^{2} y_{..k.}^2 - CF$$
$$= \frac{24.820^2 + 23.380^2}{2 \times 2 \times 3} - 90.80 = 0.08640$$

$$SS_{(ST \times \text{Pot})} = \frac{1}{n \times r} \sum_{i=1}^{2} \sum_{k=1}^{2} y_{i.k.}^2 - CF - SS_{(ST)} - SS_{(\text{Pot})}$$
$$= \frac{11.09^2 + 11.24^2 + 13.73^2 + 12.14^2}{2 \times 3}$$
$$-90.80 - 0.52215 - 0.08640 = 0.12615$$

Table of totals for variety × potassium:

	Variety			
Potassium	V1	V2	Total	Mean
K1	12.15	11.94	24.090	1.506
K2	12.67	11.44	24.110	1.507
Total	24.820	23.380		
Mean	1.551	1.461		

$$SS_{(\text{Var} \times \text{Pot})} = \frac{1}{m \times r} \sum_{j=1}^{2} \sum_{k=1}^{2} y_{.jk.}^2 - CF - SS_{(\text{Var})}$$
$$-SS_{(\text{Pot})} = \frac{12.15^2 + 12.67^2 + 11.94^2 + 11.44^2}{2 \times 3}$$
$$-90.80 - 0.00002 - 0.08640 = 0.04335$$

Table totals for variety × sowing time x potassium (treatments):

	V1		V2			
	S1	S2	S1	S2	Total	Mean
K1	5.84	6.31	5.25	7.42	12.670	2.068
K2	6.23	5.71	5.01	6.43	11.440	1.948
Total	12.070	12.020	10.260	13.850		
Mean	2.012	2.003	1.710	2.308		

$$SS_{(\text{Var} \times ST \times \text{Pot})} = \frac{1}{r} \sum_{\text{i=1}}^{2} \sum_{\text{j=1}}^{2} \sum_{\text{k=1}}^{2} y_{.jk.}^2 - CF - SS_{(\text{Var})}$$
$$- SS_{(ST)} - SS_{(\text{Pot})} - SS_{(ST \times \text{Var})} - SS_{(ST \times \text{Pot})}$$
$$- SS_{(\text{Var} \times \text{Pot})}$$
$$= \frac{5.84^2 + 6.23^2 + \ldots\ldots\ldots + 7.42^2 + 6.43^2}{3}$$
$$- 90.80 - 0.00002 - 0.52215 - 0.08640$$
$$-0.55207 - 0.12615 - 0.04335 = 0.00240$$

Each SS has 1 d.f.:

$$
\begin{aligned}
SS_{Er} &= SS_{\mathrm{TOT}} - SS_R - SS_V - SS_S - SS_{VS} \\
&\quad - SS_K - SS_{VK} - SS_{SK} - SS_{VSK} \\
&= 1.3425 - 0.0035 - 0.000017 - 0.522 \\
&\quad - 0.552 - 0.0864 - 0.043 - 0.126 - 0.0024 \\
&= 0.0064
\end{aligned}
$$

The structure of the analysis of variance for this factorial experiment in a randomized complete block design is given as follows:

SOV	*s*	*SS*	*MS*	*F*	*Tab F*
Replication	$r-1=2$	0.00351	0.00175	3.783	3.739
V	1	0.00002	0.00002	0.036 NS	4.600
S	1	0.52215	0.52215	1126.074	4.600
VS	1	0.55207	0.55207	1190.593	4.600
K	1	0.08640	0.08640	186.331	4.600
VK	1	0.04335	0.04335	93.489	4.600
SK	1	0.12615	0.12615	272.056	4.600
VSK	1	0.00240	0.00240	5.176	4.600
Error	$(r-1)$ $(2^3-1)=14$	0.00649	0.00046		
Total	$2^3.r-1=23$	1.34253			

From the above ANOVA table, it is clear that all the effects are significant, except the main effect of variety. Thus there is no varietal effect on seed weight of lentil. So far as the best sowing time and dose of potassium are concerned, the dose having higher mean values in respective cases would be preferred. So S2 and K1 would be preferred over S1 and K2, respectively.

Now we are to find out the interaction effects of different factors which are significantly different from others. For the purpose we are to calculate the critical difference values for all the three first-order and the second-order interactions using the following formulae:

$$
CD(0.05) \text{ for variety } \times \text{ sowing time } = \sqrt{\frac{2 \times ErMS}{pr}} \times t_{q_{f_2;\text{error } d.f.}} = \sqrt{\frac{2 \times 0.00046}{2 \times 3}} \times t_{0.025;14.}
$$

$$
= \sqrt{\frac{2 \times 0.00046}{2 \times 3}} \times 2.144 = 0.0265
$$

$$
\begin{aligned}
&CD(0.05) \text{ for sowing time } \times \text{ potassium} \\
&= \sqrt{\frac{2 \times ErMS}{mr}} \times t_{\alpha/2;\text{error d.f.}} \\
&= \sqrt{\frac{2 \times 0.00046}{2 \times 3}} \times t_{0.025;14.} = \sqrt{\frac{2 \times 0.00046}{2 \times 3}} \times 2.144 \\
&= 0.0265 CD(0.05) \text{ for variety } \times \text{ potassium} \\
&= \sqrt{\frac{2 \times ErMS}{nr}} \times t_{\alpha/2;\text{error } d.f.} \\
&= \sqrt{\frac{2 \times 0.00046}{2 \times 3}} \times t_{0.025;14.} = \sqrt{\frac{2 \times 0.00046}{2 \times 3}} \times 2.144 \\
&= 0.0265 CD(0.05) \text{ for variety } \times \text{ sowing time } \times \text{ potassium} \\
&= \sqrt{\frac{2 \times ErMS}{r}} \times t_{\alpha/2;\text{error } d.f.} \\
&= \sqrt{\frac{2 \times 0.00046}{2 \times 3}} \times t_{0.025;14.} = \sqrt{\frac{2 \times 0.00046}{2 \times 3}} \times 2.144 \\
&= 0.037
\end{aligned}
$$

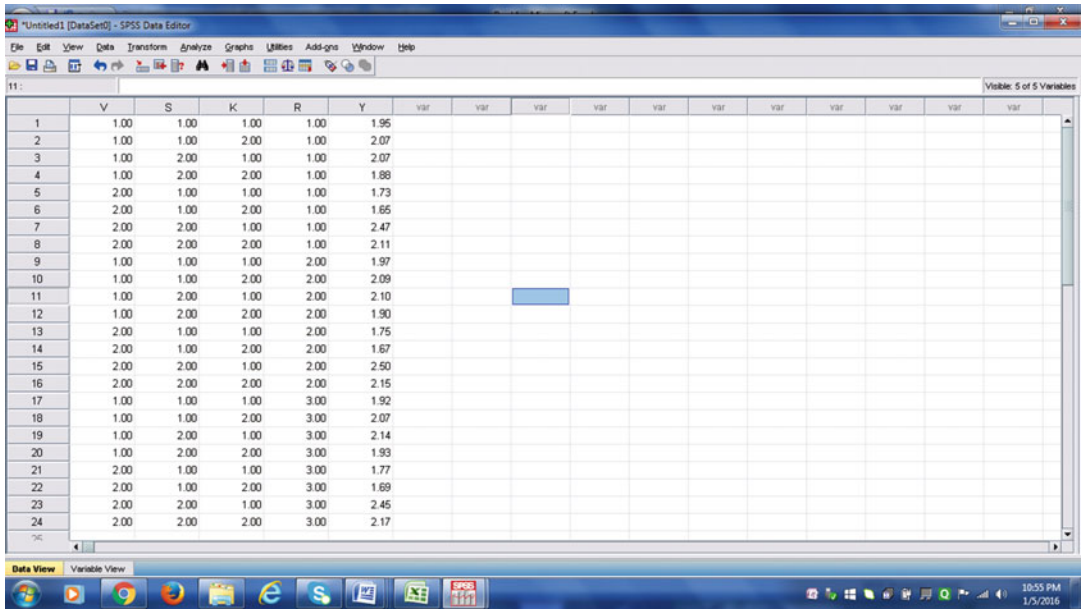
Our next step is to construct the mean table.

	Yield		CD (0.05)
Variety X Sowing time			
V2S2	2.308		0.0265
V1S1	2.012	|	
V1S2	2.003		
V2S1	1.710		
Variety X Potassium			
V1K2	2.112		0.0265
V1K1	2.025		
V2K1	1.990		
V2K2	1.907		
Sowing Time X Potassium			
S2K1	2.288		0.0265
S2K2	2.023		
S1K2	1.873	|	
S1K1	1.848		
Variety X Sowing Time X Potassium			
V2S2K1	2.473		0.037
V2S2K2	2.143		
V1S2K1	2.103	|	
V1S1K2	2.077		
V1S1K1	1.947		
V1S2K2	1.903		
V2S1K1	1.750		
V2S1K2	1.670		

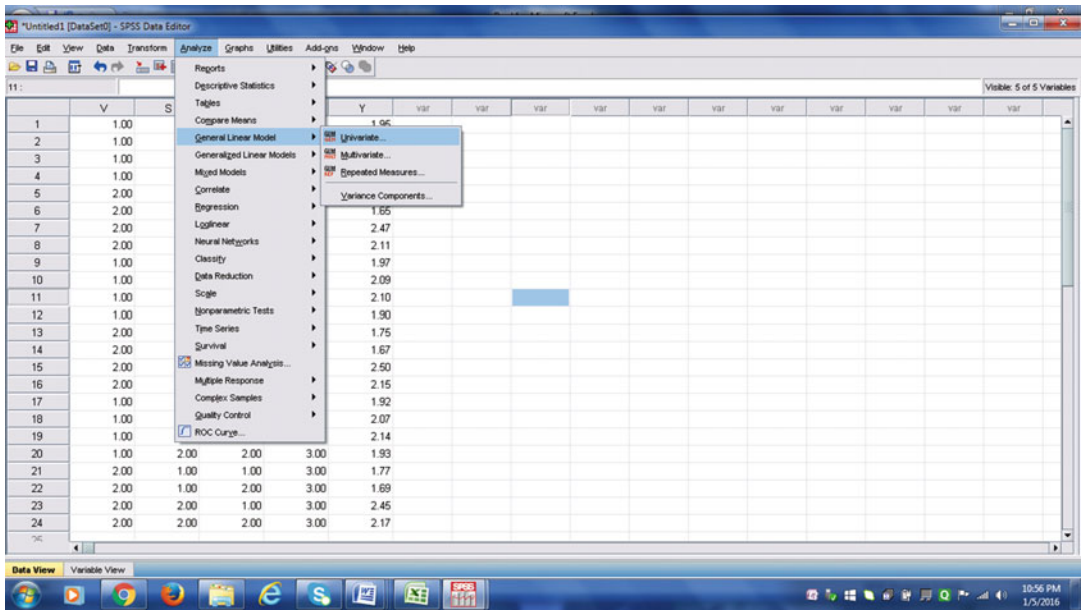
Hence from the analyses, we can conclude that:

1. Two varieties are equally effective w.r.t seed wt.
2. Sowing time (S2) is better than S1.
3. Potassium level K1 is better than K2.
4. In the case of interaction effect variety × sowing time, V2S2 is superior over others.
5. All the interaction effects of variety × potassium are giving different effects. Treatment combination V1K2 is best among them.
6. Among the sowing time × potassium interactions, S2K1 is better than reaming.
7. In the case of the second-order interaction, i.e., variety × sowing time × potassium, V2S2K1 is giving significantly higher yield over reaming all the interactions, whereas V2S1K2 is giving less yield.

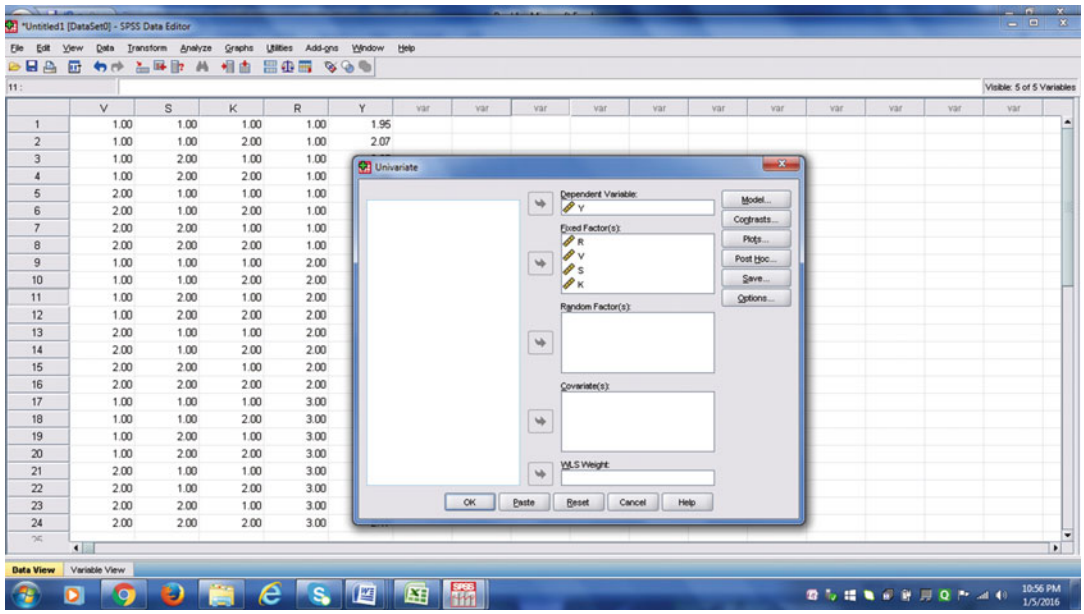
Example 11.8 Now let us demonstrate how this 2^3 analysis can be done using SPSS.



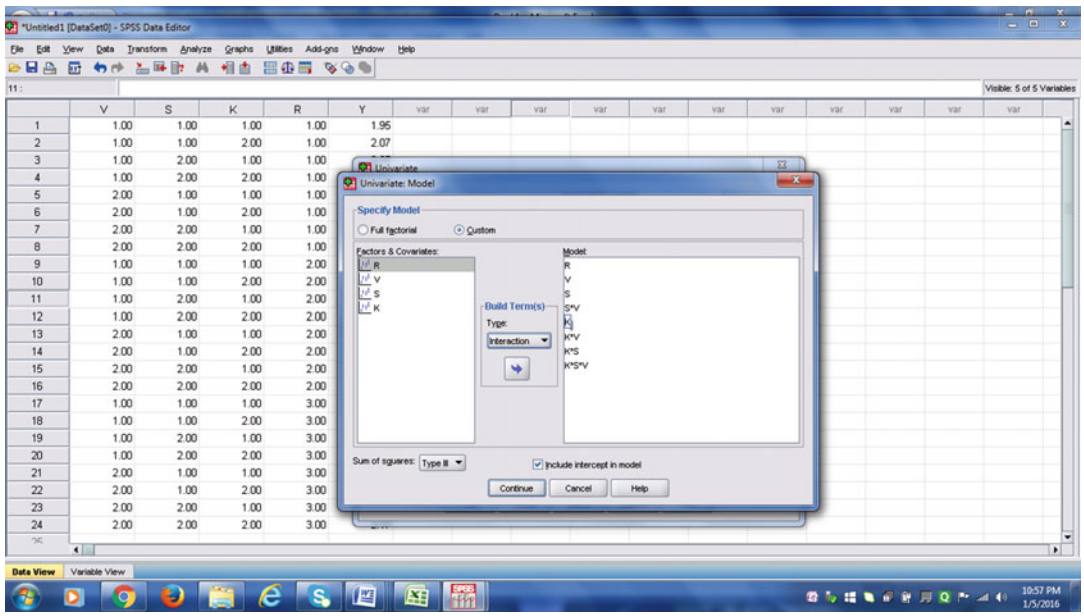
Step 1: Enter data as shown above.



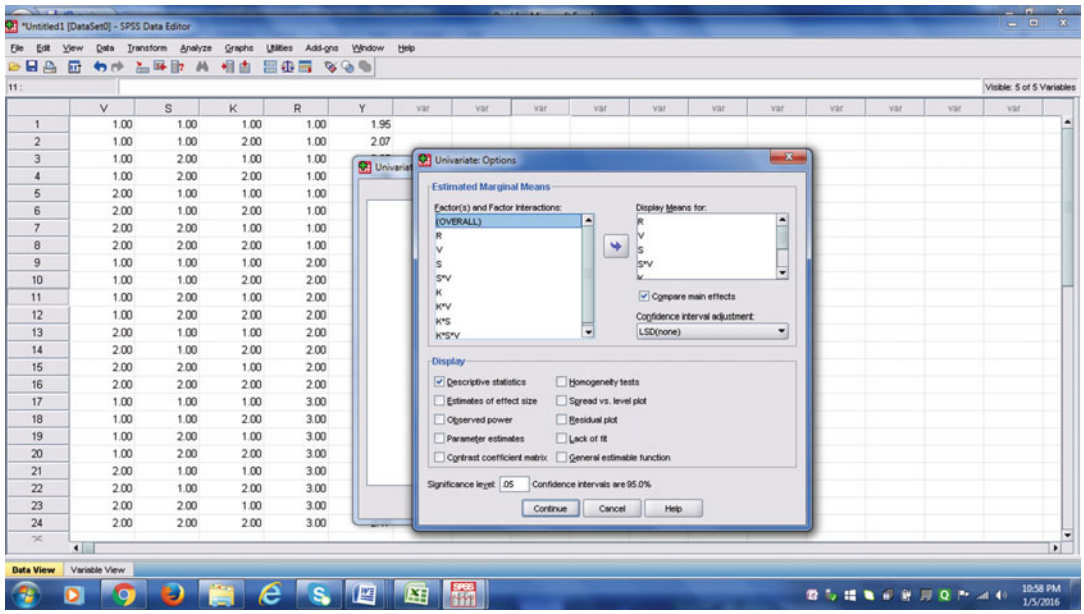
Step 2: Select the General Linear Model followed by Univariate option.



Step 3: Select the variables in the appropriate box.



Step 4: Specify the model.



Step 5: Select appropriate options to get the desired output.

Step 6: Select Continue and go to get the following output.

Univariate analysis of variance:

Between-Subjects Factors

		N
R	1	8
	2	8
	3	8
V	1	12
	2	12
S	1	12
	2	12
K	1	12
	2	12

Dependent Variable:Y

R	V	S	K	Mean	Std. Deviation	N
1	1	1	1	1.9500	.	1
			2	2.0700	.	1
			Total	2.0100	.08485	2
		2	1	2.0700	.	1
			2	1.8800	.	1
			Total	1.9750	.13435	2
		Total	1	2.0100	.08485	2
			2	1.9750	.13435	2
			Total	1.9925	.09394	4
	2	1	1	1.7300	.	1
			2	1.6500	.	1
			Total	1.6900	.05657	2
		2	1	2.4700	.	1
			2	2.1100	.	1
			Total	2.2900	.25456	2
		Total	1	2.1000	.52326	2
			2	1.8800	.32527	2
			Total	1.9900	.37771	4
	Total	1	1	1.8400	.15556	2
			2	1.8600	.29698	2
			Total	1.8500	.19391	4
		2	1	2.2700	.28284	2
			2	1.9950	.16263	2
			Total	2.1325	.24636	4
		Total	1	2.0550	.31043	4
			2	1.9275	.21046	4
			Total	1.9912	.25481	8
2	1	1	1	1.9700	.	1
			2	2.0900	.	1
			Total	2.0300	.08485	2
		2	1	2.1000	.	1
			2	1.9000	.	1
			Total	2.0000	.14142	2
		Total	1	2.0350	.09192	2

			2	1.9950	.13435	2
			Total	2.0150	.09678	4
	2	1	1	1.7500	.	1
			2	1.6700	.	1
			Total	1.7100	.05657	2
		2	1	2.5000	.	1
			2	2.1500	.	1
			Total	2.3250	.24749	2
		Total	1	2.1250	.53033	2
			2	1.9100	.33941	2
			Total	2.0175	.38413	4
	Total	1	1	1.8600	.15556	2
			2	1.8800	.29698	2
			Total	1.8700	.19391	4
		2	1	2.3000	.28284	2
			2	2.0250	.17678	2
			Total	2.1625	.24958	4
		Total	1	2.0800	.31507	4
			2	1.9525	.21639	4
			Total	2.0162	.25934	8
3	1	1	1	1.9200	.	1
			2	2.0700	.	1
			Total	1.9950	.10607	2
		2	1	2.1400	.	1
			2	1.9300	.	1
			Total	2.0350	.14849	2
		Total	1	2.0300	.15556	2
			2	2.0000	.09899	2
			Total	2.0150	.10786	4
	2	1	1	1.7700	.	1
			2	1.6900	.	1
			Total	1.7300	.05657	2
		2	1	2.4500	.	1
			2	2.1700	.	1
			Total	2.3100	.19799	2
		Total	1	2.1100	.48083	2
			2	1.9300	.33941	2
			Total	2.0200	.35534	4
	Total	1	1	1.8450	.10607	2

			2	1.8800	.26870	2
			Total	1.8625	.16800	4
		2	1	2.2950	.21920	2
			2	2.0500	.16971	2
			Total	2.1725	.21360	4
		Total	1	2.0700	.29541	4
			2	1.9650	.20809	4
			Total	2.0175	.24312	8
Total	1	1	1	1.9467	.02517	3
			2	2.0767	.01155	3
			Total	2.0117	.07333	6
		2	1	2.1033	.03512	3
			2	1.9033	.02517	3
			Total	2.0033	.11290	6
		Total	1	2.0250	.09006	6
			2	1.9900	.09654	6
			Total	2.0075	.09087	12
	2	1	1	1.7500	.02000	3
			2	1.6700	.02000	3
			Total	1.7100	.04733	6
		2	1	2.4733	.02517	3
			2	2.1433	.03055	3
			Total	2.3083	.18247	6
		Total	1	2.1117	.39671	6
			2	1.9067	.26028	6
			Total	2.0092	.33733	12
	Total	1	1	1.8483	.10962	6
			2	1.8733	.22322	6
			Total	1.8608	.16817	12
		2	1	2.2883	.20449	6
			2	2.0233	.13382	6
			Total	2.1558	.21517	12
		Total	1	2.0683	.27797	12
			2	1.9483	.19216	12
			Total	2.0083	.24160	24

Tests of Between-Subjects Effects

Dependent Variable:Y

Source	Type III Sum of Squares	df	Mean Square	F	Sig.
Corrected Model	1.336[a]	9	.148	320.147	.000
Intercept	96.802	1	96.802	2.088E5	.000
R	.004	2	.002	3.783	.049
V	1.667E-5	1	1.667E-5	.036	.852
S	.522	1	.522	1.126E3	.000
V * S	.552	1	.552	1.191E3	.000
K	.086	1	.086	186.331	.000
V * K	.043	1	.043	93.489	.000
S * K	.126	1	.126	272.056	.000
V * S * K	.002	1	.002	5.176	.039
Error	.006	14	.000		
Total	98.144	24			
Corrected Total	1.343	23			

a. R Squared = .995 (Adjusted R Squared = .992)

Multiple Comparisons

Y

LSD

(I) R	(J) R	Mean Difference (I-J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
1	2	-.0250*	.01077	.036	-.0481	-.0019
	3	-.0263*	.01077	.029	-.0493	-.0032
2	1	.0250*	.01077	.036	.0019	.0481
	3	-.0013	.01077	.909	-.0243	.0218
3	1	.0263*	.01077	.029	.0032	.0493
	2	.0013	.01077	.909	-.0218	.0243

Based on observed means.

The error term is Mean Square(Error) = .000.

*. The mean difference is significant at the .05 level.

4. S * V

Dependent Variable:Y

S	V	Mean	Std. Error	95% Confidence Interval	
				Lower Bound	Upper Bound
1	1	2.012	.009	1.993	2.031
	2	1.710	.009	1.691	1.729
2	1	2.003	.009	1.984	2.022
	2	2.308	.009	2.289	2.327

6. K * V

Dependent Variable:Y

K	V	Mean	Std. Error	95% Confidence Interval	
				Lower Bound	Upper Bound
1	1	2.025	.009	2.006	2.044
	2	2.112	.009	2.093	2.131
2	1	1.990	.009	1.971	2.009
	2	1.907	.009	1.888	1.926

7. K * S

Dependent Variable:Y

K	S	Mean	Std. Error	95% Confidence Interval	
				Lower Bound	Upper Bound
1	1	1.848	.009	1.829	1.867
	2	2.288	.009	2.269	2.307
2	1	1.873	.009	1.854	1.892
	2	2.023	.009	2.004	2.042

8. K * S * V

Dependent Variable:Y

K	S	V	Mean	Std. Error	95% Confidence Interval	
					Lower Bound	Upper Bound
1	1	1	1.947	.012	1.920	1.973
		2	1.750	.012	1.723	1.777
	2	1	2.103	.012	2.077	2.130
		2	2.473	.012	2.447	2.500
2	1	1	2.077	.012	2.050	2.103
		2	1.670	.012	1.643	1.697
	2	1	1.903	.012	1.877	1.930
		2	2.143	.012	2.117	2.170

Estimates

Dependent Variable:Y

K	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
1	2.068	.006	2.055	2.082
2	1.948	.006	1.935	1.962

Pairwise Comparisons

Dependent Variable:Y

(I) K	(J) K	Mean Difference (I-J)	Std. Error	Sig.[a]	95% Confidence Interval for Difference[a]	
					Lower Bound	Upper Bound
1	2	.120*	.009	.000	.101	.139
2	1	-.120*	.009	.000	-.139	-.101

Based on estimated marginal means

*. The mean difference is significant at the .05 level.

a. Adjustment for multiple comparisons: Least Significant Difference (equivalent to no adjustments).

Univariate Tests

Dependent Variable:Y

	Sum of Squares	df	Mean Square	F	Sig.
Contrast	.086	1	.086	186.331	.000
Error	.006	14	.000		

Estimates

Dependent Variable:Y

S	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
1	1.861	.006	1.848	1.874
2	2.156	.006	2.143	2.169

Pairwise Comparisons

Dependent Variable:Y

(I) S	(J) S	Mean Difference (I-J)	Std. Error	Sig.[a]	95% Confidence Interval for Difference[a]	
					Lower Bound	Upper Bound
1	2	-.295*	.009	.000	-.314	-.276
2	1	.295*	.009	.000	.276	.314

Based on estimated marginal means

*. The mean difference is significant at the .05 level.

a. Adjustment for multiple comparisons: Least Significant Difference (equivalent to no adjustments).

	Sum of Squares	df	Mean Square	F	Sig.
Contrast	.522	1	.522	1.126E3	.000
Error	.006	14	.000		

The F tests the effect of S. This test is based on the linearly independent pairwise comparisons among the estimated marginal means.

Estimates

Dependent Variable:Y

V	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
1	2.008	.006	1.994	2.021
2	2.009	.006	1.996	2.022

Pairwise Comparisons

Dependent Variable:Y

(I) V	(J) V	Mean Difference (I-J)	Std. Error	Sig.[a]	95% Confidence Interval for Difference[a]	
					Lower Bound	Upper Bound
1	2	-.002	.009	.852	-.021	.017
2	1	.002	.009	.852	-.017	.021

Based on estimated marginal means

a. Adjustment for multiple comparisons: Least Significant Difference (equivalent to no adjustments).

Univariate Tests

Dependent Variable:Y

	Sum of Squares	df	Mean Square	F	Sig.
Contrast	1.667E-5	1	1.667E-5	.036	.852
Error	.006	14	.000		

The F tests the effect of V. This test is based on the linearly independent pairwise comparisons among the estimated marginal means.

Dependent Variable:Y

R	Mean	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
1	1.991	.008	1.975	2.008
2	2.016	.008	2.000	2.033
3	2.018	.008	2.001	2.034

Pairwise Comparisons

Dependent Variable:Y

(I) R	(J) R	Mean Difference (I-J)	Std. Error	Sig.[a]	95% Confidence Interval for Difference[a]	
					Lower Bound	Upper Bound
1	2	-.025*	.011	.036	-.048	-.002
	3	-.026*	.011	.029	-.049	-.003
2	1	.025*	.011	.036	.002	.048
	3	-.001	.011	.909	-.024	.022
3	1	.026*	.011	.029	.003	.049
	2	.001	.011	.909	-.022	.024

Based on estimated marginal means

*. The mean difference is significant at the .05 level.

a. Adjustment for multiple comparisons: Least Significant Difference (equivalent to no adjustments).

Univariate Tests

Dependent Variable:Y

	Sum of Squares	df	Mean Square	F	Sig.
Contrast	.004	2	.002	3.783	.049
Error	.006	14	.000		

It is to be noted that the output, not only through SPSS, but from any statistical software depends on programme concerned and the instruction fed to the programme during execution. The experimenter, must have clear idea about the particular type of analysis required and the corresponding instruction to be provided during analysis using a particular software, otherwise interpretation of the results would be difficult as well as may be misleading.

11.3.2 $m \times n \times p$ Asymmetrical Factorial Experiment

The more general class of three-factor factorial experiments is the $m \times n \times p$ factorial experiments, in which three factors are included in the experiment, each having different levels, viz., m, n, and p levels. Thus, we are talking about three-factor asymmetrical factorial experiments. In three-factor asymmetrical factorial experiment, at least one factor will have a different level than the other two factors. Three-factor symmetrical factorial experiments are the special case of three-factor factorial experiments in which all the three factors have the same level. A three-factor factorial experiment can be conducted using basic CRD, RBD, or LSD design. But the problem with LSD is that even at the lowest level of three-factor symmetrical factorial experiment, i.e., 2^3 factorial experiment, we require an experimental plot of at least 8×8 experimental unit and for the lowest three-factor asymmetrical factorial experiment, i.e., $2 \times 2 \times 3$ factor asymmetrical factorial experiment, require at least a plot of 12×12 number of experimental units. In reality the number of experimental units required to conduct a factorial experiment under LSD setup is much higher compared to either CRD or RBD design. As such three-factor and more than three-factor factorial experiments are generally conducted in CRD or RBD design.

The analysis of three-factor asymmetrical factorial experiment will be similar to that of the three-factor symmetrical factorial experiment with different levels of the factors under experimentation. As such the calculation procedure to get different sums of squares would be the same as we have discussed in three-factor symmetrical factorial experiments. We shall demonstrate the analysis of three-factor asymmetrical factorial experiment using practical problem.

Example 11.9 ($3 \times 3 \times 4$ Three-Factor Asymmetrical Factorial CRD)

An experiment was conducted with 108 cows of almost similar nature to know the fat content of milk from three breeds of cows feed with three different concentrates from four localities. Three cows were subjected to each of the 36 treatment combinations. Analyze the data to find out the best cow breed, best feed, best locality, and best interaction effects among the factors with high milk fat content:

Breed	B1											
Feed	F1				F2				F3			
Locality	L1	L2	L3	L4	L1	L2	L3	L4	L1	L2	L3	L4
Cow1	5.12	5.21	5.14	5.16	5.23	5.22	5.14	5.2	5.21	5.12	5.18	5.27
Cow2	5.07	5.20	5.13	5.11	5.19	5.16	5.13	5.15	5.17	5.06	5.14	5.24
Cow3	5.18	5.23	5.16	5.22	5.28	5.30	5.16	5.26	5.26	5.20	5.23	5.30
Breed	*B2*											
Feed	*F1*				*F2*				*F3*			
Locality	L1	L2	L3	L4	L1	L2	L3	L4	L1	L2	L3	L4
Cow1	5.32	5.51	5.64	5.46	5.63	5.32	5.64	5.5	5.31	5.52	5.28	5.37
Cow2	5.37	5.46	5.55	5.48	5.61	5.41	5.55	5.52	5.36	5.54	5.33	5.39
Cow3	5.27	5.50	5.63	5.41	5.59	5.26	5.63	5.45	5.27	5.46	5.24	5.35
Breed	*B3*											
Feed	*F1*				*F2*				*F3*			
Locality	L1	L2	L3	L4	L1	L2	L3	L4	L1	L2	L3	L4
Cow1	5.21	5.34	5.36	5.29	5.40	5.26	5.36	5.33	5.25	5.29	5.22	5.31
Cow2	5.26	5.38	5.41	5.36	5.47	5.32	5.41	5.40	5.29	5.38	5.26	5.34
Cow3	5.18	5.33	5.35	5.26	5.38	5.23	5.35	5.30	5.23	5.26	5.20	5.30

Solution From the given information, it is clear that the response data from the experiment could be analyzed using the procedure of asymmetrical ($3 \times 3 \times 4$) factorial experiment conducted with three replications under laboratory condition. So the data can be analyzed as per the analysis of three-factor factorial completely randomized design, and the appropriate statistical model for the analysis will be

$$y_{ijkl} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + \gamma_k + (\alpha\gamma)_{ik} + (\beta\gamma)_{jk} + (\alpha\beta\gamma)_{ijk} + e_{ijkl}$$

where $i = 3$, $j = 3$, $k = 4$, and $l = 3$

y_{ijkl} = response in lth cow of ith breed feeding with jth concentrates from kth locality

μ = general effect

α_i = additional effect due to ith breed, $\sum \alpha_i = 0$

β_j = additional effect due to jth concentrates, $\sum \beta_j = 0$

γ_k = additional effect due to kth locality, $\sum \gamma_k = 0$

$(\alpha\beta)_{ij}$ = interaction effect of the ith breed and jth concentrate, $\sum_i (\alpha\beta)_{ij} = \sum_j (\alpha\beta)_{ij} = 0$

$(\alpha\gamma)_{ik}$ = interaction effect of the ith breed and kth of locality, $\sum_i (\alpha\gamma)_{ik} = \sum_k (\alpha\gamma)_{ik} = 0$

$(\beta\gamma)_{jk}$ = interaction effect of the jth concentrate and kth locality, $\sum_j (\beta\gamma)_{jk} = \sum_k (\beta\gamma)_{jk} = 0$

$(\alpha\beta\gamma)_{ijk}$ = interaction effect of the ith breed feeding with jth concentrates in kth locality, $\sum_i (\alpha\beta\gamma)_{ijk} = \sum_j (\alpha\beta\gamma)_{ijk} = \sum_k (\alpha\beta\gamma)_{ijk} = 0$

e_{ijkl} = error component associated with lth cow of ith breed feeding with jth concentrates from kth locality and $e_{ijkl} \sim$ i.i.d. N(0, σ^2)

Hypothesis to be tested:

$$H_{01} : \alpha_1 = \alpha_2 = \alpha_3 = 0$$
$$H_{02} : \beta_1 = \beta_2 = \beta_3 = 0$$
$$H_{03} : \gamma_1 = \gamma_2 = \gamma_3 = \gamma_4 = 0$$

H_{04} : all interaction (first- and second-order) effects are equal to zero

against

H_{11} : all α's are not equal to zero

H_{12} : all β's are not equal to zero

H_{13} : all γ's are not equal to zero

H_{14} : all interaction (first- and second-order) effects are not equal to zero

Let the level of significance be $\alpha = 0.01$.

$$\text{Grand total } (GT) = 5.12 + 5.07 + \ldots\ldots + 5.34 + 5.30 = 574.13$$

$$\text{Correction factor } (CF) = \frac{GT^2}{mnpr} = \frac{574.13^2}{3 \times 3 \times 4 \times 3} = 3052.085$$

$$\text{Total sum of square } (SS_{\text{Tot}}) = 5.12^2 + 5.07^2 + \ldots\ldots + 5.34^2 + 5.30^2 - 3052.085 = 2.062$$

$$\text{Treatment sum of square } (SS_{\text{T}}) = \frac{46.98^2 + 48.16^2 + \ldots\ldots\ldots + 47.08^2 + 47.87^2}{3} - 3052.085 = 1.9229$$

$$\text{Error sum of square } (SS_{Er.}) = SS_{\text{Tot}} - SS_{\text{T}} = 2.0625 - 1.9229 = 0.1396$$

From the given data, let us construct the following tables of totals and from the tables get the following quantities:

	Breed			Total	Mean
Feed	B1	B2	B3		
F1	61.93	65.60	63.73	191.26	5.31
F2	62.42	66.11	64.21	192.74	5.35
F3	62.38	64.42	63.33	190.13	5.28
Total	186.73	196.13	191.27		
Mean	5.19	5.45	5.31		

$$SS_{(\text{Breed})} = \frac{1}{npr}\sum_{i=1}^{3} y_{i\ldots}^2 - CF = \frac{186.73^2 + 196.13^2 + 191.27^2}{36} - 3052.085 = 1.227$$

$$SS_{(\text{Feed})} = \frac{1}{mpr}\sum_{j=1}^{3} y_{\cdot j\cdot}^2 - CF = \frac{191.26^2 + 192.74^2 + 190.13^2}{36} - 3052.085 = 0.0951$$

$$SS_{(\text{Breed} \times \text{Feed})} = \frac{1}{pr}\sum_{i=1}^{3}\sum_{j=1}^{3} y_{ij..}^2 - CF - SS_{\text{Breed}} - SS_{\text{Feed}}$$
$$= \frac{61.93^2 + 62.42^2 + \ldots\ldots\ldots\ldots + 64.21^2 + 63.33^2}{12} - 3052.085 - 1.227 - 0.0951$$
$$= 0.0747$$

Location	Breed			Total	Mean
	B1	B2	B3		
L1	46.71	48.73	47.67	143.11	5.30
L2	46.70	48.98	47.79	143.47	5.31
L3	46.41	49.49	47.92	143.82	5.33
L4	46.91	48.93	47.89	143.73	5.32
Total	186.73	196.13	191.27		
Mean	5.19	5.45	5.31		

$$SS_{(\text{Loc.})} = \frac{1}{mnr}\sum_{j=1}^{4} y_{..k.}^2 - CF = \frac{143.11^2 + 143.47^2 + 143.82^2 + 143.73^2}{9} - 3052.0857$$
$$= 0.0112$$

$$SS_{(\text{Breed}\times\text{Loc})} = \frac{1}{mr}\sum_{i=1}^{3}\sum_{k=1}^{4} y_{i.k.}^2 - CF - SS_{\text{Breed}} - SS_{\text{Loc}}$$
$$= \frac{46.71^2 + 46.70^2 + \ldots\ldots\ldots + 47.92^2 + 47.89^2}{9} - 3052.0857 - 1.2276 - 0.0951$$
$$= 0.0420$$

Location	Feed			Total	Mean
	F1	F2	F3		
L1	46.98	48.78	47.35	143.11	5.30
L2	48.16	47.48	47.83	143.47	5.31
L3	48.37	48.37	47.08	143.82	5.33
L4	47.75	48.11	47.87	143.73	5.32
Total	191.26	192.74	190.13		
Mean	5.31	5.35	5.28		

$$SS_{(\text{Feed}\times\text{Loc})} = \frac{1}{nr}\sum_{j=1}^{3}\sum_{k=1}^{4} y_{.jk.}^2 - CF - SS_{\text{Feed}} - SS_{\text{Loc}}$$
$$= \frac{46.98^2 + 48.16^2 + \ldots\ldots\ldots + 47.08^2 + 47.87^2}{9} - 3052.0857 - 0.0951 - 0.0112$$
$$= 0.2620$$

		Breed										
		B1			B2			B3				
	Feed	F1	F2	F3	F1	F2	F3	F1	F2	F3	Total	Mean
Location	L1	15.37	15.70	15.64	15.96	16.83	15.94	15.65	16.25	15.77	143.11	5.30
	L2	15.64	15.68	15.38	16.47	15.99	16.52	16.05	15.81	15.93	143.47	5.31
	L3	15.43	15.43	15.55	16.82	16.82	15.85	16.12	16.12	15.68	143.82	5.33
	L4	15.49	15.61	15.81	16.35	16.47	16.11	15.91	16.03	15.95	143.73	5.32
Total		61.93	62.42	62.38	65.60	66.11	64.42	63.73	64.21	63.33		
Mean		5.16	5.20	5.20	5.47	5.51	5.37	5.31	5.35	5.28		

$$SS_{(\text{Breed}\times\text{Feed}\times\text{Loc})} = \frac{1}{r}\sum_{i=1}^{3}\sum_{j=1}^{3}\sum_{k=1}^{4} y_{ijk.}^2 - CF - SS_{\text{Breed}} - SS_{\text{Feed}} - SS_{\text{Loc}}$$
$$- SS_{\text{Breed}\times\text{Feed}} - SS_{\text{Breed}\times\text{Loc}} - SS_{\text{Feed}\times\text{Loc}}$$
$$= \frac{15.37^2 + 15.64^2 + \ldots\ldots\ldots + 15.68^2 + 15.95^2}{3} - 3052.085 - 1.227$$
$$-0.0951 - 0.0112 - 0.0747 - 0.0420 - 0.2620$$
$$= 0.2099$$

ANOVA table					
SOV	d.f.	*SS*	*MS*	Cal F	Tab F at 1 %
Treatment	35	1.9229	0.0549	28.323	1.919
Breed	2	1.2277	0.6138	316.447	4.913
Feed	2	0.0952	0.0476	24.533	4.913
Breed × feed	4	0.0748	0.0187	9.634	3.591
Location	3	0.0113	0.0038	1.935 NS	4.066
Breed × location	6	0.0420	0.0070	3.609	3.063
Feed × location	6	0.2621	0.0437	22.516	3.063
Breed × feed × location	12	0.2100	0.0175	9.020	2.442
Error	72	0.1397	0.0019		
Total	107	2.0626			

It is clear from the above table that levels of all the factors, viz., breed, feed, and location, including all interaction effects except the location effect are significantly different from each other. So our next task is to find out the best level of these factors and their combinations. For the purpose we are to calculate the critical difference values for different factors and their combinations using the following formulae:

$$CD_{0.01}\ (\text{breed}) = \sqrt{\frac{2MS_{Er}}{r.np}}t_{0.005,\text{err}.d.f}$$

$$= \sqrt{\frac{2 \times 0.0019}{3 \times 3 \times 4}}2.645 = 0.027$$

$$CD_{0.01}\ (\text{feed}) = \sqrt{\frac{2MS_{Er}}{r.mp}}t_{0.005,\text{err}.d.f}$$

$$= \sqrt{\frac{2 \times 0.0019}{3 \times 3 \times 4}}2.645 = 0.027$$

$$CD_{0.01}\ (\text{breed} \times \text{feed}) = \sqrt{\frac{2MS_{Er}}{rp}}t_{0.005,\text{err}.d.f}$$

$$= \sqrt{\frac{2 \times 0.0019}{3 \times 4}}2.645 = 0.047$$

$$CD_{0.01}\ (\text{breed} \times \text{location})$$

$$= \sqrt{\frac{2MS_{Er}}{rn}}t_{0.005,\text{err}.d.f} = \sqrt{\frac{2 \times 0.0019}{3 \times 3}}2.645$$

$$= 0.054$$

$$CD_{0.01}\ (\text{feed} \times \text{location})$$

$$= \sqrt{\frac{2MS_{Er}}{rm}}t_{0.005,\text{err}.d.f} = \sqrt{\frac{2 \times 0.0019}{3 \times 3}}2.645$$

$$= 0.054$$

$$CD_{0.01}\ (\text{breed} \times \text{feed} \times \text{location}) = \sqrt{\frac{2MS_{Er}}{r}}$$

$$t_{0.005,\text{err}.d.f} = \sqrt{\frac{2 \times 0.0019}{3}}2.645 = 0.095$$

Now our next task is to make the mean tables for comparison.

Breed	Mean	CD
B2	5.448	0.027
B3	5.313	
B1	5.187	
Feed	**Mean**	**CD**
F2	5.354	0.027
F1	5.313	
F3	5.281	
Breed X Feed	**Mean**	**CD**
B2F2	5.509	0.047
B2F1	5.467	
B2F3	5.368	
B3F2	5.351	
B3F1	5.311	
B3F3	5.278	
B1F2	5.202	
B1F3	5.198	
B1F1	5.161	
Breed X Location	**Mean**	**CD**
B2L3	5.499	0.054
B2L2	5.442	
B2L4	5.437	
B2L1	5.414	
B3L3	5.324	
B3L4	5.321	
B3L2	5.310	
B3L1	5.297	
B1L4	5.212	
B1L1	5.190	
B1L2	5.189	
B1L3	5.157	
Feed X Location	Mean	CD
F2L1	5.420	0.054
F1L3	5.374	
F2L3	5.374	
F1L2	5.351	
F2L4	5.346	
F3L4	5.319	
F3L2	5.314	
F1L4	5.306	
F2L2	5.276	
F3L1	5.261	
F3L3	5.231	
F1L1	5.220	

Breed X Feed X Loca	Mean	CD
B2F2L1	5.610	0.095
B2F1L3	5.607	
B2F2L3	5.607	
B2F3L2	5.507	
B2F1L2	5.490	
B2F2L4	5.490	
B2F1L4	5.450	
B3F2L1	5.417	
B3F1L3	5.373	
B3F2L3	5.373	
B2F3L4	5.370	
B3F1L2	5.350	
B3F2L4	5.343	
B2F2L2	5.330	
B2F1L1	5.320	
B3F3L4	5.317	
B2F3L1	5.313	
B3F3L2	5.310	
B3F1L4	5.303	
B2F3L3	5.283	
B3F2L2	5.270	
B1F3L4	5.270	
B3F3L1	5.257	
B1F2L1	5.233	
B1F2L2	5.227	
B3F3L3	5.227	
B3F1L1	5.217	
B1F1L2	5.213	
B1F3L1	5.213	
B1F2L4	5.203	
B1F3L3	5.183	
B1F1L4	5.163	
B1F1L3	5.143	
B1F2L3	5.143	
B1F3L2	5.127	
B1F1L1	5.123	

Example 11.10 (Three-Factor Asymmetrical Factorial RBD)

A field experiment with three varieties of potato and four levels of potassium on potato was tested in two spacings in a randomized block design. Yields (q/ha) for different treatment combinations are given below for three replications. Analyze the data to find out the best variety, best dose of potassium, best spacing, and best interaction effects among the factors:

Spacing	S1												S2											
Varieties	V1				V2				V3				V1				V2				V3			
Potassium	K0	K1	K2	K3	K0	K1	K2	K3	K0	K1	K2	K3	K0	K1	K2	K3	K0	K1	K2	K3	K0	K1	K2	K3
R1	197	198	201	205	197	196	202	203	197	199	204	205	199	201	201	204	200	204	205	206	199	202	203	207
R2	198	200	204	207	200	200	207	207	200	203	206	208	201	204	205	206	203	206	207	210	202	208	209	209
R3	200	201	205	208	199	199	206	206	198	202	205	207	205	206	204	205	203	207	208	209	203	203	206	210

Solution From the given information, it is clear that the experiment was an asymmetrical ($2 \times 3 \times 4$) factorial experiment conducted in randomized block design, so the appropriate statistical model for the analysis will be

$$y_{ijkl} = \mu + \alpha_i + \beta_j + (\alpha\beta)_{ij} + \gamma_k + (\alpha\gamma)_{ik} + (\beta\gamma)_{jk} + (\alpha\beta\gamma)_{ijk} + \delta_l + e_{ijkl}$$

where $i = 2, j = 3, k = 4$, and $l = 3$

y_{ijkl} = response in lth replicate due to ith level of the first factor (spacing) and jth level of the second factor (variety) and kth level of the third factor (potassium)

μ = general effect

α_i = additional effect due to the ith level of the first factor (spacing), $\sum \alpha_i = 0$

β_j = additional effect due to the jth level of the second factor (variety), $\sum \beta_j = 0$

γ_k = additional effect due to the kth level of the third factor (potassium), $\sum \gamma_k = 0$

$(\alpha\beta)_{ij}$ = interaction effect of the ith level of the first factor (spacing) and jth level of the second factor (variety), $\sum_i (\alpha\beta)_{ij} = \sum_j (\alpha\beta)_{ij} = 0$

$(\alpha\gamma)_{ik}$ = interaction effect of the ith level of the first factor (spacing) and kth level of the third factor (potassium), $\sum_i (\alpha\gamma)_{ik} = \sum_k (\alpha\gamma)_{ik} = 0$

$(\beta\gamma)_{jk}$ = interaction effect of the jth level of the second factor (variety) and kth level of the third factor (potassium), $\sum_j (\beta\gamma)_{jk} = \sum_k (\beta\gamma)_{jk} = 0$

$(\alpha\beta\lambda)_{ijk}$ = interaction effect of the ith level of the first factor (spacing), jth level of the second factor (variety), and kth level of the third factor (potassium), $\sum_i (\alpha\beta\lambda)_{ijk} = \sum_j (\alpha\beta\lambda)_{ijk} = \sum_k (\alpha\beta\lambda)_{ijk} = 0$

δ_l = additional effect due to lth replication, $\sum \delta_l = 0$

e_{ijkl} = error component associated with lth replicate due to the ith level of the first factor (spacing) and jth level of the second factor (variety) and kth level of the third factor (potassium) and $e_{ijkl} \sim$ i.i.d. N(0, σ^2)

Hypothesis to be tested:

$$H_0 : \alpha_1 = \alpha_2 = 0$$
$$\beta_1 = \beta_2 = \beta_3 = 0$$
$$\gamma_1 = \gamma_2 = \gamma_3 = \gamma_4 = 0$$
$$\delta_1 = \delta_2 = \delta_3 = 0$$

All interaction effects = 0 against

H_1 : allα's are not equal
allβ's are not equal
allγ's are not equal
allδ's are not equal

All interaction effects are not equal

Let the level of significance be 0.05.

From the given data table, let us calculate the following quantities:

$$\text{Grand total } (GT) = \sum_{i=1}^{2}\sum_{j=1}^{3}\sum_{k=1}^{4}\sum_{l=1}^{3} y_{ijkl} = 14650$$

$$\text{Correction factor } (CF) = \frac{GT^2}{2 \times 3 \times 4 \times 3} = \frac{14650^2}{72} = 2980868.056$$

$$SS_{\text{TOT}} = \sum_{i=1}^{2}\sum_{j=1}^{3}\sum_{k=1}^{4}\sum_{l=1}^{3} y_{ijkl}^2 - CF = 901.944$$

$$SS_R = \frac{1}{m.n.p}\sum_{l=1}^{3} y_{oool}^2 - CF = \frac{4835^2 + 4910^2 + 4905^2}{24} - 2980868.056 = 146.527$$

From the above table, first let us form the following tables and from the table get the following quantities:

Table of totals for spacing × variety:

	Spacing			
Variety	S1	S2	Total	Mean
V1	2424	2441	4865	202.708
V2	2422	2468	4890	203.750
V3	2434	2461	4895	203.958
Total	7280	7370		
Mean	202.222	204.722		

$$SS_{(\text{Spa})} = \frac{1}{n \times p \times r} \sum_{i=1}^{2} y_{iooo}^2 - CF = \frac{7280^2 + 7370^2}{3 \times 4 \times 3} - 2980868.056 = 112.5$$

$$SS_{(\text{Var})} = \frac{1}{m \times \text{p} \times r} \sum_{j=1}^{3} y_{ojoo}^2 - CF = \frac{4865^2 + 4890^2 + 4895^2}{2 \times 4 \times 3} - 2980868.056$$
$$= 21.527$$

$$SS_{(\text{Spa} \times \text{Var})} = \frac{1}{n \times r} \sum \sum y_{ijoo}^2 - CF - SS_{(Var)} - SS_{(Spa)}$$
$$= \frac{2424^2 + 2441^2 + 2422^2 + 2468^2 + 2434^2 + 2461^2}{4 \times 3} - 2980868.056 - 112.500 - 21.527$$
$$= 18.083$$

Table of totals for spacing × potassium:

	Spacing			
Potassium	S1	S2	Total	Mean
K0	1786	1815	3601	200.056
K1	1798	1841	3639	202.167
K2	1840	1848	3688	204.889
K3	1856	1866	3722	206.778
Total	7280	7370		
Mean	202.222	204.722		

$$SS_{(\text{Pot})} = \frac{1}{m \times n \times r} \sum_{k=1}^{4} y_{ooko}^2 - CF = \frac{3601^2 + 3639^2 + 3688^2 + 3722^2}{2 \times 3 \times 3} - 2980868.056$$
$$= 473.611$$

$$SS_{(\text{Spa} \times \text{Pot})} = \frac{1}{n \times r} \sum_{i=1}^{2} \sum_{k=1}^{4} y_{ioko}^2 - CF - SS_{(\text{Spa})} - SS_{(\text{Pot})}$$
$$= \frac{1786^2 + 1815^2 + \ldots\ldots\ldots + 1856^2 + 1866^2}{3 \times 3} - 2980868.056 - 112.500 - 473.611$$
$$= 46.055$$

Table of totals for variety × potassium:

	Variety				
Potassium	V1	V2	V3	Total	Mean
K0	1200	1202	1199	3601	200.055
K1	1210	1212	1217	3639	202.166
K2	1220	1235	1233	3688	204.888
K3	1235	1241	1246	3722	206.777
Total	4865	4890	4895	14650	
Average	202.708	203.75	203.958	610.417	

$$SS_{(\text{Var} \times \text{Pot})} = \frac{1}{m \times r}\sum_{j=1}^{3}\sum_{k=1}^{4} y_{0jko}^2 - CF - SS_{(\text{Var})} - SS_{(\text{Pot})}$$
$$= \frac{1200^2 + 1202^2 + 1199^2 + \ldots\ldots + 1241^2 + 1246^2}{2 \times 3} - 2980868.056 - 21.527 - 473.611$$
$$= 15.805$$

Table of totals for spacing × variety × potassium (treatments):

	S1			S2				
	V1	V2	V3	V1	V2	V3	Total	Mean
K0	595	596	595	605	606	604	3601	200.056
K1	599	595	604	611	617	613	3639	202.167
K2	610	615	615	610	620	618	3688	204.889
K3	620	616	620	615	625	626	3722	206.778
Total	2424	2422	2434	2441	2468	2461		
Mean	202.000	201.833	202.833	203.417	205.667	205.083		

$$SS_{(\text{Spa}\times\text{Var}\times\text{Pot})} = \frac{1}{r}\sum_{i=1}^{2}\sum_{j=1}^{3}\sum_{k=1}^{4} y_{0jko}^2 - CF - SS_{(\text{Spa})} - SS_{(\text{Var})} - SS_{(\text{Pot})} - SS_{(\text{Spa}\times\text{Var})}$$
$$-SS_{(\text{Spa}\times\text{Pot})} - SS_{(\text{Var}\times\text{Pot})}$$
$$= \frac{595^2 + 596^2 + 595^2 + \ldots\ldots + 625^2 + 626^2}{3} - 2980868.056$$
$$- 112.500 - 225.505 - 21.527 - 18.083 - 46.055 - 15.805$$
$$= 17.694$$

$$SS_{(Er)} = SS_{\text{TOT}} - SS_R - SS_{(\text{Spa})} - SS_{(\text{Var})} - SS_{(\text{Pot})} - SS_{(\text{Spa}\times\text{Var})} - SS_{(\text{Spa}\times\text{Pot})} - SS_{(\text{Var}\times\text{Pot})}$$
$$-SS_{(\text{Spa}\times\text{Var}\times\text{Pot})}$$
$$= 901.944 - 146.527 - 112.500 - 21.527 - 473.611 - 18.083 - 46.055 - 15.805 - 17.694$$
$$= 50.138$$

Now using the above values, we frame the following ANOVA table:

SOV	d.f.	SS	MS	F ratio	Table value of F at	
					$p = 0.05$	$p = 0.01$
Replication	2	146.528	73.264	67.216	3.21	5.12
Spacing	1	112.500	112.500	103.213	4.07	7.25
Variety	2	21.528	10.764	9.875	3.21	5.12
S × V	2	18.083	9.042	8.295	3.21	5.12
Potassium	3	473.611	157.870	144.838	2.83	4.26
S × K	3	46.056	15.352	14.085	2.83	4.26
V × K	6	15.806	2.634	2.417	2.22	3.23
S × V × K	6	17.694	2.949	2.706	2.22	3.23
Error	46	50.139	1.090			
Total	71	901.944				

It is clear from the above table that all the effects are significant at 5 % level of significance, while all the effects except the $V \times K$ and $S \times V \times K$ are significant at 1 % level also. But as we have fixed the level of significance at 5% all the null hypotheses are rejected.

Now we are to find out the levels of different factors which are significantly different from others and also the best level of each factor. For the purpose we are to calculate the critical difference values for spacing, variety, potassium, and all the interaction effects using the following formula:

$$CD(0.05) \text{ for spacing}$$
$$= \sqrt{\frac{2 \times ErMS}{npr}} \times t_{\alpha/2;\text{error } d.f.}$$
$$= \sqrt{\frac{2 \times 1.090}{3 \times 4 \times 3}} \times t_{0.025;46.}$$
$$= \sqrt{\frac{2 \times 1.090}{3 \times 4 \times 3}} \times 2.016 = 0.495$$

$$CD(0.05) \text{ for variety}$$
$$= \sqrt{\frac{2 \times ErMS}{mpr}} \times t_{\alpha/2;\text{error } d.f.}$$
$$= \sqrt{\frac{2 \times 1.090}{2 \times 4 \times 3}} \times t_{0.025;46.}$$
$$= \sqrt{\frac{2 \times 1.090}{2 \times 4 \times 3}} 2.016 = 0.606$$

$$CD(0.05) \text{ for potassium}$$
$$= \sqrt{\frac{2 \times ErMS}{mnr}} \times t_{\alpha/2;\text{error } d.f.}$$
$$= \sqrt{\frac{2 \times 1.090}{2 \times 3 \times 3}} \times t_{0.025;46.}$$
$$= \sqrt{\frac{2 \times 1.090}{2 \times 3 \times 3}} 2.016 = 0.700$$

$CD(0.05)$ for spacing $\times$ variety

$$= \sqrt{\frac{2 \times ErMS}{pr}} \times t_{\alpha/2;\text{error } d.f.}$$

$$= \sqrt{\frac{2 \times 1.090}{4 \times 3}} \times t_{0.025;46.}$$

$$= \sqrt{\frac{2 \times 1.090}{4 \times 3}} \times 2.016 = 0.857$$

$CD(0.05)$ for spacing $\times$ potassium

$$= \sqrt{\frac{2 \times ErMS}{nr}} \times t_{\alpha/2;\text{error } d.f.}$$

$$= \sqrt{\frac{2 \times 1.090}{3 \times 3}} \times t_{0.025;46.}$$

$$= \sqrt{\frac{2 \times 1.090}{3 \times 3}} \times 2.016 = 0.990$$

$CD(0.05)$ for variety $\times$ potassium

$$= \sqrt{\frac{2 \times ErMS}{mr}} \times t_{\alpha/2;\text{error } d.f.}$$

$$= \sqrt{\frac{2 \times 1.090}{2 \times 3}} \times t_{0.025;46.}$$

$$= \sqrt{\frac{2 \times 1.090}{2 \times 3}} 2.016 = 1.213$$

$CD(0.05)$ for spacing $\times$ variety $\times$ potassium

$$= \sqrt{\frac{2 \times ErMS}{r}} \times t_{\alpha/2;\text{error } d.f.} = \sqrt{\frac{2 \times 1.090}{3}} \times t_{0.025;46.}$$

$$= \sqrt{\frac{2 \times 1.090}{3}} 2.016 = 1.715$$

Table of means:

Spacing	Yield(q/ha)		CD(0.05)
S2	204.722		**0.495**
S1	202.222		
Variety			
V3	203.958		**0.607**
V2	203.750		
V1	202.708		
Potassium			
K3	206.778		**0.701**
K2	204.889		
K1	202.167		
K0	200.056		
Spacing x Variety (S x V)			
S2V2	205.667		**0.858**
S2V3	205.083		
S2V1	203.417		
S1V3	202.833		
S1V1	202.000		
S1V2	201.833		
Spacing× Potassium(S×N)			
S2K3	207.333		**0.991**
S1K3	206.222		
S2K2	205.333		
S2K1	204.556		
S1K2	204.444		
S2K0	201.667		
S1K1	199.778		
S1K0	198.444		
Variety × Potassium (V x N)			
V3K3	207.667		**1.213**
V2K3	206.833		
V1K3	205.833		
V2K2	205.833		
V3K2	205.500		
V1K2	203.333		
V3K1	202.833		
V2K1	202.000		
V1K1	201.667		
V2K0	200.333		
V1K0	200.000		
V3K0	199.833		
Spacing x Variety x Potassium (S x V x P)			

S2V3K3	208.667		**1.716**
S2V2K3	208.333		
S1V1K3	206.667		
S1V3K3	206.667		
S2V2K2	206.667		
S2V3K2	206.000		
S2V2K1	205.667		
S1V2K3	205.333		
S1V2K2	205.000		
S1V3K2	205.000		
S2V1K3	205.000		
S2V3K1	204.333		
S2V1K1	203.667		
S1V1K2	203.333		
S2V1K2	203.333		
S2V2K0	202.000		
S2V1K0	201.667		
S1V3K1	201.333		
S2V3K0	201.333		
S1V1K1	199.667		
S1V2K0	198.667		
S1V1K0	198.333		
S1V2K1	198.333		
S1V3K0	198.333		

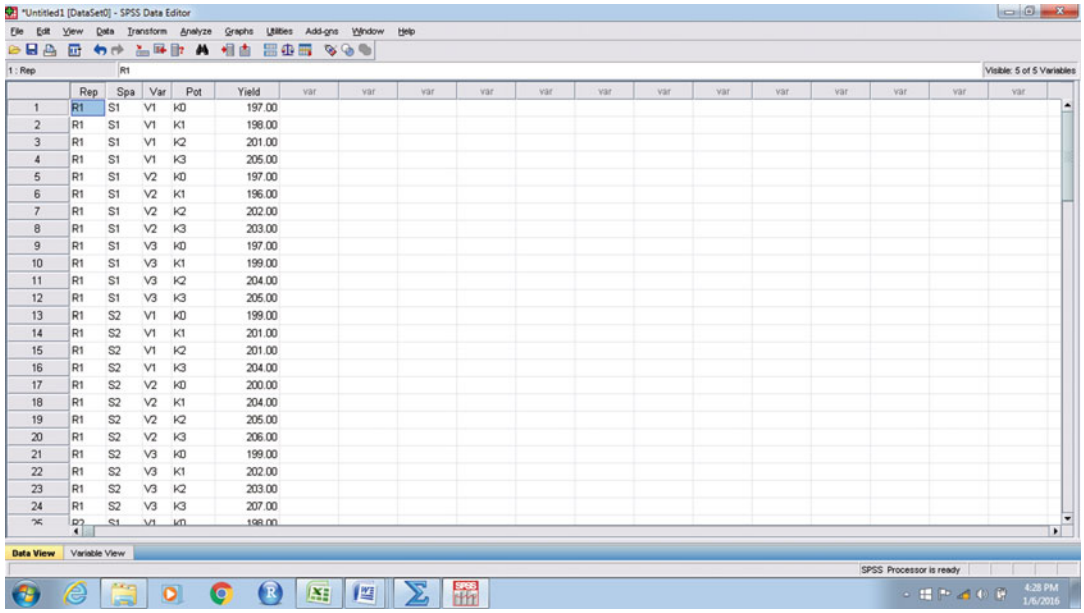
From the above table, we have the following conclusions:

(i) S2 spacing is significantly better than the S1 spacing.
(ii) Variety V3 is the best variety which is on par with V2.
(iii) All the doses of potassium are significantly different from each other and the best dose of potassium is K3.
(iv) Among the interaction effects of spacing and varieties, S2V2 is the best which is at par with S2V3 and so on.
(v) Among the interaction effects of spacing and potassium, S2K3 is the best followed by S1K3, S2K2, and so on.
(vi) Among the interaction effects of varieties and potassium, V3K3 and V2K3 are the best followed by V1K3, V2K3, and so on.
(vii) Among the three-factor interactions, S2V3K3 and S2V2K3 are the best interaction effect followed by S1V1K3, S1V3K3, S2V2K2, and so on.

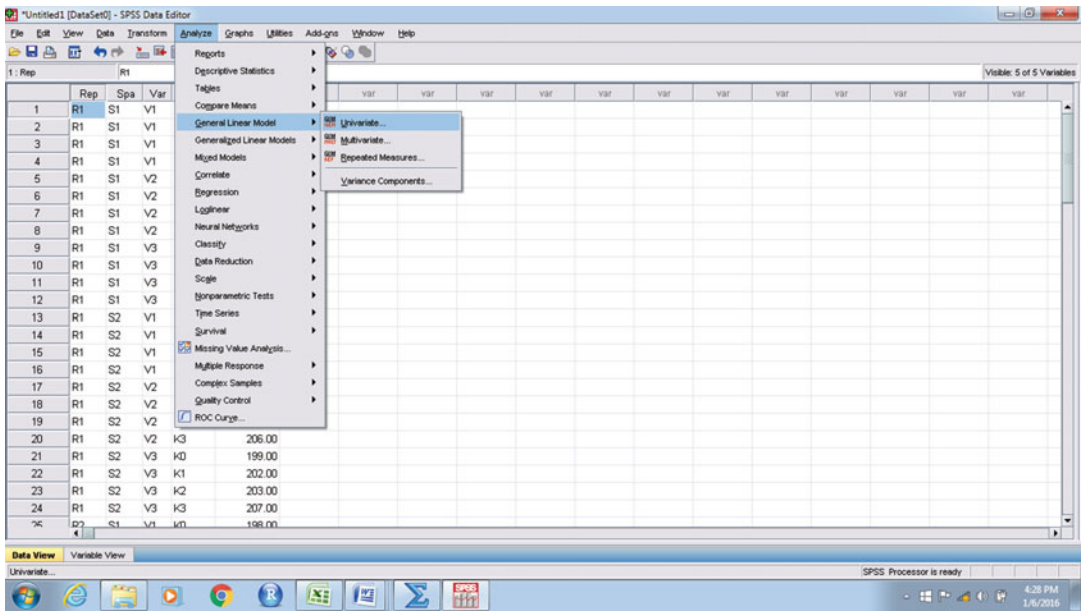
Example 11.10

In the following few slides, we shall demonstrate how the above analysis could be done using SPSS:

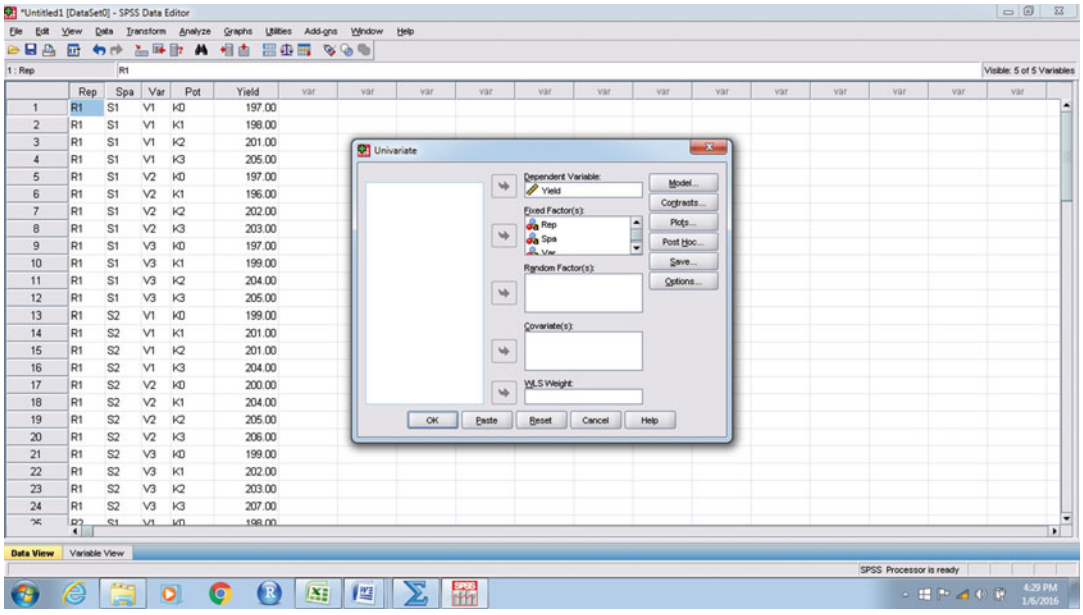
Step 1: Enter the data in SPSS data view as below; change the variable names.



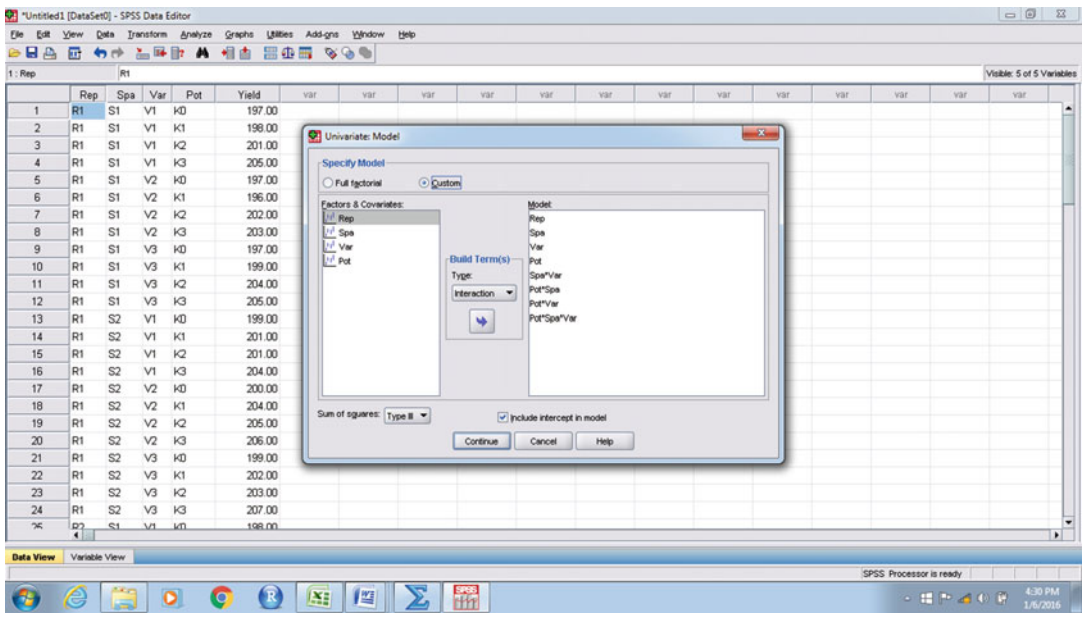
Step 2: Go to Analysis → Generalized linear model → Click on Univariate as below.



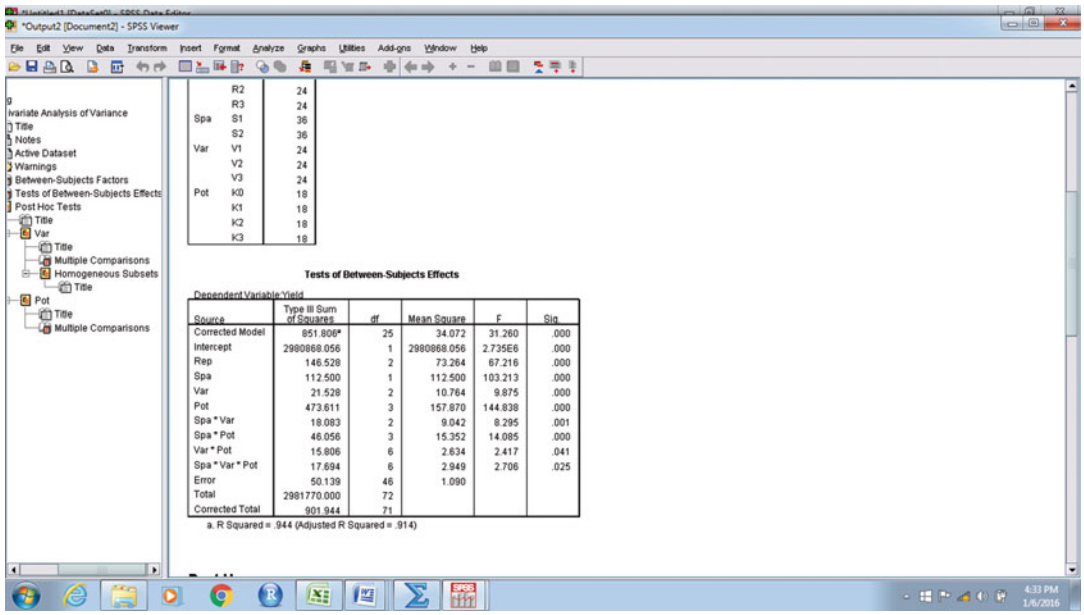
Step 3: Pass the dependent variable (in our case Yield) into the Dependent variable option and fixed variable into the Fixed variable (in our case Rep, Spa, Var, and Pot) as below.



Step 4: Click on Model → Change the option to custom → Pass the Rep, Spa, Var, Pot, Spa*Var, Spa*Pot, Var*Pot, and Pot*Spa*Var (by selecting Nitrogen and Sulfur with shift) into the Model as below.



Step 5: Click on Continue and then OK to get the output as below.



11.4 Incomplete Block Design

As we go on increasing the number of treatments in simple experiments or number of factors and/or their levels in factorial experiments and following the basic randomized block design, one has to accommodate a large number of treatments in each replication of a single block. Replications and blocks have so long been used synonymously. In practice, it is very difficult to obtain a complete block which can accommodate relatively large number of treatments. It becomes very difficult to accommodate such huge number of treatments in a complete block, as we do it with a randomized complete block design (randomized block design). For example, in 3^3 factorial experiment, we need to accommodate 27 treatment combinations in one block/replication. If one wants to conduct the same experiment using LSD, then he needs 27×27 numbers of experimental units which are to be homogenous in perpendicular way. The problem of getting such huge blocks of homogenous experimental units becomes more and more difficult as we further increase the number of treatments. Moreover, in factorial experiments using RBD, we test the significance of replication, main effects, and the interaction effects of different orders against only one error variance, which means all the effects are measured with equal precision. Thus this type of experimental setup should be used only when all the factors/treatment combinations are of equal importance and we require equal precision for all the factors/treatment combinations. On the other hand, if the factors are of unequal importance and are required to be estimated with differential precision, we are to think for some other setup of experimental design. Moreover for the sake of meticulous conduction of experimental protocol, one may require experimental units of different sizes for practical feasibility under field condition; for example, if one wants to accommodate different types of irrigation and different doses of nitrogen to be accommodated in one factorial experiment, it is quite usual that the irrigation treatment required larger plot size compared to the nitrogen factor. There are many instances in practical fields for such requirement. In all these cases, the conventional factorial experiment with RCB design will

not serve the purpose. With this backdrop including many other points, the idea of incomplete blocks came under consideration. According to this idea, *each replication is no longer constituted of a single block of size equal to the huge number of treatments included in the experiment rather each replication is being constituted of a number of small blocks of homogenous experimental units which can accommodate a part of the total treatments*. Thus, the blocks are incomplete in the sense that these are not constituted of or are not accommodating all the treatments of the experiment. In doing so the idea of a complete block equivalent to a replication changes to a replication constituted of number of incomplete blocks. As usual, the experimental units within a block are homogeneous compared to the experimental units among the blocks. In the process, the blocks are becoming one more source of variation in the analysis of variance. In this section, we are mainly concerned with initial experimental designs with incomplete blocks depending upon the need of the situations, and mainly we shall discuss the split plot and strip plot designs.

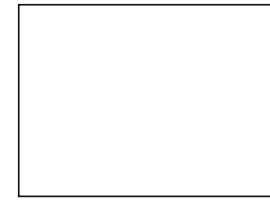
11.4.1 Split Plot Design

While accommodating different factors in a single experiment, particularly under field condition, the experimenter may have differential precision requirement for different factors or combinations. Moreover factors like types of irrigation, types of tillage, types of pest management, drainage management, weed management, etc. require comparatively larger size of plots for convenience compared to the factors like variety, fertilizer, dose, etc. To an experimenter conducting experiment with irrigation and the variety or doses of nitrogen, the varietal effect or the doses of nitrogen or the combination may be more important than the irrigation types; for irrigation treatments the experimenter may need comparatively larger plots than for variety/fertilizer. Thus in such experiments, we are to handle two situations, viz., requirement of differential plot size and differential precision for different treatments. In such cases we opt for split plot designs.

Each and every replication in split plot design is constituted of number of blocks equal to the number of levels of the factor requiring higher plot size and lesser precision, known as the *main plot factor*. Again each and every block should be constituted of as many numbers of homogenous experimental units as the levels of the other factor which require lesser plot size compared to the main plot factor and higher precision, known as the *subplot factor*.

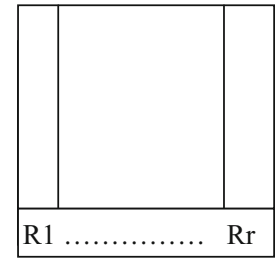
Layout and Randomization

Let there be two factors A and B at p and q levels, respectively, included in a split plot experiment and the factor A is the main plot factor, while the factor B is the subplot factor**.** The step-by-step procedure of the layout for a $p \times q$ split plot design with r replications is as follows:

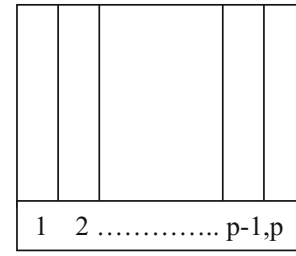


Whole experimental area

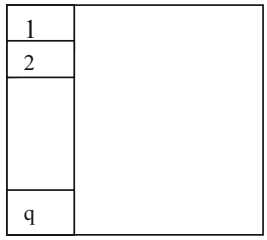
Step 1: The whole experimental area is divided into r replications across the fertility gradient of the field.



Step 2: Each and every replication should be subdivided into p number of blocks (main plot) of equal size as shown below.

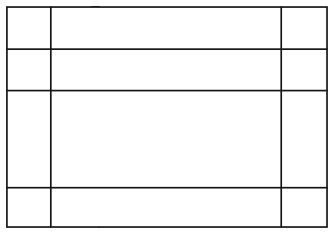


Step 3: Each and every main plot should be constituted of q number of homogenous experimental units of equal size.



Step 4: The p levels of the main plot factor are randomly distributed among p blocks in each and every replication separately.

Step 5: The q levels of the subplot factor are randomly allocated to q subplots of each and every p main plot factor separately.



Separate sets of random numbers are to be used in each and every step of randomization.

Statistical model and analysis:

$$y_{ijk} = \mu + \gamma_i + \alpha_j + e_{ij} + \beta_k + \upsilon_{jk} + e'_{ijk}$$

where $i = 1, 2, \ldots, r$; $j = 1, 2, \ldots, p$; and $k = 1, 2, \ldots, q$

μ = general effect

γ_i = additional effect due to the ith replication

α_j = additional effect due to the jth level of the main plot factor A and $\sum_{j=1}^{p} \alpha_j = 0$

β_k = additional effect due to the kth level of the subplot factor B and $\sum_{k=1}^{q} \beta_k = 0$

υ_{jk} = interaction effect due to the jth level of the main plot factor A and kth level of the subplot factor B and $\sum_{j} \upsilon_{jk} = \sum_{k} \upsilon_{jk} = 0$ for all k for all j

e_{ij} (error I) = error associated with the ith replication and jth level of the main plot factor.

e'_{ijk} (error II) = error associated with the ith replication, jth level of the main plot factor, and kth level of the subplot factor and $e_{ijk}{}' \sim$ i.i.d. N(0, $\sigma_s{}^2$)

Hypothesis to be tested:

$$H_0 : \gamma_1 = \gamma_2 = \ldots\ldots = \gamma_i = \ldots\ldots = \gamma_r = 0$$
$$\alpha_1 = \alpha_2 = \ldots\ldots = \alpha_j = \ldots\ldots = \alpha_p = 0$$
$$\beta_1 = \beta_2 = \ldots\ldots = \beta_k = \ldots\ldots = \beta_q = 0$$
$$\upsilon_{11} = \upsilon_{12} = \ldots\ldots = \upsilon_{jk} = \ldots\ldots = \upsilon_{pq} = 0$$

H_1 : γ's are not all equal
α's are not all equal
β's are not all equal
υ's are not all equal

Let the level of significance be 0.05.

ANOVA for split plot design

SOV	d.f.	*SS*	*MS*	Cal. *F*
Replication	$r-1$	SS_R	MS_R	$MS_R/MS_{(Er\ I)}$
Main plot factor (A)	$p-1$	$SS_{(A)}$	$MS_{(A)}$	$MS_{(A)}/MS_{(Er\ I)}$
Error I	$(r-1)(p-1)$	$SS_{(Er\ I)}$	$MS_{(Er\ I)}$	
Subplot factor (B)	$(q-1)$	$SS_{(B)}$	$MS_{(B)}$	$MS_{(B)}/MS_{(Er\ II)}$
Interaction (A × B)	$(p-1)(q-1)$	$SS_{(AB)}$	$MS_{(AB)}$	$MS_{(AB)}/MS_{(Er\ II)}$
Error II	$p\,(q-1)(r-1)$	$SS_{(Er\ II)}$	$MS_{(Er\ II)}$	
Total	$pqr-1$			

Different sums of squares and mean sum of squares are calculated as follows:

1. Grand total = $GT = \sum_{i=1}^{r}\sum_{j=1}^{p}\sum_{k=1}^{q} y_{ijk}$.
2. Correction factor = $CF = \dfrac{GT^2}{pqr}$.
3. $SS_{\text{Tot}} = \sum_{i=1}^{r}\sum_{j=1}^{p}\sum_{k=1}^{p} y_{ijk}^2 - CF$.
4. Work out the sum of square due to the main plot factor and the replication. For the purpose

Table 11.1 Totals of the main plot × replication

	A_1	A_2	. . .. . .	A_j	. . .. . .	A_p	Total	Average
R_1	$y_{11.}$	$y_{12.}$	. . .. . .	$y_{1j.}$	. . .. . .	$y_{1p.}$	$\sum y_{1..}$	$\overline{y}_{100}$
R_2	$y_{21.}$	$y_{22.}$	. . .. . .	$y_{2j.}$	. . .. . .	$y_{2p.}$	$\sum y_{2..}$	$\overline{y}_{200}$
:	:	:	:	:	:	:	:	
R_i	$y_{i1.}$	$y_{i2.}$	. . .. . .	$y_{ij.}$	. . .. . .	$y_{ip.}$	$\sum y_{i..}$	$\overline{y}_{i00}$
:	:	:	:	:	:	:	:	
R_r	$y_{r1.}$	$Y_{r2.}$	. . .. . .	$y_{rj.}$	. . .. . .	$y_{rp.}$	$\sum y_{r..}$	$\overline{y}_{r00}$
Total	$\sum y_{.1.}$	$\sum y_{.2.}$	. . .. . .	$\sum y_{.j.}$	. . .. . .	$\sum y_{.p.}$	$\sum y_{...}$	$\overline{y}_{000}$
Average	$\overline{y}_{.1.}$	$\overline{y}_{.2.}$		$\overline{y}_{.j.}$		$\overline{y}_{.p.}$		

Table 11.2 Totals of the main plot × subplot factors

	B_1	B_2	. . .. . .	B_k	. . .. . .	B_n	Total	Average
A_1	$y_{.11}$	$y_{.12}$	. . .. . .	$y_{.1k}$	. . .. . .	$y_{.1q}$	$\sum y_{.1.}$	$\overline{y}_{.1.}$
A_2	$y_{.21}$	$y_{.22}$	. . .. . .	$y_{.2k}$	. . .. . .	$y_{.2q}$	$\sum y_{.2.}$	$\overline{y}_{.2.}$
:	:	:	:	:	:	:	:	
A_j	$y_{.j1}$	$y_{.j2}$	. . .. . .	$y_{.jk}$	. . .. . .	$y_{.jq}$	$\sum y_{.j.}$	$\overline{y}_{.j.}$
:	:	:	:	:	:	:	:	
A_p	$y_{.p1}$	$y_{.p2}$	. . .. . .	$y_{.pk}$	. . .. . .	$y_{.pq}$	$\sum y_{.p.}$	$\overline{y}_{.m.}$
Total	$\sum y_{..1}$	$\sum y_{..2}$	. . .. . .	$\sum y_{..k}$	. . .. . .	$\sum y_{..q}$	$\sum y_{...}$	$\overline{y}_{...}$
Average	$\overline{y}_{..1}$	$\overline{y}_{..2}$		$\overline{y}_{..k}$		$\overline{y}_{..q}$		

the following table of totals is required to be framed (Table 11.1).

where $y_{ij.} = \sum_{k=1}^{q} y_{ijk}$

$$SS_{\text{(Table 11.1)}} = \frac{1}{q}\sum_{i}^{r}\sum_{j}^{p} y_{ij.}^2 - CF$$

$$SS_R = \frac{1}{pq}\sum_{i=1}^{r} y_{i..}^2 - CF$$

$$SS(A) = \frac{1}{qr}\sum_{j=1}^{p} y_{.j.}^2 - CF$$

$$SS_{\text{Error I}} = SS_{\text{(Table I)}} - SS_R - SS_{(A)}$$

5. Work out the sum of squares due to the subplot factor and interaction. For the purpose, the following table of totals is required to be formed (Table 11.2):

Check: In both the tables, the totals for the main factor A at different levels are the same:

$$SS_{\text{(Table 11.2)}} = \frac{1}{r}\sum_{j=1}^{p}\sum_{k=1}^{q} y_{.jk}^2 - CF$$

$$SS_{(B)} = \frac{1}{pr}\sum_{k=1}^{q} y_{..k}^2 - CF$$

$$SS_{(AB)} = SS_{\text{(Table 11.2)}} - SS_{\text{(A)}} - SS_{\text{(B)}}$$

$$SS_{\text{(Error II)}} = SS_{\text{Tot}} - SS_R - SS_{(A)} - SS_{\text{(Error I)}} - SS_{(B)} - SS_{(AB)}$$

Mean sums of squares are calculated dividing the sum of squares by corresponding degrees of freedom.

6. F ratios for replication and main plot factors are compared to the respective mean sum of squares against mean sum of squares due to error I, while the F ratios corresponding to the subplot factor and the interaction effects are worked out by comparing the respective mean sum of squares against the mean sum of squares due to error II.

7. Calculated F ratios are compared with the tabulated value of F at appropriate level of significance and degrees of freedom.
8. In the event of significance of F test, one needs to estimate the standard errors (SEs) for different types of mean comparison as follows:
   (a) The CD to compare two replication means value will be $CD_\alpha = \sqrt{\frac{2\text{MS}_{(\text{Er I})}}{pq}} \times t_{\alpha/2;\text{error}-I \;\; d.f.}$.
   (b) The CD to compare two main plot treatment means will be $CD_\alpha = \sqrt{\frac{2MS_{(Er\ I)}}{rq}} \times t_{\alpha/2;\text{error}-I \;\; d.f.}$.
   (c) The SE for the difference between two subplot treatment means $= \sqrt{\frac{2ErMS-II}{rm}}$, and the corresponding CD value will be $CD_\alpha = \sqrt{\frac{2MS_{(Er\ II)}}{rp}} \times t_{\alpha/2;\text{error}-II \;\; d.f.}$.
   (d) The CD value to compare two subplot treatment means at the same level of the main plot treatment will be $CD_\alpha = \sqrt{\frac{2\text{MS}_{(Er\ \text{II})}}{r}} \times t_{\alpha/2;\text{error}II \;\; d.f.}$.
   (e) The CD value to compare two main plot treatment means at the same or different levels of the subplot treatment $= \sqrt{\frac{2\left[(q-1)MS_{(Er\ \text{II})}+MS_{(Er\ \text{I})}\right]}{rq}}\, t^*$, where approximate value of t is calculated as

$$t^* = \frac{t_1 MS_{(Er\ \text{I})} + t_2(n-1)MS_{(Er\ \text{II})}}{MS_{(Er\ \text{I})} + (n-1)MS_{(Er\ \text{II})}}$$ where t_1 and t_2 are tabulated values at error I and error II degrees of freedom, respectively, at the chosen significance level.

Advantages and disadvantages:

Advantages:

(i) The advantage of managing different factors as per the requirement without sacrificing the information from the design is the main advantage.
(ii) Different factor effects are estimated at different precision levels which was not possible in simple experiments. In split plot designs, the subplot factor and its interaction with the main plot factor are estimated more precisely than the main plot factor effect.

Disadvantages:

(i) The factor to be assigned as the main plot factor or subplot factor is of extremely importance.
(ii) Randomization and layout along with the analysis are somewhat complicated compared to other simple experiments.
(iii) The comparison of the main plot treatment means at the same or different levels of the subplot treatment (CD e) is somewhat approximately 1.
(iv) When both the factors require larger plot size, then split plot design is not suitable.

Example 11.11 (Split Plot Experiment)
To know the effect of three different feeds and four doses of trilostane on the weight of broiler chicken, an experiment was conducted. The experiment was conducted in nine net houses comprised of three blocks each having three net houses. Each net house was then partitioned into four big cages. Three different feeds were randomly allocated to each of the three net houses separately in each and every block. Among the four cages of each and every net house, four doses of trilostane were allocated randomly. Chick weights are recorded at the age of 40 days. Analyze the data and draw your conclusion:

Feed	Feed 1				Feed 2				Feed 3			
Trilostane	T1	T2	T3	T4	T1	T2	T3	T4	T1	T2	T3	T4
Block 1	1.83	1.88	1.92	2.01	1.85	1.91	1.94	2.05	1.86	1.93	1.97	2.22
Block 2	1.84	1.89	1.93	2.03	1.86	1.92	1.95	2.09	1.86	1.93	1.96	2.17
Block 3	1.81	1.88	1.93	2.05	1.87	1.91	1.95	2.07	1.85	1.94	1.97	2.19

Solution Here in this experimenteach net house in each block can be treated as the main plot in split plot design and four cages in each net house as the subplots. Thus we have three main plot factors and four subplot factors. Main plot and subplot factors are feed and doses of trilostane, respectively. The experiment is repeated three times, i.e., in three blocks.

Thus for the above experiment, we have three levels of main plot factors and four levels of subplot factors in three replications. The appropriate statistical model is

$$y_{ijk} = \mu + \gamma_i + \alpha_j + e_{ij} + \beta_k + \upsilon_{jk} + e_{ijk}$$

where $i = 1, 2, 3$; $j = 1, 2, 3$; and $k = 1, 2, 3, 4$

μ = general effect

γ_i = additional effect due to ith replication

α_j = additional effect due to jth level of the main plot factor, i.e., feed, and $\sum_{j=1}^{3} \alpha_j = 0$

β_k = additional effect due to kth level of the subplot factor, i.e., trilostane, and $\sum_{k=1}^{4} \beta_k = 0$

υ_{jk} = interaction effect due to jth level of the main plot factor (feed) and kth level of the subplot factor (trilostane) and $\sum_{j=1}^{3} \upsilon_{jk} = \sum_{k=1}^{4} \upsilon_{jk} = 0$

e_{ij} (error I) = error associated with ith replication and jth level of the main plot factor and $e_{ij} \sim$ i.i.d. $N(0, {\sigma_m}^2)$

e'_{ijk} (error II) = error associated with ith replication, jth level of the main plot factor (feed), and kth level of the subplot factor (trilostane) and $e_{ijk} \sim$ i.i.d. $N(0, {\sigma_s}^2)$

Hypothesis to be tested:

$H_0 : \gamma_1 = \gamma_2 = \gamma_3 = 0$
$\alpha_1 = \alpha_2 = \alpha_3 = 0$
$\beta_1 = \beta_2 = \beta_3 = \beta_4 = 0$
$\upsilon's$ are all equal to zero

against

$H_1 : \alpha's$ are not all equal
$\gamma's$ are not all equal
$\beta's$ are not all equal
$\upsilon's$ are not all equal

Let the level of significance be 0.05.

The step-by-step procedure for the computation of different sums of square and mean sum of squares is given as follows:

Step 1: From raw data we have

$$GT = \sum_{i=1}^{3}\sum_{j=1}^{3}\sum_{k=1}^{4} y_{ijk} = GT = 1.83 + 1.88 + \ldots\ldots + 1.97 + 2.19 = 73.95.$$

$$\text{Correction factor } (CF) = \frac{GT^2}{mnr} = \frac{73.95^2}{3 \times 4 \times 3} = 136.9680.$$

$$SS_{\text{TOT}} = \sum_{i=1}^{3}\sum_{j=1}^{3}\sum_{k=1}^{4} y_{ijk}^2 - CF = 1.83^2 + 1.88^2 + \ldots\ldots + 1.97^2 + 2.19^2 - 136.968 = 0.3607.$$

Step 2: Work out the sum of square due to the main plot factor and the replication. The following table of totals is required to be framed (Table 11.3):

$$SS_{(\text{Table } 11.3)} = \frac{1}{q}\sum_{i=1}^{r}\sum_{j=1}^{p} y_{ij.}^2 - CF = 16.0939$$

$$SS_R = \frac{1}{pq}\sum_{i=1}^{r} y_{i..}^2 - CF = \frac{1}{3 \times 4}\sum_{i=1}^{3} y_{i..}^2 - CF = \frac{23.37^2 + 23.43^2 + 23.42^2}{12} - 136.9680 = 0.00017.$$

Table 11.3 Table of totals for feed × replication

	Replication			
Feed	R1	R2	R3	Total
F1	7.64	9.55	9.54	26.73
F2	7.75	7.82	7.80	23.37
F3	7.98	7.92	7.95	23.85
Total	23.37	25.29	25.29	73.95
Average	36.33	36.43	36.63	

$$SS_{(\text{Feed})} = \frac{1}{qr}\sum_{j=1}^{p} y_{.j}^2 - CF$$

$$= \frac{1}{4\times 3}\sum_{j=1}^{3} y_{.j}^2$$

$$-CF = \frac{23.00^2 + 23.37^2 + 23.85^2}{12} -$$

$$136.9680 = 0.03027$$

$$SS_{(\text{Error I})} = TSS_{(\text{Table I})} - SS_R - SS_{(F)}$$

$$= 0.031688 - 0.000172 - 0.030272$$

$$= 0.00124$$

Step 3: Work out the sum of square due to the subplot factor and interaction. The following table of totals is required to be formed (Table 11.4):

$$SS_{(\text{Table 11.4})} = \frac{1}{3}\sum_{j=1}^{p}\sum_{k=1}^{4} y_{.jk} - CF$$

$$= \frac{1}{3}[5.48^2 + 5.65^2 ..... + 5.90^2$$

$$+6.58^2] - 136.9680 = 0.35678$$

$$SS_{(\text{Trilostane})} = \frac{1}{pr}\sum_{k=1}^{n} y_{..k}^2 - CF = \frac{1}{3\times 3}\sum_{k=1}^{4} y_{..k}^2 - CF$$

$$= \frac{16.63^2 + 17.19^2 + 17.52^2 + 18.88^2}{3\times 3}$$

$$-136.9680 = 0.30507$$

$$SS_{(F\times T)} = SS_{(\text{tableII})} - SS_{(F)} - SS_{(T)}$$

$$= 0.35670 - 0.03027 - 0.305077$$

$$= 0.021438$$

$$SS_{Er.II} = SS_T - SS_R - SS_{(F)} - SS_{ErI} - SS_{(T)}$$

$$-SS_{(F\times T)} = 0.36078 - 0.000172$$

$$-0.030272 - 0.00124 - 0.30507$$

$$-0.0214 = 0.0025833$$

Table 11.4 Table of totals for feed × trilostane

	Trilostane					
Feed	T1	T2	T3	T4	Total	Average
F1	5.48	5.65	5.78	6.09	23.00	1.92
F2	5.58	5.74	5.84	6.21	23.37	1.95
F3	5.57	5.80	5.90	6.58	23.85	1.99
Total	16.63	17.19	17.52	18.88		
Average	1.85	1.91	1.95	2.10		

Step 4: Mean sums of squares are calculated by dividing the sum of square by corresponding degrees of freedom.

Step 5: F ratios for the replication and main plot are obtained by comparing the respective mean sum of squares against the mean sum of square due to error I. On the other hand, the F ratios corresponding to the subplot factor and the interaction effects are worked out by comparing the respective mean sum of squares against the mean sum of square due to error II:

ANOVA table for 3 × 4 split plot experiment

					Tab. F
SOV	d.f.	*MS*	*MS*	*F* ratio	p =0.05
Replication	3−1 = 2	0.000172	0.00009	0.27679	6.94
Main Plot Factor(Feed)	3−1 = 2	0.030272	0.01514	48.65179	6.94
Error I	(3–1) (3–1) =4	0.001244	0.00031		
Subplot factor (Trilostane)	(4–1) = 3	0.305078	0.10169	708.56774	3.16
Interaction (F × T)	(3–1) (4–1) = 6	0.021439	0.00357	24.89677	2.66
Error II	3 (4–1) (3–1) = 18	0.002583	0.00014		
Total	3.3.4−1 = 35	0.360789			

Calculated F ratios are compared with the tabulated value of F at $\alpha = 0.05$ and $\alpha = 0.01$ levels of significance and at appropriate degrees of freedom. It is found that the effects of feed, trilostane, and their interaction are significant at both 5 % and 1 % level of significance.

Our next task will be to estimate the SE's for different types of comparison as given below:

(i) The standard error for the difference between two feed means $= \sqrt{\frac{2ErMS-I}{rq}} = \sqrt{\frac{2(0.00031)}{3\times4}} = 0.00720$, and the corresponding CD value could be $CD_{(0.05)} = \sqrt{\frac{2ErMS-I}{rq}}\, t_{(0.025);\text{error}-I\ \ d.f.} = \sqrt{\frac{2(0.00031)}{3\times4}} \times 2.776 = 0.0199$.

(ii) The standard error for the difference between two subplot trilostane means $= \sqrt{\frac{2MS_{Er-II}}{rp}} = \sqrt{\frac{2(0.00014)}{3\times3}}$, and the corresponding CD value could be $CD_{(0.05)} = \sqrt{\frac{2MS_{Er-II}}{rp}} t_{0.025;\text{error}-II\ \ d.f.} = \sqrt{\frac{2(0.00014)}{3\times3}} \times 2.101 = 0.01186$.

(iii) The standard error for the difference between two feed means at the same or different levels of the subplot treatment trilostane $= \sqrt{\frac{2[(q-1)MS_{Er-II}+MS_{Er-I}]}{rq}} = \sqrt{\frac{2[(4-1)0.00014+0.00031]}{3.4}} = 0.0032095$, but the ratio of the treatment mean difference and the above SE does not follow t-distribution, and approximately the value of t is given by

$$t(cal) = \frac{t_1 MS_{Er-I} + t_2(q-1)MS_{Er-II}}{MS_{Er-I} + (q-1)MS_{Er-II}} = \frac{(2.776)(0.00031) + (2.101)(4-1)0.00014}{(0.00031) + (4-1)(0.00014)} = 2.3841$$

where $t_1 = t_{0.025,4}$ value and $t_2 = t_{0.025,18}$ value and the corresponding CD value could be $CD_{(0.05)} = SE_d \times t(cal) = 0.003209 \times 2.38414 = 0.00765$:

Feed	Average	CD (0.05)
F3	1.988	0.01990
F2	1.948	
F1	1.917	
Trilostane		
T4	2.098	0.01186
T3	1.947	
T2	1.910	
T1	1.848	
$F \times T$		
F3T4	2.193	0.00765
F2T4	2.070	
F1T4	2.030	
F3T3	1.967	
F2T3	1.947	
F3T2	1.933	
F1T3	1.927	
F2T2	1.913	
F1T2	1.883	
F2T1	1.860	
F3T1	1.857	
F1T1	1.827	

From the table mean comparison given below, it is clear that feed 3 is the best feed, followed by F2 and F1. All the feeds are significantly different from each other. So far as the effect of trilostane is concerned, maximum weight of chicks is obtained from T4 followed by T3, T2, and T1. All the levels of trilostane are significantly different from each other with respect to the weight of chicks at 40 days of age. The interaction of the feed and the trilostane has significantly different effects from each other; F3T4 interaction is the best.

Example 11.11 (Split Plot in SPSS Using the Syntax)

In SPSS split plot analysis can be done by using the syntax, and in the following section, we shall demonstrate the analysis of the above example using the syntax in SPSS.

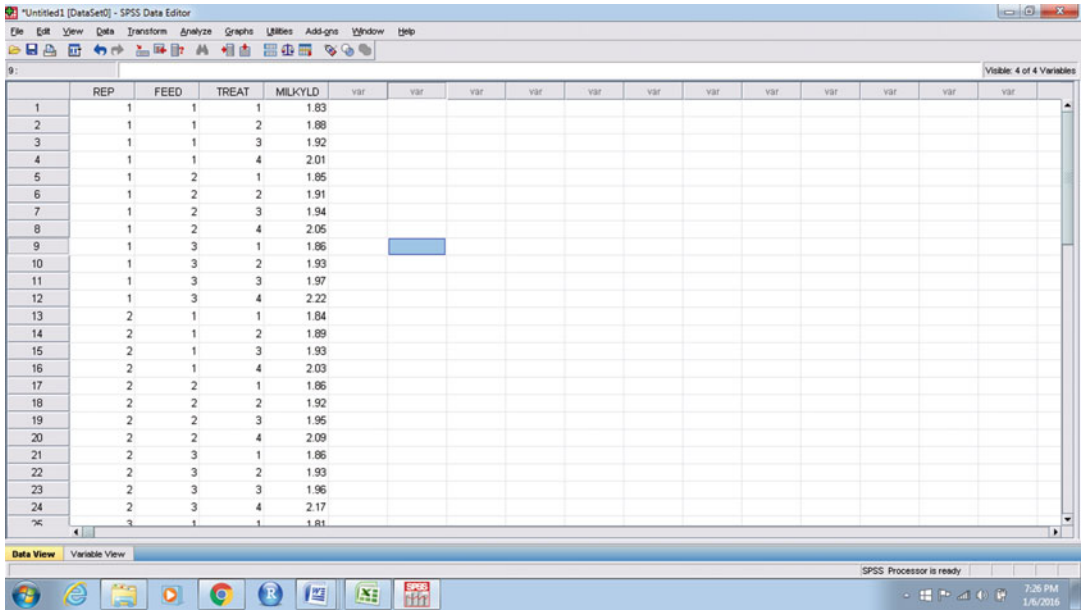
Syntax for the example taken:

```
UNIANOVA
MILKYLD BY REP FEED TREAT
/METHOD = SSTYPE(3)
/INTERCEPT = INCLUDE
/CRITERIA = ALPHA(.05)
```

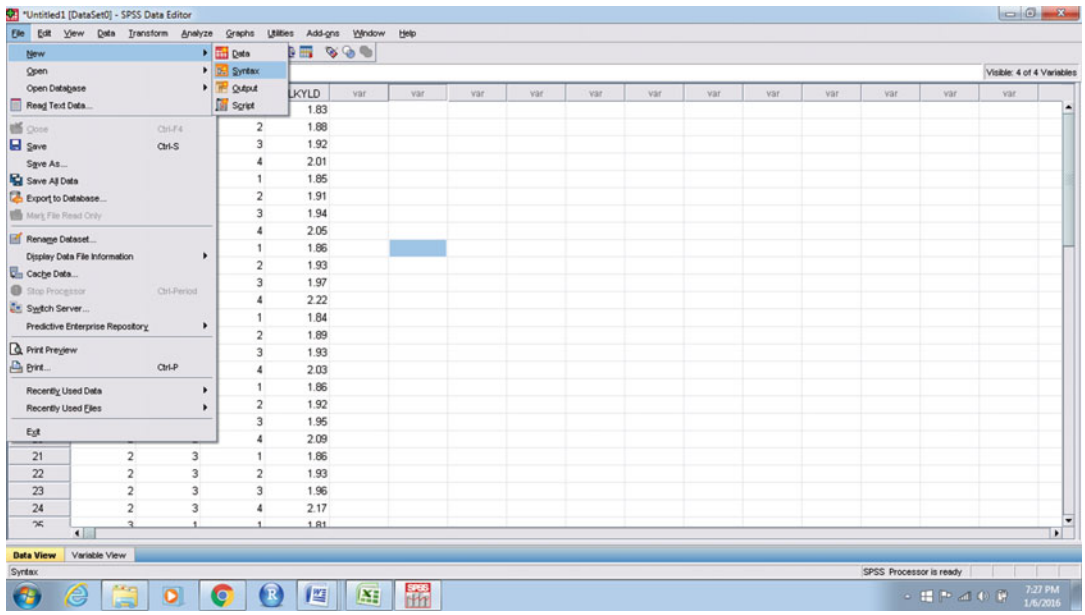
/DESIGN = REP FEED REP*FEED TREAT FEED*TREAT

/TEST FEED VS REP*FEED.

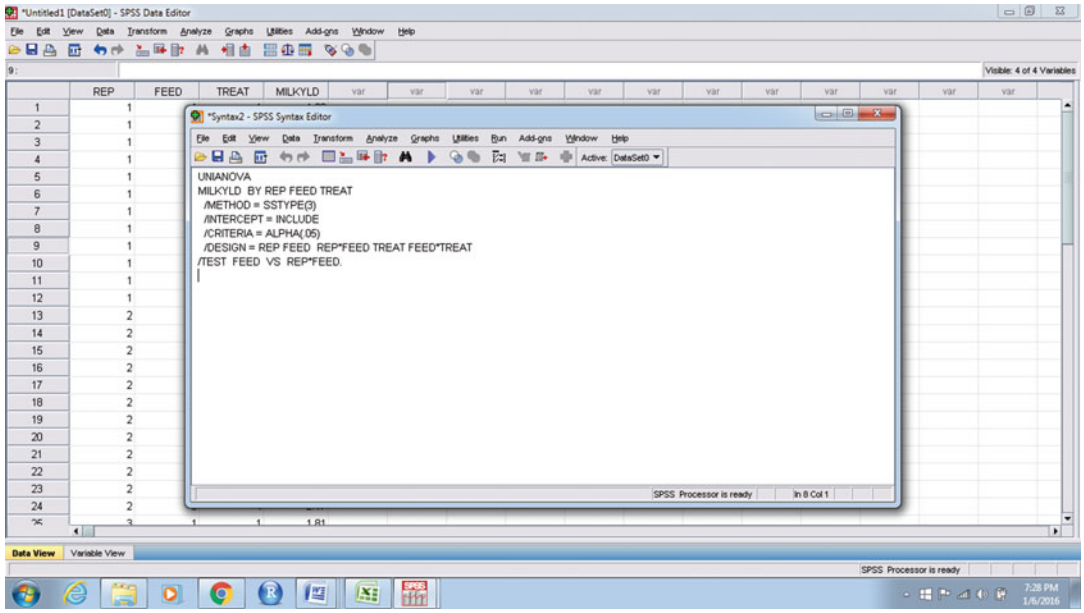
Step 1: Enter the data in SPSS data view as shown below.



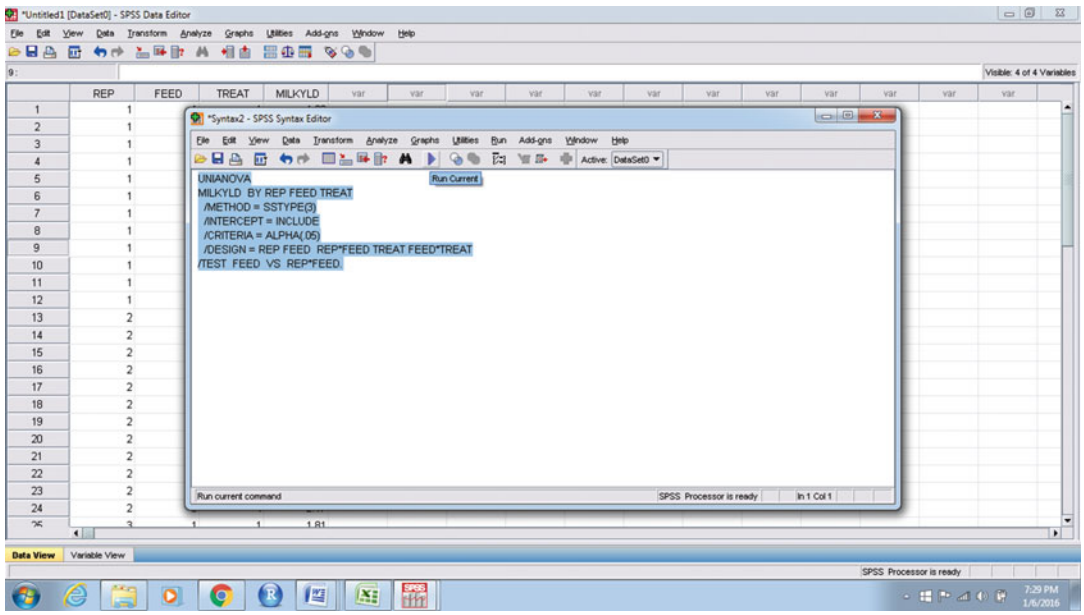
Step 2: Go to File → New → Click on "Syntax" as below.



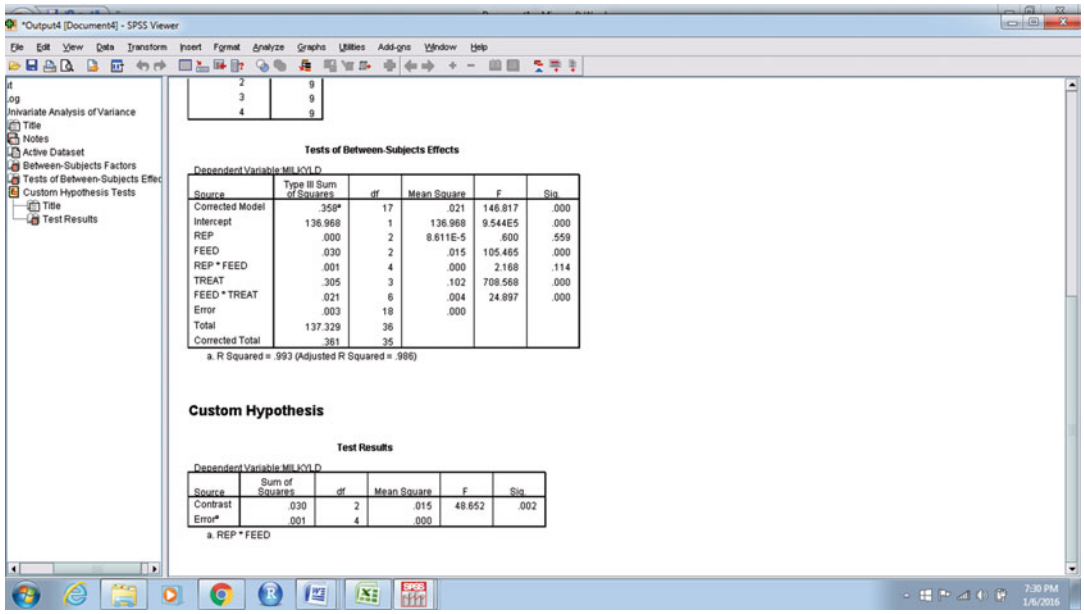
Step 3: Write the syntax as below.



Step 4: Select all the syntax lines and then press “Run Current” as mentioned below.



Step 5: The output will appear in the output window.



Note: Custom Hypothesis is for the main plot error.

CD values and the mean comparison can be taken as usual.

Example 11.12 (Split Plot Design)
A field experiment was conducted to identify the best spacing and date of sowing in *rabi* arhar. Three different spacings were randomly allocated to three main plots in each replication separately, and in each main plot, four dates of sowing were allocated randomly among the four plots in each main plot. Grain yields (t/ha) are recorded from the individual plots and given below. Analyze the data and draw your conclusion:

Spacing	Spacing-1				Spacing-2				Spacing-3			
DOS	D1	D2	D3	D4	D1	D2	D3	D4	D1	D2	D3	D4
Rep-1	17.42	11.89	8.62	7.74	11.89	10.07	3.92	3.26	9.77	4.13	2.96	2.24
Rep-2	17.45	11.93	8.67	7.78	11.95	10.10	3.96	3.32	9.82	4.18	3.04	2.29
Rep-3	17.45	11.94	8.65	7.77	11.93	10.09	3.94	3.30	9.79	4.16	2.98	2.26

For the above experiment with three levels of main plot factors and four levels of subplot factors in three replications, the appropriate statistical model is

$$y_{ijk} = \mu + \gamma_i + \alpha_j + e_{ij} + \beta_k + \upsilon_{jk} + e_{ijk}$$

where $i = 1, 2, 3$; $j = 1, 2, 3$; and $k = 1, 2, 3, 4$

μ = general effect
γ_i = additional effect due to ith replication
α_j = additional effect due to jth level of the main plot factor, i.e., spacing, and $\sum_{j=1}^{3} \alpha_j = 0$
β_k = additional effect due to kth level of the subplot factor, i.e., date of sowing, and $\sum_{k=1}^{4} \beta_k = 0$

υ_{jk} = interaction effect due to jth level of the main plot factor (spacing) and kth level of the subplot factor (date of sowing) and $\sum_{j=1}^{3} \upsilon_{jk} = \sum_{k=1}^{4} \upsilon_{jk} = 0$

e_{ij} (error I) = error associated with ith replication and jth level of the main plot factor and $e_{ij} \sim$ i.i.d. $N(0, {\sigma_m}^2)$

e_{ijk} (error II) = error associated with ith replication, jth level of the main plot factor (spacing), and kth level of the subplot factor (date of sowing) and $e_{ijk} \sim$ i.i.d. $N(0, {\sigma_s}^2)$

Hypothesis to be tested:

$H_0 : \gamma_1 = \gamma_2 = \gamma_3 = 0$
$\alpha_1 = \alpha_2 = \alpha_3 = 0$
$\beta_1 = \beta_2 = \beta_3 = \beta_4 = 0$
All interaction effects ${\upsilon_{jk}}'s$ are equal to zero

$H_1 : \alpha's$ are not all equal
$\gamma's$ are not all equal
$\beta's$ are not all equal
All interaction effects ${\upsilon_{jk}}'s$ are not equal

Let the level of significance be 0.05.

The step-by-step procedure for the computation of different sums of square and mean sum of squares are given as follows:

Step 1: From raw data we have

$$\text{Grand total } (GT) = \sum_{i=1}^{3}\sum_{j=} 1^3 \sum_{k=1}^{4} y_{ijk} =$$

$17.42 + 17.45 + \ldots\ldots + 2.29 + 2.26 = 282.66.$

$$\text{Correction factor } (CF) = GT^2\, mnr = \frac{282.66^2}{3 \times 4 \times 3}$$

$= 2219.352.$

$$\text{SS}_{\text{Tot}} = \sum_{i=1}^{3}\sum_{j=1}^{3}\sum_{k=} 1^4 y_{ijk}^2 - CF = 17.42^2 +$$

$17.45^2 + \ldots\ldots + 2.29^2 +$
$2.26^2 - 2219.352 = 717.125.$

Step 2: Work out the sum of square due to the main plot factor and the replication. The following table of totals is required to be framed (Table 11.5):

Table 11.5 Table of totals for spacing × replication

Spacing	Replication			Total	Mean
	R1	R2	R3		
S1	45.67	45.83	45.81	137.31	11.4425
S2	29.14	29.33	29.26	87.73	7.310833
S3	19.1	19.33	19.19	57.62	4.801667
Total	93.91	94.49	94.26		

$$SS_{(\text{Table 11.5})} = \frac{1}{n}\sum_{i=1}^{r}\sum_{j=1}^{m} y_{ij.}^2 - CF$$
$$= 269.884$$

$$SS_R = \frac{1}{mn}\sum_{i=1}^{r} y_{i00}^2 - CF = \frac{1}{3 \times 4}\sum_{i=1}^{3} y_{i..}^2 - CF$$

$$= \frac{93.91^2 + 94.49^2 + 94.26^2}{12}$$

$-2219.352 = 0.0142$

$$SS_{(\text{Spa})} = \frac{1}{nr}\sum_{j=1}^{m} y_{.j.}^2 - CF = \frac{1}{4 \times 3}$$

$$\sum_{j=1}^{3} y_{.j.}^2 - CF = \frac{137.31^2 + 87.73^2 + 57.62^2}{12}$$

$-2219.352 = 269.869$

$$SS_{(\text{Error I})} = SS_{(\text{Table I})} - SS_R - SS_{(\text{Spa})}$$
$$= 269.884 - 0.0142 - 269.869 = 0.0009$$

Step 3: Work out the sum of square due to the subplot factor and interaction. The following table of totals is required to be formed (Table 11.6):

Table 11.6 Table of totals for spacing × date of sowing

Spacing	Date of sowing				Total	Mean
	D1	D2	D3	D4		
S1	52.32	35.76	25.94	23.29	137.31	11.44
S2	35.77	30.26	11.82	9.88	87.73	7.31
S3	29.38	12.47	8.98	6.79	57.62	4.80
Total	117.47	78.49	46.74	39.96		
Mean	13.05	8.72	5.19	4.44		

$$SS_{(\text{Table 11.6})} = \frac{1}{3}\sum_{j=1}^{m}\sum_{k=1}^{4} y_{.jk} - CF$$

$$= \frac{1}{3}\left[52.32^2 + 35.77^2 + \ldots\ldots + 6.79^2\right] - CF$$

$$= 717.109$$

$$SS(\text{DOS}) = \frac{1}{mr}\sum_{k=1}^{n} y_{..k}^2 - CF = \frac{1}{3\times 3}\sum_{k=1}^{4} y_{..k}^2 - CF = \frac{117.47^2 + 78.49^2 + 46.74^2 + 39.96^2}{3\times 3} - 2219.352 = 418.5713$$

$$SS_{(P\times V)} = SS_{(\text{TableII})} - SS_{(Spa)} - SS_{(DOS)} = 717.109 - 269.869 - 418.571 = 28.6692$$

$$SS_{Er.\ II} = SS_{\text{Tot}} - SS_R - SS_{(\text{Spa})} - SS_{Er.I} - SS_{(\text{DOS})} - SS_{(\text{Spa}\times\text{DOS})} = 717.12 - 0.014 - 269.869 - 0.0009 - 418.571 - 28.669 = 0.0013$$

Step 4: Mean sums of squares are calculated by dividing the sum of square by corresponding degrees of freedom.

Step 5: F ratios for the replication and main plot are obtained by comparing the respective mean sum of squares against the mean sum of square due to error I. On the other hand, the F ratios corresponding to the subplot factor and the interaction effects are worked out by comparing the respective mean sum of squares against the mean sum of square due to error II:

ANOVA table for 3 × 4 split plot experiment

SOV	d.f.	*MS*	*MS*	Cal. F	Tab. F(p = 0.05)
Replication	3−1 = 2	0.0142	0.0071	31.02	6.94
Main plot factor (Spa)	3−1 = 2	269.8690	134.9345	588805.13	6.94
Error I	(3–1) (3–1) = 4	0.0009	0.0002		
Subplot factor (DOS)	(4–1) = 3	418.5713	139.5238	1982705.95	3.16
Interaction (Spa × DOS)	(3–1) (4–1) = 6	28.6692	4.7782	67900.80	2.66
Error II	3 (4–1) (3–1) = 18	0.0013	0.0001		
Total	3.3.4−1 = 35	717.1259			

Calculated F ratios are compared with the tabulated value of F at $\alpha = 0.05$ level of significance and at appropriate degrees of freedom. It is found that the effects of spacing, date of sowing, and their interaction are significant at 5 % level of significance.

Our next task will be to calculate the critical difference values for different types of mean comparison as given below:

(i) The CD to compare the difference between two main plot treatment means $= CD_{(0.05)} = \sqrt{\frac{2MS_{Er}-I}{rn}}t_{(0.025);\text{error}-I\ \ d.f.} = \sqrt{\frac{2(0.0002)}{3\times 4}} \times 2.776 = 0.1715.$

(ii) The CD to compare the difference between two subplot treatment means $= CD_{(0.05)} = \sqrt{\frac{2MS_{Er}-II}{r.m}}t_{0.025;\text{error}-II\ \ d.f.} = \sqrt{\frac{2(0.0001)}{3\times 3}} \times 2.101 = 0.0083.$

(iii) The CD to compare the difference between two main plot treatment means at the same or different levels of the subplot treatment $= \sqrt{\frac{2[(n-1)MS_{Er}II + MS_{Er}I]}{rn}}t^* = \sqrt{\frac{2[(4-1)0.0002+0.0001]}{3\times 4}}t^* = 0.01123t^*$ where

$$t^* = \frac{t_1 MS_{Er}\ I + t_2(n-1)MS_{Er}\ II}{MS_{Er}\ I + (n-1)MS_{Er}\ II} = \frac{(2.776)(0.0002) + (2.101)(4-1)0.0001}{(0.0002) + (4-1)(0.0001)} = 2.371$$

where $t_1 = t_{0.025,4}$ value and $t_2 = t_{0.025,18}$ value and the corresponding CD value could be $CD_{(0.05)} = 0.01123t^* = 0.01123 \times 2.371 = 0.0266.$

Spacing	Mean	CD
S1	11.443	0.1715
S2	7.311	
S3	4.802	
DOS	**Mean**	**CD**
D1	13.052	0.0083
D2	8.721	
D3	5.193	
D4	4.440	
Spa X DOS	**Mean**	**CD**
S1D1	17.440	0.0266
S2D1	11.923	
S1D2	11.920	
S2D2	10.087	
S3D1	9.793	
S1D3	8.647	
S1D4	7.763	
S3D2	4.157	
S2D3	3.940	
S2D4	3.293	
S3D3	2.993	
S3D4	2.263	

From the table mean comparison given below, it is clear that first spacing method is the best method, which is significantly superior to other two spacings. So far as the effect of date of sowing is concerned, maximum yield of arhar is obtained from the date of sowing 1 (D1) followed by D2, D3, and D4. All the sowing dates are significantly different from each other with respect to the yield of arhar. The interaction of the spacing method and the sowing data has significantly different effects from each other; the interaction effects which are not significantly different have been put under the same lines. Thus it is clear that spacing method 1 in combination with sowing date 1 has produced significantly higher yield than any other combination.

11.5 Strip Plot Design

Split plot design can accommodate one factor in larger plots (main plots), but while conducting experiments, sometimes the benefit of using large plot size may be required for more than one factor. In two-factor factorial experiment, if both the factors require large plots, then it is not possible through split plot design. Strip plot design is such a design where two factors can be accommodated in larger plots. Experiments with factors like methods of plowing, types of irrigation, methods of mulching, etc. require larger plot size for convenience of management. Moreover, sometimes the interaction effects are of much importance than that of the main effects of the factors. In strip plot design, the interaction effects between the two factors are measured with higher precision than either of the two factors. The basic idea of dividing each replication into blocks (main plots) in one direction is also extended to perpendicular direction, i.e., blocking is done in perpendicular directions in each replication. Thus if we are conducting a field experiment with two factors A and B having p and q levels, respectively, in r replication, then each replication is divided into p rows (horizontal rows) and q columns (vertical rows) to accommodate p levels of factor A in p horizontal rows randomly and q levels of the factor B in q vertical rows (columns) randomly or vice versa. In the process each row and each column of a replicate receive a particular level of factors A and factor B, respectively. The factor assigned to the horizontal rows is called *horizontal factor*, and the factor assigned to the columns (vertical rows) is called the *vertical factor*. The smallest plot in strip plot design is the intersection plot.

Layout and randomization:

Let there be two factors A and B at p and q levels, respectively, included in a strip plot experiment of which factor A is the horizontal plot factor, while the factor B is the vertical plot factor**.** The step-by-step procedure of the layout for a $p \times q$ strip plot design with r replications is as follows:

Step 1: The whole experimental area is divided into r replications across the fertility gradient of the field.

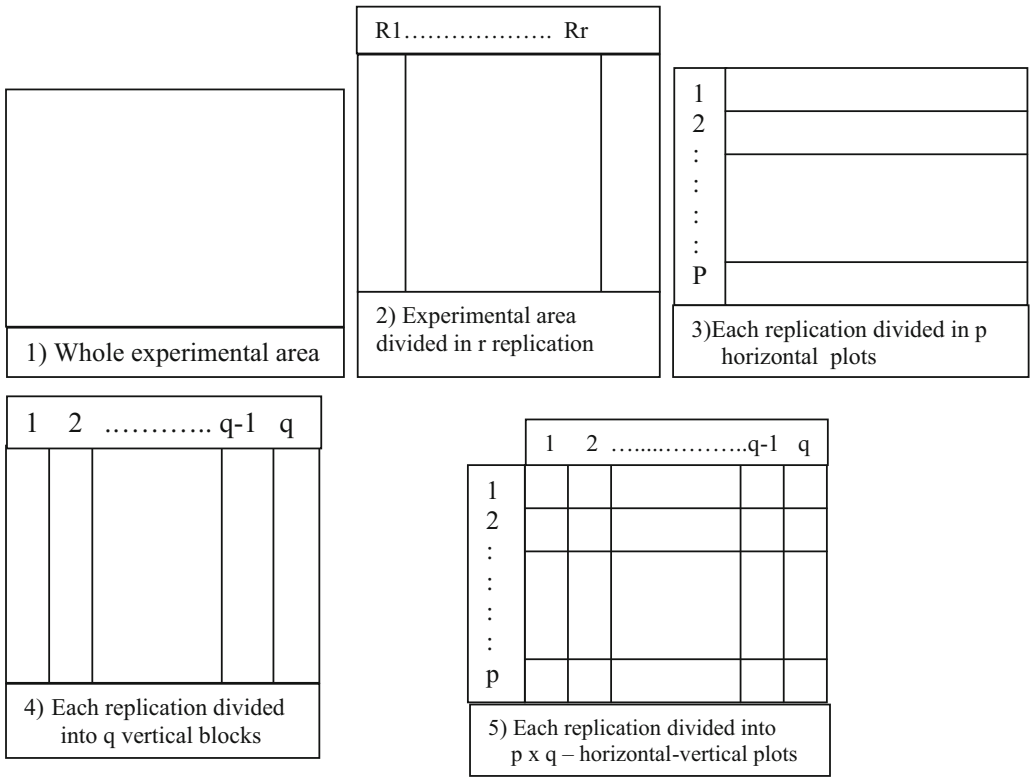
Step 2: Each and every replication should be constituted of p number of blocks (horizontal blocks) of equal size.

Step 3: Each and every replication should be constituted of q number of blocks (vertical blocks) of equal size.

Step 4: The p levels of horizontal plot factor are randomly distributed among p blocks in each and every replication separately.

Step 5: The q levels of vertical plot factor are randomly allocated to q vertical plots of each and every replication separately.

Separate sets of random numbers are to be used in each and every step of randomization.



Statistical model:

$$y_{ijk} = \mu + \gamma_i + \alpha_j + e_{ij} + \beta_k + e'_{ik} + (\alpha\beta)_{jk} + e''_{ijk}$$

where $i = 1, 2, \ldots, r$; $j = 1, 2, \ldots, p$; and $k = 1, 2, \ldots, q$

μ = general effect

γ_i = additional effect due to ith replication

α_j = additional effect due to jth level of vertical factor A and $\sum_{j=1}^{p} \alpha_j = 0$

β_k = additional effect due to kth level of horizontal factor B and $\sum_{k=1}^{q} \beta_k = 0$

$(\alpha\beta)_{jk}$ = interaction effect due to jth level of factor A and kth level of factor B and $\sum_j (\alpha\beta)_{jk} = \sum_k (\alpha\beta)_{jk} = 0$

e_{ij} (error I) = error associated with ith replication and jth level of vertical factor A and $e_{ik} \sim$ i.i.d. N(0, $\sigma_1{}^2$)

e'_{ik} (error II) = error associated with ith level of replication and kth level of horizontal factor B and $e'_{ij} \sim$ i.i.d. $N(0, \sigma_2^2)$

e''_{ijk} (error III) = error associated with ith replication, jth level of vertical factor A, and kth level of horizontal factor B and $e_{ijk} \sim$ i.i.d. N(0, σ_3^2)

Hypothesis to be tested:

$$H_0 : \gamma_1 = \gamma_2 = \ldots\ldots = \gamma_i = \ldots\ldots = \gamma_r = 0$$
$$\alpha_1 = \alpha_2 = \ldots\ldots = \alpha_j = \ldots\ldots = \alpha_p = 0$$
$$\beta_1 = \beta_2 = \ldots\ldots = \beta_k = \ldots\ldots = \beta_q = 0$$
$$(\alpha\beta)_{11} = (\alpha\beta)_{12} = \ldots\ldots = (\alpha\beta)_{jk} = \ldots\ldots$$
$$= (\alpha\beta)_{pq} = 0$$

H_1 : γ's are not all equal
α's are not all equal
β's are not all equal
$(\alpha\beta)'$s are not all equal

Let the level of significance be 0.05.

Analysis The analysis of strip plot design is performed in three steps: (a) analysis of horizontal factor effects, (b) analysis of vertical factor effects, and (c) analysis of interaction factor effects.

First we construct the three two-way tables of totals of (a) replication × horizontal factor, (b) replication × vertical factor, and (c) horizontal × vertical factor. The step-by-step procedure for the computation of different sums of square and mean sum of square is given as follows:

(i) Grand total $= G = \sum_{i=1}^{r}\sum_{j=1}^{p}\sum_{k=1}^{q} y_{ijk}$.

(ii) Correction factor $(CF) = \dfrac{G^2}{pqr}$.

(iii) $SS_{\text{Tot}} = \sum_{i=1}^{r}\sum_{j=1}^{p}\sum_{k=1}^{q} y_{ijk}^2 - CF$.

(iv) Work out the sum of squares due to the horizontal factor A and the replication. The following table of totals is required to be framed (Table 11.7).

Table 11.7 Totals for replication × factor A

	A_1	A_2	.....	A_j	.....	A_p	Total	Mean
R_1	$y_{11.}$	$y_{12.}$	.....	$y_{1j.}$	.....	$y_{1p.}$	$y_{1..}$	$\bar{y}_{1..}$
R_2	$y_{21.}$	$y_{22.}$	.....	$y_{2j.}$	.....	$y_{2p.}$	$y_{2..}$	$\bar{y}_{2..}$
:	:	:	:	:	:	:	:	
R_i	$y_{i1.}$	$y_{i2.}$	.....	$y_{ij.}$	.....	$y_{ip.}$	$y_{i..}$	$\bar{y}_{i..}$
:	:	:	:	:	:	:	:	
R_r	$y_{r1.}$	$Y_{r2.}$	.....	$y_{rj.}$	.....	$y_{rp.}$	$y_{r..}$	$\bar{y}_{r..}$
Total	$\sum y_{.1.}$	$\sum y_{.2.}$	.....	$\sum y_{.j.}$	.....	$\sum y_{.p.}$	$\sum y_{...}$	$\bar{y}_{...}$
Mean	$\bar{y}_{.1.}$	$\bar{y}_{.2.}$		$\bar{y}_{.j.}$		$\bar{y}_{.p.}$		

where $y_{ij.} = \sum_{k=1}^{q} y_{ijk}$

$$SS_{\text{(Table 11.7)}} = \frac{1}{q}\sum_{i=1}^{r}\sum_{j=1}^{p} y_{ij.}^2 - CF$$

$$SS_R = \frac{1}{pq}\sum_{i=1}^{r} y_{i..}^2 - CF$$

$$SS_{(A)} = \frac{1}{qr}\sum_{j=1}^{p} y_{.j.}^2 - CF$$

$$SS_{\text{(Error I)}} = SS_{(\text{Table}11.7)} - SS_R - SS_{(A)}$$

(v) Work out the sum of square due to the horizontal factor B and the replication. The following table of totals is required to be framed (Table 11.8).

Table 11.8 Totals for replication × factor B

	B_1	B_2	.....	B_k	.....	B_n	Total	Mean
R_1	$y_{1.1}$	$y_{1.2}$	.....	$y_{1.k}$	.....	$y_{1.q}$	$\sum y_{1..}$	$\overline{y}_{1..}$
R_2	$y_{2.1}$	$y_{2.2}$	.....	$y_{2.k}$	.....	$y_{2.q}$	$\sum y_{2..}$	$\overline{y}_{2..}$
:	:	:	:	:	:	:	:	
R_i	$y_{i.1}$	$y_{i.2}$	.....	$y_{i.k}$	.....	$y_{i.q}$	$\sum y_{i..}$	$\overline{y}_{i..}$
:	:	:	:	:	:	:	:	
R_r	$y_{r.1}$	$Y_{r.2}$	.....	$y_{r.k}$	.....	$y_{r.q}$	$\sum y_{r..}$	$\overline{y}_{r..}$
Total	$\sum y_{..1}$	$\sum y_{..2}$	.....	$\sum y_{..kj}$	.....	$\sum y_{..qp}$	$\sum y_{...}$	$\overline{y}_{...}$
Mean	$\overline{y}_{..1}$	$\overline{y}_{..2}$		$\overline{y}_{..k}$		$\overline{y}_{..q}$		

$$SS_{(\text{Table } 11.8)} = \frac{1}{p}\sum_{i=1}^{r}\sum_{k=1}^{q} y_{i.k}^2 - CF$$

$$SS_{(B)} = \frac{1}{pr}\sum_{k=1}^{q} y_{..k}^2 - CF$$

$$SS_{\text{(Error II)}} = SS_{(\text{Table } 11.8)} - SS_R - SS_{(B)}$$

(vi) Work out the sum of square due to the vertical factor and horizontal factor interaction; the following table of totals is required to be formed (Table 11.9).

Table 11.9 Totals for factor A × factor B

	B_1	B_2	.....	B_k	.....	B_n	Total	Mean
A_1	$y_{.11}$	$y_{.12}$	.....	$y_{.1k}$	.....	$y_{.1q}$	$\sum y_{.1.}$	$\overline{y}_{.1.}$
A_2	$y_{.21}$	$y_{.22}$	.....	$y_{.2k}$	.....	$y_{.2q}$	$\sum y_{.2.}$	$\overline{y}_{.2.}$
:	:	:	:	:	:	:	:	
A_j	$y_{.j1}$	$y_{.j2}$	.....	$y_{.jk}$	.....	$y_{.jq}$	$\sum y_{.j.}$	$\overline{y}_{.j.}$
:	:	:	:	:	:	:	:	
A_m	$y_{.m1}$	$y_{.m2}$	.....	$y_{.mk}$	.....	$y_{.mq}$	$\sum y_{.m.}$	$\overline{y}_{.m.}$
Total	$\sum y_{..1}$	$\sum y_{..2}$	.....	$\sum y_{..k}$	.....	$\sum y_{..q}$	$\sum y_{...}$	$\overline{y}_{...}$
Mean	$\overline{y}_{..1}$	$\overline{y}_{..2}$		$\overline{y}_{..k}$		$\overline{y}_{..n}$		

$$SS_{(\text{Table } 11.9)} = \frac{1}{r}\sum_{j=1}^{p}\sum_{k=1}^{q} y_{.jk}^2 - CF$$

$$SS_{(\text{AB})} = = SS_{(\text{Table } 11.9)} - SS_{(A)} - SS_{(B)}$$

$$SS_{\text{(Error III)}} = SS_{\text{Tot}} - SS_R - SS_{(A)} - SS_{(B)} - SS_{(AB)} - SS_{Er\ \text{I}} - SS_{Er\text{II}}$$

Mean sums of squares are calculated by dividing the sum of square by corresponding degrees of freedom:

ANOVA table for $m \times n$ strip plot design in r replication				
SOV	d.f.	*SS*	*MS*	*F* ratio
Replication	$r-1$	SS_R	MS_R	MS_R/MS_{ErI}
Factor (A)	$p-1$	$SS_{(A)}$	$MS_{(A)}$	$MS_{(A)}/MS_{ErI}$
Error I	$(r-1)(p-1)$	SS_{ErI}	MS_{ErI}	
Factor (B)	$(q-1)$	$SS_{(B)}$	$MS_{(B)}$	$MS_{(B)}/MS_{ErII}$
Error II	$(r-1)(q-1)$	SS_{ErII}	MS_{ErII}	
Interaction (A x B)	$(p-1)(q-1)$	$SS_{(AB)}$	$MS_{(AB)}$	$MS_{(AB)}/MS_{ErIII}$
Error III	$(p-1)(q-1)(r-1)$	SS_{ErIII}	MS_{ErIII}	
Total	$pqr-1$	SS_{Tot}		

(vii) Calculated F ratios are compared with the tabulated value of F at appropriate level of significance and degrees of freedom.

(viii) In the event of the significance of the F test, the next task will be to estimate the CD values for different types of comparison as given below:

(a) To compare the difference between two replication means, the CD value will be $CD_\alpha = \sqrt{\frac{2MS_{Er\text{I}}}{pq}} \times t_{\alpha/2;\text{error-I d.f.}}$

(b) To compare the difference between two horizontal plot treatment means, the CD value will be $CD_\alpha = \sqrt{\frac{2MS_{Er\text{I}}}{rq}} \times t_{\alpha/2;\text{error-I d.f.}}$

(c) To compare the difference between two vertical plot treatment means, the CD value will be $CD_\alpha = \sqrt{\frac{2MS_{Er\text{II}}}{rp}} \times t_{\alpha/2;\text{error-II d.f.}}$

(d) To compare the difference between two horizontal plot treatment means at the same or different levels of vertical plots, the CD value will be $CD_\alpha = \sqrt{\frac{2[(q-1)MS_{Er\text{III}}+MS_{Er\text{I}}]}{rq}} \times t^*_{\alpha/2;\text{errorII d.f.}}$ where $t^* = \frac{\{(q-1)MS_{\text{ErIII}} \times t_{\text{III}}\}+(MS_{Er\text{I}} \times t_{\text{I}})\}}{\{(n-1)MS_{Er\text{III}}+MS_{Er\text{I}}\}}$

(e) To compare the difference between two vertical plot treatment means at the same or different levels of horizontal plot treatment, the CD value will be $CD_\alpha = \sqrt{\frac{2[(p-1)MS_{Er\text{III}}+MS_{Er\text{II}}]}{rp}} t^{**}_{\alpha/2;\text{errorII d.f.}}$, where $t^{**} = \frac{[(p-1)MS_{Er\text{III}} \times t_{\text{III}}+MS_{Er\text{II}} \times t_{\text{II}}]}{(p-1)MS_{Er\text{III}}+MS_{Er\text{II}}}$.

Here $t_{\text{I}} = t$ value at error I degrees of freedom, $t_{\text{II}} = t$ value at error II degrees of freedom, and $t_{\text{III}} = t$ value at error III d.f. with specified level of significance.

Advantages and disadvantages:

Two different factors requiring larger plot sizes for the feasibility of management can be accommodated in this type of design. Moreover the effects of both the factors are estimated with equal precision, whereas interaction effects of the factors are estimated more precisely than the two main factor effects. But the process of randomization and layout is complicated than the designs discussed so far.

Example 11.13

To know the effect of number of baths (F) taken (once, twice, and thrice in a day) and hygiene (H) level of cattle shed (25 %, 50 %, 75 %, and 100 %) on milk yield capacity of the crossbreed cows, an experiment was conducted in strip plot design with three replications. Given below are the average milk yield data per day for different treatment combinations. Analyze the information to identify the best bathing frequency and hygiene level along with their combination toward the production of milk:

	Vertical plot (bathing frequency)											
	F1				F2				F3			
Horizontal plot / Hygiene Level	H1	H2	H3	H4	H1	H2	H3	H4	H1	H2	H3	H4
Rep-1	13.1	14.5	14.5	16.2	13.7	16.2	17.4	19.4	13.3	15.8	16.8	17.3
Rep-2	13.3	14.6	14.6	16.3	13.8	16.5	17.8	18.3	13.6	15.6	17.1	16.9
Rep-3	13.8	14.2	14.2	16.7	14.1	16.6	16.9	18.7	13.9	15.5	16.7	17

Statistical model:

$$y_{ijk} = \mu + \gamma_i + \alpha_j + e_{ij} + \beta_k + e'_{jk} + (\alpha\beta)_{jk} + e''_{ijk}$$

where $i = 3$, $j = 3$, and $k = 4$

μ = general effect

R_i = additional effect due to ith replication

α_j = additional effect due to jth level of vertical factor A (bathing frequency) and $\sum_{j=1}^{3} \alpha_j = 0$

β_k = additional effect due to kth level of horizontal factor B (hygiene level) and $\sum_{k=1}^{4} \beta_k = 0$

$(\alpha\beta)_{jk}$ = interaction effect due to jth level of bathing frequency and kth level of hygiene level and $\sum_j (\alpha\beta)_{jk} = \sum_k (\alpha\beta)_{jk} = 0$

e_{ij} (error I) = error associated with ith replication and jth level of vertical factor A and $e_{ij} \sim$ i.i.d. N(0, ${\sigma_1}^2$)

e^2_{jk} (error II) = error associated with jth level of vertical factor A (bathing frequency) and kth level of horizontal factor B (hygiene level) and $e_{jk} \sim$ i.i.d. $N(0, \sigma_2^2)$

e''_{ijk} (error III) = error associated with ith replication, jth level of vertical factor A, and kth level of horizontal factor B and $e_{ijk} \sim$ i.i.d. N(0, σ_3^2)

Hypothesis to be tested:

$$H_0 : \gamma_1 = \gamma_2 = \gamma_3 = 0$$
$$\alpha_1 = \alpha_2 = \alpha_3 = 0$$
$$\beta_1 = \beta_2 = \beta_3 = \beta_4 = 0$$
$$(\alpha\beta)_{11} = (\alpha\beta)_{12} = \ldots\ldots = (\alpha\beta)_{jk} = \ldots\ldots = (\alpha\beta)_{34} = 0$$

against

H_1 : γ's are not all equal
α's are not all equal
β's are not all equal
$(\alpha\beta)'$s are not all equal

Let the level of significance be 0.05.

First we construct the three two-way tables of the total of replication × bathing frequency, replication × hygiene level, and bathing frequency × hygiene level. The step-by-step procedure for the computation of different sums of square and mean sum of square is given as follows:

$$\text{Grand total } (GT) = \sum_{i=1}^{3}\sum_{i=1}^{3}\sum_{k=1}^{4} y_{ijk} =$$
$$13.1 + 13.3 + 13.8 + 14.5\ldots\ldots$$
$$+16.9 + 17.0 = 564.90$$

$$\text{Correction factor } (CF) = \frac{GT^2}{3 \times 4 \times 3} = \frac{564.90^2}{36} = 8864.222$$

Work out the sum of squares due to the vertical factor A and the replication. The following table of totals is required to be framed (Table 11.10):

Table 11.10 Table of totals for replication × bathing frequency

	Vertical Plot (bathing frequency)				
Replication	F1	F2	F3	Total	Mean
Rep-1	58.3	66.7	63.2	188.2	15.683
Rep-2	58.8	66.4	63.2	188.4	15.700
Rep-3	58.9	66.3	63.1	188.3	15.692
Total	176.0	199.4	189.5		
Mean	14.667	16.617	15.792		

$$SS_{(\text{Table 11.10})} = \frac{1}{4}\sum_{i=1}^{3}\sum_{j=1}^{3} y_{ij.}^2 - CF$$
$$= 8887.292 - 8864.222 = 23.07$$

$$SS_R = \frac{1}{3\times4}\sum_{i=1}^{3} y_{i..}^2 - CF = \frac{188.2^2 + 188.4^2 + 188.3^2}{12} - 8864.222 = 0.00166.$$

$$SS_{(A)} = \frac{1}{4 \times 3}\sum_{j=1}^{3} y_{.j.}^2 - CF = \frac{176.0^2 + 199.4^2 + 189.5^2}{12} - 8864.222 = 22.995.$$

$$SS_{(Error\ I)} = SS_{(TableI)} - SS_{(R)} - SS_{(A)}$$
$$= 23.07 - 0.00166 - 22.995 = 0.073$$

Work out the sum of square due to the horizontal factor B and the replication; the following table of totals is required to be framed (Table 11.11):

Table 11.11 Table of totals for replication × hygiene level $SS_{(Er.II)} = SS_{(\text{Table 11.11})} - SS_{(B)} = 69.700$

	Horizontal plot (hygiene level)					
Replication	H1	H2	H3	H4	Total	Mean
Rep-1	40.1	46.5	48.7	52.9	188.2	15.683
Rep-2	40.7	46.7	49.5	51.5	188.4	15.700
Rep-3	41.8	46.3	47.8	52.4	188.3	15.692
Total	122.6	139.5	146.0	156.8		
Mean	13.622	15.500	16.222	17.422		

$$SS_{(\text{Table 11.11})} = \frac{1}{3}\sum_{i=1}^{3}\sum_{k=1}^{4} y_{i.k}^2 - CF$$

$$= \frac{40.1^2 + 40.7^2 + \ldots\ldots + 51.5^2 + 52.4^2}{3}$$

$$-8864.222 = 69.700$$

$$SS_{(B)} = \frac{1}{3 \times 3}\sum_{k=1}^{4} y_{..k}^2 - CF = \frac{122.6^2 + 139.5^2 + 146.0^2 + 156.8^2}{9}$$

$$- 8864.222 = 68.360.$$

$$-68.360 = 1.340$$

Work out the sum of square due to the vertical factor and horizontal factor interaction. The following table of totals is required to be formed (Table 11.12):

Table 11.12 Table of totals for hygiene level × bathing frequency

	Vertical plot (bathing frequency)				
Horizontal plot (hygiene level)	F1	F2	F3	Total	Mean
H1	40.2	41.6	40.8	122.6	13.622
H2	43.3	49.3	46.9	139.5	15.500
H3	43.3	52.1	50.6	146.0	16.222
H4	49.2	56.4	51.2	156.8	17.422
Total	176.0	199.4	189.5		
Mean	14.667	16.617	15.792		

$$SS_{(A\times B)} = \frac{1}{r}\sum_{j=1}^{m}\sum_{k=1}^{n} y_{.jk}^2 - CF - SS_{(A)} - SS_{(B)}$$

$$= \frac{40.2^2 + 43.3^2 + 43.3^2 + \ldots\ldots + 50.6^2 + 51.2^2}{3}$$

$$-8864.222 - 22.995 - 68.360 = 7.398$$

$$SS_{(Er.\ III)} = SS_{(\text{Tot})} - SS_{(R)} - SS_{(A)} - SS_{(B)} - SS_{(AB)} - SS_{(Er.I)} - SS_{(Er.II)} = 100.927 - 0.0016 - 22.995 - 68.360 - 7.398 - 0.0733 - 1.340 = 0.758$$

Mean sums of squares are calculated by dividing the sum of square by corresponding degrees of freedom:

SOV	d.f.	SS	MS	F Value	Table value of F ($p = 0.05$)	($p = 0.01$)
Replication	2	0.00167	0.00083	0.04545	6.944	18.000
Vertical factor (bathing frequency)	2	22.995	11.4975	627.136	6.940	18.000
Error I	4	0.07333	0.01833			
Horizontal factor (hygiene)	3	68.3608	22.7869	102.031	4.757	9.780
Error II	6	1.34	0.22333			
F × H	6	7.39833	1.23306	19.5121	2.996	4.821
Error III	12	0.75833	0.06319			
Total	35	100.927				

(i) F ratios for replication and vertical factor effects are obtained by comparing the respective mean sum of squares against the mean sum of square due to error I. On the other hand, the F ratios corresponding to the horizontal factor and interaction between horizontal and vertical factor are worked out by comparing the respective mean sum of squares against the mean sum of square due to error II and error III, respectively.

(ii) Calculated F ratios are compared with the tabulated value of F at appropriate level of significance and degrees of freedom. It is found from the above table that except for replication effect, all other effects are significant both at 5 % and 1 % levels of significance.

(iii) Once the F test becomes significant, our next task is to estimate the SEs for different types of comparison as given below:

(a) The standard error for the difference between two vertical plot treatment means $= \sqrt{\frac{2ErMS.I}{rn}}$, and the corresponding CD value could be $CD_\alpha = \sqrt{\frac{2ErMS.I}{rn}} \times t_{\alpha/2;\text{error}-I \ \ d.f.} = \sqrt{\frac{2\times 0.01833}{3\times 4}} \times 2.776 = 0.153$.

(b) The standard error for the difference between two horizontal plot treatment means $= \sqrt{\frac{2ErMS.II}{rm}}$, and the corresponding CD value could be $CD_{(0.05)} = \sqrt{\frac{2ErMS.II}{3\times 3}} \times t_{\alpha/2;\text{error}-II \ \ d.f.} = \sqrt{\frac{2\times 0.223}{3\times 3}} \times 2.447 = 0.545$.

(c) The standard error for the difference between two vertical plot treatment means at the same level of horizontal plot treatment

$$= \sqrt{\frac{[2(n-1)ErMS.III + ErMS.I]}{rn}}$$

$$= \sqrt{\frac{2(4-1)0.063 + 0.018}{3 \times 4}} = 0.182$$

(d) The standard error for the difference between two horizontal plot treatment means at the same level of vertical plot treatment $= \sqrt{\frac{2[(m-1)ErMS.III + ErMS.II]}{rm}} = \sqrt{\frac{2[(3-1)0.063+0.223]}{3\times 3}} = 0.278$.

But the ratio of the treatment difference and the above SE in (c) and (d) does not follow the t-distribution, and the approximate weighted t is calculated as follows:

$$= \frac{\{(n-1)ErMS.III \times t_{III}\} + (ErMS.I \times t_I)}{\{(n-1)ErMS.III + ErMS.I\}}$$

$$= \frac{\{(4-1)0.063 \times 2.179\} + (0.0183 \times 2.776)}{\{(4-1) \times 0.063 + 0.0183\}}$$

$$= 2.187$$

and

$$\frac{[(m-1)ErMS.III \times t_{III} + ErMS.II \, x \, t_{II}]}{(m-1)ErMS.III + ErMS.II}$$

$$= \frac{[(3-1) \times 0.063 \times 2.179 + 0.223 \times 2.447]}{(3-1) \times 0.063 + 0.223}$$

$$= 2.350$$

where $t_I = t_{0.025,4} = 2.776$, $t_{II} = t_{0.025,6} = 2.447$, and $t_{III} = t_{0.025,12} = 2.179$. Corresponding CD values could be $CD(0.05) = SE_d \times t(\text{cal})$.

Thus, the critical difference value to compare two vertical plot treatment means at the same level of horizontal plot treatment is $CD(0.05) = SE_d \times t(\text{cal}) = 0.182 \times 2.187 = 0.398$, and the critical difference value to compare two horizontal plot treatment means at the same level of vertical plot treatment is $CD(0.05) = SE_d \times t(\text{cal}) = 0.278 \times 2.350 = 0.653$.

Now our next task is to compare the treatment means:

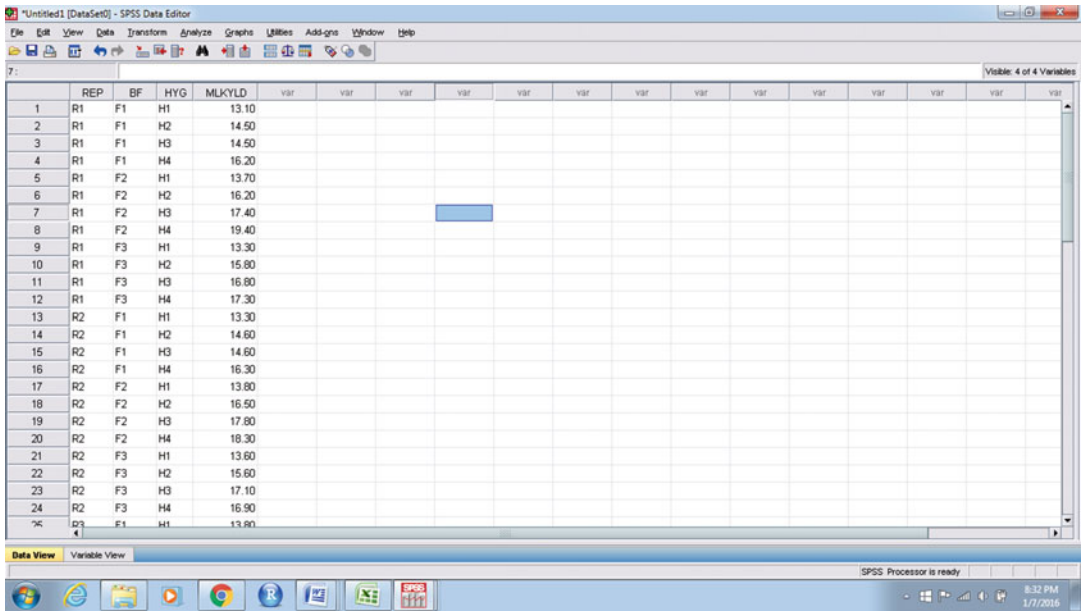
Bathing frequency	Means
F2	16.617
F3	15.792
F1	14.667
Hygiene level	
H4	17.422
H3	16.222
H2	15.500
H1	13.622

Comparing the treatment means, it can be concluded that all the levels of both the factors are significantly different from each other and bathing frequency 2 is the best among the bathing frequencies and hygiene level 4 is the best hygiene level schedule. Similarly by using appropriate critical difference values as mentioned above, one can find out the best bathing frequency at particular hygiene level and vice versa.

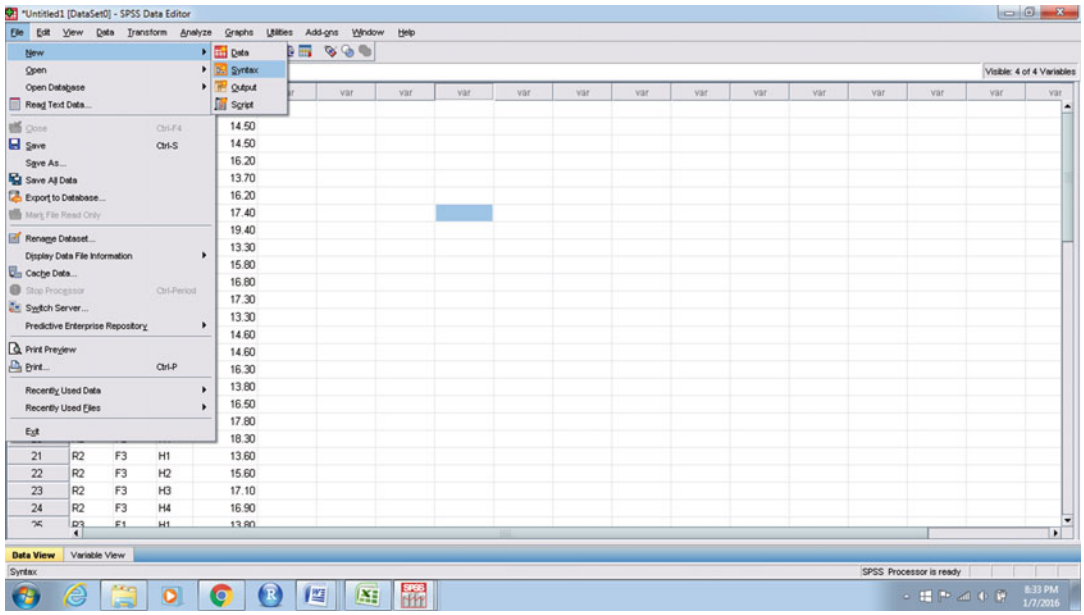
Example 11.13 (Using Customized Syntax in SPSS)

```
UNIANOVA
   MLKYLD BY REP BF HYG
   /METHOD = SSTYPE(3)
   /INTERCEPT = INCLUDE
   /CRITERIA = ALPHA(.05)
   /DESIGN = REP BF BF*REP HYG HYG*REP BF*HYG
   /TEST BF VS REP*BF.
```

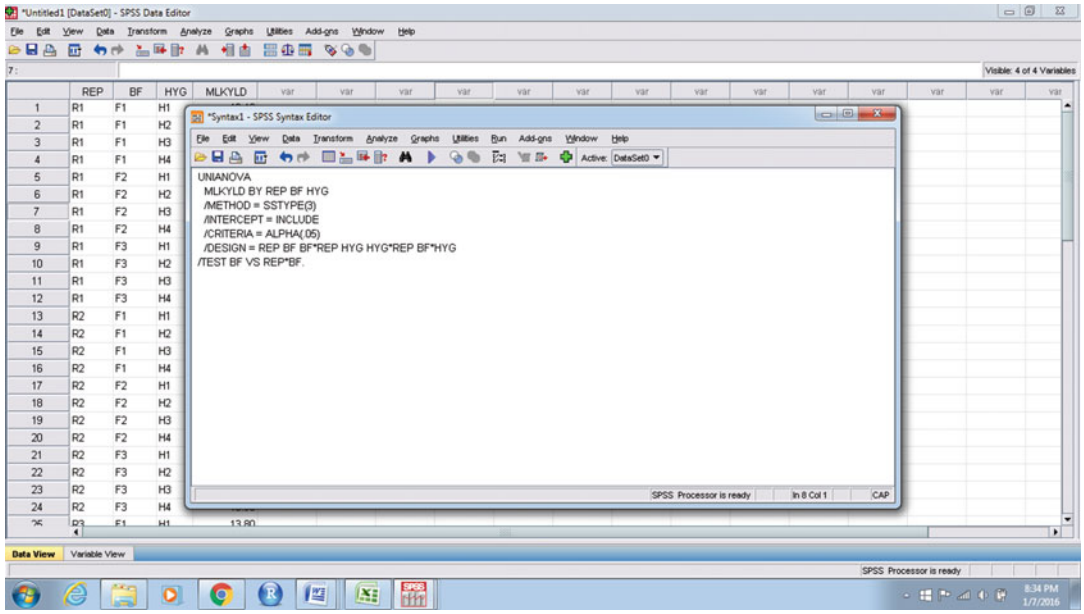
Step 1: Enter the data in SPSS data view as below; change the variable names.



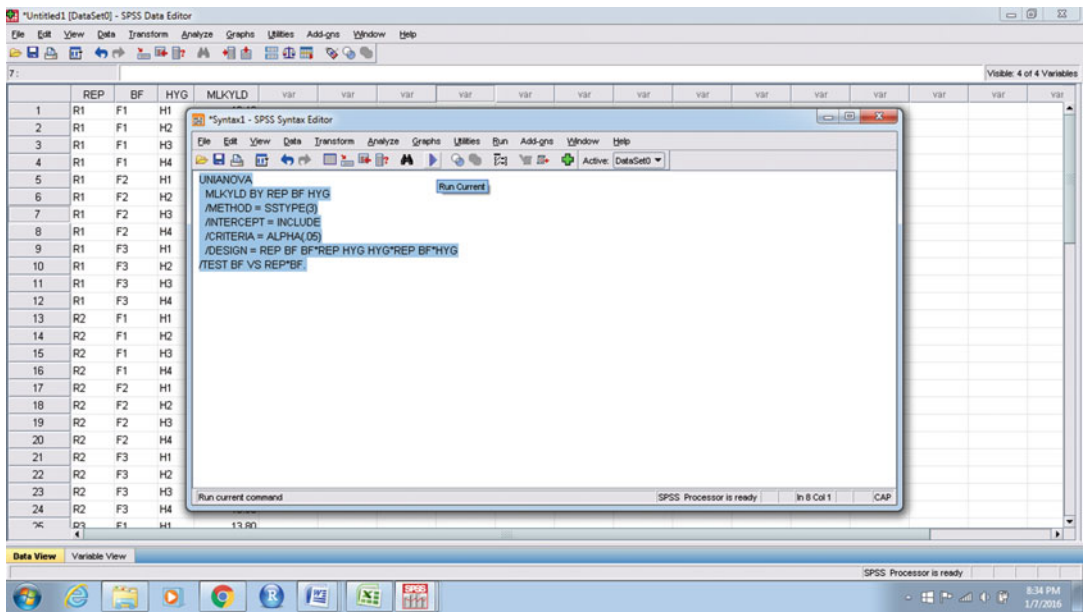
Step 2: Go to File → New → Click on "Syntax" as below.



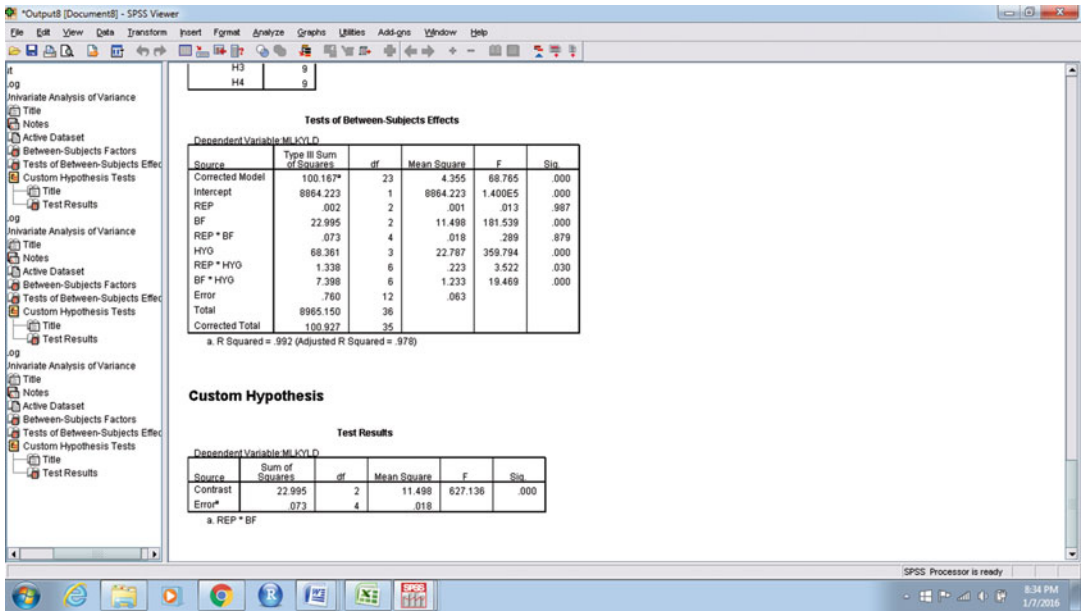
Step 3: Write the syntax as below.



Step 4: Select all the syntax; then press "Run Current" as mentioned below.



Step 5: The output will appear in the output window.



*Note: The sum of squares that corresponds to REP*BF is the error I, REP*HYG is the error II, and Error is the error III.*

Example 11.14 (Strip Plot Design)
To find the efficacy of three different times of N application and four irrigation schedules in semidry rice, an experiment was conducted in strip plot design with three replications. Given below are the yield (q/ha) data for different treatments. Analyze the information to identify the best time of application of nitrogen and irrigation schedule along with their combination:

	Vertical plot (time of N application)											
Horizontal plot (irrigation)	T1				T2				T3			
	I1	I2	I3	I4	I1	I2	I3	I4	I1	I2	I3	I4
Rep-1	30.30	31.41	32.13	31.95	28.54	30.58	31.72	28.86	31.94	33.87	34.30	33.57
Rep-2	28.00	31.77	33.15	31.12	27.87	29.47	31.07	28.57	31.51	33.76	34.23	32.44
Rep-3	29.20	31.64	32.68	31.57	28.24	30.06	31.45	28.76	31.77	33.87	34.32	33.04

Statistical model:

$$y_{ijk} = \mu + \gamma_i + \alpha_j + e_{ij} + \beta_k + e'_{jk} + (\alpha\beta)_{jk} + e''_{ijk}$$

where $i = 1, 2, 3$; $j = 1, 2,3$; and $k = 1, 2, 3, 4$
μ = general effect
γ_i = additional effect due to ith replication
α_j = additional effect due to jth level of vertical factor A (time of N application) and $\sum_{j=1}^{3} \alpha_j = 0$

β_k = additional effect due to kth level of horizontal factor B (irrigation) and $\sum_{k=1}^{4} \beta_k = 0$

$(\alpha\beta)_{jk}$ = interaction effect due to jth time of N application and kth level of irrigation and $\sum_j (\alpha\beta)_{jk} = \sum_k (\alpha\beta)_{jk} = 0$

e_{ij} (error I) = error associated with ith replication and jth level of vertical factor A and $e_{ij} \sim$ i.i.d. N(0, ${\sigma_1}^2$)

e_{jk}^2 (error II) = error associated with jth level of vertical factor A (time of N application) and kth level of horizontal factor B (irrigation) and $e_{jk} \sim$ i.i.d. N(0, σ_2^2)

e_{ijk} (error III) = error associated with ith replication jth level of vertical factor A, and kth level of horizontal factor B and $e_{ijk} \sim$ i.i.d. N(0, σ_3^2)

Hypothesis to be tested:

$$H_0 : \gamma_1 = \gamma_2 = \gamma_3 = 0$$
$$\alpha_1 = \alpha_2 = \alpha_3 = 0$$
$$\beta_1 = \beta_2 = \beta_3 = \beta_4 = 0$$
$$(\alpha\beta)_{11} = (\alpha\beta)_{12} = \ldots\ldots\ldots = (\alpha\beta)_{jk} = \ldots\ldots\ldots = (\alpha\beta)_{34} = 0$$

H_1 : γ's are not all equal
α's are not all equal
β's are not all equal
$(\alpha\beta)'$s are not all equal

Let the level of significance be 0.05.

First we construct the three two-way tables of the total of replication × time of N application, replication × irrigation, and time of N application × irrigation. The step-by-step procedure for the computation of different sums of square and mean sum of square is given as follows:

$$\text{Grand total } (GT) = \sum_{i=1}^{3}\sum_{j=1}^{3}\sum_{k=1}^{4} y_{ijk} = 30.30 + 28.00 + \ldots\ldots\ldots + 32.44 + 33.04 = 1128.73$$

$$\text{Correction factor (CF)} = \frac{GT^2}{3 \times 4 \times 3} = \frac{1128.73^2}{36} = 35389.761$$

From the following table of totals, let us work out the sum of squares due to the vertical factor A and the replication (Table 11.13).

Table 11.13 Table of totals for replication × manure

	Vertical plot (time of N application)				
Replication	T1	T2	T3	Total	Average
Rep-1	125.79	119.70	133.68	379.17	31.60
Rep-2	124.04	116.98	131.94	372.96	31.08
Rep-3	125.09	118.51	133.00	376.60	31.38
Total	374.92	355.19	398.62		
Average	31.24	29.60	33.22		

$$SS_{(\text{Table 11.13})} = \frac{1}{4}\sum_{i=1}^{3}\sum_{j=1}^{3} y_{ij.}^2 - CF = \frac{125.79^2 + 124.04^2 + \ldots\ldots\ldots + 131.94^2 + 133.00^2}{4} - 35389.761 = 80.511$$

$$SS_{(R)} = \frac{1}{3 \times 4}\sum_{i=1}^{3} y_{i00}^2 - CF = \frac{379.17^2 + 372.96^2 + 376.60^2}{12} - 35389.761 = 1.6227$$

$$SS_{(N)} = \frac{1}{4 \times 3}\sum_{j=1}^{3} y_{.j.}^2 - CF = \frac{374.92^2 + 355.19^2 + 398.62^2}{12} - 35389.761 = 78.809$$

$$SS_{(\text{Error I})} = SS_{(\text{Table 11.13})} - SS_R - SS_{(N)} = 80.511 - 1.622 - 78.809 = 0.079$$

From the following table of totals, let us work out the sum of squares due to the vertical factor A and the replication (Table 11.14).

Table 11.14 Table of totals for replication × irrigation

	Horizontal plot (irrigation)					
Replication	Irrg.1	Irrg.2	Irrg.3	Irrg.4	Total	Average
Rep-1	90.78	95.86	98.15	94.38	379.17	31.60
Rep-2	87.38	95.00	98.45	92.13	372.96	31.08
Rep-3	89.21	95.57	98.45	93.37	376.60	31.38
Total	267.37	286.43	295.05	279.88		
Average	29.71	31.83	32.78	31.10		

$$SS_{(\text{Table.11.14})} = \frac{1}{3}\sum_{i=1}^{3}\sum_{k=1}^{4} y_{i.k}^2 - CF$$

$$= \frac{90.78^2 + 87.38^2 + \ldots\ldots + 92.13^2 + 93.37^2}{3}$$

$$- 35389.761 = 48.294$$

$$SS_{(\text{Irrig.})} = \frac{1}{3 \times 3}\sum_{k=1}^{4} y_{.k}^2 - CF = \frac{267.37^2 + 286.43^2 + 295.05^2 + 279.88^2}{9}$$

$$- 35389.761 = 45.369$$

$$SS_{(Er.II)} = \frac{1}{3}\sum_{i=1}^{3}\sum_{k=1}^{4} y_{i.k}^2 - CF - SS_{(\text{Irrg.})}$$

$$= \frac{90.78^2 + 87.38^2 + \ldots\ldots + 92.13^2 + 93.37^2}{3}$$

$$- 35389.761 - 45.369 = 2.924$$

From the following table of totals, let us work out the sum of squares due to the vertical factor A and the horizontal factor B (Table 11.15).

Table 11.15 Table of totals for time of application × irrigation

	Vertical plot (time of *N* application)				
	T1	T2	T3	Total	Average
Irrg.1	87.50	84.65	95.22	267.37	29.71
Irrg.2	94.82	90.11	101.50	286.43	31.83
Irrg.3	97.96	94.24	102.85	295.05	32.78
Irrg.4	94.64	86.19	99.05	279.88	31.10
Total	374.92	355.19	398.62		

$$SS_{(N \times I.)} = \frac{1}{r}\sum_{j=1}^{m}\sum_{k=1}^{n} y_{.jk}^2 - CF - SS_{(N)} - SS_{(I.)}$$

$$= \frac{87.50^2 + 94.82^2 + 97.96^2 + \ldots\ldots + 102.85^2 + 99.05^2}{3}$$

$$- 35389.761 - 78.809 - 45.369 = 3.868$$

$$SS_{(Er.\,III)} = SS_{\text{Tot}} - SS_R - SS_{(N)} - SS_{(I.)} - SS(N \times I.) - SS_{(Er.I)} - SS_{(Er.II)} = 133.471 - 1.622 - 78.809 - 45.369 - 3.868 - 0.079 - 2.924 = 0.797$$

Mean sums of squares are calculated by dividing the sum of square by corresponding degrees of freedom:

ANOVA table

SOV	d.f.	*SS*	*MS*	Cal. F	Tab. F ($p = 0.05$)
Replication	2	1.623	0.811	40.947	6.940
Vertical factor (time of N application)	2	78.809	39.405	1988.595	6.940
Error I	4	0.079	0.020		
Horizontal factor (irrigation)	3	45.369	15.123	31.025	4.760
Error II	6	2.925	0.487		
Time of N application × irrigation	6	3.868	0.645	9.703	3.000
Error III	12	0.797	0.066		
Total	35	133.471			

(i) F ratios for replication and vertical factor effects are obtained by comparing the respective mean sum of squares against the mean sum of square due to error I. On the other hand, the F ratios corresponding to the horizontal factor and interaction between horizontal and vertical factor are worked out by comparing the respective mean sum of squares against the mean sum of square due to error II and error III, respectively.

(ii) Calculated F ratios are compared with the tabulated value of F at appropriate level of significance and degrees of freedom. It is found from the above table that all effects are significant both at 5 % and 1 % levels of significance.

(iii) Once the F test becomes significant, our next task is to estimate the *CD* for different types of comparison as given below:

The *CD* for the difference between two vertical plot treatment means $= CD_{\alpha} = \sqrt{\frac{2MS_{Er-\mathrm{I}}}{rn}} \times t_{\alpha/2;\text{error}-\mathrm{I}\ \text{d.f.}} = \sqrt{\frac{2\times 0.020}{3\times 4}} \times 2.776 = 0.1595.$

The *CD* for the difference between two horizontal plot treatment means $= CD_{(0.05)} = \sqrt{\frac{2MS_{Er-\mathrm{II}}}{3.3}} \times t_{\alpha/2;\text{error}-\mathrm{II}\ \text{d.f.}} = \sqrt{\frac{2\times 0.487}{3.3}} \times 2.447 = 0.805.$

The *CD* for the difference between two vertical plot treatment means at the same level of horizontal plot treatment

$$= \sqrt{\frac{2[(n-1)MS_{Er} - \mathrm{III} + MS_{Er} - \mathrm{I}]}{rn}} t^{*}$$
$$= \sqrt{\frac{2(4-1)0.066 + 0.0.20}{3.4}} t^{*} = 0.186t^{*}$$

where t^{*} is calculated as follows:

$$\frac{\{(n-1)MS_{Er} - \mathrm{III} \times t_{\mathrm{III}}\} + (MS_{Er} - \mathrm{I} \times t_{\mathrm{I}})}{\{(n-1)MS_{Er} - \mathrm{III} + MS_{Er} - \mathrm{I}\}}$$
$$= \frac{\{(4-1)0.066 \times 2.179\} + (0.020 \times 2.776)}{\{(4-1)\times 0.066 + 0.020\}}$$
$$= 2.244$$

Thus, the critical difference value to compare two vertical plot treatment means at the same level of horizontal plot treatment is $CD(0.05) = 0.186 \times 2.244 = 0.419$.

The *CD* for the difference between two horizontal plot treatment means at the same level of vertical plot treatment $= \sqrt{\frac{2[(m-1)MS_{Er}\mathrm{III} + MS_{Er}\mathrm{II}]}{rm}} t^{*} = \sqrt{\frac{2[(3-1)0.066+0.487]}{3\times 3}} t^{*} = 0.289t^{*} = 0.289 \times 2.392 = 0.692$

where t^{*} is calculated as follows:

$$\frac{[(m-1)MS_{Er}\mathrm{III} \times t_{\mathrm{III}} + MS_{Er} \times t_{\mathrm{II}}]}{(m-1)MS_{Er} + MS_{Er}}$$
$$= \frac{[(3-1)\times 0.066 \times 2.179 + 0.487 \times 2.447]}{(3-1)\times 0.066 + 0.487}$$
$$= 2.392$$

In both cases $t_I = t_{0.025,4} = 2.776$, $t_{II} = t_{0.025,6} = 2.447$, and $t_{III} = t_{0.025,12} = 2.179$.

Time of Application of Nitrogen	Mean	CD	
T3	33.22	0.1595	
T1	31.24		
T2	29.60		
Irrigation Level	Mean		
I3	32.78	0.805	
I2	31.83		
I4	31.10		
I1	29.71		
Time of N App X Irrig.	Mean		
T3I3	34.283	0.419 and 0.692	
T3I2	33.833		
T3I4	33.017		
T1I3	32.653		
T3I1	31.740		
T1I2	31.607		
T1I4	31.547		
T2I3	31.413		
T2I2	30.037		
T1I1	29.167		
T2I4	28.730		
T2I1	28.217		

Comparing the treatment means, it can be concluded that nitrogen application at time 3 is the best among the times of N application and irrigation schedule 3 is the best irrigation schedule. Similarly by using appropriate critical difference values as mentioned above, one can find out the best time of N application at a particular irrigation level and vice versa.

Special Experiments and Designs 12

12.1 Introduction

Throughout Chaps. 10 and 11, we have discussed different standard experimental designs. To conduct such experiments, one needs to have design-specific requirements/conditions to be fulfilled. But under practical situations, there are varieties of problems such as the dearth of experimental material, dearth of experimental plots, etc.

Suppose an experimenter is conducting an experiment with four doses of nitrogen (N1, N2, N3, N4) and three doses of potassium (K1, K2, K3). So under standard factorial setup, there will be 12 treatment combinations (N1K1, N1K2, N1K3, N2K1, N2K2, N2K3, N3K1, N3K2, N3K3, N4K1, N4K2, and N4K3), and these can be repeated/replicated as per the requirement. So the experimenter needs 12 experimental unit plots in each replication. Now in many practical situations, a question raised how far the doses of nitrogen or the doses of potassium or their combinations are superior over the standard ones, popularly known as control/check? To answer this question, one needs to introduce control as one of the treatments. In most of the cases, the checks are generally constituted of zero doses of both the factors. That means we need to introduce zero dose in both the cases, i.e., there would be five doses of nitrogen and four doses of potassium. So altogether there would be 20 treatment combinations, thereby requiring (+8) 20 experimental plots in each replication. So the experimenter is to accommodate 20 experimental units in each replication, thereby increasing the requirement of huge number of experimental units. In many practical situations, this increase in experimental units to such a great extent may not be feasible under the given experimental condition. So the question is how to tackle such situation without compromising the objective of the experimentation?

When a plant breeder is in the process of developing varieties, at the initial stage, the experimenter may not have enough material to repeat the newly developed variety more than once. Our conventional designs require each and every treatment to be repeated at least once. So the question is how to adjust such a situation?

Again one of the prerequisites of conventional breeding is to evaluate the available germplasm before these are put under breeding experiments for exploitation of potential germplasms. A large number of germplasms/lines are required to be evaluated at a time under the uniform evaluation protocol. It becomes very difficult to accommodate a huge number of germplasms under the uniform evaluation protocol using CRD setup or a RBD. This problem becomes more acute when we consider RBD setup because we are to form blocks which can accommodate such a huge number of germplasms or lines, thus

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making it very difficult to evaluate the germplasms, particularly under RBD setup.

Augmentation of the standard designs is required to be done to cope with the above situations. In fact the idea of augmented design was formulated by Federer (1956). Appropriate adjustment is made in the analysis of variance to tackle the problem of comparing treatments over the factorial treatments in the form of control treatments. Thus in the above example of factorial experiment with control treatment instead of using 20 treatments, one can set an experiment with $4 \times 3 + 1(\text{control} = \text{N0K0}) = 13$ treatments in each replication and by adjusting the sum of squares accordingly can compare the treatment effects against the control to examine the difference between the control and the treatment effects and also among treatments.

The designs which are developed by adjusting/modifying the basic designs to overcome the above problems are called augmented designs. To accommodate the experimental treatments, having material scares in nature, along with the other treatments, is given by Federer, 1956. Mostly these are used in germplasm evaluation experiments, plant breeding trials, etc. but can also be used in the field experiment of entomology, pathology, agronomy, etc. The problem of evaluating huge number of germplasms at a place and at a time could be overcome by augmenting the basic CRD or RBD. The basic idea behind such design consists of forming one set of treatments (mostly with the check varieties) against which the other set of treatments (mostly the new varieties) is tested/compared. The check varieties are available in good amount for repetition but the new varieties may not have easy availability. The check varieties are repeated number of times, but the new varieties may not be applied more than once because of scarcity. In this type of design, the check varieties are repeated and randomly allocated in each block, and a number of new varieties are placed in each block. The block size may vary, but the homogeneity among the experimental units within a block should be ensured. The adjustment for new variety total depends upon the standard design used and their placements in the design. The major advantage of this type of design is that the new varieties, no matter how discrepant their values recorded may be, do not contribute to experimental error of experiment. The total sum of squares is partitioned into sources for comparing the means of check varieties, the means of new varieties in the same or different blocks, and the means of check and new varieties. It may be noted that unwise choice of any extreme treatment in replicated experiment may result in higher experimental error, thereby making the tests nonsignificant and sometimes may spoil the whole experiment.

12.2 Comparison of Factorial Effects vs. Single Control Treatment

Let us suppose we have $m \times n$ factorial experiments to be conducted using RBD with a control. Thus we are talking about two-factor (A and B say) factorial experiments along with a control treatment conducted in RBD with r replications. Altogether we have $m \times n + 1$ treatment to be used in r replications. The layout of the $mn + 1$ number of treatments will be as usual as per the layout of the simple RBD design. But the analysis of the responses recorded from the experiment is taken up in two stages. In the first step of analysis, the data are analyzed as per the analysis of simple RBD with $(m \times n + 1)$ treatments in r blocks. In the second step, the $m \times n$ factorial treatment effects are partitioned into different components as per the analysis of two-factor factorial analysis using RBD. The control treatment is compared with the factorial treatment by using the sum of squares calculated as follows:

$$SS_{(CvsT)} = \left[\frac{(\text{Control total})^2}{r} + \frac{(m \times n \text{ treatment total})^2}{m \times n \times r}\right] - \text{CF}$$

The corresponding analysis of variance table for the above analysis will be as follows:

SOV	d.f.	SS	MSS	Cal F
Replication	$r-1$	SS_R	MS_R	MS_R/MS_{Er}
Treatments	$mn-1$	SS_{Tr}	MS_{Tr}	MS_{Tr}/MS_{Er}
$SS_{(A)}$	$m-1$	$SS_{(A)}$	$MS_{(A)}$	$MS_{(A)}/MS_{Er}$
$SS_{(B)}$	$n-1$	$SS_{(B)}$	$MS_{(B)}$	$MS_{(B)}/MS_{Er}$
$SS_{(AB)}$	$(m-1)(n-1)$	$SS_{(AB)}$	$MS_{(AB)}$	$MS_{(AB)}/MS_{Er}$
Control vs. other treatments $SS_{(CvsT)}$	1	$SS_{(CvsT)}$	$MS_{(CvsT)}$	$MS_{(CvsT)}/MS_{Er}$
Error	By subtraction	SS_{Er}	MS_{Er}	
Total	$(mn + 1)r-1$	SS_{Tot}		

The calculated values of F are compared with the respective table values of F at appropriate level of significance and degrees of freedom. In the event of significance of any one or all the F tests, the corresponding critical difference or least significant difference values are to be worked out to compare the treatment means. While comparing the treatment means concerning the factorial treatments, the usual procedure is to be adopted during the calculation of CD/LSD values, i.e.,

$$LSD/CD(\alpha)_R = \sqrt{\frac{2MS_{Er}}{mn+1}}\, t_{\alpha/2,\text{error d.f.}} \text{ for replication}$$

$$LSD/CD(\alpha)_A = \sqrt{\frac{2MS_{Er}}{nr}}\, t_{\alpha/2,\text{error d.f.}} \text{ for factor A}$$

$$LSD/CD(\alpha)_B = \sqrt{\frac{2MS_{Er}}{mr}}\, t_{\alpha/2,\text{error d.f.}} \text{ for factor B}$$

$$LSD/CD(\alpha)_{AB} = \sqrt{\frac{2MS_{Er}}{r}}\, t_{\alpha/2,\text{error d.f.}} \text{ for interaction of factors A and B}$$

The best levels of main effect or interaction effect are worked out by comparing the treatment mean difference with respective *LSD*/*CD* values. If the difference between any pair of level means is more than the corresponding *LSD*/*CD* values, then these two levels under comparison are declared significantly different, and the best level is selected on the basis of mean of the levels under comparison. On the other hand, if the difference between any pair of level means is equal to or less than the corresponding *LSD*/*CD* value, then these two levels under comparison are declared statistically at par.

To compare the means of control versus the rest of the treatments, we are to use the *LSD* value as follows:

$$LSD/CD(\alpha)_{AB} = \sqrt{MS_{Er}\left(\frac{1}{r_c}+\frac{1}{r_t}\right)}\, t_{\alpha/2,\text{error d.f.}}$$

$$= \sqrt{MS_{Er}\left(\frac{1}{r}+\frac{1}{mnr}\right)}\, t_{\alpha/2,\text{error d.f.}}$$

where r_c and r_t are the number of observations for control and factorial (t = mn) treatments, respectively.

Example 12.1

The following information is pertaining to a factorial experiment of potato conducted with four doses of nitrogen and three seed rates along with a control (i.e., conventional seed rate and dose of nitrogen) in randomized block design with three replications. Analyze the data to examine whether there exists any significant difference (a) between the control treatment and the other treatments, (b) among the doses of nitrogen, (c) among the seed rates, and (d) to find out the best dose of nitrogen and seed rate combination for the highest yield:

Nitrogen	Seed rate	R1	R2	R3
N0	S1	27.77	27.81	27.71
N0	S2	28.34	28.39	28.31
N0	S3	27.37	27.40	27.29
N1	S1	29.67	29.75	29.62
N1	S2	23.34	23.40	23.32
N1	S3	23.8	23.84	23.72
N2	S1	22.66	22.72	22.60
N2	S2	25.47	25.50	25.44
N2	S3	26.31	26.36	26.25
N3	S1	26.76	26.82	26.71
N3	S2	25.79	25.83	25.73
N3	S3	27.65	27.68	27.57
Control		22.31	22.36	22.26

Solution According to the given problem, we are to test the hypotheses:

(a) The effect of the control treatment and the factorial treatment is the same.
(b) Different doses of nitrogen are equal.
(c) Different seed rates are equal in response.
(d) Different combinations of doses of nitrogen and seed rates are equal in response.

Let the level of significance be $\alpha = 0.05$.

Total analysis of the above problem is done in two steps: in the first step, analysis of data takes place taking 13 ($4 \times 3 + 1 = 13$) treatments as per the analysis of RBD in three replications. For the purpose we frame the following table and calculate the following quantities:

Step 1:

Grand total $(GT) = 27.77 + 28.34 + \ldots\ldots + 27.57 + 22.26 = 1011.63$

$$\text{Correction factor } (CF) = \frac{GT^2}{v \times r} = \frac{1011.63^2}{13 \times 3} = 26240.904$$

Total sum of squares $(SS_{\text{TOT}}) = 27.77^2 + 28.34^2 + \ldots\ldots + 27.57^2 + 22.26^2 - CF = 192.941$

Treatment	Nitrogen	Seed rate	R1	R2	R3	Total
T1	N0	**S1**	27.77	27.81	27.71	**83.29**
T2	N0	S2	28.34	28.39	28.31	**85.04**
T3	N0	S3	27.37	27.40	27.29	**82.06**
T4	N1	**S1**	29.67	29.75	29.62	**89.04**
T5	N1	S2	23.34	23.40	23.32	**70.06**
T6	N1	S3	23.80	23.84	23.72	**71.36**
T7	N2	**S1**	22.66	22.72	22.60	**67.98**
T8	N2	S2	25.47	25.50	25.44	**76.41**
T9	N2	S3	26.31	26.36	26.25	**78.92**
T10	N3	**S1**	26.76	26.82	26.71	**80.29**
T11	N3	S2	25.79	25.83	25.73	**77.35**
T12	N3	S3	27.65	27.68	27.57	**82.90**
T13	Control		22.31	22.36	22.26	**66.93**
Total			**337.24**	**337.86**	**336.53**	**1011.63**

Sum of squares due to block $(SS_{\text{Block}}) = \frac{1}{13}\left(337.24^2 + 337.86^2 + 336.53^2\right) - CF = 0.0681.$

Sum of squares due to treatment $(SS_{Tr}) = \frac{1}{3}\left(83.29^2 + 85.04^2 + \ldots\ldots + 66.93^2\right) - CF = 192.869$

Sum of squares due to error $(SS_{Er}) = SS_{\text{TOT}} - SS_{\text{Block}} - SS_{Tr} = 192.941 - 0.068 - 192.869 = 0.0038$

To compare the factorial treatments (12 in number) with control, we work out the sum of squares due to control vs. the rest as follows:

Sum of squares due to control vs. the rest

$$= \frac{1}{3}(66.93)^2 + \frac{1}{36}(83.29 + 85.04 + \ldots\ldots + 82.90)^2 - CF = 42.806$$

Step 2:

In the second stage of analysis, the factorial treatment effects are partitioned into main effects and interaction effects due to factors as per the standard analysis of factorial experiments. For the purpose the following table of factorial treatment totals is framed, and the following quantities are worked out:

Table of totals for S × N factorial treatments:

	N0	N1	N2	N3	Total
S1	83.29	85.04	82.06	89.04	339.43
S2	70.06	71.36	67.98	76.41	285.81
S3	78.92	80.29	77.35	82.90	319.46
Total	232.27	236.69	227.39	248.35	944.70

Grand total-2 $(GT_2) = 83.29 + 70.06 + \ldots\ldots + 76.41 + 82.90 = 944.70$

Correction factor-2 $(CF2) = \frac{944.70}{12 \times 3} = 24790.502$

Table sum of squares $(SS_{\text{Tab}}) = \frac{1}{3}\left(83.29^2 + 70.06^2 + \ldots\ldots\ldots + 76.41^2 + 82.90^2\right) - CF2 = 150.062$

Sum of squares due to nitrogen $(SS_N) = \frac{1}{9}\left(232.27^2 + 236.69^2 + 227.39^2 + 248.35^2\right) - CF2 = 26.769$

Sum of squares due to seed rate $(SS_S) = \frac{1}{12}(339.43^2 + 285.81^2 + 319.46^2) - CF2 = 122.395$

Sum of squares due to interaction (SS_{NS})
$= SS_{\text{Tab}} - SS_{(N)} - SS_{(S)}$
$= 150.062 - 26.769 - 122.395 = 0.898$

With the help of the information and sum of squares worked out in step 1 and step 2, the following analysis of variance table is framed.

Analysis of variance table for 3 × 4 + 1 experiment in RBD:

SOV	d.f.	SS	MSS	F ratio
Blocks	3−1 = 2	0.06814	0.03407	211.7450
Treatments	(3 × 4 + 1)−1 = 12	192.86948	16.07246	99892.5577
Seed rate (S)	3−1 = 2	122.39522	61.19761	380351.6689
Nitrogen (N)	4−1 = 3	26.76901	8.92300	55457.7122
SN	(3–1)(4–1) = 6	0.89847	0.14975	930.6884
Control vs. others	1	42.80678	42.80678	266050.0874
Error	24	0.00386	0.00016	
Total	(3 × 4 + 1)3−1 = 38	192.94148		

For the above analysis, we have the table values

$F_{0.05;2,24} = 3.40$, $F_{0.05;3,24} = 3.01$, $F_{0.05;6,24} = 2.51$, and $F_{0.05;1,24} = 4.26$. Thus, all the treatment effects are significant at 5 % level of significance. As the test corresponding to control vs. the rest effect is significant, so one can conclude that the factorial effect has significantly different responses than the control treatment. In order to work out the best dose of nitrogen, best seed rate, and combination of seed rate and nitrogen, we calculate the following critical difference values:

$$CD_{0.05}(\text{seed rate}) = \sqrt{\frac{2MS_{Er}}{r \times n}} \times t_{0.025;\text{error df}} = \sqrt{\frac{2 \times 0.00016}{3 \times 4}} \times 2.064 = 0.0106$$

$$CD_{0.05}(\text{nitrogen}) = \sqrt{\frac{2MS_{Er}}{r \times s}} \times t_{0.025;\text{error df}} = \sqrt{\frac{2 \times 0.00016}{3 \times 3}} \times 2.064 = 0.0123$$

$$CD_{0.05}(\text{interaction}) = \sqrt{\frac{2MS_{Er}}{r}} \times t_{0.025;\text{error df}} = \sqrt{\frac{2 \times 0.00016}{3}} \times 2.064 = 0.0213$$

In order to find out the best seed rate, best dose of nitrogen, and best combination, the average yields corresponding to three seed rates, four doses of nitrogen, and 12 interaction effects are arranged in descending order separately and are presented below:

Seed rate	Mean	CD
S1	28.286	0.0106
S3	26.622	
S2	23.818	
Nitrogen	Mean	CD
N3	27.594	0.0123
N1	26.299	
N0	25.808	
N2	25.266	
Seed rate × nitrogen	Mean	CD
S1N3	29.680	0.0213
S1N1	28.347	
S1N0	27.763	
S3N3	27.633	
S1N2	27.353	
S3N1	26.763	
S3N0	26.307	
S3N2	25.783	
S2N3	25.470	
S2N1	23.787	
S2N0	23.353	
S2N2	22.660	

From the above table, one can find that all the three seed rates are significantly different from each other (as the difference between the mean responses of any two seed rates is greater than the corresponding critical difference value). Thus, the best seed rate is the S1 seed rate producing the highest yield.

Similarly, the difference between the effects of any two doses of nitrogen is greater than the

corresponding critical difference value. Hence the effects of different doses of nitrogen significantly differ from each other, and the best dose of nitrogen is N3 producing the highest yield.

So far as the interaction effects are concerned, all the combinations are significantly different from each other; the combination S1N3 is found to be the best yielder.

12.3 Augmented Designs for the Evaluation of Plant Germplasms

As has already been discussed about the problem of evaluating huge number of germplasms at a time and/or at a place; augmentation of basic CRD, RBD, and LSD can be made for the purpose. But because of drawbacks of requiring more number of experimental units compared to other two basic designs, the possibility of using LSD is not considered in this section. We shall consider augmented CRD and RBD for the purpose.

12.3.1 Augmented Completely Randomized Design

If we can have the whole experimental area constituted of a number of homogeneous experimental plots, then one can think for augmented CRD for the evaluation of germplasms. The basic experimental design used here is a completely randomized design. Let us suppose we have "t" number of test genotypes which cannot be repeated because of scarcity of material and "c" number of checks which can be repeated "r" number of times. Thus the total number of plots required is $N = t + rc$.

The whole experimental area is divided into N number of homogeneous experimental units. N number of experimental plots are randomly allotted to $t + c$ number of entries such that c number of check varieties are replicated r number of times. There shall be $t + c = e$ entries. The sum of squares is calculated as follows:

$$\text{Grand total } (G) = \sum_{i=1}^{t} T_i + \sum_{j=1}^{c}\sum_{k=1}^{r} C_{jk}, \text{where } T_i$$

is the value corresponding to ith ($i = 1, 2, \ldots, t$) genotype and C_{jk} is the value corresponding to jth ($j = 1, 2, \ldots, c$) check and kth ($k = 1, 2, \ldots, r$) replicate.

$$\text{Correction factor } (CF) = \frac{G^2}{N}$$

$$\text{Total sum of squares } (SS_{Tot}) = \sum_{i=1}^{t} T_i^2 + \sum_{j=1}^{c}\sum_{k=1}^{r} C_{jk}^2 - CF$$

$$\text{Sum of squares due to entries } (SS_e) = \sum_{i=1}^{t} T_i^2 + \frac{1}{r}\sum_{j=1}^{c}\sum_{k=1}^{r} C_{jk}^2 - CF$$

$$\text{Correction factor for checks } (CFc) = \frac{\left(\sum_{j=1}^{c}\sum_{k=1}^{r} C_{jk}\right)^2}{c \times r}$$

$$\text{Sum of squares due to checks } (SS_c) = \frac{1}{r}\sum_{j=1}^{c}\sum_{k=1}^{r} c_{\cdot j}^2 - CF_c$$

$$\text{Correction factor for genotypes } (CF_t) = \frac{\left(\sum_{i=1}^{t} T_i\right)^2}{t}$$

$$\text{Sum of squares due to genotypes } (SS_t) = \sum_{i=1}^{t} T_i^2 - CF_t$$

$$\text{Sum of squares due to check vs. genotype } (SS_{cg}) = SS_e - SS_c - SS_t$$

$$\text{Error sum of squares } (SS_{Er}) = SS_{TOT} - SS_e$$

As such the analysis of variance table will be as follows:

SOV	d.f	SS	MS	F ratio
Entries (e)	$e-1$	SS_e	MS_e	MS_e/MS_{Er}
Checks (c)	$c-1$	SS_c	MS_c	MS_c/MS_{Er}
Genotypes (t)	$t-1$	SS_t	MS_t	MS_t/MS_{Er}
Check vs. genotype	1	SS_{ct}	MS_{ct}	MS_{ct}/MS_{Er}
Error	$c(r-1)$	SS_{Er}	MS_{Er}	
Total	$N-1$	SS_{Tot}		

The calculated values of F are compared with the respective table values of F at appropriate level of significance and degrees of freedom. In the event of significance of any one or all the F tests, the corresponding critical difference or least significant difference values are to be worked out to compare the treatment means. *LSD*/*CD* (α) to compare mean difference:

(a) Between two checks: $\sqrt{\frac{2MS_{Er}}{r}}\, t_{\alpha/2,\text{err.d.f}}$

(b) Between a check and a genotype: $\sqrt{MS_{Er}\left(1+\frac{1}{r}\right)}\, t_{\alpha/2,\text{err.d.f}}$

Example 12.2 (Augmented CRD)
The following table gives the field layout and the responses in 25 experimental units in an evaluation trial with three checks (c) and ten test genotypes (g) in a homogenous experimental area where the checks are repeated five times each and test varieties are not repeated at all. Analyze the data to examine (a) whether the test genotypes are superior over the checks, (b) which of the check genotypes is superior, and (c) which of the test genotypes is superior.

Layout and response for each plot of an augmented CRD with ten test genotypes and three checks each replicated five times:

c-1, 13	g-10, 19	g-8, 36	c-1, 13	c-3, 14	g-3, 45
g-6, 13	c-1,14	g-9, 18	c-2, 16	c-3, 13	
c-2, 15	c-3, 13	g-5, 27	c-2, 19	c-1, 16	
c-3, 12	g-2, 27	c-2 16	c-1, 15	g-1, 19	
g-7, 22	c-3,11	c-2, 18	g-4, 24		

Solution From the given information, it appears that the experiment has been conducted following augmented completely randomized design, where a number of checks = 3 and are repeated five times each. A number of test genotypes = 10.

Let the level of significance be $\alpha = 0.05$.

To facilitate the analysis, first we make the following tables:

Genotypes	Response
$g-1$	19
$g-2$	27
$g-3$	45
$g-4$	24
$g-5$	27
$g-6$	13
$g-7$	22
$g-8$	36
$g-9$	18
$g-10$	19
Total	250
Mean	25

Check	R1	R2	R3	R4	R5	Total	Mean
$c-1$	13	14	13	15	16	71	14.20
$c-2$	15	16	18	16	19	84	16.80
$c-3$	12	13	11	14	13	63	12.60
						218	14.533

$$\text{Grand total}\,(GT) = \sum_{i=1}^{v} g_i + \sum_{k=1}^{r}\sum_{j=1}^{c} c_{kj}$$

$$= \sum_{i=1}^{10} g_i + \sum_{k=1}^{5}\sum_{j=1}^{3} c_{kj} = 250 + 218 = 468,$$

where g_i is the value corresponding to ith (i = 1, 2, ….., 10) genotype and c_{kj} is the value corresponding to jth (j = 1, 2, 3) check and kth (k = 1, 2, …, 5) replicate.

$$\text{Correction factor}\,(CF) = \frac{GT^2}{N} = \frac{418^2}{25}$$

$$= 8760.96$$

$$\text{Total sum of squares}\,(SS_{\text{Tot}}) = \sum_{i=1}^{v} g_i^2 + \sum_{k=1}^{r}\sum_{j=1}^{c} c_{kj}^2 - CF = \sum_{i=1}^{10} g_i^2 + \sum_{k=1}^{5}\sum_{j=1}^{3} c_{kj}^2 - CF$$
$$= \left(19^2 + 25^2 + \ldots\ldots\ldots 19^2\right) + \left(13^2 + 14^2 + \ldots\ldots\ldots + 14^2 + 13^2\right) - 8760.96 = 1529.04$$

$$\text{Sum of squares due to entries}\,\left(SS_{(e)}\right) = \sum_{i=1}^{v} g_i^2 + \frac{1}{r}\sum_{j=1}^{c} c_{\cdot j}^2 - CF = \sum_{i=1}^{10} g_i^2 + \frac{1}{5}\sum_{j=1}^{3} c_{\cdot j}^2 - CF$$
$$= \left(19^2 + 27^2 + \ldots\ldots\ldots + 19^2\right) + \frac{1}{5}\left(71^2 + 84^2 + 63^2\right) - 8760.96 = 1506.24$$

$$\text{Correction factor for checks}\,(CFc) = \frac{1}{c \times r}\left(\sum_{k=1}^{r}\sum_{j=1}^{c} c_{kj}\right)^2 = \frac{1}{3 \times 5}\left(\sum_{k=1}^{5}\sum_{j=1}^{3} c_{kj}\right)^2$$
$$= \frac{1}{15} \times 218^2 = 3168.266$$

$$\text{Sum of squares due to checks}\,(SS_c) = \frac{1}{r}\sum_{j=1}^{c}\sum_{k=1}^{r} c_{\cdot j}^2 - CF_c = \frac{1}{5}\sum_{j=1}^{3}\sum_{k=1}^{5} c_{\cdot j}^2 - 3168.266$$
$$= \frac{1}{5}\left[71^2 + 84^2 + 63^2\right] - 3168.266 = 44.933$$

$$\text{Correction factor for genotypes}\,\left(CF_g\right) = \frac{1}{v}\left(\sum_{i=1}^{v} g_i\right)^2 = \frac{1}{10}\left(\sum_{i=1}^{10} g_i\right)^2 = \frac{1}{10} \times 250^2 = 6250$$

$$\text{Sum of squares due to genotypes}\,\left(SS_{(g)}\right) = \sum_{i=1}^{v} g_i^2 - CF_g = \left(19^2 + 27^2 + \ldots\ldots\ldots + 19^2\right) - 6250$$
$$= 7054 - 6250 = 804$$

$$\text{Sum of square due to check vs. genotype}\,\left(SS_{cg}\right) = SS_e - SS_c - SS_g$$
$$= 1506.24 - 44.93 - 804.00$$
$$= 657.306$$

$$\text{Error sum of squares}\,(SS_{Er}) = SS_{\text{Tot}} - SS_e = 1529.04 - 1506.24 = 22.80$$

Thus, the ANOVA table corresponding to the above analysis will be as follows:

ANOVA table

SOV	d.f.	SS	MS	Cal F	Tab F (0.05)
Entries	12	1506.240	125.520	66.063	2.690
Checks	2	44.933	22.467	11.825	3.890
Genotypes	9	804.000	89.333	47.018	2.800
C × G	1	657.307	657.307	345.951	4.750
Error	12	22.800	1.900		
Total	24	1529.040			

From the above table, it is clear that the tabulated F value corresponding to each and every test at desired level of significance (0.05) and respective degrees of freedom is less than the respective calculated values. Hence we conclude that:

(i) There remain significant differences among the 14 entries (check plus test genotypes).
(ii) There remain significant differences among the three checks.

(iii) There remain significant differences among the ten test genotypes.

So our next objectives will be to compare the checks among themselves, among the genotypes, and among the checks and the genotypes. For that we need to calculate the critical difference values corresponding to the above comparisons.

Standard errors of mean difference for:

Between two checks: $\sqrt{\frac{2MS_{Er}}{r}} = \sqrt{\frac{2\times 1.900}{5}} = 0.871$ and corresponding

$$CD(0.05) = SEd \times t_{0.025,\text{error } df} = 0.871 \times 2.179 = 1.899$$

Between two test genotypes: $\sqrt{2MS_{Er}} = \sqrt{2 \times 1.033} = 1.437$ and corresponding

$$CD(0.05) = SEd \times t_{0.025,\text{error } df} = 1.949 \times 2.179 = 4.247$$

Between a check and a genotype:

$$\sqrt{ErMS\left(1+\tfrac{1}{r}\right)} = \sqrt{1.900 \times \left(1+\tfrac{1}{5}\right)} = 1.509$$

and corresponding

$$CD(0.05) = SEd \times t_{0.025,\text{error df}} = 1.509 \times 2.179 = 3.290$$

Checks	Mean response	CD
c-2	16.80	1.899
c-1	14.20	
c-3	12.60	
Check x Genotypes		
Genotypes	25.00	3.29
Checks	14.53	
Genotypes		
g-3	45.00	4.247
g-8	36.00	
g-2	27.00	
g-5	27.00	
g-4	24.00	
g-7	22.00	
g-1	19.00	
g-10	19.00	
g-9	18.00	
g-6	13.00	

From the above table, we conclude that:

(i) Among the checks, the check $c-2$ is having significantly higher response compared to other two checks.
(ii) The average performance of test genotypes is significantly higher than the checks.
(iii) Among the test genotypes, $g-3$ is the best performer followed by $g-8$ which is at par with $g-2$ and $g-5$.

12.3.2 Augmented Randomized Block Design

Analogous to that of simple RBD, in augmented RBD also the whole experimental field is divided into number of blocks, each consisting of homogenous experimental units. The difference between the simple RBD and augmented RBD is that in simple RBD the same treatments are applied in all the blocks,

but in augmented RBD the same check varieties are included in each block along with different test varieties. That means check varieties are repeated all blocks, but new sets of varieties appear in different blocks. Thus, in augmented randomized block design, the whole experimental area is divided into "r" number of distinct blocks such that kth block contains $(n_k + c)$ number of homogeneous experimental units. Here "n_k" is the number of test genotypes in kth block, and "c" is the number of check varieties repeated in each of the "r" blocks. Thus, for r number of blocks, we can have $\sum_{k=1}^{r} n_k = n$ number of new varieties; altogether $n + c = e$ number of entries are there in the experiment. It may be noted that the size of the blocks may vary in augmented RBD, whereas the block size remains fixed in simple RBD.

The randomization is taken up in such a way that all the checks and the n_k number of test genotypes occur only once in kth block. Thus the total number of experimental units in this design will be $(n_1 + c) + (n_2 + c) + \ldots\ldots + (n_r + c) = n + rc = N$ (say).

Randomization and Layout

1. kth block is divided into $(n_k + c)$ number of plots.
2. Randomly allocate the c number of checks among $(n_k + c)$ number of plots in kth block.
3. Randomly allocate the total $\sum_{k=1}^{r} n_k = n$ test genotypes with "n_k" test genotypes in kth block. Thus, it may be noted that randomization technique of test genotypes is just like that of allocation of treatments in CRD. While allocating the test genotypes, we are left with $N-rc = n$ number of experimental units spread over r blocks, and we are to allocate these n test genotypes in n experimental unit like the allocation in CRD.

Sometimes the check varieties are placed in a systematic manner, i.e., the check varieties are placed after a fixed number of plots. But the analysis with random allocation of check varieties and with systematic allocation of check varieties will be different. The layout of the augmented RBD with two check varieties c1 and c2 may look like as given below:

Blocks	Experimental units						
B1	g4	g15	g10	c1	c2	g9	
B2	c2	g1	g8	c2	g11		
B3	g12	c1	g19	g14	c2	g6	g22
.....							
.....							
.....							
.....							
B_{r-1}	g21	g5	c2	g3	g17	c1	
B_r	c1	c2	g16	g13	g7		

The structure of analysis of variance-augmented RBD conducted with n genotypes with random allocation of c check varieties in r blocks will be as follows:

ANOVA table

SOV	d.f.	SS	MS	F ratio
Blocks	$r-1$	SS_B	MS_B	MS_B/MS_{Er}
Entries (e)	$e-1$	SS_e	MS_e	MS_e/MS_{Er}
Checks (c)	$c-1$	SS_c	MS_c	MS_c/MS_{Er}
Genotypes (g)	$n-1$	SS_g	MS_g	MS_g/MS_{Er}
Check vs. genotype	1	SS_{cg}	MS_{cg}	MS_{cg}/MS_{Er}
Error	$(c-1)(r-1)$	$SSEr$	MS_{Er}	
Total	$N-1$	SS_{Tot}		

As only the checks are replicated but not the test genotypes, before calculating the different components of the analysis of variance, we are to adjust the effects of test genotypes:

(i) Block effects $r_k = \frac{1}{c}\left(\sum_{j=1}^{c} c_{jk} - \overline{c}\right)$, where $\overline{c} = \frac{1}{r}\sum_{j=1}^{c}\sum_{k=1}^{r} c_{jk}$ and c_{jk} is the value corresponding to jth ($j = 1, 2, \ldots, c$) check in kth ($k = 1, 2, \ldots, r$) block. It may be noted that the sum of the block effects must be equal to zero, i.e., $\sum_{k=1}^{r} r_k = 0$.

(ii) Mean effect $(m) = \frac{1}{e}[G - (r-1)\overline{c} - \sum_{k=1}^{r} n_k r_k]$, where n_k is the number of test genotypes in the kth block (we have taken $n_k = v$ for all the blocks). Thus, the mean effect for equal number test genotype in each block is $\frac{1}{e}\left[G - (r-1)\overline{c} - \sum_{k=1}^{r} n_k r_k\right]$ $\left(\text{where } \sum n_k = n, \text{ then } n\sum_{k=1}^{r} r_k = n \times 0 = 0\right)$

(iii) Check effects $\left(\mathrm{c_j}\right) = \overline{c}_j - m, (j = 1,2,\ldots,c)$ where $\overline{c}_j = \frac{1}{r}\sum_{k=1}^{r} c_{jk}$ = mean for jth check

(iv) Adjustment for genotypic responses $\left(g_i'\right) = g_i - r_{ik}$, where g_i is the response of the ith test genotype and r_{ik} is the block effect of the block in which the ith genotype occurs.

Corresponding effects of the ith test genotype is obtained by subtracting the mean effect (m) from the above adjusted effect of genotype ($g_i^{'}$), i.e., $g_i = g_i' - m$

Grand total $(G) = \sum_{i=1}^{n} g_i + \sum_{k=1}^{r}\sum_{j=1}^{c} c_{kj}$, where g_i is the value corresponding to ith ($i = 1, 2, \ldots, n$) genotype and c_{kj} is the value corresponding to jth (j = 1, 2, …, c) check and kth (k = 1, 2, …, r) replicate.

Correction factor $(CF) = \frac{G^2}{N}$

Total sum of squares $(SS_{Tot}) = \sum_{i=1}^{n} g_i^2 + \sum_{k=1}^{r}\sum_{j=1}^{c} c_{kj}^2 - CF$

Sum of squares due to block $(SS_B) = \sum_{k=1}^{r}\left(\frac{R_k^2}{n_k + c}\right) - CF$ where R_k is the sum of the observations in kth block.

Sum of squares due to entries $(SSe) = (m \times G) + \sum_{k=1}^{r} r_k R_k + \sum_{j=1}^{c} c_j\left(\sum_{k=1}^{r} c_{jk}\right) + \sum_{i=1}^{n} g_i g_i'' - \sum_{k=1}^{r}\frac{R_k^2}{(n_k + c)}$

Correction factor for checks $(CFc) = \frac{1}{c \times r}\left(\sum_{k=1}^{r}\sum_{j=1}^{c} c_{kj}\right)^2$

Sum of squares due to checks $(SSc) = \frac{1}{r}\sum_{k=1}^{r}\left(\sum_{j=1}^{c} c_{kj}\right)^2 - CF_c$

Correction factor for genotypes $(CFg) = \frac{1}{n}\left(\sum_{i=1}^{n} g_i\right)^2$

Sum of squares due to genotypes $(SSg) = \sum_{i=1}^{n} g_i^2 - CF_g$

Sum of squares for check vs. genotype $(cgSS) = SSe–SSc–SSg$

Error sum of squares $(SS_{Er}) = SS_{\text{Tot}}–SS_B–SSe$

The standard errors of difference for testing the different varietal means are given bellow:

(i) For two check means $= \sqrt{\frac{2MS_{Er}}{r}}$

(ii) For two test genotype means in the same blocks $= \sqrt{2MS_{Er}}$

(iii) For any two entries means in the same block $= \sqrt{MS_{Er} \times \left(1 + \frac{1}{c}\right)}$

(iv) For means between a check and a test genotypes $= \sqrt{MS_{Er} \times \left(1 + \frac{1}{r} + \frac{1}{c} + \frac{1}{rc}\right)}$

Merits and Demerits Augmented designs are applied only when no other designs fit best for the purpose. Experimenter should take every care to control the experimental error during experimentation. For the reason the plots in each and every block should be kept to their highest possible homogeneous condition, and the number of test genotype in each and every block should be kept the same to facilitate statistical analysis. Added advantage of this type of design is that inclusions of any number of blocks at any point of time are possible if other conditions satisfy.

Example 12.3 (Augmented RBD)
In a germplasm evaluation trial, 20 test genotypes were tested in five blocks along with three standard check varieties. Given below is the layout and responses of total 23(20 + 3) genotypes. Analyze the data to examine (a) whether the test genotypes are superior over the checks, (b) which of the check varieties is superior, and (c) which of the test genotypes is superior. Note that in the given layout, g stands for test genotypes and c stands for check varieties:

Block 1	Block 2	Block 3	Block 4	Block 5
g20, 40	C1, 9	g1,14	g4,16	C3, 8
C3, 7	g7,17	C2, 6	C2, 8	g18, 27
g3, 19	C3, 9	C3, 9	g19, 23	C2, 7
g2, 25	g15, 28	g17, 47	C1,8	g13, 12
C2, 7	g6, 13	g5, 29	g9, 44	C1, 8
C1, 9	C2, 8	C1, 9	C3,7	g10, 19
g14, 37	g12, 47		g11, 21	
g8, 33	g16, 26			

Solution From the given information, it is clear that the above experiment has been conducted in an augmented randomized block design with three checks, each being replicated in each of the five blocks; there are 20 test genotypes randomly allocated among the five blocks. The block size is varying from 6 in block 3 and 5 to 8 in block 1 and block 2.

Thus,

c = number of checks = 3.
v = number of test genotypes in different blocks = 5, 5, 3, 4, and 3, respectively, in block 1, block 2, block 3, block 4, and block 5.
r = number of blocks = 5.
And n = number of test genotypes = 18.

Let the level of significance be $\alpha = 0.05$.

Only the checks are replicated five times but not the test genotypes, so we are to adjust the effects of test genotypes as follows.

We make the following table and the following quantities are worked out:

Checks	R1	R2	R3	R4	R5	**Total**	**Mean**
C1	9	9	9	8	8	**43**	**8.6**
C2	7	8	6	8	7	**36**	**7.2**
C3	7	9	9	7	8	**40**	**8**
Total	**23**	**26**	**24**	**23**	**23**	**119**	
Genotypes	40	17	14	16	27		
	19	28	47	23	12		
	25	13	29	44	19		
	37	47		21			
	33	26					
Total	**154**	**131**	**90**	**104**	**58**	**537**	
Rep Total	**177**	**157**	**114**	**127**	**81**	**656**	

Block effects $r_k = \frac{1}{c}\left(\sum_{j=1}^{c} c_{jk} - \overline{c}\right) = \frac{1}{3}\left(\sum_{j=1}^{3} c_{jk} - \overline{c}\right)$,

where $\overline{c} = \frac{1}{r}\sum_{j=1}^{c}\sum_{k=1}^{r} c_{jk} = \frac{1}{5}\sum_{j=1}^{3}\sum_{k=1}^{5} c_{jk} = \frac{1}{5} \times 119 = 23.8$. Thus, we have

$$r_1 = \frac{1}{c}\left(\sum_{j=1}^{c} c_{j1} - \overline{c}\right) = \frac{1}{3}\left(\sum_{j=1}^{3} c_{j1} - \overline{c}\right) = \frac{1}{3}(23.0 - 23.8) = -0.267$$

$$r_2 = \frac{1}{c}\left(\sum_{j=1}^{c} c_{j2} - \overline{c}\right) = \frac{1}{3}\left(\sum_{j=1}^{3} c_{j2} - \overline{c}\right) = \frac{1}{3}(26.0 - 23.8) = 0.733$$

$$r_3 = \frac{1}{c}\left(\sum_{j=1}^{c} c_{j3} - \overline{c}\right) = \frac{1}{3}\left(\sum_{j=1}^{3} c_{j3} - \overline{c}\right) = \frac{1}{3}(24.0 - 23.8) = 0.066$$

$$r_4 = \frac{1}{c}\left(\sum_{j=1}^{c} c_{j4} - \overline{c}\right) = \frac{1}{3}\left(\sum_{j=1}^{3} c_{j4} - \overline{c}\right) = \frac{1}{3}(23.0 - 23.8) = -0.267$$

$$r_5 = \frac{1}{c}\left(\sum_{j=1}^{c} c_{j5} - \overline{c}\right) = \frac{1}{3}\left(\sum_{j=1}^{3} c_{j5} - \overline{c}\right) = \frac{1}{3}(23.0 - 23.8) = -0.267$$

It may be noted that sum of the block effects must be equal to zero, i.e., $\sum_{k=1}^{r} r_k = -0.267 - 0.733 - 0.066 - 0.267 - 0.267 = 0$.

Mean effect (m)

$$= \frac{1}{e}\left[G - (r-1)\overline{c} - \sum_{k=1}^{r} n_k r_k\right]$$

$$= \frac{1}{23}[656 - (5-1)23.8 - \{5 \times (-0.267) + 5 \times (0.733) + 3 \times (0.066) + 4 \times (-0.267) + 3 \times (-0.267)\}]$$

$$= \frac{1}{23}[656 - 95.2 + 0.666] = 24.353$$

Check effects $\left(c_j\right) = \overline{c}_j - m, (j = 1, 2, 3)$. Thus we have

$$c_1 = \overline{c}_1 - m = 8.6 - 24.353 = -15.753$$
$$c_2 = \overline{c}_2 - m = 7.2 - 24.353 = -17.153$$
$$c_3 = \overline{c}_3 - m = 8.0 - 24.353 = -16.353$$

Adjustment for genotypic responses $\left(g_i'\right) = g_i - r_{ik}$, where g_i is the response of the ith test genotype and r_{ik} is the block effect of the block in which the ith genotype occurs.

Corresponding effects of the ith test genotype is obtained by subtracting the grand mean (m) from the above adjusted effect of genotype (g_i'), i.e., $g_i'' = g_i' - m$:

Genotypes	Genotypic response (g_i)	Block (k)	Block effect (r_{ik})	Adjusted response $(g_i' = g_i - r_{ik})$	Adjusted genotype effects $(g_i'' = g_i' - m)$
g1	14	3	0.0667	−10.420	−145.875
g2	25	1	−0.2667	0.914	22.842
g3	19	1	−0.2667	−5.086	−96.640
g4	16	4	−0.2667	−8.086	−129.381
g5	29	3	0.0667	4.580	132.830
g6	13	2	0.7333	−12.086	−157.122
g7	17	2	0.7333	−8.086	−137.468
g8	33	1	−0.2667	8.914	294.151
g9	44	4	−0.2667	19.914	876.201
g10	19	5	−0.2667	−5.086	−96.640
g11	21	4	−0.2667	−3.086	−64.813
g12	47	2	0.7333	21.914	1029.942
g13	12	5	−0.2667	−12.086	−145.036
g14	37	1	−0.2667	12.914	477.806
g15	28	2	0.7333	2.914	81.583
g16	26	2	0.7333	0.914	23.755
g17	47	3	0.0667	22.580	1061.276
g18	27	5	−0.2667	2.914	78.669
g19	23	4	−0.2667	−1.086	−24.986
g20	40	1	−0.2667	15.914	636.547

Grand total (G) = grand total $(GT) = \sum_{i=1}^{n} g_i + \sum_{k=1}^{r}\sum_{j=1}^{c} c_{kj} = 537 + 119 = 656$, where g_i is the value corresponding to ith $(i = 1, 2, \ldots, 20)$ genotype and c_{kj} is the value corresponding to jth $(j = 1, 2, 3)$ check and kth $(k = 1, 2, \ldots, 5)$ replicate.

$$\text{Correction factor } (CF) = \frac{G^2}{N} = \frac{656^2}{35} = 12295.314$$

Total sum of squares (SS_{Tot})

$$= \sum_{i=1}^{n} g_i^2 + \sum_{k=1}^{r}\sum_{j=1}^{c} c_{kj}^2 - CF$$

$$= \sum_{i=1}^{20} g_i^2 + \sum_{k=1}^{5}\sum_{j=1}^{3} c_{kj}^2 - CF$$

$$= \left(20^2 + 19^2 + \ldots\ldots + 12^2 + 19^2\right) + \left(9^2 + 7^2 + \ldots\ldots + 7^2 + 8^2\right) - 12295.314$$

$$= 5474.685$$

Sum of squares due to block (SS_B)

$$= \sum_{k=1}^{r} \frac{r_k^2}{v_k + c} - CF$$
$$= \frac{1}{(5+3)}(177^2) + \frac{1}{(5+3)}(157^2) + \frac{1}{(3+3)}(114^2) + \frac{1}{(4+3)}(127^2) + \frac{1}{(3+3)}(81^2) - 12295.31$$
$$= 3916.125 + 3081.125 + 2166.00 + 2304.14 + 1093.5 - 12295.31$$
$$= 265.578$$

Sum of squares due to entries(SS_e)

$$= (m \times G) + \sum_{k=1}^{r} r_k \left(\sum_{i=1}^{v} \sum_{j=1}^{c} y_{ijk} \right) + \sum_{j=1}^{c} c_j \left(\sum_{k=1}^{r} c_{jk} \right) + \sum_{i=1}^{n} g_i g_i'' - \sum_{k=1}^{r} \frac{r_k^2}{c + v_k}$$
$$= [24.353 \times 656] + [117 \times (-0.267) + 157 \times (0.733) + 114 \times (0.066) + 127 \times (-0.267) + 81 \times (-0.267)]$$
$$+[43 \times (-24.0899) + 36 \times (-25.489) + 40 \times (-24.689)]$$
$$+[14 \times (-145.875) + 25 \times (-22.842) + 19 \times (-96.640) + \ldots\ldots + 40 \times (636.547)]$$
$$-\left[\frac{1}{(5+3)}(177^2) + \frac{1}{(5+3)}(157^2) + \frac{1}{(3+3)}(114^2) + \frac{1}{(4+3)}(127^2) + \frac{1}{(3+3)}(81^2)\right]$$
$$= 15975.976 + 20.066 + (-1949.081) + (3717.63) - 12560.892$$
$$= 5203.373$$

Correction factor for checks (CFc)

$$= \frac{1}{c \times r}\left(\sum_{k=1}^{r} \sum_{j=1}^{c} c_{kj} \right)^2 = \frac{1}{3 \times 5}(119^2) = 944.066$$

Sum of squares due to checks (SS_c)

$$= \frac{1}{r} \sum_{k=1}^{r} \left(\sum_{j=1}^{c} c_{kj} \right)^2 - CF_c$$
$$= \frac{1}{5}(43^2 + 36^2 + 40^2) - 944.066$$
$$= 4.933$$

Correction factor for genotypes (CF_g)

$$= \frac{1}{n}\left(\sum_{i=1}^{n} g_i \right)^2 = \frac{1}{20} \times 536^2 = 14418.45$$

Sum of squares due to genotypes (SS_g)

$$= \sum_{i=1}^{n} g_i^2 - CF_g$$
$$= (40^2 + 19^2 + 25^2 + \ldots\ldots + 12^2 + 19^2) - 14418.45$$
$$= 16813 - 14418.45 = 2394.55$$

Sum of squares check vs. genotype (SS_{cg})

$$= SS_e - SS_c - SS_g$$
$$= 7556.707 - 4.933 - 2394.55$$
$$= 5157.223$$

Error sum of squares (SS_{Er})

$$= SS_{Tot} - SS_B - SS_e$$
$$= 5474.685 - 265.678 - 5203.373 = 5.398$$

SOV	d.f.	SS	MSS	Cal F	Tab F
Blocks	4	265.578	66.3945	135.298	3.84
Entries (e)	22	5203.373	236.51695	481.972	3.18
Checks (c)	2	4.933	2.4665	5.026	4.46
Genotypes (g)	19	2394.55	126.02895	256.821	3.22
C vs. G	1	5157.223	5157.223	10509.347	5.32
Error	11	5.398	0.4907273		
Total	34	5474.685			

From the above ANOVA table, it is clear that the calculated F values are greater than the corresponding tabulated F values at 5 % level of significance and respective degrees of freedom. So, one can infer that:

(i) There remain significant differences among the 20 entries (check plus test genotypes).
(ii) There remain significant differences among the three checks.
(iii) There remain significant differences among the 16 test genotypes.

So our next objectives will be to compare the checks among themselves, among the genotypes, and among the checks and the genotypes. For that we need to calculate the critical difference values corresponding to the above comparisons.

Standard errors of mean difference for:

Between two checks: $\sqrt{\frac{2MS_{Er}}{r}} = \sqrt{\frac{2\times 0.490}{5}} = 0.443$ and corresponding $CD(0.05) = SEd \times t_{0.025,\text{error df}} = 0.443 \times 2.200 = 0.975$

Between any two entries in the same block: $\sqrt{MS_{Er}\left(1+\frac{1}{r}\right)} = \sqrt{0.490 \times \left(1+\frac{1}{5}\right)} = 0.767$ and corresponding $CD(0.05) = SEd \times t_{0.025,\text{error df}} = 0.767 \times 2.200 = 1.688$

(c) Between two test genotypes: $\sqrt{2MS_{Er}} = \sqrt{2 \times 0.490} = 0.990$ and corresponding $CD(0.05) = \text{SEd} \times t_{0.025,\text{error df}} = 0.990 \times 2.200 = 2.180 = 5.391$

(d) Between means of a check and a test genotypes $= \sqrt{MS_{Er} \times \left(1+\frac{1}{r}+\frac{1}{c}+\frac{1}{rc}\right)} = \sqrt{0.490 \times \left(1+\frac{1}{5}+\frac{1}{3}+\frac{1}{15}\right)} = 0.886$ and corresponding $CD(0.05) = SEd \times t_{0.025,\text{error df}}$ $0.886 \times 2.200 = 1.950$

Conclusion Using the below mean tables and corresponding *CD* values, one can compare the genotypes among themselves as well as with the checks, and one can conclude that:

(i) C1 and C3 and C3 and C2 are at par with each other. Among the three c1 is the best check.
(ii) Among the test genotypes, g12 and g17 are the best one having significantly higher response than any other genotype followed by g9, g20, g14, and so on.
(iii) Among the entries g20 in block 1, g12 in block 2, g17 in block 3, g44 in block 4, and g18 in block 5 are the best entries, respectively.
(iv) Irrespective of the block, g12 and g17 are found to be the best and the better performer compared to other test and check genotypes:

Among the checks		
	Checks	Mean
	C1	8.6
	C3	8.0
	C2	7.2
CD(0.05)	**0.975**	

Among the genotypes																			
g12	g17	g9	g20	g14	g8	g5	g15	g18	g16	g2	g19	g11	g3	g10	g7	g4	g1	g6	g13
47	47	44	40	37	33	29	28	27	26	25	23	21	19	19	17	16	14	13	12
CD(0.05)	**5.391**																		

Entries in the same block					
	B1	B2	B3	B4	B5
	9	9	9	8	8
	7	8	6	8	7
Checks	7	9	9	7	8
	40	17	14	16	27
	19	28	47	23	12
	25	13	29	44	19
	37	47		21	
Genotypes	33	26			
CD(0.05)	**1.688**				

Among the entries																						
g12	g17	g9	g20	g14	g8	g5	g15	g18	g16	g2	g19	g11	g3	g10	g7	g4	g1	g6	g13	C1	C3	C2
47	47	44	40	37	33	29	28	27	26	25	23	21	19	19	17	16	14	13	12	8.6	8	7.2
CD (0.05)	**1.950**																					

12.4 Combine Experiment

Experiments, particularly the field experiments, are required to be repeated for their consistency or otherwise in results. Agricultural experiments, experiments with living objects, are not only subjected to the treatments under investigation but also are subjected to varied range of agroclimatic situations. So the performance of the treatments is required to be assessed over the varied situations. For example, yield performance of a set of varieties/breeds is required to be assessed under different abiotic and biotic conditions for consistency before these are released for wide adoption by the farmers. A breed/variety is put under multilocational trial or experimented over different seasons/years for their consistency or otherwise in performance. In doing so the experimental treatments come across with a varied range of abiotic and/or biotic conditions. At the same time, such repetitions of the experiments open up the scopes of the experiment with respect to its applicability over the situations. Moreover the presence and estimations of the treatment × situation interaction effects are needed to be worked out. A treatment or a set of treatments having nonsignificant interaction effects will imply consistency of the treatment(s) over different situations. On the other hand, if the treatment × situation interaction be significant, then the best place where a particular treatment is of much adoptability could be identified and exploited.

In the process, a particular experiment is repeated under different situations, viz., seasons, years, locations, etc., essentially under the same experimental protocol. Now to have the overall effect of a treatment or treatments, the experimenter needs to combine the responses of the experiments conducted under different situations. *Such type of analysis which combines the analysis of the same experiment conducted in different situations is known as combined analysis. Essentially, combined analysis is performed in two phases: in the first phase, it includes situation-wise analyses of the experiment separately and then to combine the results of all the situations to have a comprehensive idea about the treatments.*

Let us discuss the step-by-step analytical procedure of multilocational trial conducted with t treatments using RBD with r replications in each of the *l* locations:

Step 1:

We are provided with the information of an experiment conducted with t treatments in RBD with r replications from each of the *l* locations**.** Following the usual procedure of RBD analysis, let us analyze the data from each of the *l* locations separately and summarize the same as follows.

The location-wise mean sum of squares for different sources of variations is as follows:

		Location (L)			
SOV	d.f.	L_1	L_2	…….	L_l
Replication	r-1	MS_R-1	MS_R-2	…….	MS_R-*l*
Treatment	t-1	MS_{Tr}-1	MS_{Tr}-2	…….	MS_{Tr}- *l*
Error	(r-1)(t-1)	MS_{Er}-1	MS_{Er}-2	…….	MS_{Er}- *l*

Step 2:

The combined analysis starts with the testing of homogeneity of the error mean squares from different locations. This is because of the fact that in the event of acceptance of homogeneity of the error mean squares, further analysis will be different from that of in the presence of heterogeneity among the error mean squares. We know that error mean square is nothing but the estimated variance. So if the homogeneity of variances is established, then one should go for

unweighted combined analysis of variance otherwise *weighted combined analysis of variance*. So the test for homogeneity of error mean squares (variance) is necessary before taking up the combined analysis of variance. Bartlett's test or Hartley's test for homogeneity variance can be adopted for the purpose:

(i) Bartlett's test for homogeneity of variances can be performed following the procedure described in Chap. 6.2.1.2.ix. Bartlett's test for homogeneity of variance can be performed even when error mean squares are arising out of experiments having different replications.

(ii) But the combined analysis of variance is taken up generally for the experiments conducted under the same protocol, i.e., the number of replications used in all the sets is equal. In that case Hartley's test becomes more useful and simple. Hartley's test is given as

$$F_{\max} = \frac{\text{Largest error mean square among the situations}}{\text{Smallest error mean square among the situations}} = \frac{MxMS_{Er}}{MnMS_{Er}}$$

For different treatments (t) and replication combinations, the value of $F_{\max}$ statistics has been tabulated by Hartley. If the observed value of $F_{\max}$ is less than or equal to the table value at specified level of significance, then the error mean squares (variances) are declared homogeneous; otherwise these are heterogeneous. *As a rule of thumb, if the above ratio be less than 3, then the variances are generally taken as homogeneous otherwise not*. That means

$$F_{\max} = \frac{\text{Largest error mean square among the situations}}{\text{Smallest error mean square among the situations}} = \frac{MxMS_{Er}}{MnMS_{Er}} < 3.$$

Step 3:

Appropriate model for the combined analysis would be as follows:

$$y_{ijk} = \mu + \alpha_i + \beta_k + \gamma_{ik} + \delta_{jk} + e_{ijk}$$

where $i = 1, 2, \ldots, t$; $j = 1, 2, \ldots\ldots, r$; and $k = 1, 2, \ldots\ldots, l$

y_{ijk} = response of ith treatment in jth replication of kth location

μ = general effect

α_i = additional effect due to ith treatment and $\sum_{i=1}^{t} \alpha_i = 0$

β_k = additional effect due to kth location and $\sum_{k=1}^{r} \beta_k = 0$

γ_{ik} = interaction effect due to ith treatment in kth location and $\gamma_{ik} \sim$ i.i.d. N(0, σ^2)

δ_{jk} = effect of the jth replication in the kth location and $\sum_{j=1}^{r}\sum_{k=1}^{l} \delta_{jk} = 0$

e_{ijk} = error component associated with ith treatment and jth replication and kth location and $e_{ijk} \sim$ i.i.d. N(0, σ^2)

The combined analysis of variance table would be as follows:

SOV	Degrees of freedom	S.S.
Location	$l-1$	SS_L
Replication within locations	$l(r-1)$	SS_R
Treatments	$(t-1)$	SS_{Tr}
Treatment × location	$(t-1)(l-1)$	$SS_{(LT)}$
Error	$l(r-1)(t-1)$	SS_{Er}

Step 4:

(a) *Unweighted analysis:*

When the error mean squares are homogeneous, one should adopt unweighted analysis, and the different steps for unweighted analysis of variances are as follows:

(i) Correction factor $(CF) = \frac{1}{ltr}\left(\sum_{i=1}^{t}\sum_{j=1}^{r}\sum_{k=1}^{l} y_{ijk}\right)^2$.

(ii) *Total sum of square* $(TSS) = \sum_{i=1}^{t}\sum_{j=1}^{r}\sum_{k=1}^{l} y_{ijk}^2 - C.F.$

(iii) Replication within location sum of square $= \sum_{k=1}^{l} R_k SS$
where $R_k SS$ is the sum of square due to replication in kth location.

(iv) A treatment × location table of totals is formed and from which the treatment sum of square, location sum of square, and treatment × location sum of square are computed as per the methods used in factorial experiments.

(v) Error sum of square $(SS_{Er}) = \sum_{k=1}^{l} SS_{Er_k}$, where SS_{Er_k} is the error sum of square in kth location.

(vi) The significance of treatment × location is tested first using

$$F = \frac{\text{Treatment} \times \text{location } MS}{MS_{\text{Er}}}.$$

(vii) If the above interaction effect be significant, then the significance of treatment effect is worked out using

$$F = \frac{\text{Treatment } MS}{\text{Interaction } MS}.$$

If the interaction effect is not significant, then interaction MS is added to MS_{Er} for a single F test.

(b) *Weighted analysis:*

In the case of heterogeneous error mean square, the weighted analysis of variance is taken up:

(i) The weight for different locations is calculated as $W_k = \frac{r_k}{MS_{Er_k}}$ and $W = \sum_{k=1}^{l} W_k$. One thing should be remembered that for $W_k's$ to be sufficiently accurate, the degrees of freedom for error components in individual experiments should be 15 or more.

(ii) The grand total is calculated using the formula $\sum_{k=1}^{l} W_k L_k$, where L_k is the grand total for the location k and $CF = \frac{1}{tW}(GT)^2$.

(iii) The total sum of square $= \sum_{k=1}^{l}\left(W_k \sum_{i=1}^{t} T_{ik}^2\right) - CF$

(iv) Location sum of square $= \frac{1}{t}\sum_{k=1}^{l} W_k \left(\sum_{k=1}^{l} L_k\right)^2 - C.F.$

(v) Treatment sum of square $= \frac{1}{W}\sum_{i=1}^{t}\left(W_k L_k^2\right) - CF$

(vi) Location × treatment sum of square = total SS – location SS – treatment SS.

(vii) In the case of heterogeneous MS_{Er}, the significance of interaction effects is worked out using

$$x^2 = \frac{(m-4)(m-2)}{m(+t-3)} \times \text{interaction} MS.$$

(viii) The appropriate degrees of freedom for χ^2 are calculated as

$$(l-1)(t-1)\frac{(m-4)}{(m+t-3)}.$$

(ix) The treatment means are computed as

$$\overline{T}_i = \frac{1}{W}\sum_{k=1}^{l} W_k L_{ki}.$$

(x) The critical difference value for comparison of different treatment effects is given by $CD(\alpha) = \sqrt{\frac{2\times\text{interaction } MS}{W}} t_{\alpha/2,\text{interaction df}}$. On the other hand, if the error mean squares are heterogeneous, the interaction effect is nonsignificant. The analysis of variance may be carried out as per RBD using mean values for different treatments, and in that case the standard error for comparison of treatment mean is given

by $CD(\alpha) = \sqrt{\frac{2 \times \text{interaction } MS}{l}} t_{\alpha/2, \text{interaction df}}$, where l is the number of locations.

Example 12.4 Unweighted Combined RBD Analysis

An experiment was conducted with 18 different treatment combinations to study the effect of various weed controlling measures on growth attributed in 0 till wheat for three consecutive years during the same seasons. The following data gives the replication-wise dry matter production (gm^{-2}) for different treatments during the three years of experimentation. Analyze the data to identify the best treatment with respect to dry matter production:

	Year 1			Year 2			Year 3		
Treatment	**R1**	**R2**	**R3**	**R1**	**R2**	**R3**	**R1**	**R2**	**R3**
T1	801.00	803.01	803.86	801.13	803.21	803.91	801.25	803.64	804.19
T2	856.50	858.62	859.44	856.61	858.95	859.58	856.72	858.93	859.59
T3	822.50	824.81	825.53	822.63	824.93	825.59	822.74	824.76	825.61
T4	755.30	757.61	758.30	755.40	757.79	758.35	755.53	757.78	758.39
T5	761.50	763.58	764.44	761.62	763.65	764.41	761.74	763.86	764.68
T6	723.50	725.66	726.33	723.60	725.82	726.54	723.72	725.77	726.52
T7	745.50	747.54	748.44	745.63	747.89	748.64	745.74	747.91	748.62
T8	771.00	773.27	773.91	771.11	773.32	774.10	771.22	773.22	773.96
T9	746.90	749.17	749.86	747.00	749.23	749.93	747.10	749.22	750.02
T10	750.40	752.59	753.21	750.51	752.55	753.38	750.62	752.87	753.57
T11	756.70	758.81	759.51	756.80	758.97	759.73	756.92	759.07	759.72
T12	848.43	850.74	851.35	848.56	850.91	851.60	848.66	850.86	851.51
T13	880.90	883.10	883.78	881.01	883.34	884.05	881.11	883.49	884.12
T14	798.95	801.06	801.76	799.07	801.07	801.99	799.19	801.50	802.09
T15	796.67	798.70	799.43	796.79	798.89	799.64	796.90	798.90	799.73
T16	753.45	755.64	756.25	753.55	755.82	756.55	753.65	755.87	756.50
T17	749.68	752.02	752.65	749.78	752.17	752.71	749.89	752.13	752.87
T18	786.90	789.10	789.75	787.03	789.19	789.84	787.14	789.28	790.05

Solution According to the given information, the experiment has been conducted for three consecutive years following the same 18 treatments in randomized block design. So we are to perform the combined analysis of variance for randomized block design. The step-by-step procedure is given below:

Step 1:

Year-wise analysis of variance for RBD:

	Year 1				Year 2				Year 3			
Treatment	R1	R2	R3	Total	R1	R2	R3	Total	R1	R2	R3	Total
T1	801.00	803.01	803.86	2407.87	801.13	803.21	803.91	2408.25	801.25	803.64	804.19	2409.08
T2	856.50	858.62	859.44	2574.56	856.61	858.95	859.58	2575.15	856.72	858.93	859.59	2575.25
T3	822.50	824.81	825.53	2472.84	822.63	824.93	825.59	2473.15	822.74	824.76	825.61	2473.11
T4	755.30	757.61	758.30	2271.21	755.40	757.79	758.35	2271.55	755.53	757.78	758.39	2271.71
T5	761.50	763.58	764.44	2289.52	761.62	763.65	764.41	2289.68	761.74	763.86	764.68	2290.29
T6	723.50	725.66	726.33	2175.49	723.60	725.82	726.54	2175.96	723.72	725.77	726.52	2176.00
T7	745.50	747.54	748.44	2241.48	745.63	747.89	748.64	2242.15	745.74	747.91	748.62	2242.27
T8	771.00	773.27	773.91	2318.18	771.11	773.32	774.10	2318.52	771.22	773.22	773.96	2318.40
T9	746.90	749.17	749.86	2245.93	747.00	749.23	749.93	2246.16	747.10	749.22	750.02	2246.34
T10	750.40	752.59	753.21	2256.20	750.51	752.55	753.38	2256.44	750.62	752.87	753.57	2257.07
T11	756.70	758.81	759.51	2275.02	756.80	758.97	759.73	2275.51	756.92	759.07	759.72	2275.71
T12	848.43	850.74	851.35	2550.52	848.56	850.91	851.60	2551.06	848.66	850.86	851.51	2551.03
T13	880.90	883.10	883.78	2647.78	881.01	883.34	884.05	2648.39	881.11	883.49	884.12	2648.71
T14	798.95	801.06	801.76	2401.77	799.07	801.07	801.99	2402.12	799.19	801.50	802.09	2402.78
T15	796.67	798.70	799.43	2394.79	796.79	798.89	799.64	2395.32	796.90	798.90	799.73	2395.54
T16	753.45	755.64	756.25	2265.34	753.55	755.82	756.55	2265.93	753.65	755.87	756.50	2266.03
T17	749.68	752.02	752.65	2254.35	749.78	752.17	752.71	2254.67	749.89	752.13	752.87	2254.88
T18	786.90	789.10	789.75	2365.74	787.03	789.19	789.84	2366.05	787.14	789.28	790.05	2366.46
Total	14105.77	14145.02	14157.80	42408.60	14107.82	14147.69	14160.55	42416.06	14109.85	14149.07	14161.72	42420.65

For year 1:

$$\text{Grand total } (GT) = 42408.60$$

$$\text{Correction factor } (CF) = \frac{GT^2}{r \times t} = \frac{42408.60^2}{3 \times 18} = 33305352.33$$

$$\text{Total sum of squares } (SS_{\text{Tot}}) = \left(801.00^2 + 856.50^2 + \ldots\ldots + 752.65^2 + 789.75^2\right) - 33305352.33 = 98982.60$$

$$\text{Sum of squares due to block } (SS_B) = \frac{1}{18}\left(14105.77^2 + 14145.02^2 + 14157.80^2\right) - 33305352.33 = 81.676$$

$$\text{Sum of squares due to treatments } (SS_{Tr}) = \frac{1}{3}\left(2407.87^2 + 2574.56^2 + \ldots\ldots + 2254.35^2 + 2365.74^2\right) - 33305352.33 = 98900.783$$

$$\text{Sum of squares due to error } (SS_{Er}) = SS_{\text{TOT}} - SS_B - SS_{Tr} = 98982.60 - 81.676 - 98900.783 = 0.14$$

ANOVA Table for year 1				
SOV	**df**	**SS**	**MS**	**F ratio**
Block	2	81.6761	40.8381	9793.5250
Treatment	17	98900.7831	5817.6931	1395162.4298
Error	34	0.1418	0.0042	
Total	53	98982.6010		

For year 2:

$$\text{Grand total } (GT) = 42416.06$$

$$\text{Correction factor } (CF) = \frac{GT^2}{r \times t} = \frac{42416.06^2}{3 \times 18} = 33317072.00$$

$$\text{Total sum of squares } (SS_{\text{Tot}}) = \left(801.13^2 + 856.61^2 + \ldots\ldots + 752.71^2 + 789.84^2\right) - 33317072.00 = 99064.03$$

$$\text{Sum of squares due to block } (SS_B) = \frac{1}{18}\left(14107.82^2 + 14147.69^2 + 14160.55^2\right) - 33317072.00 = 83.979$$

$$\text{Sum of squares due to treatments } (SS_{Tr}) = \frac{1}{3}\left(2408.25^2 + 2575.15^2 + \ldots\ldots + 2254.67^2 + 2366.05^2\right) - 33317072.00 = 98979.881$$

$$\text{Sum of squares due to error } (SS_{Er}) = SS_{\text{TOT}} - SS_B - SS_{Tr} = 99064.03 - 83.979 - 98979.881 = 0.17$$

ANOVA Table for year 2				
SOV	**df**	**SS**	**MS**	**F ratio**
Block	2	83.9800	41.9900	8315.5069
Treatment	17	98979.8814	5822.3460	1153030.8005
Error	34	0.1717	0.0050	
Total	53	99064.0331		

For year 3:

$$\text{Grand total } (GT) = 42420.65$$

$$\text{Correction factor } (CF) = \frac{GT^2}{r \times t} = \frac{42420.65^2}{3 \times 18} = 33324287.72$$

$$\text{Total sum of squares } (SS_{\text{TOT}}) = \left(801.25^2 + 856.72^2 + \ldots\ldots + 752.87^2 + 790.05^2\right) - 33324287.72 = 99056.77$$

$$\text{Sum of squares due to block } (SS_B) = \frac{1}{18}\left(14109.85^2 + 14149.07^2 + 14161.72^2\right) - 33324287.72 = 81.272$$

$$\text{Sum of squares due to treatments } (SS_{Tr}) = \frac{1}{3}\left(2409.08^2 + 2575.25^2 + \ldots\ldots + 2254.88^2 + 2366.46^2\right) - 33324287.72 = 98975.344$$

$$\text{Sum of squares due to error } (SS_{Er}) = SS_{\text{TOT}} - SS_B - SS_{Tr} = 99056.77 - 81.27 - 98975.344 = 0.15$$

ANOVA Table for year 3				
SOV	**df**	**SS**	**MS**	**F ratio**
Block	2	1.4971	0.7485	436.6411
Treatment	17	208.4576	12.2622	7152.8643
Error	34	0.0583	0.0017	
Total	53	210.0129		

Step 2:

The mean squares for different analysis of variance can be represented as follows:

SOV	d.f.	MS for the years		
		Year 1	Year 2	Year 3
Replication	2	40.8381	41.9900	40.6362
Treatment	17	5817.6931	5822.3460	5822.0791
Error	34	0.0042	0.0050	0.0044

Step 3: *(Test for homogeneity of variances)*

As per Hartley's test for homogeneity of variance,

$$F_{\max} = \frac{\text{Largest error mean square}}{\text{Smallest error mean square}} = \frac{0.0050}{0.0042} = 1.210 < 3$$

Thus we can assume homogeneous variance and go for unweighted analysis of variance.

Step 4:

The model for combined analysis of variance is as follows:

$$y_{ijk} = \mu + \alpha_i + \beta_k + \gamma_{ik} + \delta_{jk} + e_{ijk}$$

where $i = 1, 2, \ldots, 18; j = 1, 2, 3;$ and $k = 1, 2, 3$

y_{ijk} = response of ith treatments in jth blocks of kth year

μ = general effect

α_i = additional effect due to ith treatment and $\sum_{i=1}^{18} \alpha_i = 0$

β_k = additional effect due to kth year and $\sum_{k=1}^{3} \beta_k = 0$

γ_{ik} = interaction effect due to ith treatment in kth year and $\gamma_{ik} \sim$ i.i.d. N(0, σ^2)

δ_{jk} = effect of the jth block in the kth year and $\sum_{j=1}^{3}\sum_{k=1}^{3} \delta_{jk} = 0$

e_{ijk} = error component associated with ith treatment and jth block and kth year and $e_{ijk} \sim$ i.i.d. N(0, σ^2)

and the corresponding analysis of variance structure will be as follows:

SOV	d.f	*SS*
Year	3−1 = 2	YSS
Block within year	3(3–1) = 6	BSS
Treatment	(18–1) = 17	*TrSS*
Treatment x year	(18–1)(3–1) = 34	*SS*(YT)
Error	3(18–1)(3–1) = 102	*ErSS*

Unweighted Analysis When the error mean squares are homogeneous, one should adopt unweighted analysis, and the different steps

for unweighted analysis of variances are as follows:

$$\text{Correction factor } (CF) = \frac{1}{ytr}\left(\sum_{i=1}^{t}\sum_{j=1}^{r}\sum_{k=1}^{l} y_{ijk}\right)^2 = \frac{1}{3 \times 18 \times 3}(42408.60 + 42416.06 + 42420.65)^2$$
$$= 99946710.60$$

$$\text{Total sum of square } (SS_{\text{Tot}}) = \sum_{i=1}^{t}\sum_{j=1}^{r}\sum_{k=1}^{l} y_{ijk}^2 - C.F$$
$$= 801.00^2 + 856.50^2 + 822.50^2 + \ldots\ldots + 752.87^2 + 790.05^2$$
$$-99946710.68$$
$$= 297104.770$$

$$\text{Replication within the year sum of square} = \sum_{k=1}^{y} R_k SS = \sum_{k=1}^{3} R_k SS = 81.676 + 83.980 + 81.272$$
$$= 246.928$$

A treatment × year table is formed and from which the treatment sum of square, year sum of square, and treatment × year sum of square are computed as per the methods used in factorial experiments and as given below:

Treatment	Year 1	Year 2	Year 3	Total
T1	2407.87	2408.25	2409.08	7225.20
T2	2574.56	2575.15	2575.25	7724.95
T3	2472.84	2473.15	2473.11	7419.11
T4	2271.21	2271.55	2271.71	6814.47
T5	2289.52	2289.68	2290.29	6869.49
T6	2175.49	2175.96	2176.00	6527.45
T7	2241.48	2242.15	2242.27	6725.89
T8	2318.18	2318.52	2318.40	6955.09
T9	2245.93	2246.16	2246.34	6738.43
T10	2256.20	2256.44	2257.07	6769.71
T11	2275.02	2275.51	2275.71	6826.24
T12	2550.52	2551.06	2551.03	7652.61
T13	2647.78	2648.39	2648.71	7944.88
T14	2401.77	2402.12	2402.78	7206.67
T15	2394.79	2395.32	2395.54	7185.65
T16	2265.34	2265.93	2266.03	6797.29
T17	2254.35	2254.67	2254.88	6763.90
T18	2365.74	2366.05	2366.46	7098.26
Total	42408.60	42416.06	42420.65	127245.30

From the above table, we have

$$SS_{\text{Table}} = \frac{\left(2407.87^2 + 2574.56^2 + \ldots\ldots + 2254.88^2 + 2366.46^2\right)}{3} - \frac{127245.30^2}{(3 \times 18 \times 3)} = 296857.379$$

$$SS_{\text{year}} = \frac{1}{3 \times 18}\left[42408.60^2 + 42416.06^2 + 42420.65^2\right] - CF = 99946712.05 - 99946710.68 = 1.370$$

$$SS_{Tr.} = \frac{1}{3 \times 3}\left[7225.20^2 + 7724.95^2 + \ldots\ldots + 7098.26^2\right] - CF$$
$$= 100243566.40 - 99946710.68 = 296855.709$$

$$SS_{Tr. \times \text{Year}} = SS_{\text{Table}} - SS_{Yr} - SS_{Tr.} = 296857.379 - 1.370 - 296855.709 = 0.299$$

$$\text{Error sum of square } (SS_{Er.}) = \sum_{k=1}^{y} Er_k SS = \sum_{k=1}^{3} Er_k SS = 0.1418 + 0.1717 + 0.1494 = 0.4629,$$

where Er_kSS is the error sum of square in kth year.

The significance of treatment × year interaction is tested first using

$$F = \frac{\text{Treatment} \times \text{year } MS}{ErMS} = \frac{0.299}{0.0045} = 65.988.$$

At 5 % level of significance and at 34,102 d.f., the value of F statistic is 1.57 (approx.), so the test is significant. Now we use the significance test of treatment effect as follows:

$$F = \frac{\text{Treatment } MS}{\text{Interaction } MS} = \frac{296855.709}{0.2994} = 991227.24$$

Thus the combined analysis of variance table will be as follows:

SOV	d.f.	SS	MSS	F ratio
Year	2	1.3707	0.6853	
Block within years	6	246.9286	41.1548	
Treatment	17	296855.7091	17462.1005	991227.241
Treatment x Year	34	0.2995	0.0088	65.998
Error	102	0.4629	0.0045	
Total	161	297104.7707		

Our next step is to calculate the critical difference value using the following formula:

$$CD = \sqrt{\frac{2\text{MS}_{Er}}{r.l}} \times t_{0.05,\text{error.df}}$$

$$CD = \sqrt{\frac{2\text{x}0.0045}{3*3}} \times 1.983 = 0.0629$$

In the next step, calculate the treatment means to find out the best treatment as below:

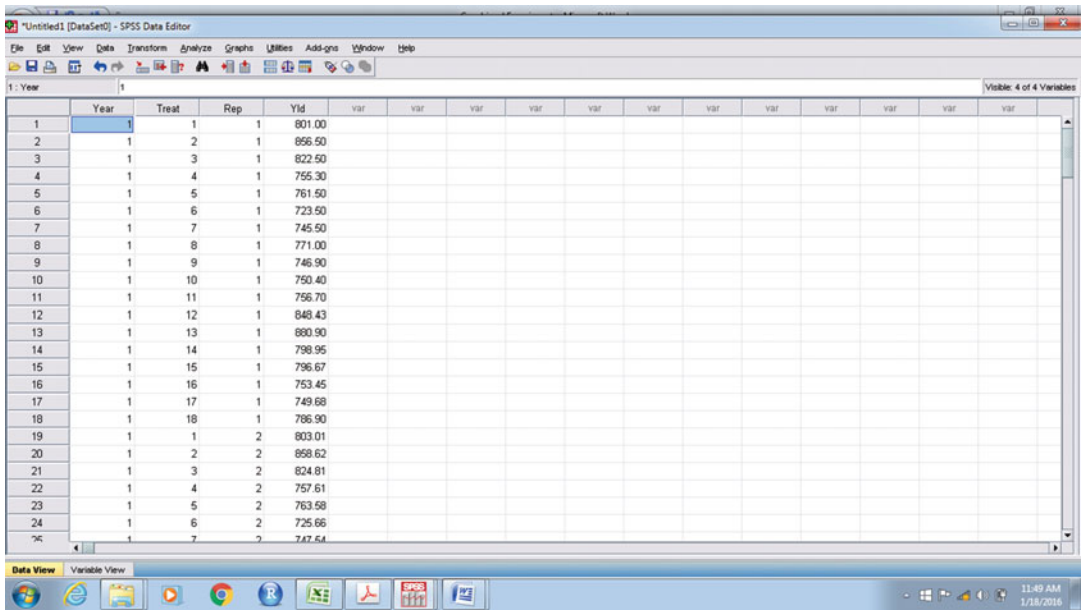
Treatment	Mean	CD
T13	882.76	0.0629
T2	858.33	
T12	850.29	
T3	824.35	
T1	802.80	
T14	800.74	
T15	798.41	
T18	788.70	
T8	772.79	
T5	763.28	
T11	758.47	
T4	757.16	
T16	755.25	
T10	752.19	
T17	751.54	
T9	748.71	
T7	747.32	
T6	725.27	

The above analysis can very well be carried out using SPSS using syntax as given below:

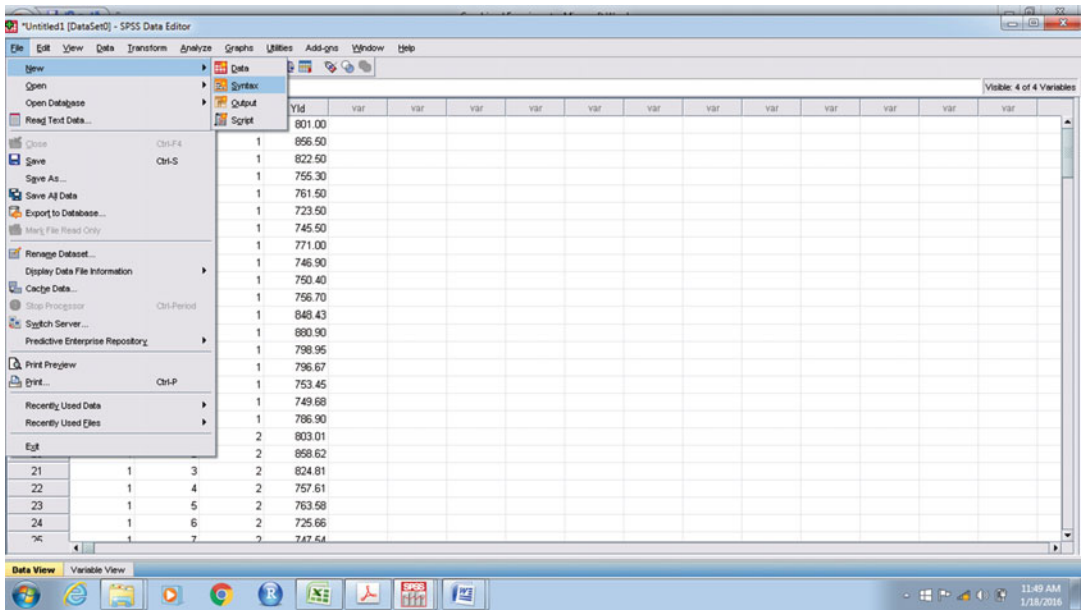
```
UNIANOVA
Yld BY Year Rep Treat
/METHOD = SSTYPE(3)
/INTERCEPT = INCLUDE
/CRITERIA = ALPHA(0.05)
/DESIGN = Year Rep(Year) Treat Year*Treat
/test Treat vs Year*Treat
```

Step 1: Conduct the individual RBD analysis in SPSS as mentioned earlier, and obtain the error mean sum of squares and perform the Bartlett's test for homogeneity of variance.

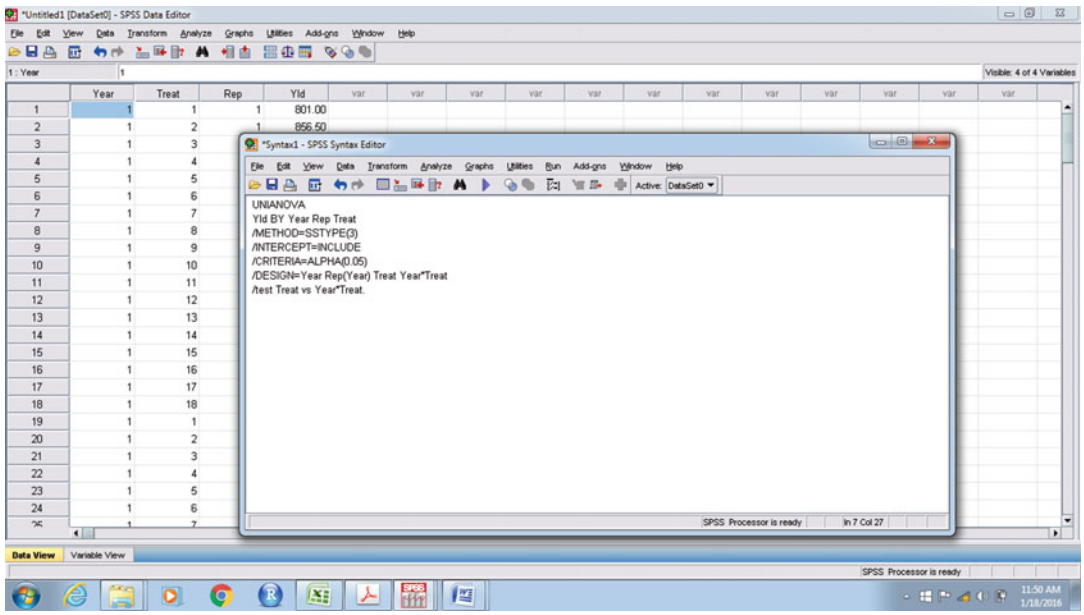
Step 2: Enter the data into the SPSS as mentioned below.



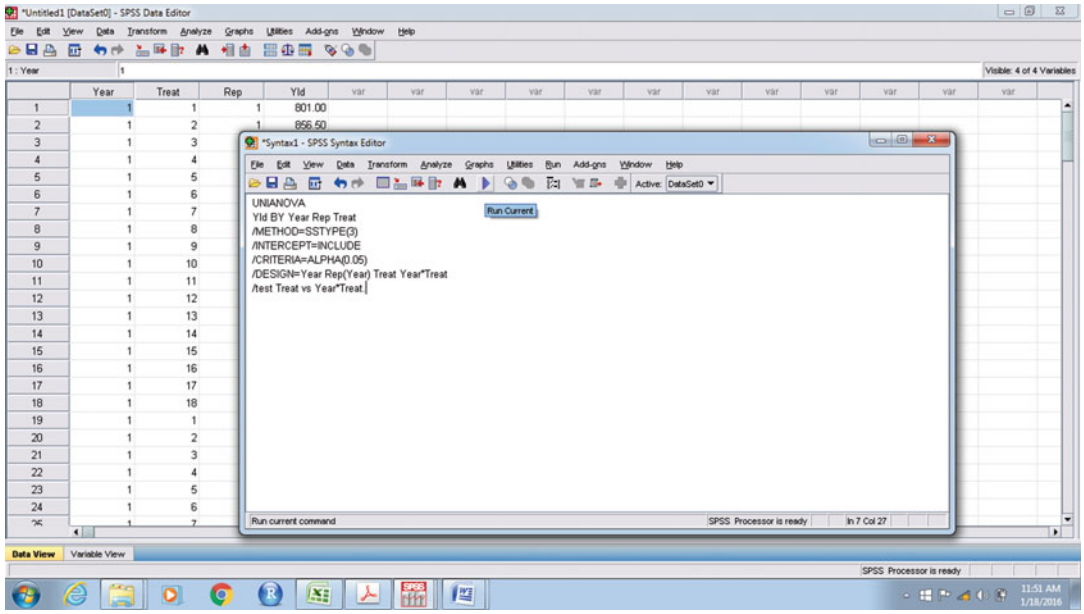
Step 3: File → New → Click on Syntax as shown below.



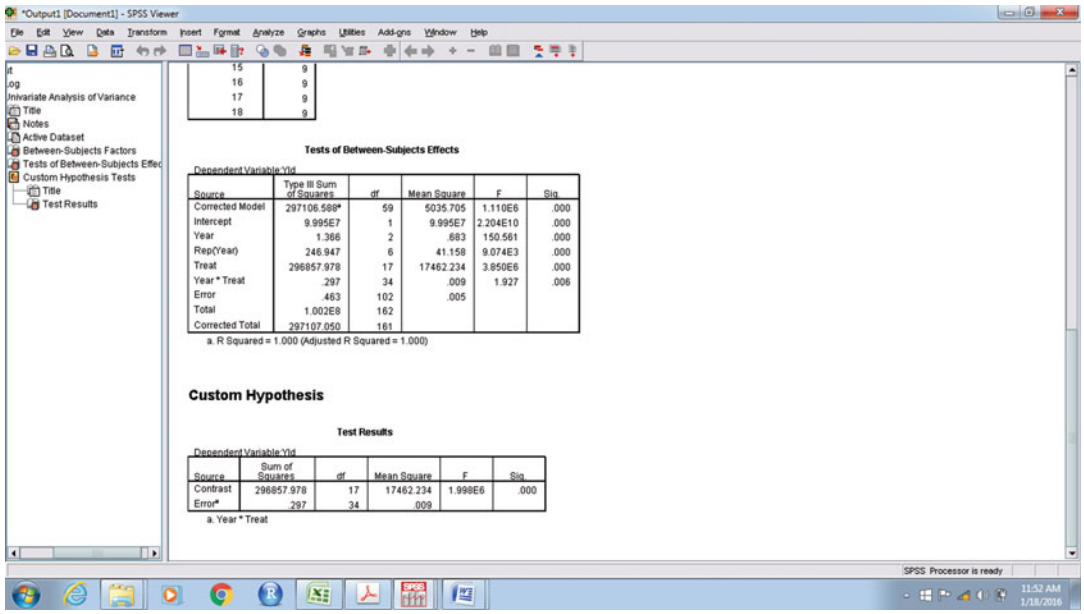
Step 4: Enter the syntax as mentioned below.



Step 5: Select all the syntax and click on run current as below.



Step 6: The output will appear in the output window as provided below.



From the above output, one can find that the results are almost the same for both the analyses. The only thing is that because of inbuilt options, there are more information in the output obtained through SPSS than usual manual calculation.

Example 12.5: (Weighted Combined RBD Analysis)

An experiment was conducted with 18 different treatment combinations of potash fertilizer in potato for three consecutive years during the same seasons. The following data gives the replication-wise yield (*t*/ha.) for different treatments during the three years of experimentation. Analyze the data to identify the best treatment with respect to the yield of potato:

Treatment	Year 1			Year 2			Year 3		
	R1	R2	R3	R1	R2	R3	R1	R2	R3
T1	20.07	20.28	19.86	21.76	22.01	22.17	20.31	20.53	20.64
T2	22.32	22.55	22.01	23.32	23.57	23.73	22.58	22.95	23.12
T3	20.54	20.76	20.33	20.65	20.92	21.06	20.77	21.06	21.15
T4	17.94	18.19	17.74	19.12	19.36	19.54	18.19	18.37	18.55
T5	18.12	18.31	18.33	20.23	20.49	20.60	18.35	18.54	18.67
T6	17.70	17.91	17.48	18.32	18.57	18.74	17.93	18.16	18.28
T7	21.12	21.37	20.86	23.12	23.46	23.60	21.41	21.64	21.81
T8	25.23	25.50	24.88	26.23	26.53	26.69	25.58	25.98	26.13
T9	20.78	21.02	20.55	21.71	21.98	22.21	21.05	21.36	21.53
T10	20.45	20.69	20.71	21.18	21.47	21.59	20.68	20.89	21.09
T11	18.64	18.83	18.40	19.78	20.06	20.18	18.86	19.09	19.19
T12	18.08	18.31	17.89	19.40	19.66	19.73	18.30	18.55	18.62
T13	18.30	18.53	18.11	19.58	19.89	19.96	18.49	18.72	18.88
T14	19.13	19.38	18.86	20.79	21.09	21.22	19.38	19.68	19.86
T15	21.93	22.21	21.61	23.32	23.68	23.76	22.38	22.61	22.82
T16	21.32	21.54	21.06	22.54	22.83	22.97	21.54	21.87	21.92
T17	21.61	21.90	21.39	22.55	22.90	23.06	21.88	22.12	22.28
T18	20.17	20.42	19.95	21.16	21.42	21.50	20.50	20.76	20.87

Solution According to the given information, the experiment has been conducted for three consecutive years following the same 18 treatments in randomized block design. So we are to perform the combined analysis of variance for randomized block design. The step-by-step procedure is given below:

Step: 1

Year-wise analysis of variance for RBD:

Treatment	Year 1			Total	Year 2			Total	Year 3			Total
	R1	R2	R3		R1	R2	R3		R1	R2	R3	
T1	20.07	20.28	19.86	60.21	21.76	22.01	22.17	65.94	20.31	20.53	20.64	61.48
T2	22.32	22.55	22.01	66.88	23.32	23.57	23.73	70.62	22.58	22.95	23.12	68.65
T3	20.54	20.76	20.33	61.63	20.65	20.92	21.06	62.64	20.77	21.06	21.15	62.97
T4	17.94	18.19	17.74	53.87	19.12	19.36	19.54	58.01	18.19	18.37	18.55	55.11
T5	18.12	18.31	18.33	54.76	20.23	20.49	20.60	61.32	18.35	18.54	18.67	55.56
T6	17.70	17.91	17.48	53.09	18.32	18.57	18.74	55.63	17.93	18.16	18.28	54.36
T7	21.12	21.37	20.86	63.35	23.12	23.46	23.60	70.17	21.41	21.64	21.81	64.86
T8	25.23	25.50	24.88	75.61	26.23	26.53	26.69	79.45	25.58	25.98	26.13	77.69
T9	20.78	21.02	20.55	62.35	21.71	21.98	22.21	65.89	21.05	21.36	21.53	63.94
T10	20.45	20.69	20.71	61.84	21.18	21.47	21.59	64.25	20.68	20.89	21.09	62.67
T11	18.64	18.83	18.40	55.88	19.78	20.06	20.18	60.02	18.86	19.09	19.19	57.13
T12	18.08	18.31	17.89	54.28	19.40	19.66	19.73	58.80	18.30	18.55	18.62	55.46
T13	18.30	18.53	18.11	54.95	19.58	19.89	19.96	59.43	18.49	18.72	18.88	56.09
T14	19.13	19.38	18.86	57.37	20.79	21.09	21.22	63.10	19.38	19.68	19.86	58.91
T15	21.93	22.21	21.61	65.75	23.32	23.68	23.76	70.76	22.38	22.61	22.82	67.81
T16	21.32	21.54	21.06	63.93	22.54	22.83	22.97	68.33	21.54	21.87	21.92	65.33
T17	21.61	21.90	21.39	64.89	22.55	22.90	23.06	68.52	21.88	22.12	22.28	66.27
T18	20.17	20.42	19.95	60.54	21.16	21.42	21.50	64.09	20.50	20.76	20.87	62.12
Total	363.46	367.69	360.03	1091.18	384.77	389.89	392.32	1166.98	368.16	372.85	375.40	1116.41

For year 1:

$$\text{Grand total } (GT) = 1091.18$$

$$\text{Correction factor } (CF) = \frac{GT^2}{r \times t} = \frac{1091.18^2}{3 \times 18} = 22049.36$$

$$\text{Total sum of squares } (SS_{\text{Tot}}) = \left(20.07^2 + 22.32^2 + \ldots\ldots + 21.39^2 + 19.95^2\right) - 22049.36 = 193.40$$

$$\text{Sum of squares due to block } (SS_B) = \frac{1}{18}\left(363.46^2 + 367.69^2 + 360.03^2\right) - 22049.36 = 1.633$$

$$\text{Sum of squares due to treatments } (SS_{Tr}) = \frac{1}{3}\left(60.21^2 + 66.88^2 + \ldots\ldots + 64.89^2 + 60.54^2\right) - 22049.36 = 191.450$$

$$\text{Sum of squares due to error } (SS_{Er}) = SS_{\text{TOT}} - SS_B - SS_{Tr} = 193.40 - 1.633 - 191.450 = 0.32$$

ANOVA Table for year 1				
SOV	**df**	**SS**	**MS**	**F ratio**
Block	2	1.6336	0.8168	88.0472
Treatment	17	191.4502	11.2618	1213.9524
Error	34	0.3154	0.0093	
Total	53	193.3993		

For year 2:

$$\text{Grand total } (GT) = 1166.98$$

$$\text{Correction factor } (CF) = \frac{GT^2}{r \times t} = \frac{1166.98^2}{3 \times 18} = 25219.26$$

Total sum of squares (SS_{TOT})

$$= \left(21.76^2 + 23.32^2 + \ldots\ldots + 23.06^2 + 21.50^2\right) - 25219.26 = 195.00$$

Sum of squares due to block (SS_B)

$$= \frac{1}{18}\left(384.77^2 + 389.89^2 + 392.32^2\right) - 25219.26 = 1.650$$

Sum of squares due to treatments (SS_{Tr})

$$= \frac{1}{3}\left(65.94^2 + 70.62^2 + \ldots\ldots + 68.52^2 + 64.09^2\right) - 25219.26 = 193.316$$

Sum of squares due to error (SS_{Er})

$$= SS_{\text{TOT}} - SS_B - SS_{Tr} = 195.00 - 1.650 - 193.316 = 0.03$$

ANOVA Table for year 2				
SOV	**df**	**SS**	**MS**	**F ratio**
Block	2	1.6500	0.8250	960.1994
Treatment	17	193.3164	11.3716	13234.9976
Error	34	0.0292	0.0009	
Total	53	194.9956		

For year 3:

$$\text{Grand total } (GT) = 1116.41$$

$$\text{Correction factor } (CF) = \frac{GT^2}{r \times t} = \frac{1116.41^2}{3 \times 18} = 23080.91$$

Total sum of squares (SS_{TOT})

$$= \left(20.31^2 + 22.58^2 + \ldots\ldots + 22.28^2 + 20.87^2\right) - 23080.91 = 210.01$$

Sum of squares due to block (SS_B)

$$= \frac{1}{18}\left(368.16^2 + 372.85^2 + 375.40^2\right) - 23080.91 = 1.497$$

Sum of squares due to treatments (SS_{Tr})

$$= \frac{1}{3}\left(61.48^2 + 68.65^2 + \ldots\ldots + 66.27^2 + 62.12^2\right) - 23080.91 = 208.457$$

Sum of squares due to error (SS_{Er})

$$= SS_{\text{TOT}} - SS_B - SS_{Tr} = 210.01 - 1.497 - 208.457 = 0.06$$

ANOVA Table for year 3				
SOV	**df**	**SS**	**MS**	**F ratio**
Block	2	1.4971	0.7485	436.6411
Treatment	17	208.4576	12.2622	7152.8643
Error	34	0.0583	0.0017	
Total	53	210.0129		

Step 2:

The mean squares for different analyses of variance can be represented as follows:

		MS for the years		
SOV	d.f.	Year 1	Year 2	Year 3
Replication	2	0.8168	0.8250	0.7485
Treatment	17	11.2618	11.3716	12.2622
Error	34	0.0093	0.0009	0.0017

Step 3: (Test for homogeneity of variances)

As per Hartley's test for homogeneity of variance,

$$F_{\max} = \frac{\text{Largest error mean square}}{\text{Smallest error mean square}} = \frac{0.0093}{0.0009} = 10.797 > 3$$

Thus we can assume heterogeneous variance and go for weighted analysis of variance.

Step 4:

The model for combined analysis of variance is as follows:

$$y_{ijk} = \mu + \alpha_i + \beta_k + \gamma_{ik} + \delta_{jk} + e_{ijk}$$

where $i = 1, 2, \ldots, 18$; $j = 1, 2, 3$; and $k = 1, 2, 3$

y_{ijk} = response of ith treatments in jth blocks of kth year

μ = general effect

α_i = additional effect due to ith treatment and $\sum_{i=1}^{18} \alpha_i = 0$

β_k = additional effect due to kth year and $\sum_{k=1}^{3} \beta_k = 0$

γ_{ik} = interaction effect due to ith treatment in kth year and $\gamma_{ik} \sim$ i.i.d. N(0, σ^2)

δ_{jk} = effect of the jth block in the kth year and $\sum_{j=1}^{3}\sum_{k=1}^{3} \delta_{jk} = 0$

e_{ijk} = error component associated with ith treatment and jth block and kth year and $e_{ijk} \sim$ i.i.d. N(0, σ^2)

and the corresponding analysis of variance structure will be as follows:

SOV	d.f.	SS
Year	3−1 = 2	*YSS*
Block within year	3(3–1) = 6	*BSS*
Treatment	(18–1) = 17	*TrSS*
Treatment × year	(18–1)(3–1) = 34	*SS*(YT)
Error	3(18–1)(3–1) = 102	*ErSS*

In the case of heterogeneous error mean square, the weighted analysis of variance is taken up:

(i) The weight for different locations is calculated as $W_k = \frac{r_k}{Er_k MS}$ and $W = \sum_{k=1}^{l} W_k$.

Thus

$$W_1 = \frac{r_1}{MS_{Er_1}} = \frac{3}{0.0093} = 323.382$$

$$W_2 = \frac{r_2}{MS_{Er_2}} = \frac{3}{0.0009} = 3491.607$$

$$W_3 = \frac{r_3}{MS_{Er_3}} = \frac{3}{0.0017} = 1749.977$$

Treatment	Year 1 (Y1)	Year 2 (Y2)	Year 3 (Y3)	$\sum_{i=1}^{3} W_k Y_{ki}$	$\bar{T} = \frac{1}{W}\sum_{i=1}^{3} W_k Y_{ki}$	T_i^2		
						y_{i1}^2 Year 1 (Y1)	y_{i2}^2 Year 2 (Y2)	y_{i3}^2 Year 3 (Y3)
T1	60.21	65.94	61.48	357296.057	64.205	3624.976	4348.365	3779.319
T2	66.88	70.62	68.65	388357.866	69.786	4472.785	4987.754	4713.065
T3	61.63	62.64	62.97	348836.936	62.684	3798.113	3923.346	3965.848
T4	53.87	58.01	55.11	316421.993	56.860	2902.134	3365.488	3037.217
T5	54.76	61.32	55.56	329057.209	59.130	2998.752	3760.746	3086.737
T6	53.09	55.63	54.36	306529.021	55.082	2818.531	3094.389	2955.226
T7	63.35	70.17	64.86	378991.562	68.103	4013.352	4923.952	4206.248
T8	75.61	79.45	77.69	437796.521	78.670	5716.316	6311.618	6035.548
T9	62.35	65.89	63.94	362132.370	65.074	3887.761	4342.133	4088.055
T10	61.84	64.25	62.67	354007.125	63.614	3824.579	4128.157	3927.437
T11	55.88	60.02	57.13	327622.199	58.872	3122.229	3602.675	3263.976
T12	54.28	58.80	55.46	319904.445	57.485	2946.461	3457.008	3076.027
T13	54.95	59.43	56.09	323430.951	58.119	3019.283	3532.193	3145.538
T14	57.37	63.10	58.91	341960.551	61.449	3291.572	3981.414	3470.471
T15	65.75	70.76	67.81	387007.550	69.544	4322.500	5007.409	4598.492
T16	63.93	68.33	65.33	373589.409	67.132	4086.421	4669.377	4267.986
T17	64.89	68.52	66.27	376195.282	67.601	4211.300	4694.535	4392.108
T18	60.54	64.09	62.12	352053.229	63.262	3665.379	4107.172	3858.817
Total (Y_k)	1091.18	1166.98	1116.41	6381190.27		66722.444	76237.730	69868.116
W_k	323.382	3491.607	1749.978	$\sum W_k = 5564.967$				
$W_k Y_k$	352866.835	4074632.5	1953690.936	$\sum W_k Y_k = 6381190.274$				

The grand total is calculated using the formula

$$\sum_{k=1}^{y} W_k \sum_{i=1}^{18} Y_{ki} = \sum_{k=1}^{3} W_k Y_k = 6381190.274,$$

where Y_k is the grand total for the year k.

$$CF = \tfrac{1}{tW}(GT)^2 = \frac{1}{18 \times 5564.967}\left(6381190.274^2\right) = 406507250.90.$$

$$\text{Total sum of square}\,(SS_{\text{TOT}}) = \sum_{k=1}^{l}\left(W_k \sum_{i=1}^{t} y_{ik}^2\right) - C.F = \sum_{k=1}^{3}(W_k s_k) - C.F$$

$$= (323.382 \times 66722.444 + 3491.607 \times 76237.730 + 1749.978 \times 69868.116) - 406507250.90$$

$$= 3529438.546$$

$$\text{Year sum of square}\,(SS_{\text{Year}}) = \frac{1}{t}\sum_{k=1}^{l} W_k \left(\sum_{k=1}^{l} Y_k\right)^2 - C.F$$

$$= \frac{1}{18}\left[323.382 \times 1091.18^2 + 3491.607 \times 1166.98^2 + 1749.978 \times 1116.41^2\right] - 406507250.90$$

$$= 224360.957$$

$$\text{Treatment sum of square}\,(SS_{Tr}) = \frac{1}{W}\sum_{i=1}^{t}\left(\sum_{k=1}^{l} W_k Y_{ki}\right)^2 - C.F = \frac{1}{5564.967}\sum_{i=1}^{18}\left(\sum_{k=1}^{3} W_k Y_{ki}\right)^2 - 406507250.90$$

$$= \frac{1}{5564.967}[357296.057^2 + 388357.866^2 + \ldots\ldots + 376195.282^2 + 352053.229^2] - 406507250.90$$

$$= \left(\frac{1}{5564.967} \times 2280320386463.640\right) - 406507250.90 = 3256260.115$$

$$\text{Year x treatment sum of square}\,(SS_{Y\times T}) = SS_{\text{Tot}} - SS_{\text{Year}} - SS_{Tr}$$

$$= 3529438.546 - 224360.957 - 3256260.11$$
$$= 48817.474$$

In the case of heterogeneous error mean squares, the significance of interaction effects is worked out using

$$\chi^2 = \frac{(m-4)(m-2)}{m(m+t-3)} \times \text{interaction } MS$$
$$= \frac{(34-4)(34-2)}{34(34+18-3)} \times 1435.808$$
$$= 827.356$$

where m = average error degrees of freedom = 34.

The appropriate degrees of freedom for χ^2 are calculated as

$$(l-1)(t-1)\frac{(m-4)}{(m+t-3)}$$
$$= (3-1)(18-1)\frac{(34-4)}{(34+18-3)} = 20.816$$
$$\simeq 21$$

At 5 % level of significance with 20.82° of freedom, the calculated value of χ^2 (827.356) is highly significant. Hence the interaction is significant. The analysis of variance table for combined analysis of the given problem is as follows.

Weighted ANOVA for combined analysis:

SOV	d f	S.S.	M.S.
Year	3-1 = 2	224360.9571	112180.5
Treatments	(18-1) = 17	3256260.115	191544.7
Treatment × year	(18-1)(3-1) = 34	48817.474	1435.808
Total	(18)(3)-1=53	3529438.546	

The treatment means are computed as $\overline{T}_i = \frac{1}{W}\sum_{k=1}^{l} W_k Y_{ki.}$

The standard error of difference for comparison of different treatment effects is given by SEd = $\sqrt{\frac{2\times\text{interaction } MS}{W}}$, and the corresponding critical difference is given as $CD = SE_d \times t_{\alpha/2,\text{interaction df}} = \sqrt{\frac{2 \times 1435.808}{5564.967}} \times 2.034 = 1.461$.

Treatment	Mean	CD
T8	78.670	**1.461**
T2	69.786	
T15	69.544	
T7	68.103	
T17	67.601	
T16	67.132	
T9	65.074	
T1	64.205	
T10	63.614	
T18	63.262	
T3	62.684	
T14	61.449	
T5	59.130	
T11	58.872	
T13	58.119	
T12	57.485	
T4	56.860	
T6	55.082	

The treatment effects are arranged in descending order and are compared with the critical difference value as calculated above. It is found that the treatment T8 is having a maximum yield of potato followed by T2 and T15 which are statistically at par. The treatment T6 is showing the significant lowest yield of potato.

12.5 Analysis of Experimental Data Measured Over Time

There are certain parameters which vary during the period of experimentation when measurements are taken on the same unit at different points of time. Growth parameters (like number of tillers, plant height, number of branches, etc.), blood sugar/hormone content, milk yield of cow during lactation, intensity of diseases, and pest etc. are measured at different points of time over the periods. The main problem in this type of measurement is that the consecutive measurements on the same units are not independent. So there exist treatment x period interactions in such measurements. The objective of such experiments is not only to study the effects of different treatments but also to study the pattern of interaction between the treatment and the stages of growth or time intervals. The analysis of variance obtained separately at different growth stages or durations for the characters will not serve the purpose. Instead a common approach is to combine data from all times of observations into a single analysis of variance.

By taking time as a factor in the analysis, such situations could be explained in the analysis of variance. Combined analysis of variance with time or stages as one of the factors is considered. Another way to tackle such situation is to use split plot analysis with the inclusion of stage as a factor. The basic structure of analysis of variance remains the same with the inclusion of time as additional subplot factor for single-factor or factorial experiments, sub-subplot factor for split plot experiments, and so on. Before pooling the data from observations recorded at different time periods for combined analysis of variance, homogeneity of error variance is required to be verified as per the methods described in 12.4. Depending upon the nature of the variance, either unweighted or weighted analysis of variance is required to be performed. We shall not deal with details of step-by-step procedure of analysis, but rather just discuss a sketch of the analyses under different experimental setups, in the following sections.

12.5.1 Observations Taken Over Time in RBD

Let us suppose there are "t" treatments tested following RBD with "r" replications and the character recorded over "n" number of times. The analysis of variance for each of the time period is required to be taken up at first, and then the homogeneity of error mean squares from all these time periods is tested for homogeneity, and combined analysis is taken up with the inclusion of time as one of the factors in the analysis either through unweighted or weighted method. The combined analysis of variance structure will be as follows:

SOV	d.f.	SS	MSS	F ratio
Replication	$r-1$			
Treatment (T)	$t-1$			
Error(I)	$(r-1)\ (t-1)$			
Time of observation (N)	$(n-1)$			
Interaction (T x N)	$(t-1)(n-1)$			
Error (II)	$t(r-1)(n-1)$			
Total	$rnt-1$			

Conclusion is to be drawn accordingly. It may be noted that treatments, time, and interactions are tested with different precisions. In fact time and interaction between time and treatment are estimated more precisely than the treatments.

12.5.2 Observations Taken Over Time in Two-Factor RBD

Let there be "B" breeds of cows tested forming blocks of r cows in each for the efficacy of "f" feeds toward milk yield during lactation over "n"

number of times. The analysis of variance structure would be as follows:

SOV	d.f.	SS	MSS	F ratio
Replication	$r-1$			
Breed(B)	$b-1$			
Feed (F)	$f-1$			
Interaction (B x F)	$(b-1)\,(f-1)$			
Error(I)	$b(r-1)\,(f-1)$			
Time of observation (N)	$(n-1)$			
Interaction (B × N)	$(b-1)(n-1)$			
Interaction (F × N)	$(f-1)(n-1)$			
Interaction (B × F × N)	$(b-1)(n-1)(f-1)$			
Error (II)	$bf(r-1)(n-1)$			
Total	$rbfn-1$			

12.5.3 Observations Taken Over Time in Split Plot Design

Suppose we are testing t varieties of paddy in subplots tested in a split plot design for the efficacy of "p" levels of plowing in main plots with "r" replications and the character recorded over "n" number of times. The analysis of variance structure will be as follows:

SOV	d.f.	SS	MSS	F ratio
Replication	$r-1$			
Irrigation (I)	$p-1$			
Error (I)	$(r-1)(p-1)$			
Variety (t)	$(t-1)$			
Interaction (T × P)	$(t-1)\,(p-1)$			
Error (II)	$p(r-1)(t-1)$			
Time of observation (N)	$(n-1)$			
Interaction (P × N)	$(p-1)(n-1)$			
Interaction (T × N)	$(t-1)(n-1)$			
Interaction (P × T × N)	$(p-1)(t-1)$ $(n-1)$			
Error (II)	$pt(r-1)$ $(n-1)$			
Total	$rptn-1$			

12.6 Experiments at Farmers' Field

One of the major areas of activity of rural development, particularly in agriculture and allied sectors, is *Lab-to-Land* program. Experimental results/findings/recommendations/better technologies/management practices generated at the research stations, mostly under ideal experimental conditions, are required to be tested for their wide applicability under the stakeholder conditions. Farmers are the main stakeholders in such rural development program. Farmers or the targeted users vary in their socioeconomic conditions, skills, educations, cultures, managerial abilities, climatic conditions, availability of inputs and disposal of outputs, etc. which ultimately affect their pragmatism in adopting experimental results/findings/recommendations/better technologies/management practices. So it becomes necessary to test these experimental results/findings/recommendations/technologies/management practices under the biophysical constraints encountered by the users and the realistic situations prevailing at the ground level before the extension personals take up these for dissemination at the field level. The idea of *on-farm research or farmer field demonstration* came into practice as such.

On farm trials are mainly objected toward situation-specific technology generation/modification or toward technology verification. However, majority of the trials fall on the second category. On farm researches are carried out mainly:

(i) To identify the location-/region-/zone-specific constraints
(ii) To study the gap between the existing technology at the farm level and the anticipated outcome as a result of innovation at the experimental station
(iii) To identify the major components in boosting the adoption of new technology/recommendation (innovation)
(iv) To modify the innovation in the light of the availability of local conditions

(v) To study the adoptability/suitability of the innovated technology under varied conditions
(vi) To demonstrate the utility/superiority of the innovated technology

Steps in On-Farm Research

In spite of situation-specific variations, by and large the whole process of on-farm research may be thought of comprising three major steps, viz.:

(a) Diagnostic survey
(b) Planning and designing of experiment at farmers' field
(c) Experimentation at farmers' field

Survey helps in characterizing the ground truth with respect to socioeconomic conditions, biophysical conditions, constraints faced by the users, and of course the state of technology in practice compared to the innovated technologies. In the second phase, providing due consideration to the available information of diagnostic survey modification/refinement of the innovation under local condition is attempted to. Planning and designing of experiments are made accordingly. In the third stage, experiments at the farmers' field are conducted with active participation of the farmers. As the experiments at the farmers' field progress, the dissemination of the technology starts gaining momentum. Extension personals start their activities to propagate the success of the experimental results/findings/recommendations/better technologies/management practices.

12.6.1 Major Considerations During Experimentations at Farmers' Fields

Farmers, particularly under Indian context, vary with respect to their biophysical resources, managements, and other conditions. Most of the farmers, particularly in the populous countries, are having small and marginal land holdings compared to developed countries. Till today the main objective of the farmers is to maximize return using limited resources at their disposal. Farmers at the initial stage are mostly reluctant to such experimentations at their farms. So to win over the confidence of the farmers is a major task before starting experimentation. As such selection of farmers to demonstrate the importance or superiority of technology developed plays a vital role. However, though not a unique one, the following points are to be kept in mind before finalizing the experimentation at farmers' fields:

(i) The experiment should be kept as simple as possible; treatments should be such that the probability of loss due to any treatment should be as minimum as possible, that treatment must have demonstrative effect, and that there should be scope for compensating the loss to the farmer due to treatment(s).
(ii) Selection of farms: Farmers/farmers' field should be selected in such a way that these actually represent the targeted population of farms. Unbiased selection of farms is necessary to have valid estimation of the farm responses. Sometimes it is advocated for selection of farms based on personal judgment. But in spite of the advantages like minimization of cost, accessibility, feasibility, etc., nonrandom sampling even by the experts fails to provide adequate representation of the population, thereby leading to biased estimation for the population parameters. As such, random sampling, especially the stratified random sampling, would be the most likely option for selection of farms, and stratification may be taken up at different levels followed by random sampling.
(iii) The experimental design: Farmers' field experiments should be framed with minimum number of treatments having promising demonstrative effects. Adoption of simple experimental design will help in overall management of the experiments. The simplest experimental design is the randomized block design; it is very difficult

to provide replication for the treatments at a particular farm. However, by repeating the experiment at different farmers' fields, repeated observations on a particular treatment may be obtained and, of course due adjustments, are to be made during the analysis of experimental data. The whole experimental area at a particular farmer's field is divided into number of plots of equal sizes as the number of treatments, including the treatment with farmers' practice. In each farmer's field, the treatments are allotted to the plots at random separately; the same randomization scheme should not be adopted for all farmers' fields. The principle of local control should be followed as much as possible under the given situation. Strictly speaking, this is also not important from the objective point of view of the experiment; we are interested in estimating the average response of the treatments over the situation as a whole not for a specified field. Analysis of the experiment will be as per the analysis of combined experiments and the scheme of stratification. Depending upon the number of stages of stratification, the analysis of variance may be partitioned accordingly. Generally hierarchical or nested designs are followed.

Let us suppose we have selected three blocks (b) from a list of blocks at random and from each of these three blocks, three villages (v) are selected at random, and again from each of these three villages, three farmers (n) are selected at random. So the analysis of variance model may be as follows:

$$Y_{ijk} = \mu + \alpha_i + \beta(\alpha)_{ij} + \varepsilon_{ijk}; i = 1,2,3; j = 1,2,3; k = 1,2,3$$

where Y_{ijk} = the response due to kth farmer in ith block and jth village

μ = the overall mean

α_i= additional effect due to ith block

$\beta(\alpha)_{ij}$ = additional effect due to jth village within ith block

ε_{ijk} = is the error component due to kth farmer in ith block and jth village and $\varepsilon_{ijk}{}'s \sim iidN(0, \sigma^2)$

And the corresponding analysis of variance table would be as follows:

SOV	d.f.	SS	MS	Tab F
Block	$b-1 = 3-1 = 2$	$SS_{(B)}$	$MS_{(B)} = SS_{(B)}/(b-1)$	$MS_{(B)}/MS_{V(B)}$
Village with in block	$b(v-1) = 3(3-1) = 6$	$SS_{V(B)}$	$MS_{V(B)} = SS_{V(B)}/b(v-1)$	$MS_{V(B)}/MS_{(within)}$
Within village	$b.v.(n-1) = 3.3(3-1) = 18$	$SS_{(within)}$	$MS_{(within)} = SS_{(within)}/b.v.(n-1)$	
Total	$b.v.n-1 = 3.3.3.-1 = 26$	$SS_{(Tot)}$		

In the above example, if village effects are taken as random, while the effects of blocks are considered as fixed, then the error to test the effect of blocks is $MS_{V(B)}$, while to test the effect of villages, the error is $MS_{(within)}$. As such, the F statistic for testing block effects is $F = MS_{(B)}/MS_{V(B)}$ and to test the effect of villages is $F = MS_{V(B)}/MS_{(within)}$. Likewise, depending upon the situations, different effects can be estimated and tested.

(iv) Recording of ancillary information: As farmers' filed experimentations are conducted under varied range of situations, information on situation parameters like

soil color, texture, structure, pH, constituent soil nutrients before and after experimentation, weather parameters (like temperature, relative humidity, rainfall, wind speed, sunshine hours), land topography, etc. may help in getting unbiased and precise estimation of the population parameters toward better explanation of the experimental results and its subsequent impact on agriculture and rural development.

Example 12.6

To determine the effects of different levels of nitrogen in wheat crop, a nested design was used: four places were randomly chosen with three farmers per places and six varieties. The following data gives the information on wheat yield at harvest. Analyze the data and then draw the conclusion:

Place	1	1	1	2	2	2	3	3	3	4	4	4
Farmer	1	2	3	4	5	6	7	8	9	10	11	12
Variety	Yield (q/ha)											
V1	12.24	12.24	12.24	13.26	14.28	14.28	15.30	16.32	13.40	13.40	13.50	14.60
V 2	12.24	12.24	12.24	13.26	15.30	16.32	13.26	17.34	13.50	13.60	13.30	14.70
V 3	12.24	11.22	13.26	14.28	14.28	12.24	15.30	17.34	13.40	12.20	14.50	15.70
V 4	13.26	12.24	13.26	14.28	17.34	15.30	16.32	17.34	14.70	13.50	14.60	15.70
V 5	11.22	12.24	12.24	13.26	13.26	14.28	15.30	16.32	12.30	13.40	13.50	14.60
V 6	12.24	11.22	12.24	13.26	13.26	12.24	14.28	15.30	13.30	12.20	13.40	14.50

Solution

$$GT = 12.24 + 12.24 + 12.24..... + 14.60 + 14.50 = 995.52$$

$$CF = \frac{GT^2}{\text{Total no. of obs.}} = \frac{995.52^2}{72} = 13764.723$$

$$SS_{\text{Tot}} = 12.24^2 + 12.24^2 + 12.24^2 + ... + 14.60^2 + 14.50^2 - 13764.723 = 168.355$$

From the given information, construct the following tables and obtain the following quantities:

	Place				
V	1	2	3	4	Total
1	36.72	41.82	45.02	41.50	165.06
2	36.72	44.88	44.10	41.60	167.30
3	36.72	40.80	46.04	42.40	165.96
4	38.76	46.92	48.36	43.80	177.84
5	35.70	40.80	43.92	41.50	161.92
6	35.70	38.76	42.88	40.10	157.44
Total	220.32	253.98	270.32	250.90	

Sum of square for place $= SS_{\text{Place}}$

$$= \frac{\left[220.32^2 + 253.98^2 + 270.32^2 + 250.90^2\right]}{18} - CF = 72.524$$

Place	1	1	1	2	2	2	3	3	3	4	4	4	
Farmer	1	2	3	4	5	6	7	8	9	10	11	12	Total
Variety	Yield (q/ha)												
1	12.24	12.24	12.24	13.26	14.28	14.28	15.30	16.32	13.40	13.40	13.50	14.60	165.06
2	12.24	12.24	12.24	13.26	15.30	16.32	13.26	17.34	13.50	13.60	13.30	14.70	167.30
3	12.24	11.22	13.26	14.28	14.28	12.24	15.30	17.34	13.40	12.20	14.50	15.70	165.96
4	13.26	12.24	13.26	14.28	17.34	15.30	16.32	17.34	14.70	13.50	14.60	15.70	177.84
5	11.22	12.24	12.24	13.26	13.26	14.28	15.30	16.32	12.30	13.40	13.50	14.60	161.92
6	12.24	11.22	12.24	13.26	13.26	12.24	14.28	15.30	13.30	12.20	13.40	14.50	157.44
Total	73.44	71.40	75.48	81.60	87.72	84.66	89.76	99.96	80.60	78.30	82.80	89.80	995.52

Sum of square for place within farmer

$$= SS_{\text{Place(Farmer)}}$$

$$= \frac{\left[73.44^2 + 71.40^2 + \ldots\ldots\ldots + 82.80^2 + 89.80^2\right]}{6}$$

$$- SS_{\text{Place}} - CF \quad = 46.967$$

Sum of square within the variety

$$= SS_{\text{Variety(Farmer)}}$$

$$= SS_{\text{TOT}} - SS_{\text{Place}} - SS_{\text{Farmer(Place)}}$$

$$= 168.355 - 72.524 - 46.967 = 48.863$$

From the above quantities, the following ANOVA table is constructed:

SOV	df	SS	MS	F	Tab. F at 5 %
Place	3	72.524	24.175	4.118	4.066
Farmer within place	8	46.967	5.871	7.209	2.097
Variety within farmer	60	48.864	0.814		
Total	71	168.355			

It was assumed that the effects of place and farmer are random. The experimental error for place is the mean square for farmer within place, and the experimental error for farmer is the mean square for variety within farmer. The critical value for place is $F_{0.05,3,8} = 4.07$, and the critical value for farmer within place is $F_{0.05,8,60} = 2.097$. The calculated F values are greater than the critical values and thus the effects of place and farmer are significant.

Use-Misuse of Statistical Packages

13

Since time immemorial statistics is being used knowingly or unknowingly. In this modern scientific era, one can hardly find any area where statistics is not playing a vital role. Statistics deals with the study of population as a whole rather than the individual unit of the population. Statistics is concerned with aggregated information on a particular subject in a population providing due importance to each and every element of the population. Wide range of application of statistics is found in the field of agriculture, biology, education, economics, business, management, medical, engineering, psychology, environment, and space; even in the management of war, statistics is playing a vital role. One can hardly find any human activity where statistics is not used. Statistical theories are applied on set of data to extract the inner meaning, to unearth the so long hidden information embedded within a particular data set and make it more and more informative for the betterment of the human civilization.

Statistics has developed itself along with the development of human civilization. Because of the need of the society and inquisitiveness of human beings, science has developed in every sphere so also the subject statistics. Various branches/disciplines of science have emerged, and in each of this development usefulness of statistics has been felt ever increasing. "Necessity is the mother of invention." To cater these necessities, a number of theories and areas of statistics have been developed due to the demand of other disciplines of science. As a result, in every sphere of human civilization, statistics has become an indispensable part.

For quite a long period, in spite of its tremendous development as an indispensible discipline, its application was restricted mainly because of the fact that many of the statistical theories require knowledge of mathematics and require extensive calculation. The quick and continued increase in computing facilities particularly after the second half of the twentieth century has tremendous impact on the use of statistical tools. Instead of almost linear models, nonlinear and multivariate statistical tools have been used to a greater extent. With the advancement in computing facilities, the use of statistics has increased manifold. Starting from the era of manual Facit to modern supercomputers through desk/pocket/scientific calculators and different generations of computers, the computing facilities have increased tremendously. With the ever increasing facility, the use of different statistical theories in various fields which were not feasible earlier has become possible nowadays. Statistical theories are more extensively used nowadays to make the data more and more informative.

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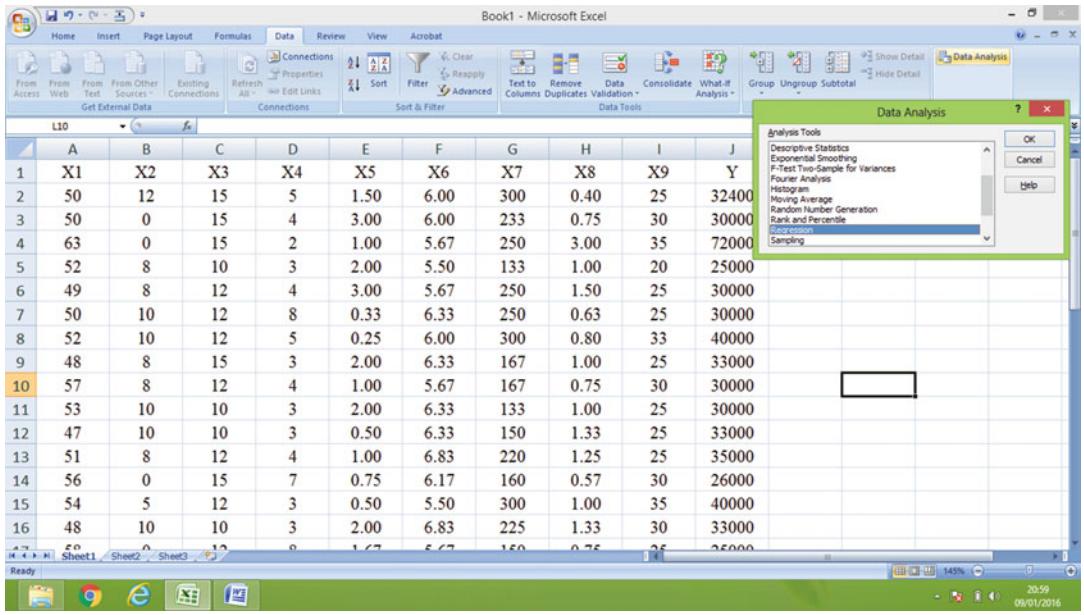
Like a coin having two faces, the development of statistics and computing facilities is also not unidirectional or flawless. Statistical theories and the set of data are best informative at the hands of a good statistician with an appropriate computing facility. The knowledge of both statistics, the subject concern where statistics is to be used, the data, and the computing facility available are the important contributory factors to unearth the hidden information in a set of data. The absence of any one of these will lead to misinformation. A set of data can be analyzed in numerous ways, but a very few of these possible ways can only deliver the actual information. For effective use of data, knowledge of statistical tools available, knowledge of generation of data, and objective of the analysis of data are the main points to be kept in mind. A number of instances are there where calculations have been made with the help of the computer packages, without understanding the theories and situations where actually the specific calculation are required to be taken up, the nature of data and its limitations, and also the objective. In brief, statistical analyses have been taken up without knowing the logic and utilities in these cases. Statistical theories are used best by the subject matter specialists in consultation with an efficient statistician under the given knowledge base about the software to be used for the purpose of calculation. Understanding of both the specialists toward the field of each other to a certain degree is essential for efficient use of statistical theories toward advancement of human civilization. Misuse of statistics has become a greater concern particularly with the development of softwares.

This has been clearly stated by Marino 2014, with particular reference to the biomedical research. The author has stated that "descriptive, exploratory, and inferential statistics are necessary components of hypothesis-driven biomedical research. Despite the ubiquitous need for these tools, the emphasis on statistical methods in pharmacology has become dominated by inferential methods often chosen more by the availability of user-friendly software than by any understanding of the data set or the critical assumptions of the statistical tests. Such frank misuse of statistical methodology and the quest to reach the mystical $\alpha < 0.05$ criteria have hampered research via the publication of incorrect analysis driven by rudimentary statistical training. Perhaps more critically, a poor understanding of statistical tools limits the conclusions that may be drawn from a study by divorcing the investigator from their own data. The net result is a decrease in quality and confidence in research findings, fueling recent controversies over the reproducibility of high profile findings and effects that appear to diminish over time." Even when statistical techniques are correctly applied, the results can be difficult to interpret for those lacking expertise, so interpretation of results emerging out of statistical analysis through computer packages is a must. Misuse can occur when conclusions are overgeneralized and claimed to be representative of more than they really are, often by either deliberately or unconsciously overlooking sampling bias. To make data gathered from statistics believable and accurate, the sample taken must be representative of the whole.

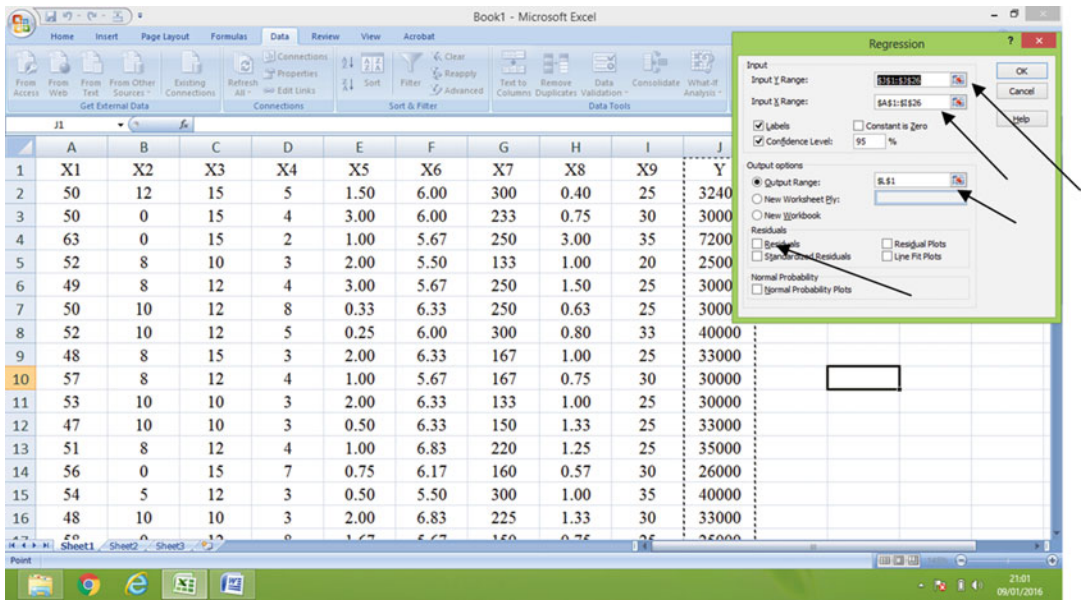
Softwares developed for statistical calculations have their advantages and limitations. One needs to be very much selective in finalizing the use of a particular module of particular software to be used for a specific purpose. Statistical softwares are multipurpose in nature; these are developed in such a way that a varied range of user can use the software and for the purpose one must have a clear idea about the different commands to answer during execution of software. One must have a clear idea about what are the requirements, what input to be fed to the computer, whether it is feasible to get the information fed to the computer using statistical theories, what should be the directions to the computer, and what are the output generated by the computer and how to interpret the output. Let us demonstrate the same by taking one example on regression analysis using MS Excel and SPSS as follows:

Data entered in to the MS Excel spreadsheet.



	A	B	C	D	E	F	G	H	I	J
1	X1	X2	X3	X4	X5	X6	X7	X8	X9	Y
2	50	12	15	5	1.50	6.00	300	0.40	25	32400
3	50	0	15	4	3.00	6.00	233	0.75	30	30000
4	63	0	15	2	1.00	5.67	250	3.00	35	72000
5	52	8	10	3	2.00	5.50	133	1.00	20	25000
6	49	8	12	4	3.00	5.67	250	1.50	25	30000
7	50	10	12	8	0.33	6.33	250	0.63	25	30000
8	52	10	12	5	0.25	6.00	300	0.80	33	40000
9	48	8	15	3	2.00	6.33	167	1.00	25	33000
10	57	8	12	4	1.00	5.67	167	0.75	30	30000
11	53	10	10	3	2.00	6.33	133	1.00	25	30000
12	47	10	10	3	0.50	6.33	150	1.33	25	33000
13	51	8	12	4	1.00	6.83	220	1.25	25	35000
14	56	0	15	7	0.75	6.17	160	0.57	30	26000
15	54	5	12	3	0.50	5.50	300	1.00	35	40000
16	48	10	10	3	2.00	6.83	225	1.33	30	33000

From Data Analysis tool, Regression menu has been activated.



	A	B	C	D	E	F	G	H	I	J
1	X1	X2	X3	X4	X5	X6	X7	X8	X9	Y
2	50	12	15	5	1.50	6.00	300	0.40	25	3240
3	50	0	15	4	3.00	6.00	233	0.75	30	3000
4	63	0	15	2	1.00	5.67	250	3.00	35	7200
5	52	8	10	3	2.00	5.50	133	1.00	20	2500
6	49	8	12	4	3.00	5.67	250	1.50	25	3000
7	50	10	12	8	0.33	6.33	250	0.63	25	3000
8	52	10	12	5	0.25	6.00	300	0.80	33	40000
9	48	8	15	3	2.00	6.33	167	1.00	25	33000
10	57	8	12	4	1.00	5.67	167	0.75	30	30000
11	53	10	10	3	2.00	6.33	133	1.00	25	30000
12	47	10	10	3	0.50	6.33	150	1.33	25	33000
13	51	8	12	4	1.00	6.83	220	1.25	25	35000
14	56	0	15	7	0.75	6.17	160	0.57	30	26000
15	54	5	12	3	0.50	5.50	300	1.00	35	40000
16	48	10	10	3	2.00	6.83	225	1.33	30	33000

Dependent and independent variables range, output range, and other options have been selected in the proper dialogue box to get the following output:

SUMMARY OUTPUT

Regression Statistics	
Multiple R	0.845928
R Square	0.715594
Adjusted R Square	0.54495
Standard Error	9352.489
Observations	25

ANOVA

	df	*SS*	*MS*	*F*	*Significance F*
Regression	9	3.3E+09	3.67E+08	4.193495	0.00719
Residual	15	1.31E+09	87469057		
Total	24	4.61E+09			

	Coefficients	*Standard Error*	*t Stat*	*P-value*	*Lower 95%*	*Upper 95%*
Intercept	31080.11	43562.31	0.713463	0.486512	-61770.8	123931
X1	0.440054	378.9411	0.001161	0.999089	-807.254	808.134
X2	-190.143	598.963	-0.31745	0.755276	-1466.8	1086.517
X3	-157.755	1282.193	-0.12303	0.903713	-2890.68	2575.175
X4	-88.7728	1712.524	-0.05184	0.959342	-3738.93	3561.387
X5	-2749.45	2561.26	-1.07348	0.300024	-8208.65	2709.746
X6	-2497.02	3875.447	-0.64432	0.5291	-10757.3	5763.301
X7	51.80299	37.28408	1.389413	0.184988	-27.6661	131.2721
X8	19587.13	4653.429	4.209182	0.000759	9668.581	29505.68
X9	-139.831	486.211	-0.28759	0.777594	-1176.16	896.5035

Note that in the previous selections, residual box was left blank as such there was no residual or predicted value in the output above. But if one selects residual dialogue box, then we would expect the following output:

SUMMARY OUTPUT

Regression Statistics	
Multiple R	0.845928
R Square	0.715594
Adjusted R Square	0.54495
Standard Error	9352.489
Observations	25

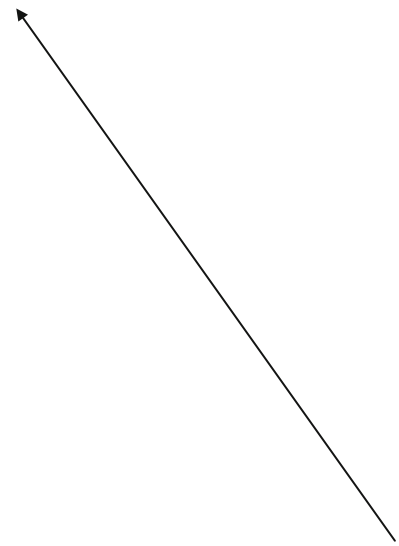
ANOVA

	df	*SS*	*MS*	*F*	*Significance F*
Regression	9	3.3E+09	3.67E+08	4.193495	0.00719
Residual	15	1.31E+09	87469057		
Total	24	4.61E+09			

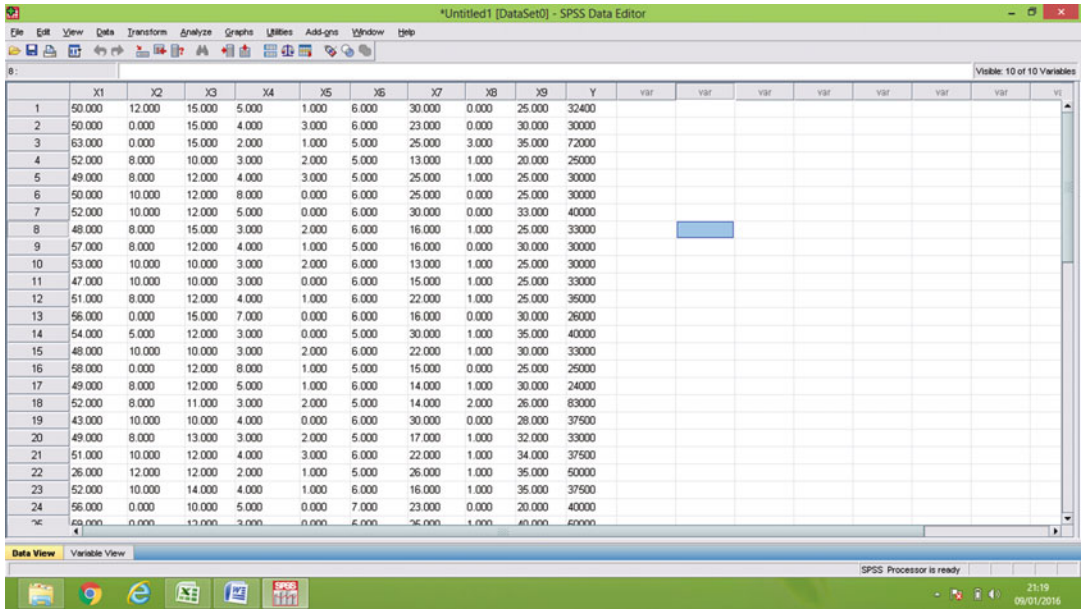
	Coefficients	*Standard Error*	*t Stat*	*P-value*	*Lower 95%*	*Upper 95%*
Intercept	31080.11	43562.31	0.713463	0.486512	-61770.8	123931
X1	0.440054	378.9411	0.001161	0.999089	-807.254	808.134
X2	-190.143	598.963	-0.31745	0.755276	-1466.8	1086.517
X3	-157.755	1282.193	-0.12303	0.903713	-2890.68	2575.175
X4	-88.7728	1712.524	-0.05184	0.959342	-3738.93	3561.387
X5	-2749.45	2561.26	-1.07348	0.300024	-8208.65	2709.746
X6	-2497.02	3875.447	-0.64432	0.5291	-10757.3	5763.301
X7	51.80299	37.28408	1.389413	0.184988	-27.6661	131.2721
X8	19587.13	4653.429	4.209182	0.000759	9668.581	29505.68
X9	-139.831	486.211	-0.28759	0.777594	-1176.16	896.5035

RESIDUAL OUTPUT

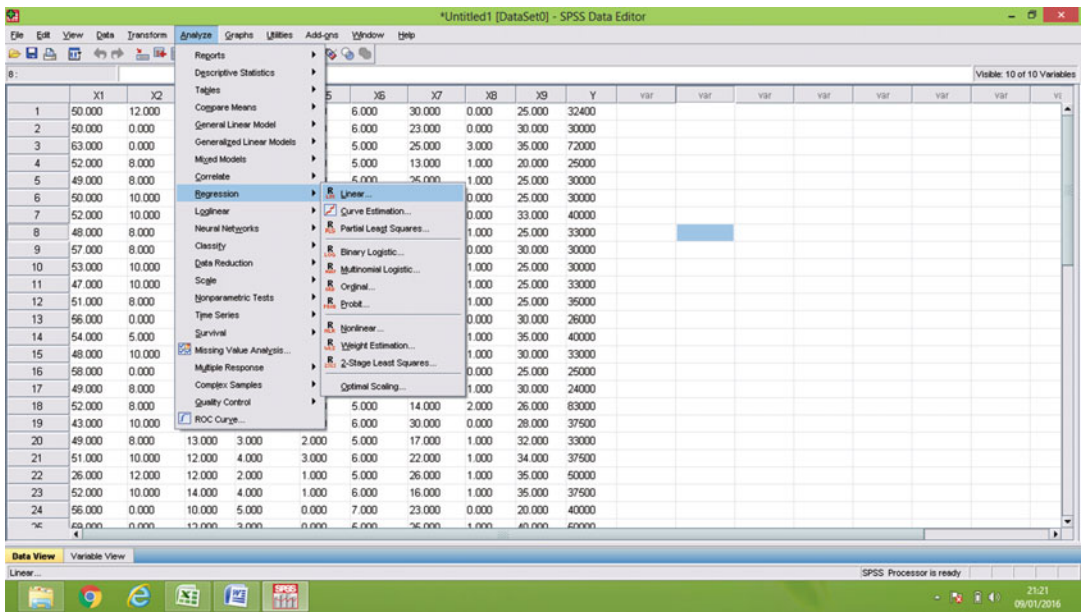
Observation	*Predicted Y*	*Residuals*
1	26783.91	5616.089
2	27715.76	2284.236
3	78474.49	-6474.49
4	32185.8	-7185.8
5	43761.61	-13761.6
6	31580.94	-1580.94
7	37791.36	2208.64
8	30384.89	2615.113
9	29574.88	425.1152
10	29034.27	965.7268
11	40500.21	-7500.21
12	39913.98	-4913.98
13	25906.55	93.44523
14	43119.41	-3119.41
15	38314.04	-5314.04
16	28717.75	-3717.75
17	28709.43	-4709.43
18	58581.99	24418.01
19	36443.01	1056.987
20	39097.22	-6097.22
21	29387.06	8112.94
22	47750.19	2249.813
23	35960.65	1539.351
24	29539.33	10460.67
25	47671.27	2328.732



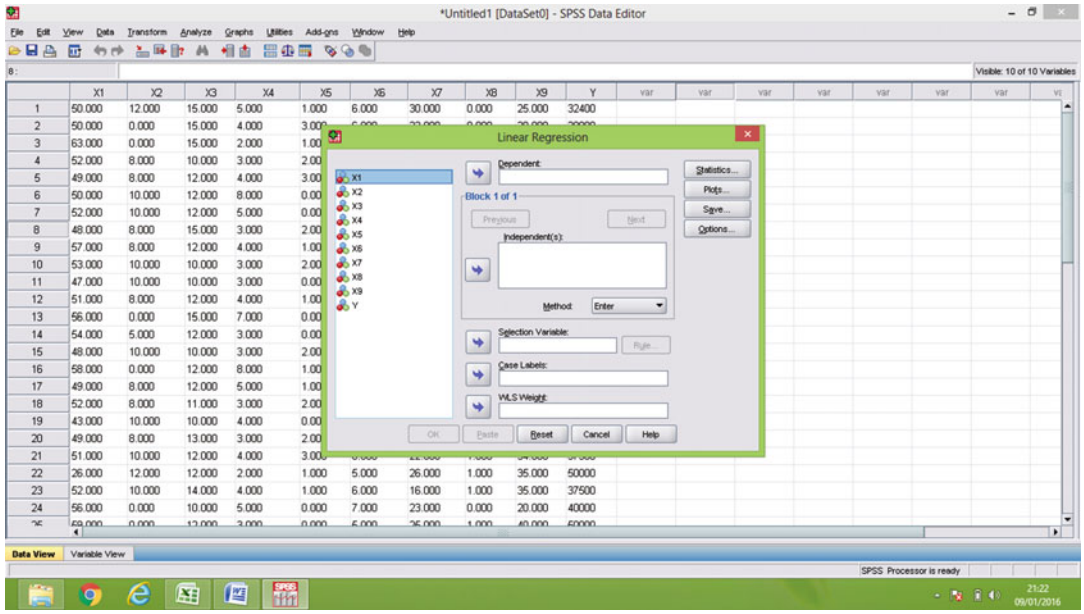
Now we shall use the same example to be worked out using SPSS as follows:



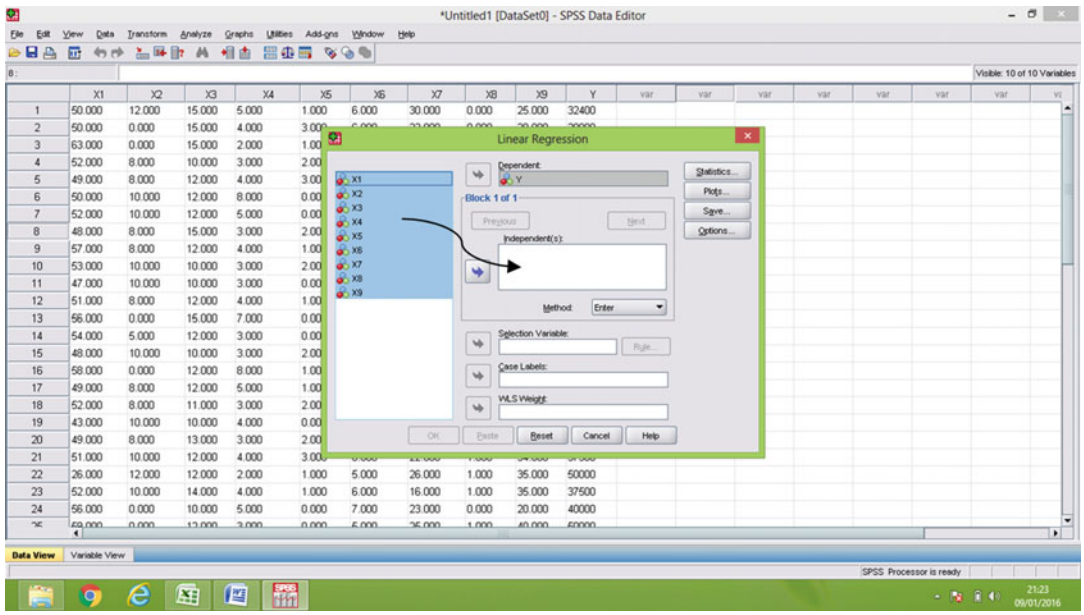
Data entered in SPSS data editor.



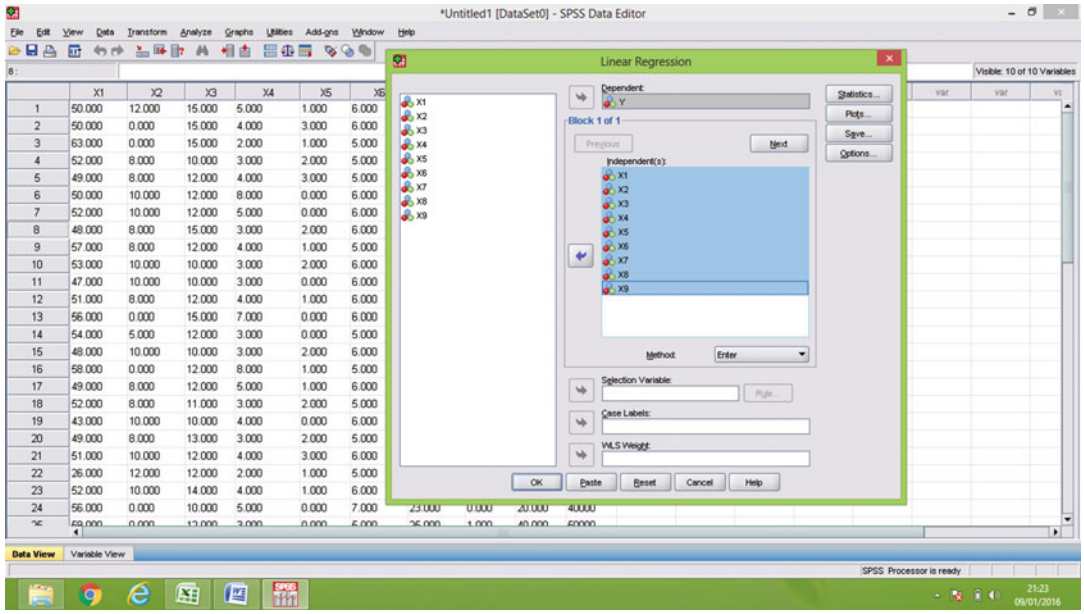
Linear Regression in Analysis tool has been activated.



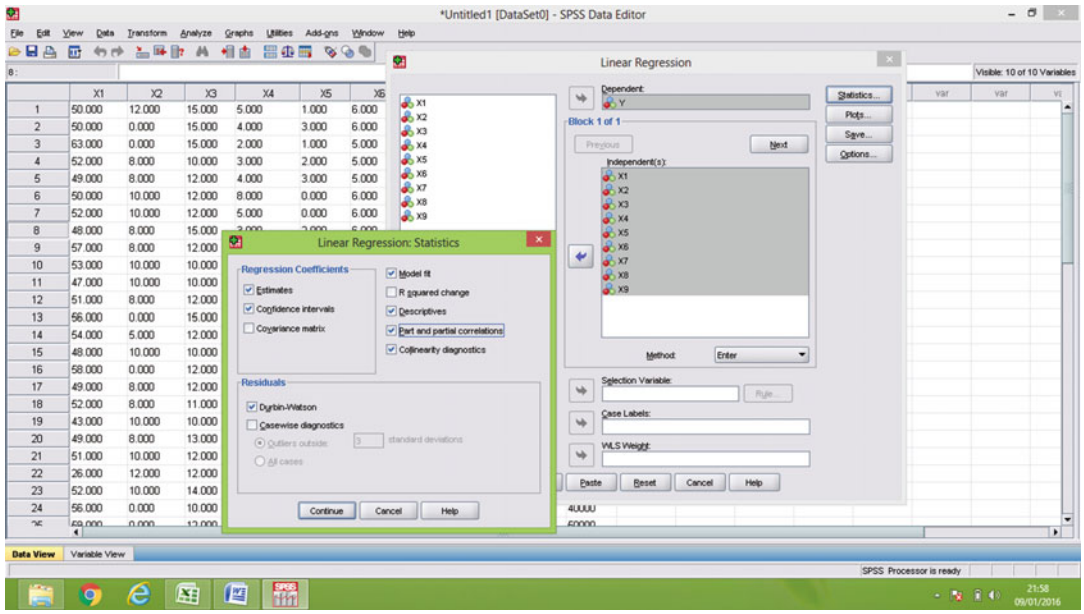
About to select the dependent and the independent set of variables.



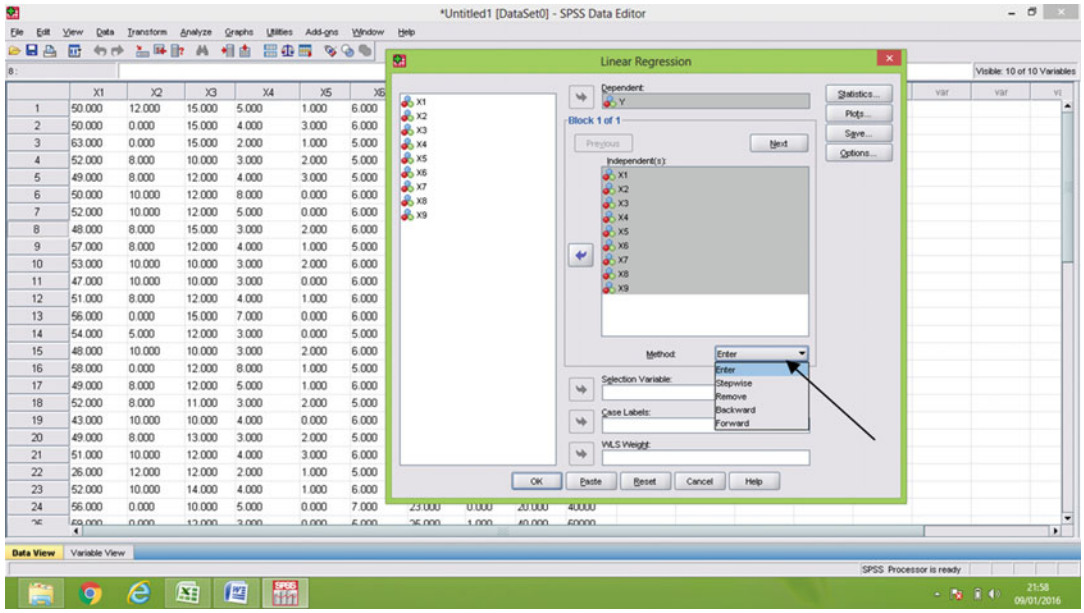
Dependent variable selected, independent variables ready to be selected.



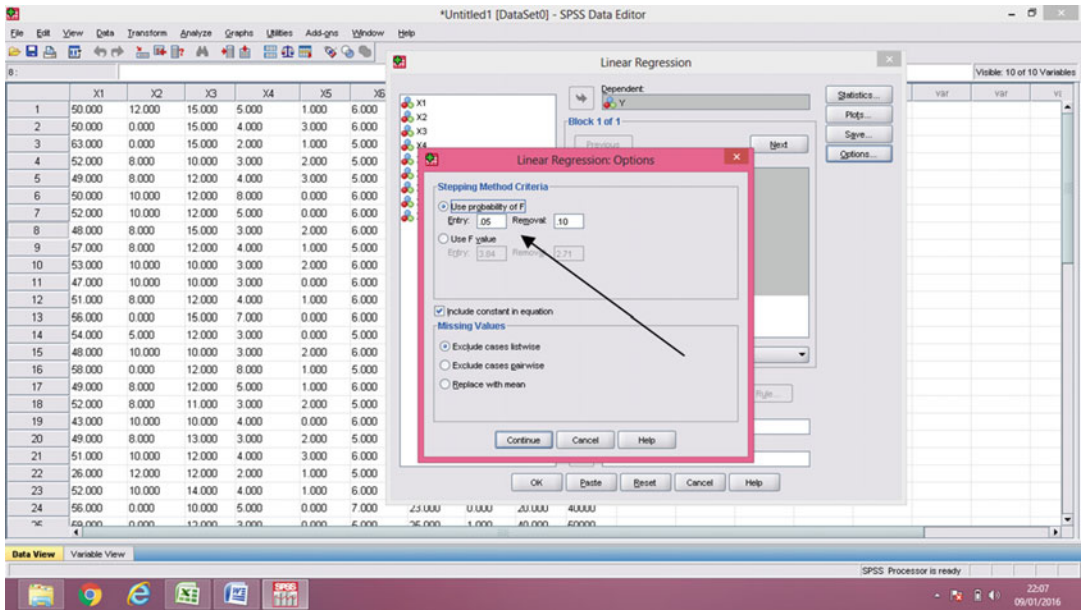
Dependent and independent set of variables have been selected.



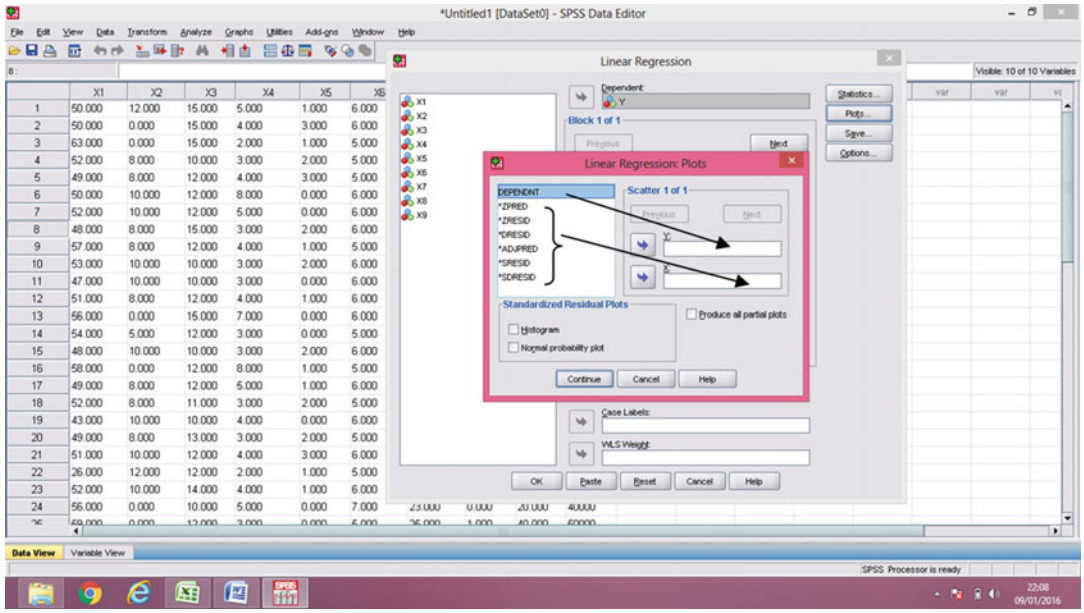
Statistics required during analysis are to be specified. Note, there are many options; one needs to know all these and select the desired one(s).



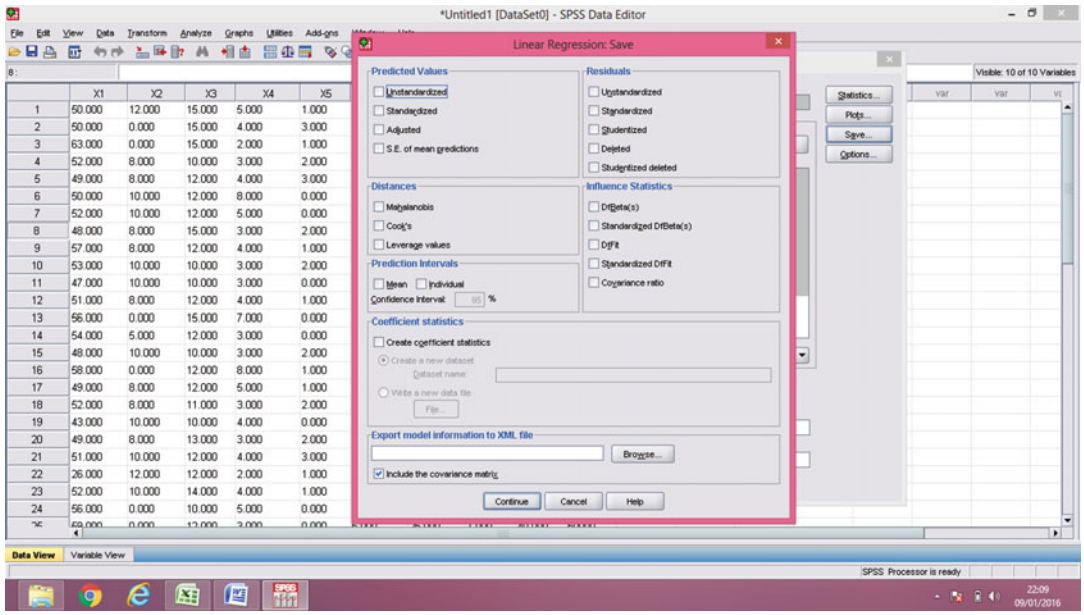
There are different methods of getting linear regression equation, viz., simple multiple regression, stepwise regression, backward, forward, etc., but one needs to have a clear idea about the differences in these methods and the situations where these can be applied before selecting a particular method.



The level of significance plays an important role in statistical inference, so also in regression analysis. The probability at which the different estimates are required to be significant is dependent on the nature of the analysis and type of data being handled. As such, specific level of significance is required to be entered as per the requirement of the analysis.



There are options for *X*-plotting; required plotting must be specified in the specific dialogue box.



There are options for saving various variables generated through analysis. One should be selective in choosing the actual variables/measures to be saved and insert the same in the appropriate dialogue box. One can see that there are comparatively many options than what we used to get in

usual regression analysis using MS Excel. Once after fulfilling the above dialogue box, the output what we get is reproduced below. While going through the analytical steps as well as output, one can find that there are more options in SPSS compared to MS Excel. Thus, not only the analysis but also the information generated through different analyses varies across the statistical packages; each statistical package has their advantages as well as disadvantages.

Regression

[Data set0]

Descriptive Statistics

	Mean	Std. Deviation	N
Y	3.75E4	13864.291	25
X1	5.10000E1	6.763875	25
X2	6.92000	4.222164	25
X3	1.22000E1	1.755942	25
X4	4.08000	1.605200	25
X5	1.16000	1.027943	25
X6	5.64000	.568624	25
X7	2.09200E1	5.908468	25
X8	.76000	.723418	25
X9	2.89200E1	5.081994	25

Correlations

		Y	X1	X2	X3	X4	X5	X6	X7	X8	X9
Pearson Correlation	Y	1.000	.075	-.118	.036	-.458	-.042	-.321	.176	.669	.323
	X1	.075	1.000	-.620	.172	.249	-.114	-.043	-.176	.102	-.005
	X2	-.118	-.620	1.000	-.284	-.214	.147	.092	.048	-.007	-.105
	X3	.036	.172	-.284	1.000	.127	.120	-.050	.114	.039	.329
	X4	-.458	.249	-.214	.127	1.000	-.311	.307	-.017	-.665	-.295
	X5	-.042	-.114	.147	.120	-.311	1.000	-.182	-.293	.278	-.125
	X6	-.321	-.043	.092	-.050	.307	-.182	1.000	.065	-.421	-.328
	X7	.176	-.176	.048	.114	-.017	-.293	.065	1.000	-.180	.320
	X8	.669	.102	-.007	.039	-.665	.278	-.421	-.180	1.000	.267
	X9	.323	-.005	-.105	.329	-.295	-.125	-.328	.320	.267	1.000
Sig. (1-tailed)	Y	.	.361	.287	.433	.011	.421	.059	.200	.000	.058
	X1	.361	.	.000	.206	.115	.294	.419	.200	.313	.491
	X2	.287	.000	.	.084	.152	.241	.332	.410	.488	.308
	X3	.433	.206	.084	.	.272	.284	.406	.294	.426	.054
	X4	.011	.115	.152	.272	.	.065	.068	.468	.000	.076
	X5	.421	.294	.241	.284	.065	.	.191	.078	.089	.276
	X6	.059	.419	.332	.406	.068	.191	.	.378	.018	.055
	X7	.200	.200	.410	.294	.468	.078	.378	.	.194	.059
	X8	.000	.313	.488	.426	.000	.089	.018	.194	.	.099
	X9	.058	.491	.308	.054	.076	.276	.055	.059	.099	.
N	Y	25	25	25	25	25	25	25	25	25	25
	X1	25	25	25	25	25	25	25	25	25	25
	X2	25	25	25	25	25	25	25	25	25	25
	X3	25	25	25	25	25	25	25	25	25	25
	X4	25	25	25	25	25	25	25	25	25	25
	X5	25	25	25	25	25	25	25	25	25	25
	X6	25	25	25	25	25	25	25	25	25	25
	X7	25	25	25	25	25	25	25	25	25	25
	X8	25	25	25	25	25	25	25	25	25	25
	X9	25	25	25	25	25	25	25	25	25	25

Variables Entered/Removed[b]

Model	Variables Entered	Variables	Method
1	X9, X1, X5, X6,	.	Enter

a. All requested variables entered.

b. Dependent Variable: Y

Model Summary[b]

Model	R	R Square	Adjusted R Square	Std. Error of the	Durbin-Watson
1	.762[a]	.581	.329	11356.378	2.047

a. Predictors: (Constant), X9, X1, X5, X6, X3, X7, X8, X2, X4

b. Dependent Variable: Y

ANOVA[b]

Model		Sum of Squares	df	Mean Square	F	Sig.
1	Regression	2.679E9	9	2.976E8	2.308	.073[a]
	Residual	1.935E9	15	1.290E8		
	Total	4.613E9	24			

a. Predictors: (Constant), X9, X1, X5, X6, X3, X7, X8, X2, X4

b. Dependent Variable: Y

Coefficients[a]

Model	Unstandardized Coefficients		Standardized Coefficients	t	Sig.	95% Confidence Interval for B		Correlations			Collinearity Statistics	
	B	Std. Error	Beta			Lower Bound	Upper Bound	Zero-order	Partial	Part	Tolerance	VIF
1 (Constant)	35124.781	45623.708		.770	.453	-62119.852	132369.413					
X1	-115.629	470.951	-.056	-.246	.809	-1119.438	888.181	.075	-.063	-.041	.530	1.888
X2	-477.816	733.003	-.146	-.652	.524	-2040.175	1084.543	-.118	-.166	-.109	.561	1.782
X3	-292.465	1579.859	-.037	-.185	.856	-3659.855	3074.924	.036	-.048	-.031	.698	1.432
X4	-73.366	2312.781	-.008	-.032	.975	-5002.942	4856.209	-.458	-.008	-.005	.390	2.565
X5	-2185.980	2719.390	-.162	-.804	.434	-7982.222	3610.262	-.042	-.203	-.134	.688	1.454
X6	-1046.739	4745.050	-.043	-.221	.828	-11160.575	9067.096	-.321	-.057	-.037	.738	1.355
X7	626.659	457.114	.267	1.371	.191	-347.655	1600.974	.176	.334	.229	.737	1.357
X8	14271.662	4979.086	.745	2.866	.012	3658.991	24884.333	.669	.595	.479	.414	2.414
X9	-3.273	593.970	-.001	-.006	.996	-1269.290	1262.745	.323	-.001	.000	.590	1.696

a. Dependent Variable: Y

Collinearity Diagnostics[a]

Model	Dimension	Eigenvalue	Condition Index	Variance Proportions									
				(Constant)	X1	X2	X3	X4	X5	X6	X7	X8	X9
1	1	8.635	1.000	.00	.00	.00	.00	.00	.00	.00	.00	.00	.00
	2	.612	3.756	.00	.00	.00	.00	.01	.13	.00	.00	.16	.00
	3	.347	4.990	.00	.00	.05	.00	.00	.44	.00	.00	.17	.00
	4	.258	5.787	.00	.00	.43	.00	.01	.15	.00	.00	.00	.00
	5	.079	10.464	.00	.00	.06	.00	.21	.04	.00	.33	.13	.01
	6	.029	17.171	.00	.01	.00	.02	.41	.06	.01	.60	.37	.11
	7	.020	20.873	.01	.07	.02	.06	.20	.00	.10	.03	.01	.29
	8	.011	27.565	.00	.08	.00	.78	.05	.10	.02	.00	.01	.30
	9	.007	34.800	.00	.57	.30	.13	.09	.02	.38	.02	.13	.11
	10	.002	66.360	.99	.27	.15	.01	.01	.06	.49	.01	.02	.17

a. Dependent Variable: Y

Residuals Statistics[a]

	Minimum	Maximum	Mean	Std. Deviation	N
Predicted Value	23417.06	74253.70	3.75E4	10564.753	25
Residual	-1.224E4	3.352E4	.000	8978.005	25
Std. Predicted Value	-1.331	3.481	.000	1.000	25
Std. Residual	-1.078	2.952	.000	.791	25

a. Dependent Variable: Y

Another Example In the following example, we shall demonstrate how many types of statistical analysis can be taken up with a given set of data. But the question is which one is the appropriate one?

F1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1
F2	1	1	1	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2	2	2
F3	1	1	2	2	3	3	4	4	5	5	1	1	2	2	3	3	4	4	5	5
Obs	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2
Ch1	148	153	157	154	162	159	149	153	150	142	167	153	160	155	163	169	149	144	146	139
F1	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2
F2	1	1	1	1	1	1	1	1	1	1	2	2	2	2	2	2	2	2	2	2
F3	1	1	2	2	3	3	4	4	5	5	1	1	2	2	3	3	4	4	5	5
Obs	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2	1	2
Ch1	164	168	168	163	169	164	140	144	140	136	164	169	162	169	175	169	143	134	149	139

The information is pertaining to a three factor experiment conducted with factors F1 (2 levels), F2 (2 levels), and F3 (5 levels), and on each treatment combination (20 in total), there are two observations and corresponding responses. *What type of analysis should be undertaken on the given set of data? Before taking analysis, one should be satisfied with the following queries: What was (were) the objective of the study? Where was the study undertaken? In the laboratory or in the field? What type of information are needed? Only the effects of factors or their interactions also? What type of experimental design is followed? And so on...*

These are required because without going details into the experimental procedure, one can analyze the given information as per the standard procedure of analysis of experimental data adopting one of the following designs among many other possibilities taking help from statistical software:

1. CRD with 20 treatments
2. RBD with 20 treatments
3. Three factor factorial ($2 \times 2 \times 5$) CRD
4. Three factor factorial ($2 \times 2 \times 5$) RBD
5. Split factorial analysis with F1 in main plots and F2 and F3 in factorial arrangement
6. Split factorial analysis with F2 in main plots and F1 and F3 in factorial arrangement
7. Split factorial analysis with F3 in main plots and F2 and F3 in factorial arrangement
8. Split-split plot arrangement with F1 in main plots, F2 in sub plots, and F3 in sub-sub plots
9. Split-split plot arrangement with F1 in main plots, F3 in sub plots, and F2 in sub-sub plots
10. Split-split plot arrangement with F2 in main plots F1 in sub plots and F3 in sub-sub plots
11. Split-split plot arrangement with F2 in main plots, F3 in sub plots, and F1 in sub-sub plots
12. Split-split plot arrangement with F3 in main plots, F1 in sub plots, and F2 in sub-sub plots
13. Split-split plot arrangement with F3 in main plots, F2 in sub plots, and F1 in sub-sub plots
14. And other variant designs of experiment

But it must be kept in mind that each and every above mentioned design has their own specificity with respect to model, assumptions, and analysis also in applicability. All are not suitable or applicable for a specific situation. With the help of statistical software, without going details into the statistical principles and or adopted method of experimentation, one can analyze the data and draw conclusion accordingly. But how far the information generated in the process is useful is of million dollar question. So one must be very careful in analyzing the experimental data on hand providing due consideration to all the aspects.

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