



## Education and Training

The Institute conducts post graduate teaching and in-service courses in Agricultural Statistics, Computer Application and Bioinformatics for human resource development. Institute is conducting M.Sc. and Ph.D. programmes in Agricultural Statistics since 1964, M.Sc. in Computer Application since 1985-86, Ph.D. in Computer Application since 2013-14, M.Sc. in Bioinformatics since 2011-12 and Ph.D. in Bioinformatics from current academic year. A brief description of human resource development during the year is given in the sequel.

### Degree Courses

The Institute is conducting the following degree courses in collaboration with the Post Graduate School of Indian Agricultural Research Institute (IARI), New Delhi which has the status of a Deemed University:

- (i) Ph.D. (Agricultural Statistics)
- (ii) M.Sc. (Agricultural Statistics)
- (iii) Ph.D. (Computer Application)
- (iv) M.Sc. (Computer Application)
- (v) Ph.D. (Bioinformatics)
- (vi) M.Sc. (Bioinformatics)

Both Ph.D. and M.Sc. students are required to study courses not only in their major area but also in other areas in Agricultural Sciences like Genetics, Agronomy, Agricultural Economics, etc. The Courses in Mathematics, Agricultural Statistics, Computer Application and Bioinformatics are offered at this Institute while the courses in Agricultural Sciences are offered at IARI.

### Number of students admitted / completed various courses during 2014-15

Courses	Number of students	
	Admitted	Completed
Ph.D. (Agricultural Statistics)	6	5
M.Sc. (Agricultural Statistics)	8	6
Ph.D. (Computer Applications)	0	0
M.Sc. (Computer Application)	7	2
Ph.D. (Bioinformatics)	6	0
M.Sc. (Bioinformatics)	5	5

### DISSERTATIONS APPROVED

#### Ph.D. (Agricultural Statistics)

- (i) **Shashi Shekhar**  
Chairperson: **Dr. LM Bhar**

#### A Study on Multiple Biological Assays

Bioassays or biological assays are used in many fields of sciences, especially in life sciences. In many practical situations for conducting experiments on biological assays, the interest of the experimenter lies in comparing several test preparations with a single standard preparation. Multiple bioassays have been proved to be a more practical approach and are also significantly less resource intensive. The main purpose of a bioassay is the estimation of the relative potency of test preparation with respect to standard preparation. Therefore, only some specific contrasts are required to be estimated. It is desired that when a block design is used for the assay, these contrasts of interest are estimated with high efficiency. This study deals with the construction of such high efficient designs for

multiple biological assays both for parallel line and slope ratio assay. A general method of construction of A-optimal binary block designs for symmetric parallel line assays has been obtained which has been extended for multiple parallel line assays as well. Another method of constructing A-optimal binary block designs for asymmetrical parallel line assays has also been proposed. Two cases have been considered. In the first case, designs obtained are of equal replications of the doses and in the second case, designs with unequal replications are obtained. This methodology has also been extended for multiple asymmetric cases. Methods of constructing block designs for multiple parallel line assays based on balanced incomplete block design have also been considered. Designs obtained here are highly efficient as all the contrasts of interest can be estimated with high efficiency. For the case of multiple slope ratio assays, a general method of constructing efficient block designs for symmetric case has been proposed. Catalogue of the designs so generated is also prepared.

(ii) **Ankur Biswas**  
Chairperson: **Dr. Anil Rai**

**A Study of Spatial Bootstrap Techniques for Variance Estimation in Finite Population**

In agricultural surveys, the important parameters of crop production are often spatial in nature, in which observations from neighbouring units tend to share similar statistical properties. In literature, spatial sampling designs are suggested to provide reliable spatial statistics using the spatial dependency among the sampling units. Here, a new efficient approach, viz. spatial estimation procedure, for estimation of the mean of spatially correlated finite population units is developed by incorporating the spatial dependency at the estimation stages of traditional without replacement sampling designs like Simple Random Sampling (SRS) and Ranked Set Sampling (RSS). In this approach, Spatial Estimators (SE) of population mean were developed following prediction approach in which unobserved population units were predicted based on their distances with observed sampling units following Inverse Distance Weighting (IDW) method. Since the proposed SE's were non-linear in nature, Rescaled Spatial Bootstrap (RSB) techniques were developed for unbiased estimation of variance of the SE under both the designs. Also, a spatial simulation study was carried out in order to study the performance of

proposed SE with respect to the corresponding classical estimators of population mean under both the designs along with its variance estimation following proposed RSB methods. Proposed SE under both designs were found to be almost unbiased, consistent, stable and more efficient for estimation of population mean. Further, in the context of without replacement sampling both by SRS as well as RSS designs for spatially correlated finite population, naive bootstrap approach results in considerably high amount of bias in the estimator of variance of the SE of population mean, whereas, the proposed RSB methods were found to be approximately unbiased. Further, the statistical properties of these RSB methods were not desirable in presence of missing observations. Thus, Proportional Spatial Bootstrap (PSB) methods were proposed using spatial imputation techniques for unbiased variance estimation of SE under SRS without replacement design. Efficient rescaling Jackknife and Bootstrap methods for unbiased estimation of variance of the RSS mean estimator in case of finite population was also studied.

(iii) **Prabina Kumar Meher**  
Chairperson: **Dr. AR Rao**

**Development of Statistical Procedures for Genome Sequence Analysis**

Several functional elements like Transcription Factor Binding Sites (TFBS), splice sites, Single Nucleotide Polymorphisms (SNPs) are present on genome and identification of these elements in wet-lab experiments is quite expensive. Hence, development of computational methods for the prediction of functional elements on genome is essential to understand the underlying complex biological phenomena. One such phenomenon involves the prediction of disease risk of an individual using whole genome level information on SNPs. However, disease risk prediction studies involve imbalanced case-control data, where controls are higher than the cases. Moreover, the number of SNPs remains larger than sample size. Another important area in genomics is to predict splice sites, which in turn helps to predict gene structures in eukaryotes. However, the existing procedures suffer from drawbacks like assumption of independency between positions at splice sites, larger window size and transformation of sequence information to numeric form. This study was taken up to develop a procedure to classify cases and controls under imbalanced data and predict disease risk of an individual, determine a suitable

window length and propose an approach to predict donor splice sites in rice and identify TFBS in a family of genes of Arabidopsis using Gibbs sampling. For the classification of imbalanced case-control data, Combined Random Forest (CRF) was proposed and its performance was found to be better in terms of prediction accuracy as compared with the Balanced Random Forest and Weighted Random Forest. For the prediction of splice sites in rice, an encoding approach with SVM, ANN and RF were proposed. A comparison revealed that the encoding approach with RF predicts the splice sites with higher accuracy. Similar result was found while comparing the performance of RF with the existing approaches: NNsplice, Splice view, MM1, WMM, MDD and MEM. In addition, a 9bp window length having 3bp at the exon end and 6bp at the intron start was found to discriminate the true splice sites from false splice sites. Based on the proposed approach, a web server was also developed to predict the donor splice sites in eukaryotes. In order to identify the TFBS, a MAD box family of genes in Arabidopsis was considered and Gibbs sampling methodology was applied. Motifs of 10bp length in 1K upstream region of genes were found as probable TFBS. Thus, application of Gibbs sampler was recommended over other techniques for TFBS identification.

(iv) **Rohan Kumar Raman**  
Chairperson: **Dr. UC Sud**

**Some Contributions to Calibration Estimators in Survey Sampling in the Presence of Non-Response**

The mail questionnaire method is commonly used to collect data in surveys as the cost in this method is considerably reduced. However, non-response can be serious problem in this method and may result in biased estimates, particularly, when the respondents differ from the non-respondents. The calibration technique is widely used to obtain precise estimators of population parameters and provides a systematic approach for incorporation of auxiliary information at the estimation stage. Calibration implies that a set of starting weights (usually the sampling design weights) are transformed into a set of new weights, called calibrated weights. Here, estimators for population total have been proposed through the calibration approach, for different situations. Expressions for variance and estimator of variance, to the first order of approximation, of proposed calibrated estimators in presence of non-response have been developed. The

performance of developed calibrated estimators is evaluated through a simulation study where the study population is generated through an assumed model and also by making use of real data. The estimator is developed for the situation where the information on auxiliary variable is assumed known for the entire sampled units and the proposed calibrated estimators outperform the Hansen and Hurwitz estimators in terms of efficiency. Further, estimators using multiple sets of weights in the context of non-response are considered. In terms of percent relative biases, the calibrated estimator based on known auxiliary information dominates the other estimators i.e., Hansen and Hurwitz estimator, Cochran ratio estimator and double sampling ratio estimator. For positive correlation between known auxiliary variable and the study variable, the proposed calibrated estimator outperforms in terms of relative root mean square error. The double sampling approach based calibrated estimator is developed when auxiliary information is unknown. Simulation results reveal that maximum improved performance occurs for large sample size as well as for high correlation between study and auxiliary variable. When information on a auxiliary variable is negatively correlated, the proposed calibrated product estimator has consistently smaller values of the percent relative root mean square error. However, if auxiliary information is not available for entire population, the double sampling approach based calibrated product estimator is preferable.

(v) **Rupam Kumar Sarkar**  
Chairperson: **Dr. AR Rao**

**Statistical Evaluation of Complex Traits Based on Genomic Information**

An empirical procedure involving six different combined distance measures, seven clustering methods, three allocation strategies have been applied on the germplasm data of rice to identify mini-core sets. Based on a proposed evaluation criteria for core set identification, a combination of combined distance measure  $A_1B_2$  – the distance based on the “average of the range-standardized absolute difference” for quantitative data with the “rescaled distance based on the average absolute difference” for qualitative data; k-means clustering method; and proportional allocation strategy was found best for the identification of mini-core set of rice germplasm. Also, the optimum values of tuning parameters of Random Forest (RF) have been identified to predict the breeding value of the trait – kernel

length in maize crop. Besides, the comparison of RF with Least Absolute Shrinkage and Selection Operator (LASSO), Elastic net (EN) and Ridge Regression (RR) for genomic prediction reveals that the correlation between the predicted and observed trait response is higher in RF than the others. In case of planning the RNA-Seq experiments, the Area Under Curve (AUC) for three different design setups (Un-blocked designs (A), Balanced block designs (B) and Incomplete Block designs (C)) and four simulated conditions (with batch effect and lane effect (S1), batch effect and no lane effect (S2), no batch effect and lane effect (S3) and no batch effect and no lane effect (S4)) have been obtained. The results reveal that the performance of incomplete block designs (C) are at par with that of Balanced Block designs (B) and superior to Unblocked designs (A) in terms of testing the difference in expression of genes under different treatment conditions. Moreover, a decrease in the noise increases the AUC marginally.

### **M.Sc. (Agricultural Statistics)**

#### **(i) Pramod Kumar Moury**

**Chairperson: Dr. Tauqueer Ahmad**

#### **A Study on Estimation of Average Yield of Cotton**

An alternative sampling methodology has been developed for estimation of average yield of cotton using limited number of pickings. The component sampling approach under uni-stage sampling design framework for estimating average yield of cotton at district level has been proposed and the same has been extended to stratified three stage sampling. Under component sampling approach, it is proposed to consider the yield of different pickings as the components of total yield. Estimates of average yield of cotton along with percentage standard error (%S.E.) have been obtained for Amravati and Aurangabad districts of Maharashtra and Warangal and Guntur districts of Andhra Pradesh for the year 2012-2013 using component sampling approach under uni-stage as well as stratified three stage sampling design framework. The estimate obtained using the proposed methodology is reliable and almost at par with the estimates obtained using General Crop Estimation Survey (GCES) methodology and an alternative methodology using double sampling regression procedure under stratified two stage sampling design framework. The proposed methodology will save cost of the survey significantly and will also be operationally

more convenient than GCES procedure. Also double sampling technique under stratified two stage sampling design framework has been proposed for estimation of average yield of cotton at tehsil level considering third picking of cotton crop as auxiliary variable. Using the proposed estimation procedure, estimates of average yield of cotton along with %S.E. have been obtained at tehsil level for Amravati and Aurangabad for 2012-2013. The estimates obtained are fairly reliable at tehsil level.

#### **(ii) Md. Harun**

**Chairperson: Dr. Cini Varghese**

#### **Statistical Designs Involving Three-way Crosses**

The objective of a breeding programme is to create variability and to select genotypes for raising or for further breeding purpose. The most common designs used by a geneticist to study genetic parameters and their interpretations are diallel (single cross), triallel (three-way cross) and quadriallel (double cross). Three-way crosses are intermediate between single and double cross hybrids with respect to uniformity, yield, stability and the relative simplicity of selecting and testing and hence are increasingly gaining popularity among breeders. Considering a full model including general and specific combining ability effects and a reduced model ignoring specific combining ability effects, the information matrices for the estimation of combining ability effects have been derived for designs involving three-way crosses. Four methods of constructing designs for breeding trials involving complete/partial three-way crosses have been developed. Among these, two methods are based on Mutually Orthogonal Latin Squares (MOLS), which yield variance balanced designs involving three-way crosses arranged in blocks. The other methods are derived from Association Schemes and Partially Balanced Incomplete Block (PBIB) designs. Also, for experimental situations in which the interest of the experimenter is in comparing a number of test lines with a control line, four series of designs involving complete/partial three-way crosses have been obtained using MOLS, PBIB designs and their association schemes. In all the designs obtained, three-way crosses are arranged in incomplete blocks. SAS codes have been developed using PROC IML to compute the information matrices and variances pertaining to general combining ability effects of full parents as well as half parents for different groups of interline comparisons.

**(iii) Saurav Guha****Chairperson: Dr. Hukum Chandra****Some Investigations on Outlier Robust Survey Inference**

In many surveys, like agriculture, income and expenditure surveys, data are typically outlier contaminated that contain few extreme values and linear model assumptions are questionable. Influential observations may appear due to imperfections of the survey design that cannot fully account for the dynamic and heterogeneous nature of the population. An observation may become influential due to a relatively large survey weight, extreme value or combination of the both. The generalized regression (GREG) estimator is widely used in survey sampling when the auxiliary data are available. However, the GREG estimator is vulnerable in the presence of outliers. Many robust procedures have a smaller variance than non-robust procedures in the presence of outliers. However, the bias can be dominant in the mean square error when the sample sizes become large. A winsorized approach based estimator of population total was proposed with a choice of cutoff points that guarantees that the resulting mean squared error is lower than the variance of the original survey weighted estimator. The upper and lower bias parameter estimates depends on the values of the top and bottom weighted residuals. If the data used to generate the cutoff values is same as the data for which the winsorized cutoff values are to be applied, then those units with the values of the top and bottom weighted residuals will be winsorized. However, if the data used to generate the cutoff values is different, then it is assumed that the data for which the winsorized cutoff values are to be applied fits the same model as the data used to generate the cutoff values. The expression for its mean squared error estimator is obtained. The improved performance of proposed estimator was demonstrated using a Monte Carlo simulation study. The developed estimator was also applied to a real life survey data.

**(iv) Prateesh P. Gopinath****Chairperson: Dr. Rajender Parsad****Two Dimensional Balanced Sampling Plans Excluding Adjacent Units**

A two dimensional balanced sampling plan excluding adjacent units are the sampling plans in which all the first order inclusion probabilities are equal and second order inclusion probabilities for pairs of adjacent units are zero and constant for all other pairs of non-adjacent units. These plans

are useful for the situations in which units in the population are arranged in two dimensions and it is expected that the adjacent units provide similar information. Two dimensional balanced sampling plans excluding adjacent units [2-BSA(m), where m denotes the distance between units] have been developed for populations with circular ordering of units for the situations when adjacent units that share a common border may provide similar response on characteristics under study (sharing a border adjacency scheme) and when all the units surrounding a selected unit may provide similar observations regarding the observed character (island adjacency scheme). In both these situations, it is assumed that  $m = 1$  or  $2$ . Algorithm based on linear programming approach was developed for construction of 2-BSA(m) plans under both adjacency schemes for  $m \leq 2$ . For execution of linear programming formulation, codes were written using PROC IML and PROC LP of SAS. Some results on existence of 2-BSA(m) plans have also been obtained for each adjacency scheme separately. Catalogues of 2-BSA(m) plans for the parameters satisfying  $RC \leq 50$ ,  $n \leq 5$  and  $m \leq 2$  have been prepared for both adjacency schemes. Here, R is the number of rows, C the number of columns,  $RC = N$ , the population size and n is the sample size.

**(v) Rajeev Ranjan Kumar****Chairperson: Dr. Girish Kumar Jha****Co-integration Approach for Energy-Use in Agriculture**

In view of increasing share of energy in the cost of cultivation as well as deregulation of prices of some petroleum products, agricultural commodity prices are vulnerable to the rise in energy prices, particularly of crude oil. In this study, an attempt has been made to examine the co-movement between energy and agricultural commodity prices with the help of Johansen co-integration technique using monthly wholesale price indices for the period April 1994 to March 2014. Since the process of deregulation started from April 2002 onward, the entire period was divided in two equal parts, so that before and after period analysis will provide a clear picture of a potential link between prices. The results clearly revealed that energy and selected agricultural commodity prices are integrated in the long-run since 2004 while fruits prices were integrated even before deregulation of petroleum price. This means that there is an increasing tendency for price changes in selected agricultural commodities

corresponding to changes in international crude oil prices in recent years. Further, an effort was also made to examine energy growth linkage in major states of India with the help of panel co-integration using annual time series data of real GSDP from agriculture and allied sectors and corresponding electricity consumption for agriculture during 1990-2010. The empirical analysis fully supported a positive long-run co-integrated relationship between GSDP and electricity consumption when the heterogeneous state effect was taken into account. There is long-run unidirectional causality running from energy consumption to agricultural growth. This implies that reducing energy consumption does not adversely affect agricultural growth in the short-run but would in the long-run and thus energy demand will increase in future in order to achieve higher agricultural growth.

**(vi) Sadikul Islam**

**Chairperson: Dr. UC Sud**

**An Application of Calibration Approach for Estimation of Finite Population Ratio under Two-Phase Sampling Design**

The calibration approach is frequently used to develop precise estimators of important population parameters. Further, the chi-square type distance function is usually used for determination of revised or calibrated weights. A higher level calibration approach has also been proposed for improving the variance estimator. The calibration approach is used to estimate finite population ratio under two phase sampling design. Different types of calibrated weights are obtained for different situations of available auxiliary information as well as for single and double system of weights. The two situations of auxiliary information considered are the totals of both the auxiliary variables pertaining to numerator and denominator is available for first phase sample separately and only the ratio of the totals of auxiliary variable is available for first phase sample. The expression for variance and estimator of variance of the estimators are developed for general sampling design as well as for SRSWOR as a special case. The performance of the different calibrated estimators is studied through a simulation study. It revealed that simple ratio estimator which does not make use of auxiliary information perform equally to calibrated estimators when the study variables are highly correlated but the correlation between study and auxiliary variable is very low.

But for fixed correlation value between study variable, increase in correlation between study and auxiliary variable efficiency of calibrated estimator gradually increases. Further, the calibrated estimator based on two systems of weights is found to perform better than the other calibrated estimators based on single weight.

**M.Sc. (Computer Application)**

**(i) Sanchita Naha**

**Chairperson: Dr. Sudeep Marwaha**

**Recommender System for Crop Variety Selection**

The internet is growing with tremendous speed and is developing rapidly regarding both content and users. This has led to an information overload problem and it is difficult to locate the right information at the right time. Recommender systems overcome this problem by guiding users through the big ocean of information. It uses the opinion of members of a community to help individuals to identify the information interesting to them or relevant to their needs. These systems use the similarity between the users' choices and the content of the items to form recommendation list for the user. However, these systems have not been exploited to that extent in agricultural domain. Therefore, an innovative idea that enables to integrate the recommendation technique with the word-of-mouth information exchange between farmers has been attempted. This study presents recommender system for crop variety selection with a focus on maize and a prototype system has been developed. The system creates a personal Farmer Agent for each registered farmer. The farmer agent stores the socio-economic profile of the farmer as well as his experiences of growing a crop variety. Java Agent Development Environment (JADE) has been used to develop these agents as well as to provide the message passing among these agents. A registered farmer can get the variety recommendation through its agent which in turn asks the recommendation from the peer farmer agents having the similar socio-economic profile. All the received recommendations are ranked and top five are shown to the requesting farmer. The system has been built on modular approach and facilitates integration of other complex recommendation algorithms. It also allows creating agents on distributed servers. The cold start problem has been tackled by registering the farmers selected for front line demonstration for maize as well as scientists who have conducted

experimental trials on the released varieties. The system has a capability to transfer agricultural technologies using both top-down as well as through peer to peer interaction approaches and will help in faster adoption of new crop varieties/ technologies.

(ii) **Linkon Kumar Saha**

**Chairperson: Dr. Alka Arora**

**Information Module on Integrated Pest Management for AGRIdaksh**

Integrated Pest Management (IPM) is the careful consideration of all available pest control techniques and subsequent integration of appropriate measures that discourage the development of pest populations and keep pesticides and other interventions to levels that are economically justified and reduce or minimize risks to human health and the environment. IPM emphasizes the growth of healthy crops with the least possible disruption to agro-ecosystems and encourages natural pest control mechanisms. AGRIdaksh is an online knowledge management tool developed at ICAR-IASRI which facilitates creation of expert system with the help of domain experts for different crops and has the capability to transfer location specific technologies and advice to the farmers efficiently and effectively. System has database of varieties, diseases and pest etc. With the increasing demand of IPM practices in agriculture, IPM module is developed and linked with AGRIdaksh for dissemination of information of IPM practices for different crops. System has been developed using web based three tier architecture and it provides information about diseases, pests and IPM practices to control them. Java Server Pages (JSP) technology has been used for programming the business logic and input forms developed using HyperText Markup Language (HTML) and validation done using java script. Database has been implemented using SQL Server 2008. Source code for developing user interfaces has been written using Netbeans 7.4 Integrated Development Environment (IDE). System has been tested using data of Tomato crop which is important vegetable crop in India. Data about IPM practices for tomato has been taken from the technical bulletin, IPM strategies for vegetables crops published from NCIPM. System provides information about different insects, weeds, diseases, nematodes of tomato crop and their corresponding IPM practices. This system also provides images for different disease and pests. These images are helpful for the identification of disease and pests.

**M.Sc. (Bioinformatics)**

(i) **Amit Kairi**

**Chairperson: Dr. AR Rao**

**Development of Information System on Buffalo Genome**

India has the largest herds of buffalo and cattle and produces highest amount of milk in the world. Among the livestock species, buffalo has remained an integral part of the Indian rural economy. With the advent of genome sequencing technologies, the whole-genome sequence assembly of Murrah breed of water buffalo has been done recently in India. Also, significant amount of information on different functional elements of various breeds of buffalo genome are available in public domain. However, the annotations of functional elements on the genome are not available. In addition, the 3D structures of buffalo proteins are not available and there exist no browser to visualize the genic information on buffalo genome. The nucleotide and protein sequence information was retrieved from NCBI and parsed. The 3D structures of proteins were predicted, validated, refined and stabilized. The parsed sequence information and protein's sequence and structure information has been imported into a database. An information system on buffalo genome with 3-tier architecture has been developed with MySQL database as bottom layer, PHP as server side application-middle layer, HTML, CSS and JavaScript at top layer as client side application layer. The developed information system contains 930 complete CDS, 1154 partial CDS, 656 Exon sequences, 237 Intron sequences, 1709 Mitochondrial DNAs, 73 sequences of Promoter Region and 67 sequences of UTR region. Out of 930 buffalo genes, 837 have been found to be mapped onto *Bubalus bubalis* (female Murrah breed). The developed genome browser shows that maximum number of genes have been distributed on chromosome 4 followed by chromosome 18 with 324 and 155 number of genes respectively. The results from the study also reveal that 837 out of 930 buffalo genes have been mapped onto *Bubalus bubalis* genome whereas, 561 buffalo genes are mapped onto *Bos taurus* genome. Further, 202 genes have been found to be predicted as orthologues between cattle and buffalo genomes. The developed information system provides several user-friendly facilities like search, filter, download, print, visualisation and browsing. The system on buffalo genome can be accessed at <http://cabingrid.res.in/bgjs/homepage.html>.

**(ii) Priya Prabhakar****Chairperson: Dr. Anil Rai****In Silico Study of Host-Pathogen Interaction under Mutation Effect on Blast Resistance Genes in Rice**

The effect of mutation on proteins of blast resistance gene was analysed by detecting and comparing the natural variations (SNPs and InDels) present in 30 alleles of *Pi-ta* gene in *Oryza* spp. *O. sativa indica*. Three-dimensional structure of *Pi-ta* proteins were predicted through I-TASSER software. 3D refine web server (<http://sysbio.mnet.missouri.edu/3Drefine/>) was used to bring the initial model closer to the native structure. The stereo chemical quality of the model was checked using the 'Protein Quality Assessment' parameter option of Discovery Studio. Quantitative structural evaluations were performed to find out the stability and disease response of *Pi-ta* alleles upon mutation. Average number of nucleotide difference between two sequences was found lower in *Oryza indica* in comparison with the nucleotide difference surveyed from *O. rufipogon*. InDel diversity per site ( $\Pi_i = 0.00061$ ) was found lower than nucleotide diversity per site ( $\Pi = 0.00255$ ) in the selected accessions of *Pi-ta* gene. More number of synonymous substitutions were observed in non-coding region. Susceptible *indica* cultivar C101A51 showed maximum number of InDels events in the gene. Most of the changes in secondary structure elements were observed in NBS-LRR region. More number of coils were found in LRR region in comparison to helix. The predicted *in silico* protein structure of the *Pi-ta* alleles was observed to be affected by mutation *i.e.* SNPs and InDels. Quantitative assessments of these structures showed differences in value of ASA, SFE and number of H-bonds. Normal mode analysis of modelled proteins showed differences in region of maximum atomic displacements between different alleles of *Pi-ta* gene. A total of 101 accessions of *Avr-Pita* proteins were found in NCBI from which 12 dominant effectors *Avr-pita* proteins and 8 recessive *Avr-pita* proteins were selected from 19 isolates of *M. oryzae* strain. All these sequences were not 100% similar. Value of SFE and number of H-bonds were less in recessive *Avr* proteins in comparison to dominant effector proteins. An approximate degree of flexibility for proteins was determined by secondary structure elements present in the structure. BAK40873.1 and BAK40874.1 contain more number of coils as compared to other structures which can lead to more degree of flexibility than others. CCD21951.1 contains least number of coils than

others, so it is most rigid structure. In normal mode analysis, region of maximum atomic displacements was found different in recessive and dominant effector proteins. In another experiment, direct interaction between proteins of *Pi-ta* alleles and their corresponding *Avr-pita* was observed by two methods. First method is interaction in gene-for-gene manner and second is *in silico* mutagenesis and interaction of polymorphic sites in the LRR region of R proteins. Maximum BE was observed in complex of BAF91347.1 and BAK40873.1. It also contained maximum number of hydrogen-bonds. Least BE was observed between docking complexes of *Pi-ta* proteins from susceptible *Oryza* cultivars and recessive *Avr* proteins. Mutation analysis of the polymorphic sites in the LRR region showed that mutability of these sites is different. The mean of the binding free energy change distribution over 19 mutations was found negative for 8 out of 11 sites. A very less correlation was found between mutations that increase stability and mutations that favour complex formation.

**(iii) Sayanti Guha Majumdar****Chairperson: Dr. AR Rao****Development of Epigenetic Database in Livestock Species**

Demand for livestock products is constantly increasing with the continuous population growth. To meet such demand it is essential to understand molecular mechanisms of livestock species. With the advent of new technologies, it has become possible to understand the underlying mechanisms present in the growth and development of important traits of livestock species. Epigenetics is an emerging field which deals with the study of mitotic and meiotic (or both) heritable changes in gene function that cannot be explained by changes in DNA sequence. Broadly, three epigenetic mechanisms, viz., DNA methylation, Histone modification and RNA interference (RNAi) occur in nature. However, the information related to the said epigenetic mechanisms in livestock species is not available at one place. Moreover, analysis of epigenetic information is required for improvement in production traits and controlling diseases in livestock. The gene and protein sequence information related to epigenetic mechanisms of livestock species was downloaded from NCBI, UCSC and CABin. Besides, the microRNA information of cattle and sheep was retrieved from miRBase. Subsequently, a tool known as "Sequence Manipulation Suit: CpG Islands" was used to obtain the probable methylation sites present in the 1k upstream region of 10,990

genes in cattle. The results reveal that the CpG islands are found in 8033 genes. In addition, the three dimensional structures of histone proteins of cow, sheep, goat, camel have been predicted, validated, refined and stabilized. Also, the probable genomic regions of histone proteins in buffalo were identified by using tBLASTn tool. The BLAST results were then parsed and kept in a suitable format to populate a database. In case of RNAi, the secondary and tertiary structures of microRNAs of cattle and sheep were predicted by RNAfold and RNAcomposer respectively. Since the miRNA information in buffalo species is not available, the genomic regions of the same were mapped by considering miRNAs of cattle as query sequences in BLASTn. For ready use of the parsed data by users, a web-based "Livestock Epigenetic Information System" has been developed with MySQL database as bottom layer, PHP as server side application-middle layer and HTML, CSS and JavaScript at top layer. The developed information system can be accessed at <http://bioinformatics.iasri.res.in/edil/>.

(iv) **Neeraj Budhlakoti**

**Chairperson: Dr. Anil Rai**

**Web Application for Classification of Proteins Responsible for Abiotic Stress in Cereals**

Abiotic stress severely limits plant growth and development as well as crop yield. Various proteins of the plants are responsible for regulation of these abiotic stresses. Therefore *in silico* prediction of function of an unknown protein is very important as this helps in regulation of related biological process of the plant for mitigation of adverse effects of abiotic stress. In order to predict function of different proteins numbers, *in silico* approaches are being followed but it was found that physicochemical properties plays very important role in determination of different functions of protein. Perl script has been written for calculating the physicochemical properties of unknown sequences instead of using ProtParam tool. This library of different physicochemical properties is used in this web application for calculating the physicochemical properties automatically for protein sequences which is provided by user as an input for prediction of function through this web server. Then this server calls the model for prediction separately for each abiotic stress which runs at backend. This server is capable to predict the function of sequences into five classes of abiotic stress. Predicting protein into a particular class does not ensure that it cannot be related to other stress. This web application filters out this

problem by predicting the protein sequences into all overlapping classes i.e. Heat, Cold, Drought, Salinity, ABA with corresponding accuracy of falling into particular classes. Presently this web application only predicts sequences which are related to cereals only. In future same approach can be extended to other crop also.

(v) **Purru Supriya**

**Chairperson: Dr. KV Bhat**

**Assembly, Annotation, Functional Classification of Transcriptomes and identification of Key Genes for Moisture Stress Tolerance in *Cucumis Melo***

Musk melon (*Cucumis melo* L., *Cucurbitaceae*) is an important fruit crop. It is considered to be the most variable species in the genus *Cucumis* and one of the most diverse among the cultivated vegetables. Moisture stress is one of the major restraining factors for its production. To minimize the yield losses caused by moisture stress, there is a need to identify the genes possessing stress tolerance. The main objective of present study was to identify key genes that play a major role in moisture stress tolerance by *de novo* assembly and annotation of musk melon transcriptome. Transcriptomic analyses of plant responses to stress are an effective way in which genes, pathways and processes responsible for plant stress tolerance can be identified. A high-throughput, SOLiD sequencing technology was employed to characterize the *de novo* transcriptome of musk melon. A total of 47,035,393 and 45,152,235 high quality unique reads for *cucumis melo* control sample and stress sample were assembled into 12859 and 13448 transcripts, respectively using CAP3, DNA STAR and CLC *de novo* assembly programs. Merging of assemblies by CAP3 resulted in larger and robust transcripts instead of using a single program alone. This *de novo* assembly of melon transcriptome from control and stress samples provides a rich source for gene identification. These transcripts were annotated with gene ontology (GO) terms. All the GO terms were classified into 37 functional groups including biological processes, cellular component and molecular function. Comparison of gene expression levels between control and stress transcriptomes by RNA-Seq mapping revealed that 122 stress responsive genes were commonly expressed in both the samples whereas 72 genes were highly up regulated in stress sample such as kinases, DREB genes, heat shock proteins, MYB transcription factors, Zinc-finger, and AP2 / ERF domain containing transcription factors. Among these, 4 genes are

involved in path ways such as plant-hormone signal transduction, protein processing in endoplasmic reticulum and Inositol phosphate metabolism. These selected genes will not only facilitate understanding of genetic basis of moisture stress response, but also accelerate genetic improvement through marker-assisted selection in musk melon.

### Certificate Course

#### Senior Certificate Course in Agricultural Statistics and Computing

Senior Certificate Course in Agricultural Statistics and Computing was organized for the benefit of research workers engaged in handling statistical data collection, processing, interpretation and employed in research Institutes of the Council, State Agricultural Universities, State Government Departments, and foreign countries including SAARC countries. The main objective of the course was to train the participants in the use of latest statistical techniques as well as use of computers and software packages. The course was organized during the period June 17 to Nov. 22, 2014. The Course comprised of two

independent modules of three months duration each. Module – I was organized during June 17 to August 19, 2014 and Module-II was organized during September 2 to November 22, 2014. The courses covered under both the modules are as given:

Topic	Instructor
<b>Module – I</b>	
Statistical Methods	Dr. Prawin Arya, Dr. Prabina Kumar Meher and Dr. Arpan Bhowmik
Official Agricultural Statistics	Dr. A K Gupta
Use of Computers in Agricultural Research	Dr. Amrit Kumar Pal, Md. Wasi Alam, Sh. Pal Singh and Sh. Upendra Kumar Pradhan
<b>Module – II</b>	
Sampling Techniques	Dr. Prachi Misra Sahoo and Dr. Kaustav Aditya
Econometrics and Forecasting Techniques	Dr. Prawin Arya and Md. Wasi Alam
Design of Experiments	Dr. Eldho Varghese and Dr. Arpan Bhowmik

Category	No. of Training Programmes	No. of Participants
CAFT	6	122
NAIP	13	403
Resource Generation	4	67
Others	2	44
<b>Total</b>	<b>25</b>	<b>636</b>

#### Details of Training Programmes Organised

S. No.	Title	Venue	Date	Sponsored by	No. of Participants
<b>Centre of Advanced Faculty Training</b>					
1.	Forecast Modelling Analytics in Crops Coordinator : Dr. Prawin Arya Co-Cordinator : Dr. Sanjeev Panwar	IASRI, New Delhi	30 May - 19 June 2014	Education Division ICAR	23
2.	Agricultural Web Applications Development using Content Management Tools Coordinator : Dr. Mukesh Kumar Co-Cordinator : Dr. N Srinivasa Rao	IASRI, New Delhi	24 September - 14 October, 2014	Education Division ICAR	16
3.	Recent Advances in Survey Design and Analysis of Survey Data using Statistical Software Coordinator : Dr. Hukum Chandra Co-Cordinator : Dr. Kaustav Aditya	IASRI, New Delhi	28 October - 17 November, 2014	Education Division ICAR	20
4.	Advances in Omics Data Analysis: Learning by Examples Coordinator : Sh. Sanjeev Kumar Co-Cordinator : Dr. DC Mishra	IASRI, New Delhi	03-23 December 2014	Education Division ICAR	22

5.	Advanced Statistical Techniques in Horticulture Science Research Coordinator : Dr. Sukanta Dash Co-Cordinator : Dr. Susheel Kumar Sarkar	IASRI, Delhi	New	02-22 January 2015	Education Division ICAR	15
6.	Recent Advances in Statistical Genetics Coordinator : Dr. AK Paul Co-Cordinator : Dr. RK Paul	IASRI, Delhi	New	03-23 February 2015	Education Division ICAR	26
<b>National Agricultural Innovative Project</b>						
7.	Basic Training on Discovery Studio Coordinators : Dr. MA Iquebal : Dr. Sarika	IASRI, Delhi	New	01-03 May 2014	NAIP	20
8.	High Performance Computing with the collaboration of C-DAC, Pune Coordinator : Sh. KK Chaturvedi	IASRI, Delhi	New	12-17 May 2014	NAIP	20
9.	Oracle Database 11g: Administration Workshop Coordinator : Sh. KK Chaturvedi	KLJ Solution Ltd. Motinagar, New Delhi		19-23 May 2014	NAIP	16
10.	Six Modules of SAS Software Coordinator : Md. Samir Farooqi <ul style="list-style-type: none"> <li>• SAS Data Integration Studio: Fast Track</li> <li>• Data Flux Data Management Studio: Fast Track</li> <li>• Text Analytics Using SAS Text Miner</li> <li>• Managing SAS Analytical Models Using SAS Model Manager</li> <li>• Grid Computing (SAS Enterprise Scheduling with Platform Suite for SAS)</li> <li>• SAS Content Categorization Studio: Building Models</li> </ul>	IASRI, Delhi	New	26 May - 19 June 2014 26-30 May 2014 02-06 June 2014 09-10 June 2014 11-13 June 2014 16-17 June 2014 18-19 June 2014.	NAIP	20
11.	Advance Training on Discovery Studio Software Coordinators : Dr. Sarika : Dr. MA Iquebal	IASRI, Delhi	New	17-21 June 2014	NAIP	20
12.	Post ICAR-ERP Implementation Coordinator: Dr. AK Choubey	IGFRI, Jhansi		21-22 July, 2014	NAIP	10
13.	Knowledge Enhancement Session or MIS/FMS Solution by IBM Coordinator : Dr. NS Rao	IASRI, Delhi NAARM, Hyderabad	New	22-24 December 2014 10-11 October, 2014	NAIP NAIP	28 50
14.	Post Go-Live Knowledge Enhancement Session for MIS/FMS Solution Cordinator : Dr. NS Rao Co-Cordinator : Dr. AK Choubey	IASRI, Delhi	New	01-05 August 2014	NAIP	67
	Cordinator : Dr. Anshu Bhardwaj Co-Cordinator : Dr. Alka Arora			August 20- 23 2014		46
	Cordinator : Dr. Alka Arora Co-Cordinator : Dr. Sudeep			15-18 September 2014		16
	Cordinator : Dr. Anshu Bhardwaj Co-Cordinator : Dr. Mukesh Kumar			23-26 September 2014		35
	Cordinator : Dr. AK Choubey Co-Cordinator : Dr. Alka Arora			29-30 September 2014		27
	Cordinator : Dr. Mukesh Kumar Co-Cordinator : Dr. AK Choubey			22-24 December 2014		28

Resource Generation					
15.	Data Analysis and Interpretation for ISS Probationers of XXXV Batch Course Director : Dr. Rajender Parsad Co- Course Director : Dr. Eldho Varghese	IASRI, New Delhi	05-23 May 2014	Central Statistics Office, Ministry of Statistics and Programme Implementation	21
16.	A Refresher Training Programme on Statistical Techniques Course Director : Dr. Hukum Chandra	IASRI, New Delhi	08-12 September, 2014	Livestock Department Government of Chhattisgarh	20
17.	International Training Programme on Importance of Statistical and Experimental Designs, Data Analysis and Biometrical Techniques in Agriculture Research Course Director : Dr. Rajender Parsad Co- Course Directors : Dr. Eldho Varghese Dr. Sukanta Dash	IASRI, New Delhi	17 November, 2014 -07 February, 2015	Ministry of Agriculture, Irrigation and Livestock (MAIL), Afghanistan	16
18.	International Training Programme on Applications of Remote Sensing and GIS in Agricultural Surveys Course Director : Dr. Prachi Misra Sahoo Co- Course Director : Dr. Tauqueer Ahmad	IASRI, New Delhi	12 February - 04 March 2015	African-Asian Rural Development Organization (AARDO)	10
Others					
19.	Office Automation using Oracle ERP for Technical Personnels of ICAR Coordinator : Dr. Sudeep Co- Coordinator : Dr. Anshu Bhardwaj	IASRI, New Delhi	09-13 March 2015	ICAR	22
20.	Office Automation using Oracle ERP for Technical Personnels of ICAR Coordinator : Dr. Alka Arora Co- Coordinator : Dr. N Srinivasa Rao	IASRI, New Delhi	16-20 March 2015	ICAR	22

### Faculty Members of PG School, IARI In Agricultural Statistics

S. No.	Name	Year of Induction
1.	Dr. UC Sud, Director	1995
2.	Dr. VK Gupta, National Professor	1984
3.	Dr. Seema Jaggi, Professor (Agricultural Statistics) from July 23, 2014	1995
4.	Dr. Anil Rai, Professor (Bioinformatics) and Head (Centre for Agricultural Bioinformatics)	1995
5.	Dr. KN Singh, Principal Scientist and Head (Forecasting and Agricultural System Modelling)	2011
6.	Dr. Rajender Parsad, Principal Scientist and Professor Agricultural Statistics till July 22, 2014	1995
7.	Sh. SD Wahi, Principal Scientist	1987
8.	Dr. KK Tyagi, Principal Scientist (Retired on September 30, 2014)	1995
9.	Dr. Lal Mohan Bhar, Principal Scientist	1998
10.	Dr. Amrit Kumar Paul, Principal Scientist	1998
11.	Dr. Tauqueer Ahmad, Principal Scientist	1998
12.	Dr. AR Rao, Principal Scientist	1998

S. No.	Name	Year of Induction
13.	Dr. Girish Kumar Jha, Principal Scientist (at IARI)	1999
14.	Dr. Cini Varghese, Principal Scientist	2000
15.	Dr. Himadri Ghosh, Principal Scientist	2004
16.	Dr. Hukum Chandra, National Fellow	2003
17.	Dr. Anil Kumar, Principal Scientist	2010
18.	Dr. Prachi Misra Sahoo, Senior Scientist	2002
19.	Dr. Amrender Kumar, Senior Scientist (at IARI)	2003
20.	Md. Wasi Alam, Scientist	2003
21.	Dr. Prawin Arya, Senior Scientist	2003
22.	Dr. Sanjeev Panwar, Scientist	2011
23.	Dr. Ranjit Kumar Paul, Scientist	2011
24.	Dr. Mir Asif Iqbal, Scientist	2011
25.	Dr. BN Mandal, Scientist	2011
26.	Dr. Susheel Kumar Sarkar, Scientist	2011
27.	Dr. Eldho Varghese, Scientist	2011
28.	Dr. Kaustav Aditya, Scientist	2012
29.	Dr. Bishal Gurung, Scientist	2013
30.	Dr. Sukanta Dash, Scientist	2013
31.	Dr. Arpan Bhowmik, Scientist	2014

### Faculty Members of PG School, IARI in Computer Application

S. No.	Name	Year of Induction
1.	Dr. PK Malhotra, Professor (Computer Application) (Retired on September 30, 2014)	1991
2.	Dr. Seema Jaggi, Professor (Computer Application) from October 1, 2014	
3.	Dr. Anjani Kumar Choubey, Head (Computer Applications)	2014
4.	Dr. Alka Arora, Senior Scientist	2001
5.	Dr. Sudeep, Senior Scientist	2002
6.	Ms. Shashi Dahiya, Scientist	2001
7.	Md. Samir Farooqi, Scientist	2001
8.	Sh. KK Chaturvedi, Scientist	2002
9.	Ms. Anu Sharma, Scientist	2004
10.	Sh. SN Islam, Scientist	2004
11.	Sh. SB Lal, Scientist	2004
12.	Dr. Anshu Bhardwaj, Scientist	2004
13.	Dr. Sangeeta Ahuja, Scientist	2002
14.	Dr. Rajni Jain, Principal Scientist (at NIAP)	2007
15.	Sh. Pal Singh, Scientist	2010
16.	Dr. Mukesh Kumar, Senior Scientist	2014
17.	Dr. N Srinivasa Rao, Senior Scientist	2014
18.	Dr. AK Mishra, Senior Scientist	2014

### Faculty Members of PG School, IARI in Bioinformatics

S. No.	Name	Year of Induction
1.	Dr. Anil Rai, Professor (Bioinformatics) and Head (Centre for Agricultural Bioinformatics)	2010
2.	Dr. KC Bansal, Director, NBPGR	2010
3.	Dr. Rajender Parsad, Principal Scientist	2010
4.	Dr. Seema Jaggi, Principal Scientist and Head (Off.) Design of Experiments	2010
5.	Dr. AR Rao, Principal Scientist	2010
6.	Dr. Sudeep, Senior Scientist	2010
7.	Sh. SB Lal, Scientist	2010
8.	Md. Samir Farooqi, Scientist	2010
9.	Ms. Anu Sharma, Scientist	2010
10.	Dr. TR Sharma, Director, NRCPB	2010

11.	Dr. Kishore Gaikwad, Senior Scientist	2010
12.	Dr. T Napoleon, Senior Scientist	2010
13.	Dr. PK Singh, Senior Scientist	2010
14.	Dr. KV Bhat, Principal Scientist	2010
15.	Dr. SS Marla, Principal Scientist	2010
16.	Dr. Sunil Archak, Senior Scientist	2010
17.	Dr. DC Mishra, Scientist	2010
18.	Dr. Sarika, Scientist	2010
19.	Sh. Sanjeev Kumar, Scientist	2010
20.	Dr. AK Mishra, Senior Scientist	2010
21.	Dr. Mir Asif Iquebal, Scientist	2013
22.	Dr. Monendra Grover, Senior Scientist	2013
23.	Dr. UB Angadi, Senior Scientist	2014
24.	Sh. KK Chaturvedi, Scientist	2014

### Research Fellowships

During this period, 27 Ph.D. and 41 M.Sc. students received research fellowship. 22 Ph.D. students received IASRI fellowship at the rate of Rs.13,125/- p.m. in addition to Rs 10,000/- per annum as the contingent grant. 01 Ph.D. student received ICAR SRF Scholarship @12,000/- p.m. in addition to Rs.10,000/- per annum as contingent grant. There was 01 departmental candidate.

03 Ph.D. students received DST-Inspire scholarship @ 18,000/-+30% HRA P.M. in addition to Rs.20,000/- per annum as contingent grant.

13 M.Sc. students received ICAR Junior Research Fellowship at the rate of Rs. 8640 /- p.m. in addition to Rs. 6000/- per annum as the contingent grant and 25 M.Sc. students received IASRI fellowship at the rate of Rs.7560 /- p.m. in addition to Rs. 6000 /- per annum as the contingent grant. There are 03 foreign students who have not received the fellowship from the institute.

### Strengthening of Post Graduate Programme

On the basis of funds received from PG School, IARI, the teaching program in the discipline of Agricultural Statistics, Computer Application and Bioinformatics were strengthened.

### Management System PG School, IARI

PG School, IARI Management System developed at IASRI is helping in achieving the objective of giving online access to various resources and making the PG programme paperless. The system

is available to students, faculty members, scientists and administrative staff of PG School, IARI. It has following sub modules:

- Courses Management
- Student Management
- Faculty Management
- Administration Management
- E-Learning

The system is being updated regularly by adding new features.

### 53<sup>rd</sup> Convocation of Post Graduate School IARI

53<sup>rd</sup> Convocation of Post Graduate School IARI was held during 16-20 February 2015. A total of 18

students in the disciplines of Agricultural Statistics, Computer Application and Bioinformatics have been awarded with Ph.D. / M.Sc. degrees. The discipline-wise number of students who got degrees are as follows:

- 5 Ph.D and 6 M.Sc. (Agricultural Statistics)
- 2 M.Sc. (Computer Application)
- 5 M.Sc. (Bioinformatics)

A session on 'Significant Educational Achievements 2014-15' was also organized in which Dr. Seema Jaggi, Professor (Agricultural Statistics and Computer Application) and Dr. Anil Rai, Professor (Bioinformatics) made presentation of their respective disciplines.



### Courses taught during the Academic Year 2013-14 in Agricultural Statistics

Trimester - III				
Code	Course Title	Credits		Instructors
		L	P	
PGS 504	Basic Statistical Methods in Agriculture	2	1	Susheel Kumar Sarkar, Sarika, Kaustav Aditya
AS 503	Basic Sampling and Non-parametric Methods	2	1	KK Tyagi, Anil Rai, Wasi Alam
AS 563	Statistical Inference	4	1	KN Singh, LM Bhar, Hukum Chandra
AS 564	Design of Experiments	3	1	Seema Jaggi, VK Gupta, Rajender Parsad
AS 566	Statistical Genetics	3	1	SD Wahi, Amrit Kumar Paul
AS 662	Advanced Design for Multi-factor Experiments	2	1	Rajender Parsad, Eldho Varghese, Sukanta Dash
AS 664	Inferential Aspects of Survey Sampling and Analysis of Survey Data	2	1	UC Sud, Hukum Chandra
AS 667	Forecasting Techniques	1	1	Amrender Kumar, Wasi Alam
AS 691	Seminar	1	0	Kanchan Sinha

### Courses taught during the Academic Year 2014-15 in Agricultural Statistics

Trimester - I				
Code	Course Title	Credits		Instructors
		L	P	
PGS 504	Basic Statistical Methods in Agriculture	2	1	Eldho Varghese, AK Gupta, Upendra Pradhan
AS 501	Basic Statistical Methods	2	1	Mir Asif Iquebal, Kaustav Aditya
AS 550	Mathematical Methods	4	0	Cini Varghese, Himadri Ghosh
AS 560	Probability Theory	2	0	KN Singh
AS 561	Statistical Methods	2	1	Seema Jaggi, RK Paul, Eldho Varghese
AS 567	Applied Multivariate Analysis	2	1	AR Rao, Bishal Gurung
AS 568	Econometrics	2	1	Prawin Arya, GK Jha
AS 569	Planning of Surveys/Experiments	2	1	UC Sud, KK Tyagi, BN Mandal
AS 572	Statistical Quality Control	2	0	Wasi Alam, Kanchan Sinha
AS 600	Advanced Design of Experiments	1	1	Rajender Parsad, Cini Varghese
AS 601	Advanced Sampling Techniques	1	1	Hukum Chandra, Prachi Misra Sahoo
AS 602	Advanced Statistical Genetics	1	1	SD Wahi, AK Paul
AS 603	Regression Analysis	1	1	LM Bhar, RK Paul
AS 604	Linear Models	2	0	Rajender Parsad, VK Gupta
AS 606	Optimization Techniques	1	1	Amrender Kumar, RK Paul
AS 691	Seminar	1	0	Bishal Gurung
Trimester - II				
Code	Course Title	Credits		Instructors
		L	P	
PGS 504	Basic Statistical Methods in Agriculture	2	1	Amrit Kumar Paul, Eldho Varghese, Arpan Bhowmik
AS 502	Basic Design of Experiments	2	1	Susheel Kumar Sarkar, Sukanta Dash
AS 551	Mathematical Methods in Statistics	4	0	Cini Varghese, Sukanta Dash, Samrendra Das
AS 562	Advanced Statistical Methods	2	1	Seema Jaggi, RK Paul, Arpan Bhowmik
AS 565	Sampling Techniques	3	1	Tauqueer Ahmad, Prachi Misra Sahoo, Kaustav Aditya
AS 570	Statistical Modeling	2	1	RK Paul, Bishal Gurung
AS 571	Bioinformatics	3	1	AR Rao, Samrendra Das
AS 573	Demography	2	0	Bishal Gurung, AK Gupta
AS 605	Advanced Statistical Inference	1	1	KN Singh, LM Bhar
AS 607	Stochastic Process	3	0	Himadri Ghosh, Kanchan Sinha
AS 661	Advanced Designs for Single Factor Experiments	2	1	LM Bhar, VK Gupta
AS 663	Advanced Theory of Sample Surveys	2	1	Hukum Chandra, Tauqueer Ahmad
AS 691	Seminar	1	0	Sanjeev Panwar

**Courses taught during the Academic Year 2013-14 in Computer Application**

Trimester - III				
Code	Course Title	Credits		Instructors
		L	P	
CA 503	Statistical Computing in Agriculture	1	2	Rajender Parsad, RK Paul, Sukanta Dash
CA 563	Operating System	2	1	Yogesh Gautam, N Srinivasa Rao
CA 567	Computer Networks	2	1	SN Islam, Mukesh Kumar
CA 568	Software Engineering	2	0	AK Choubey
CA 571	Modeling and Simulation	2	1	PK Malhotra
CA 613	Artificial Neural Networks	2	1	Anshu Bhardwaj, GK Jha
CA 614	Knowledge Database Systems for Semantic Web	2	1	Sudeep
CA 691	Seminar	1	0	PK Malhotra

**Courses taught during the Academic Year 2014-15 in Computer Application**

Trimester - I				
Code	Course Title	Credits		Instructors
		L	P	
CA 502	Introduction to Computer Application	1	1	SN Islam, Samir Farooqi
CA 551	Mathematical Foundations in Computer Application	4	0	Sukanta Dash, Samrendra Das
CA 552	Computer Oriented Numerical Methods	2	1	Pal Singh, Upendra Pradhan
CA 560	Computer Organization and Architecture	3	0	N Srinivasa Rao
CA 561/ BI 505	Principles of Computer Programming	2	1	SB Lal, KK Chaturvedi
CA 565	Compiler Construction	2	1	Sangeeta Ahuja
CA 569	Web Technologies and Applications	2	1	Alka Arora, SB Lal
CA 575	Artificial Intelligence	2	1	Rajni Jain, Sudeep
CA 691	Seminar	1	0	SN Islam
Trimester - II				
Code	Course Title	Credits		Instructors
		L	P	
CA 501	Computer Fundamentals and Programming	3	1	Pal Singh, Sangeeta Ahuja
CA 562	Object Oriented Analysis and Design	2	1	Sudeep, N Srinivasa Rao
CA 564	Data Structures and Algorithms	2	1	AR Rao
CA 566 /BI 507	Data Base Management System	2	2	SB Lal, Mukesh Kumar
CA 572	GIS and Remote Sensing Techniques	2	1	Prachi Misra Sahoo, Anshu Bhardwaj
CA 573	Data Warehousing	2	1	Samir Farooqi, KK Chaturvedi
CA 577	Data Mining and Soft Computing	2	1	Alka Arora, Anshu Bhardwaj
CA 691	Seminar	1	0	Pal Singh

### Courses taught during the Academic Year 2013-14 in Bioinformatics

Trimester - III				
Code	Course Title	Credits		Instructors
		L	P	
BI 510	Biological Databases and Data Analysis	2	1	Sanjeev Kumar, Samir Farooqi, MA Iquebal, MNV Parsad Gajula
BI 511	RNA/Protein Structure Prediction and Molecular Modeling	1	2	Sarika, Soma S Marla, Anil Rai
BI 512/ AS 608	Advanced Bioinformatics	2	1	AR Rao, M Grover, DC Mishra
BI 691	Seminar	1	0	Mir Asif Iquebal

### Courses taught during the Academic Year 2014-15 in Bioinformatics

Trimester - I				
Code	Course Title	Credits		Instructors
		L	P	
BI 501/ MBB 509 /GP 540	Introduction to Bioinformatics	2	1	AR Rao, TR Sharma, K Gaiwad
BI 503	Mathematical Foundation in Computer Application	4	0	NK Sharma, Sukanta Dash
BI 505	Principles of Computer Programming	2	1	SB Lal, KK Chaturvedi
BI 510 – 2014	Principles of Biotechnology	4	0	Ramcharan Bhattacharya
BI 511 – 2014	Basic Biochemistry	4	1	Raj Deo Rai
BI 524	Tools and Techniques for Biological Data Mining	2	1	Sanjeev Kumar, MA Iquebal
BI 525	Advanced Programming in Bioinformatics	2	1	SB Lal, KK Chaturvedi
BI 601 - 2014	Genome Assembly and Annotation	1	2	Sanjeev Kumar, DC Mishra
BI 602	Bimolecular Modeling & Simulation	2	1	UB Angadi, Sudhir Srivastava
BI 691	Seminar	1	0	Sarika
Trimester - II				
Code	Course Title	Credits		Instructors
		L	P	
BI 506 – 2014	Computational Genomics	3	1	Mir Asif Iquebal, DC Mishra, Sarika
BI 507/ CA 566	Database Management System	2	2	SB Lal, Mukesh Kumar
BI 508	Computer Applications in Bioinformatics	2	1	SB Lal, KK Chaturvedi
BI 604 – 2014	Computational Techniques of Transcriptomics and Metabolomics	1	1	AR Rao, Md. Samir Farooqi
BI 642 – 2014	Genome Wide Association Study	2	1	KV Bhatt, Sunil Archak, T Napoleon
BI 691	Seminar	1	0	Md. Samir Farooqi

## Board of Studies for Academic Year 2014-15

### Agricultural Statistics

1.	Dr. Seema Jaggi, Professor (Agricultural Statistics)	Chairperson
2.	Dr. UC Sud, Director	Member (Ex-officio)
3.	Dr. KN Singh, Head (F&ASM)	Member
4.	Dr. Cini Varghese, Senior Scientist	Member
5.	Sh. Wasi Alam, Scientist	Member Secretary
6.	Sh. Pratyush Dasgupta, Student	Students' Representative

### Computer Application

1.	Dr. P.K. Malhotra, Professor (Computer Application)	Chairman (till September 30, 2014)
2.	Dr. Seema Jaggi, Professor (Computer Application)	Chairperson (since October 1, 2014)
3.	Dr. UC Sud, Director	Member (Ex-officio)
4.	Dr. AK Choubey, Head, (CA)	Member
5.	Dr. Rajni Jain, Principal Scientist	Member
6.	Sh. KK Chaturvedi, Scientist	Member
7.	Dr. Alka Arora, Senior Scientist	Member Secretary
8.	Sh. Chandan Kumar Deb, Student	Students' Representative

### Bioinformatics

1.	Dr. Anil Rai, Professor (Bioinformatics)	Chairman
2.	Dr. UC Sud, Director	Member (Ex-officio)
3.	Dr. AR Rao, Principal Scientist	Member
4.	Dr. SS Marla, Principal Scientist	Member
5.	Dr. UB Angadi, Senior Scientist	Member
6.	Dr. Kishore Gaikward, Principal Scientist	Member

7.	Dr. MA Iqbal, Scientist	Member Secretary
8.	Students' Representative	Md. Asif Khan, Student

## Central Examination Committee for Academic Year 2014-15

### Agricultural Statistics

1.	Dr. UC Sud, Director
2.	Dr. Seema Jaggi, Professor (Agricultural Statistics)
3.	Dr. Tauqueer Ahmad, Principal Scientist
4.	Dr. LM Bhar, Principal Scientist and Head (Statistical Genetics)
5.	Dr. AR Rao, Principal Scientist
6.	Dr. Himadri Ghosh, Principal Scientist

### Computer Application

1.	Dr. UC Sud, Director
2.	Dr. P.K. Malhotra, Professor (Computer Application) Till September 30, 2014 Dr. Seema Jaggi, Professor (Computer Application) w.e.f. October 1, 2014
3.	Dr. Rajni Jain, Principal Scientist
4.	Dr. Sudeep, Senior Scientist
5.	Dr. Alka Arora, Senior Scientist
6.	Sh. KK Chaturvedi, Scientist
7.	Sh. SB Lal, Scientist
8.	Dr. Tauqueer Ahmad, Principal Scientist

### Bioinformatics

1.	Dr. UC Sud, Director
2.	Dr. Anil Rai, Professor (Bioinformatics)
3.	Dr. AR Rao, Principal Scientist
4.	Dr. KV Bhatt, Principal Scientist
5.	Dr. Kishore Gaikwad, Senior Scientist
6.	Dr. UB Angadi, Senior Scientist