



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 since 2014-15. 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.

DISSERTATIONS APPROVED

Ph.D. (Agricultural Statistics)

- i) **Sankalp Ojha**
Chairperson: Dr. LM Bhar

Outliers in Designed Experiments with Correlated Errors

In designed experiments, the assumption of independence of observations gets violated because of various types of dependence among the observations within a block viz. autoregressive, moving average type and equi-correlation. Also the departures from the basic assumptions may take place in presence of disturbances like outlier(s). In the present study an attempt has been made to tackle outliers in block designs with correlated errors. Mainly, Cook-statistic and AP statistic are developed in general for any t outliers. Simplified expressions are obtained for the case of a single outlier and the case of two outliers. Two types of correlation structures in each block have been considered. One is auto-regressive [AR(1)] and the other one is equi-correlation structure. Developed statistics are illustrated with real experimental data. Tackling of multiple outliers is very difficult owing to the presence of masking. Following the logic used in linear regression model, two methods have been developed for detecting outliers in presence of masking. One method is based on the eigenvalues of a well defined influence matrix and the other one is based on conditional Cook-statistic. Both the methods

are also illustrated with real experimental data by considering the above mentioned two correlation structures. Another way of tackling outliers is to adopt a design that is insensitive to the presence of outliers. Such designs are called robust designs. In the present study, a robustness criterion has been proposed for block designs with correlated errors. Block designs for one-way elimination of heterogeneity that are robust by this criterion have been identified. However, only equi-correlation structure in each block has been considered for identifying the robust designs.

ii) **Anindita Datta**

Chairperson: Dr. Seema Jaggi

Generalized Row-Column Designs for Single and Multi-Factor Experiments

In field and animal experiments, where there are two sources of variation in experimental units that may influence the response variable, row-column designs are used. Most of the row-column designs developed in the literature have only one unit corresponding to the intersection of row and column. However, for the instances when the number of treatments is large with limited experimental resources, Generalized Row-Column (GRC) designs are used where there is more than one unit in each row-column intersection. The GRC designs developed in the literature are to study all possible pair-wise treatment comparisons. There may arise experimental situations where it is desired to compare treatments belonging to two disjoint sets and the interest is to estimate the contrasts pertaining to treatments from different sets with as high precision as possible. Balanced Bipartite Generalized Row-Column (BBP-GRC) designs have been defined and series of BBP-GRC designs have been developed in which the contrast of first set versus second set of treatments is estimated more precisely. The presence of missing observations, outliers in the data, etc. are some of the disturbances that may occur during experimentation. These disturbances may lead to less precise comparisons among treatments. Robustness of different classes of GRC designs against missing of one or more observations has been investigated. It is found that the efficiency is quite high (more than 90%) for most of the designs and the designs

are robust and there is a decreasing trend in efficiency with increase in number of missing observations. The GRC designs developed in the literature are mostly for single factor experiments. Situations may arise wherein the experiment consist of more than one factor with each factor having more than one levels. Generalized confounded row-column (GCRC) designs, generalized partially confounded row-column (GPCRC) designs and fractional GCRC designs have been developed which ensure that all lower order interactions including main effects are estimable. For easy accessibility of GRC designs, a web solution named WebGRC has been developed that provides the online generation of randomized layout of these designs along with an online catalogue within a permissible range.

iii) **Ram Kumar Choudhary**

Chairperson: Dr. AR Rao

Multi-Location Trials and Genomic Data Analysis in Perennial Crops Exhibiting Bienniality

Most of the perennial fruit crops, like mango exhibit biennial rhythm in fruiting, i.e. it bears heavy fruiting in one year called 'on' year and less or no fruiting in the next year called 'off' year. Due to bienniality, growers are facing economic loss during 'off' year with poor yield or no yields and selling of heavy yield at low price during 'on' year due to oversupply in the market. Detection and quantification of bienniality is important to assess the amount of risk. There is a need to select genotypes which can bear fruiting consistently over the years or select the genotypes after eliminating bienniality through proper treatment. Multi-Location Trials (MLTs) are being conducted for performance testing of the genotypes over environments. However, the perennial crops which exhibit biennial rhythm may mislead the selection of genotypes unless the bienniality is removed through suitable statistical procedures. Besides, some of the observations of MLTs data are missing due to disease and pest attack, adding or dropping of genotypes from year to year, bad weather etc. This leads to a situation involving incomplete genotype x environment data matrix. Identification of superior genotypes remains a challenging task in the presence of bienniality under complete/

incomplete genotype × environment data situations that too when trials are conducted over years. The AMMI model which is widely used model to study stability of genotypes for selection may not be suitable to deal with in the presence of bienniality. Also, there is a need to device procedures to handle the incomplete data situation for the selection of genotypes in presence of bienniality. In this study, a moving average approach has been adopted to eliminate bienniality factor in the AMMI model. In order to show the effect of bienniality on selection of genotypes, the correlations between ranks of genotypes assigned based on the performance of yield, stability variance and simultaneous selection indices prior to elimination and after elimination of bienniality were estimated. It was found that the estimated correlations have deviated from unity due to the effect of bienniality. The results have been verified through simulation and assessed the changes in genotype ranking as well as in the proportion of genotypes selected in the top 50% of the total genotypes under real data situation. Also, the biennial bearing tendency in mango for the trait “*number of fruits per tree*” has been confirmed in the real data collected from AICRP-STF, Lucknow. The ‘Mallika’ genotype of mango consistently exhibited the bienniality over locations followed by Dashehari and Kishan bhog genotypes. Further, the trait was found to be moderate to highly repeatable. The results also reveal that the effect of bienniality increased on the rank correlation of genotypes evaluated on the basis of simultaneous selection indices with increased weightage on stability component. Thus, selecting genotypes in MLTs in the presence of bienniality is recommended after eliminating the bienniality from the data. The application of EM-AMMI procedure in the presence of bienniality was found to be more robust than FITCON against increasing rate of missing observations. The results reveal that EM-AMMI can be safely used up to 10% missing observations. With the advent of next generation sequencing technology huge amount of genomic data are available in public domain. Since, mango proteomics has not been fully explored, the genes responsible for bienniality need to be identified through omics approaches. Twenty nine *putative* genes responsible for mango

bienniality have been identified by *in silico* methods and a database consisting of genic/genomic information has been developed. Moreover, ‘Arginine’ amino acid residue has been identified as a key conserved residue possibly responsible for bienniality in mango. The phylogenetic analysis revealed that most of the bienniality responsible genes of mango have shown close relationship with that of apple. The three dimensional structures of bienniality responsible genes were predicted from functionality view point. A new distance measure has also been proposed to compare any two 3D protein structures.

M.Sc. (Agricultural Statistics)

- i) **Sushil Kumar**
Chairperson: Dr. Hukum Chandra

Some Investigations on Small Area Estimation of Proportions using Unit Level Survey Data

Sample surveys are usually planned to produce reliable direct estimates for larger domains or areas and are not appropriate to produce small area statistics due to small sample sizes. Small area estimation (SAE) techniques are used to produce reliable estimates for such areas or domains. Binary data are often of interest in surveys. When small area estimates are required for such binary data, use of standard estimation methods based on linear mixed models becomes problematic. In this case, generalized linear mixed model with logit link function is often used in SAE and the empirical best predictor (EBP) approach is widely used for the estimation of small area proportions under this model and proven to be efficient as well. However, the EBP requires the availability of population level auxiliary data. Sometimes population level auxiliary data is either not available or not consistent with the survey data. As a result, EBP approach cannot be used. We propose three small area predictors for population proportion under generalized linear mixed model with logit link function based on availability of level of auxiliary information. The performance of proposed method of SAE was evaluated through simulation studies. In the simulation studies, both generated data under the model and the real data from the National Sample Survey Office survey was used. The

results clearly indicated that the developed method of SAE works well for generating the estimates of small area proportions and represents a practical alternative to the EBP when population level auxiliary data is known.

ii) **Sumeet Saurav**
Chairperson: Dr. Cini Varghese

Statistical Design for Multi-Session Sensory Trials in Food and Nutrition

Sensory trials are included as an integral part of food and nutrition experiments involving agricultural/animal produce to demonstrate some sensory fact. In order to draw definite conclusion from the study, it is important to eliminate or minimize all sources of error, recognize and control all factors that may influence or interfere with the result. In addition to the potential sources associated with the preparation of the test products, there is variability due to measurement or assessment process, order effects and carryover effects. In sensory trials involving large number of products, there are mainly two operational constraints that limit the choice of experimental design. On one hand, the assessor constraint sets a maximum number of products that an assessor can evaluate within a session before onset of sensory fatigue. On the other hand, preparation constraint limits the number of products that can be prepared for a given session without loss of experimental control. Therefore, it is many times necessary to split sensory evaluations into sessions. Three general methods to construct designs for multi-session sensory trials with/without carry over effects are developed. Sometimes, designs are required that provide higher precision estimates for the crucial product comparisons, at the expense of the comparisons of lesser interest, which will be estimated with lower precision. One situation where there is special interest in a subset of product contrasts arises when control products are included in the trial. A control product may also be helpful to the panel as it provides a calibration standard, which provides a basis for comparison of results across studies. Thus, three series of treatment vs. control designs for multi-session trials are obtained to deal with such situations. Also, SAS programs are developed to calculate variances and efficiency factors of various designs obtained.

iii) **Shyamsundar Parui**
Chairperson: Dr. Rajender Parsad

Construction of Latin Hypercube Designs

Latin hypercube designs (LHD) are widely used as space-filling designs in the field of computer experiments. Choice of a good LHD closely depends upon space-filling and orthogonality criteria. Space-filling criterion provides maximum coverage to the whole design space and orthogonality criterion helps to estimate effects independently. These two criteria are not dependent upon each other. A good space-filling LHD may not be orthogonal and vice-versa. So efforts are directed to two different directions to obtain LHDs. One is to find LHDs for good space-filling and another is to find orthogonal Latin hypercube designs (OLHD). A method has been developed for construction of LHDs for two factors and any number of runs which provides good space-filling property. Space-filling values of Latin hypercube (LH) from proposed method are compared with LH obtained from methods available in literature and LH obtained from JMP software. LHs from proposed method provide good space-filling property in terms of small runs with two factors. Methods of constructing OLHDs for two and three factors have also been developed for any number of runs for which OLHDs can exist. OLH of 8 and 9 runs with three factors have same space filling property with that of the best designs obtained by taking all possible three columns combinations from 8 and 9 runs with 4 factors OLH. Catalogues have been prepared with complete list of designs and their space-filling values up to 20 runs for both the cases viz. LHD with good space filling properties and OLHDs.

iv) **Rahul Banerjee**
Chairperson: Dr. KN Singh

Pre-Harvest Forecasting of Crop Yield using Detrended Yield: A New Approach

Crop yield forecast models have been developed using weekly data on weather variables such as maximum temperature, rainfall, minimum temperature and relative humidity. Detrended yield approach has been used for developing the forecast models. Time series data on the yield of Wheat crop (*Triticum aestivum*) in five districts of Uttar Pradesh

namely, Lucknow, Kanpur, Banda, Jhansi and Faizabad was taken which were subsequently treated as the dependent variable and weekly data on the weather variables (weather indices) were used as the regressor variables in the model. The yield was detrended by obtaining the parameter estimates of the model and subsequently the detrended yield was used to forecast the yield of the crop using Autoregressive Integrated Moving Average (ARIMA) model. The proposed method of obtaining Pre-harvest forecasting of yield of crops was compared with the traditional approaches of forecasting and the proposed method was evaluated in terms of criterion such as goodness of fit of the model which was evaluated using standard statistical measures such as Mean Square Error, Mean Absolute Error and the Relative Mean Absolute Error and the forecasting performance of the proposed model was also developed using statistical measures such as Mean Squared Prediction Error (MSPE), Mean Absolute Prediction Error (MAPE) and Relative Mean Absolute Prediction Error (RMAPE). It was observed that in all the districts, the proposed model performed better as compared to the traditional method both in terms of goodness of fit as well as forecasting performance as the values of this measures were lower for all the districts as compared to the traditional approach for modeling as well as for forecasting the yield of the crop.

v) **Nitin Varshney**

Chairperson: Sh. SD Wahi

Discrimination of Coding and Non-Coding Regions in Cattle based on Epigenetic Mechanism

In the present study, discrimination of coding and non-coding regions of cattle genome, collected from the UCSC Browser, has been done based on Epigenetic Mechanism. The CDS as well as the intron sequences were divided into the training set that comprised 80% of the sequences whereas the rest of the sequences are retained in the test set. Intron sequences are encoded by using different indices meant for DNA methylation and spontaneous deamination. Content sensors that can discriminate between CDS and introns, based on the sequence pattern created by DNA methylation. Five different indices

namely Deviation of Nucleotide, Deviation of Dinucleotide, Intensity of methylation effect, Triplet avoidance index and tendency of Polypurine and Polypyrimidine that could encode exon and intron sequences have been used. Dispersion matrix was estimated based on the performance of the five indices in the training set. PCA is performed and PC scores are computed for both the CDS as well as the intron sequences in the training set. On the basis of length in base pairs the sequences have been classified into six different categories viz. $L_{0,1}, L_{0,2}, L_{0,3}, L_1, L_2, L_3$ and the number of CDS as well as intron sequences in each of the six categories have also been evaluated and the category containing the largest and the smallest number of CDS as well as intron sequences also has been found out. The relative abundance of the five indices has also been worked out in the three categories. The area under the ROC and the PR curve along with their standard errors were also computed. The proposed method has been compared with the methods based on LDA and QDA based on the area under the ROC and the PR curves, whereby the proposed method proved to be better as compared to LDA and QDA.

vi) **Rajeev Kumar**

Chairperson: Dr. Rajender Parsad

Polygonal Designs for Sampling from Naturally Ordered Populations

Balanced sampling plans excluding adjacent units {BSA(m) plans} are useful for sampling from populations in which the nearer units provide similar observations due to natural ordering of the units in time or space. The ordering of units in the population may be circular or linear. For BSA(m) plans, all the first order inclusion probabilities are equal whereas second order inclusion probabilities for pairs of adjacent units at a distance less than or equal to m are zero and constant for all other pairs of non-adjacent units which are at a distance greater than m. An important series of incomplete block designs called polygonal designs are useful for obtaining BSA(m) plans. Considering the blocks of polygonal designs as samples and the treatments as units, a BSA(m) plan can be obtained by assigning equal probability of selection to the blocks. The computer algorithm based on linear

integer programming approach available for generating efficient binary incomplete block designs has been modified for obtaining polygonal designs for both the circular and linear ordered structure of population units. Computer aided search of polygonal designs is made in the parametric range $v \leq 30$, $k \leq 5$, $m \leq 5$. In this range, 1037 designs satisfy the parametric relations for circular ordering of units and 817 for linear ordering of units. Computer aided search gives almost all the existent polygonal designs except 34 designs in case of circular ordering of units and 22 designs in case of linear ordering of units. Further, 9 new polygonal designs for the situation in which units are arranged in circular order and 14 new polygonal designs for the situation in which units are arranged in linear order are also obtained.

vii) Pankaj Das
Chairperson: Dr. AK Paul

Estimation of Growth Parameters using Non-Linear Mixed Model and Comparison with Fixed Model in Animals

A growth model defines the mathematical relationship between size of an organism and a unit of time. Repeated measurements designs are mostly used in animal experiment as there may be correlation among repeated measurements of an individual. In case of longitudinal growth data, there are within and between individuals variation. The variability between individuals are not included in fixed effect model. The problem can be solved by using non-linear mixed effect models (NLMM). NLMM have flexible covariance structure to handle unbalanced data, estimates the random covariates and control autocorrelation in repeated measures. It also provides a scope for multiple sources of heterogeneity in data by including random effects in the models. In this study, growth data of Goat and Pig has been used. Attempt has been made to develop the Von-Bertalanffy mixed model. Logistic, Gompertz and Von-Bertalanffy fixed and mixed models have been explored for these data. Comparison of the models i.e. between fixed and mixed type of the same model and among different fixed and mixed models has been attempted. The goodness of fit statistics i.e. Mean Square Error (MSE) and Root Mean

Square Error (RMSE) of the fitted models has been computed. The parameters of the best fitted models along with their corresponding standard error are estimated. Logistic mixed effect model is found to be the best for the Goat and Pig data. The prediction of this model is also better.

viii) Moagisi Innocent Ithuteng
Chairperson: Dr. LM Bhar

Time Series Regression of Aphid Count Data

Aphid population data on mungbean crop from five different locations of India, viz., Pantnagar, Behrampur, ICAR-IARI, Mohanpur and Bharatpur farms along with the meteorological data on rainfall, maximum temperature, minimum temperature, maximum relative humidity, minimum relative humidity, sunshine hours, wind speeds etc. for December, January, February, March, and April from 2001 to 2004 have been used to fit various models appropriate for modeling pest count data. It has been found that results obtained through negative binomial (NB) model are the best among other models considered, viz., OLS and Quasi-Poisson models. Even though OLS was performing better than Quasi-Poisson in terms of forecasting performance, still OLS model cannot be used to predict time series count data as this violated its assumptions, hence the regression coefficients estimates are questionable. On the other hand the Quasi-Poisson model produced highly erroneous significance tests for the coefficients that some explanatory variables are significantly related to aphid rates while the NB didn't show any significance. The problem of over-dispersion associated with aphid counts was more addressed in NB regression model as there was evidence that NB was fitting better than Quasi-Poisson and OLS models in all the locations. Based on AIC and BIC scores, NB was chosen as the better fitting model. Regarding statistics for evaluating the forecasting performance, the NB model had the smallest statistics followed by OLS and Quasi-Poisson model was clearly inferior to all other fits. Finally, most of explanatory variables included in the models were not statistically significant in predicting the aphid counts. The use of DM test also support the claim that

the NB model outperforms Poisson and OLS regression as far as modelling and forecasting of aphid pest count is concerned.

M.Sc. (Computer Application)

i) Surchand Mayanglambam Chairperson: Dr. Rajni Jain

Software for Agricultural Productivity Analysis

Productivity growth in agriculture has become a serious issue over the last five decades. Analysis of agricultural productivity data of different regions can help to find factors affecting the growth of productivity. There is a wide difference in the agricultural performance within state due to its variation in resource available, climatic, topography etc. so district level study of agricultural data will be a step to give a better result. Keeping in pace with the development of the internet technology, there is need to develop web based data analysis tools in agriculture research. Therefore, Software for Agricultural Productivity Analysis (SAPA) was required. The software is completely menu driven and offers user-friendly screens to reduce efforts in understanding the software. User can register, login, analyze agricultural productivity and can save result in Excel file. Software results are validated using a suitable dataset.

ii) Niranjan Nayak Chairperson: Dr. Alka Arora

Development of a Web Enabled System for Estimation of Canal Water Availability in a Selected Area

The Indian farming community is facing a lot of problem in increasing the crop production. Water is one of the major factors that influence the crop cultivation or crop production. Conservation of water is becoming increasingly important. Farmers rely on irrigation and canal irrigation is important component of the same. Canal irrigation system consists of network of canals which include main canal, distributary canal, minor canal and outlets. The source of water to main canal could be river water or water stand reservoir. From the sources water is released to main canal then it goes to distributary canal after that it goes to minor canal then to the field through outlet. Not all the

water released in the main canal at river water reaches to the farmer's field. A considerable portion of water released in main canal is lost in the form of seepage when it is flowing through the different canal. From irrigation point of view, the water that is available at field level is important. Normally the water available at the field level is estimated manually using the various methods to accomplish seepage losses. An online software has been developed to account for seepage losses for estimating the water available at the field level. This system has been developed using standard three tier web architecture. The client side interface layer has been implemented using HTML, CSS and JavaScript. The server side application layer has been implemented using JSP technology and the database layer has been implemented using Microsoft SQL server. This software provides information about the seepage loss for the main canal, distributary canal, minor and outlets. The system also provides how much water is available at the field level and the time taken to irrigate the field. This system can serve the Dam managers by providing them information about the seepage loss calculation, water available at field level and time taken to irrigate field.

iii) Saravanakumar R. Chairperson: Dr. Rajni Jain

Web Based Application for Apportioning Temporal Data at District Level

Agriculture performance generally differs widely within state due to varying regional characteristics in terms of resource endowments and climate. Apportioning is an important process to distribute or allocate with proportion obtained from geographical area over three decade of time period. Methodology for apportioned data for district is not available in any format in any software or in documented form. Therefore, a need for web based application for apportioning temporal data at district level was felt and attempt was made to develop the user friendly online software. User can register, login, Apportion district data, and can see the results and save data in excel file for future use. Administrator interface of the software helps in development and maintenance of user database. Software results are validated using real data.

iv) **Mayanglambam Subashchandra Singh**
Chairperson: Dr. Alka Arora

Online Software for Forewarning of Onion Thrips

Onion, *Allium cepa* is important vegetable crop and onion thrips is most damaging pest for this crop. Timely forecast can help in taking remedial measures for the same. Statistical models have been developed at ICAR-IASRI based on weather parameters for forecasting different aspects relating to thrips. The models have been developed for different planting dates for the data taken from ICAR-DOGR. Models have been developed for thirteen dates of sowing for the forewarning of crop age at first appearance of thrips, crop age at peak population of thrips and maximum thrips population. The models have been tested and used by DOGR for forewarning purpose. To disseminate the information in effective manner, online software has been developed based on the weather models. Online system for Onion Thrips Forewarning System (OTFS) has been developed using three-tier architecture. Client layer is implemented using Hypertext Markup Language (HTML), Cascading Style Sheet (CSS) and Java script. In application layer all the programming for models have been done using Java Server Pages (JSP). Database layer for storing the weather data has been implemented in Microsoft SQL Server. User can access the system using web browser. Administrator is another user to whom access rights for data management has been provided. Administrator can upload the weather data in excel sheet to the system. Results have been validated by running the models in SAS software and online software. The developed system will help the farmers, agro-advisors and agricultural extension personnel in forewarning of disease in a timely manner.

v) **Ipshita Roy Chowdhury**
Chairperson: Dr. Anshu Bharadwaj

Web Based Tool for Interpolation of Climate Data

In agriculture and environmental planning, climate plays a very important role. It is a measure to learn the relationship between biological and environmental phenomenon. Developing countries like India are facing

the problem of lack of accurate climate data. This problem affects integrated planning on the environment and agriculture. Agricultural and natural resource management activities require the understanding of spatial variation in climatic conditions. Estimates of climatic variables which are spatially distributed are required for use in geographical information systems and models. This means that the effectiveness of agricultural research depends on the techniques which can handle variability in crop and soil, weather parameters and spatial interpolation, that represents estimation of value of data points at the sites from where no sample is drawn and it is in an area which is already known with sampled points, by using the data obtained from the sampled points. There is necessity of accurate and inexpensive quantitative approaches to interpolate climate data in developing countries. Climate data in India is acquired from the weather stations located at different locations in each state. In India, when required climate data for the locations where no weather stations are located, the average (mean) of the climate data from the surroundings locations is considered. Each state doesn't have enough weather stations to even cover each district. (e.g Uttar Pradesh (UP) has 75 districts and only 47 weather stations. Source: IMD). Interpolated climate data is a necessity for better planning, forecasting and research related to global climate change scenario. Some softwares have already been developed and are being used for interpolating climate data but these are all either stand alone or have been developed for specific locations. Thus, a web based tool for interpolation of climate data was needed which can help researchers, students and ecological workers to have an access to the data at unsampled locations for their respective works. The present study was, therefore taken upon to design and develop a Web-based Tool to interpolate the climate data. In this system, the geo-statistical method of local interpolation i.e. Kriging has been used.

vi) **Murari Kumar**
Chairperson: Mohammad Samir Farooqi

Developing Agents for Bibliographic Data Retrieval St

Bibliographic records are used quantitatively by a "Bibliometrician" for analysis and

dissemination purpose but with the increasing rate of literature publication in open access journals such as Nucleic Acids Research (NAR), Springer, Oxford Journals etc., it has become difficult to retrieve structured bibliographic information in desired format. A digital bibliographic database contains necessary and structured information about published literature. Bibliographic records of different articles are scattered and resides on different web pages. This work presents the retrieval system for bibliographic data of NAR at a single place. For this purpose, parser agents have been developed which access the web pages of NAR and parse the scattered bibliographic data and finally store it into a local bibliographic database. Based on the bibliographic database, “three-tier architecture” has been developed to display the bibliographic information in systematized format. Using this system, it would be possible to build the network between different authors and affiliations and also other analytical reports can be generated.

vii) PN Somana

Chairperson: Mr. Shah Nawazul Islam

A Web Based Information System for Agricultural Equipment and Products

India being a large and diverse country with a majority of the population dependant on agriculture and allied activities, the availability of information regarding latest agricultural products, technologies and inputs to the farmers is of vital importance. Information is key to better production and productivity as a large percentage of the farmers in rural areas still follow traditional inefficient products and practices resulting in less remunerative returns. A web based information system will greatly help farmers seeking relevant information regarding products and the traders selling such products. The specific information provided aims to improve operation, better management and easier decision making. Indian Council of Agricultural Research (ICAR) has come up with a single window delivery system for services and products of research of agricultural research institutes all over the country called the Agricultural Technology Information Centre (ATIC). They provide farmers with the latest agricultural innovations and products developed at their respective

research institutes. But the information on such centres is not easily available to farmers. Information about the various products available at such centres needs to be disseminated to the rural areas. Utilization of fast expanding internet services as a medium of information transfer will greatly help farmers in remote locations of the country. This thesis presents the design and development of a web based information system which provides information on prices of seeds and planting material of latest varieties and hybrids, advanced agricultural equipments being developed by ICAR and traders of agricultural commodities.

(viii) Sanober Alam

Chairperson: Md. Shah Nawzul Islam

Development of Distributed Framework for Crop Protection

India is the second largest populated country in the world. Its population is continuously increasing and is expected to reach 1.396 billion by 2025. In the near future, the production of agricultural commodities must be increased, to meet the food requirement of increasing human population. For this, crop protection plays an important role in increasing the yield of crop by identifying the disease, insect and weed infestation and also suggests several treatment and control measures to protect the crop from all these threats. In India, around 30% losses occur in crop due to these pests. Number of information systems and expert systems for different crops are already operational. These information systems and expert systems provide an information on various aspects of crop protection to farming community. The user has to access different expert systems for different crops, so there is a need for building a single window application to provide disease, insect and weed advisory on multiple crops at the same place. For this reliable distributed framework has been developed. A distributed framework is a framework which captures, stores, retrieves, manipulates and displays information from different sources. The fundamental purpose of a distributed framework is to access data from different sources that is logically related and physically distributed. This thesis presents the design and development of distributed framework for crop protection which provides

disease, insect and weed related information from different sources at a single place of wheat and several spices crop. These information will help the farmer in identifying disease, insect and weed infecting the crop and will also suggests control measure to protect the crop from all these threats. The developed system also consists of a form based alert system which provides an online form in which the farmer has to fill some detail. On the basis of temperature, humidity and rainfall value provided by the farmer after filling the form, it gives an alert about the disease, which is going to affect the crop at that particular value.

M.Sc. (Bioinformatics)

(i) Saket Kumar Karn

Chairperson: Dr. Sudeep Marwah

Strengthening and Enhancing Microbial Taxonomy Ontology

Ontology is the latest knowledge representation technique. It is devised for the web based systems to provide the capability to deal with the semantics of the concepts in the specific knowledge domain. It has potential to be used in a distributed environment like Internet and provides the dynamic and reusable capability to the knowledge base. Ontology defines domain concept and the relationship between them and thus provides a domain language that is meaningful to both humans and machines. On the other hand, taxonomy describes real world concepts in well-defined hierarchy and exists in standard form for various knowledge domains of science. The present study deals with the taxonomy of microorganisms. The Three Domain System taxonomy is most widely adopted taxonomy in this domain. It covers Bacteria, Archaea and Eukarya domains. A Microbial Ontology has been developed for Bacteria Domain by Biswas, 2012 which covers concepts from Domain to Genus level to convert unstructured knowledge into structured knowledge. In this work, the existing ontology has been extended to cover Archaea domain up to the species level. A web based interface is also developed using N-tier architecture of web applications. Net Beans IDE 8.0, Java Server Pages (JSP), Jena and SPARQL. Jena is a Semantic Web Framework for querying and reasoning OWL ontologies, OWL editor-Protégé 3.5

has been used for building and populating ontologies. In the developed ontology, newly found microorganisms can be easily classified in microbial taxonomy by matching their characteristics. Domain experts can insert, delete and edit any new information about the microbial taxonomy. The web interface also provides search facility for finding information about the concepts and 16S rRNA sequences of various Archaea species, Information can be searched from microbial taxonomy of Archaea up to the Species level, for two Phyla, nine Classes, twelve Orders, twenty Families, sixty eight Genera, and sixty six Species. By using this software also facilities name based search for microorganism's taxonomic terms. The use of ontologies to represent the taxonomic information and the ability of the software to provide this knowledge to other applications increases the utility of this work to greater extent.

ii) Arfa Anjum

Chairperson: Dr. Seema Jaggi

Mixture Distribution Models for Differential Gene Expression Analysis

Gene expression is the process by which information from a gene is used in the synthesis of a functional gene product which may be proteins. A gene is declared differentially expressed if an observed difference or change in read counts or expression levels between two experimental conditions is statistically significant. To identify differentially expressed genes between two conditions, it is important to find statistical distributional property of the data to approximate the nature of differential genes. In the present study, the focus is mainly to investigate the differential gene expression analysis for sequence data based on mixture distribution model. Mixture model is popular because it provides a mechanism to incorporate extra variation and correlation in the data, add model flexibility and are a natural approach for modelling data that arise in multiple stages or when populations are composed of sub populations. Compound mixture distribution approach was also explored to identify the differentially expressed genes. These approaches were applied in Microarray data and RNA-seq data of *Arabidopsis thaliana*. Comparison was made between mixture distribution/ compound distribution with single

distribution with respect to the identification of differentially expressed genes. Fitting of two-component mixture normal model in case of microarray data is found to be more capable of capturing the variability as compared to single component normal distribution and hence identified differentially expressed genes more accurately. Further, it has been found that in case of RNA-seq data, negative binomial as compound Poisson distribution is more appropriate to capture the variability as compared to Poisson distribution. Thus, fitting of appropriate distribution to gene expression data provides statistically sound cut-off values for identifying differentially expressed genes.

(iii) **Md. Asif Khan**

Chairperson: Dr. Sunil Archak

Development of Crop Wild Relatives Resources (CWR) Database for *Vigna* and *Phaseolus* Species

Crop Wild Relatives (CWR) Resources database was developed for *Vigna* and *Phaseolus* species. Taxonomic data on 56 species, Genebank passport data on 53,870 accessions and 1,017,292 entries from GenBank (nucleotide, EST, protein and gene) were collected from different open source databases. The data were curated, compiled and arranged in six tables (Taxonomy, Germplasm, Nucleotide, EST, Protein and Gene) in relational manner using MSSQL Server. A web based graphic user interface was developed using ASP.NET and MS Visual Studio. This work constituted first of its kind in joining GenBank and Genebank data. The application identified as many as 41776 germplasm accessions whose genomic information is available in GenBank. Linking a specific gene, EST, nucleotide and protein of known functional importance to a germplasm accession is expected to assist molecular breeders in precision breeding programme in addition to adding value to the germplasm conserved in the genebanks.

(iv) **Priyanka Guha Majumdar**

Chairperson: Md. Samir Farooqi

Codon Usage Bias Based Comparative Genome Analysis of *Rhizobium* Species

The bacteria belonging to the genus *Rhizobium* are capable of fixing atmospheric nitrogen in

symbiosis with leguminous plants by forming root nodules. These rhizobial inoculants are used as biofertilizers and act as an alternate source of nitrogenous fertilizers. But the limitation is that the *Rhizobium* can infect only leguminous plants and they are species specific. In this era of genetic engineering we can try to transform crops other than legumes with the novel genes of *Rhizobium* responsible for nitrogen fixation. For this we need to know the codon usage patterns of the nitrogen fixing genes in order to improve the exogenous gene expression. And that is why the study of codon usage pattern of the *Rhizobium* is gaining increasing attention over the times. Efforts have been made continuously to understand the codon usage patterns and identify some conserved features of the genus *Rhizobium*. In the present study three strains of *Rhizobium* namely *Sinorhizobium melliloti* 1021, *Bradyrhizobium japonicum* USDA110 and *Rhizobium tropici* CIAT899 whose complete genome sequence are available were taken from NCBI (www.ncbi.nlm.nih.gov) for the analysis of codon usage bias and further a comparative analysis was also done among these three strains and other six strains of *Rhizobium* which had already been studied for codon usage bias by other researchers. The overall codon usage analysis showed that G and C ending codons are predominant in the rhizobial genome than A and T ending codons. Nc plot revealed that translational selection along with compositional constraints are the major causes of codon usage bias. The correspondence analysis (COA) showed the first two axes mainly accounted for the variation in the codon usage data. The Pearson correlation analysis identified significant correlation between the first axes of COA and CAI and other factors of codon usage bias, which indicated that gene expression level played an important role in shaping codon usage pattern of the genus. The comparative analysis showed that the use of Cys codons varied among the different genes in the genus *Rhizobium*. Our study of the three strains identified 17 optimal codons that were shared among these strains. The comparative analysis finally revealed that there were 16 codons that were shared amongst them and was identified as a conserved feature of the genus *Rhizobium*.

(v) **Animesh Kumar**
Chairperson: Md. Samir Farooqi

Prediction of miRNA Related to Late Blight Disease of Potato

Late blight of potato is the most important fungal disease in potato cultivation worldwide, caused by *Phytophthora infestans*. Many recent studies show that microRNA (miRNA) is an important gene expression regulator in plants also it plays a very important role in host-pathogen interaction. Several methods such as forward genetics or direct cloning are available to detect miRNA which are time consuming as well as costly. Discovering miRNA related to late blight of potato through computational means is not only efficient but also helpful in understanding of plant-pathogen molecular interaction mechanisms. It provides theoretical idea to facilitate germplasm for disease resistance for the management of late blight of potato. In the present study, prediction and characterization of novel miRNA related to late blight disease were done using computational means. A total of 23571 non-redundant mature miRNA sequences from miRBase database and 262,006 whole *Solanum tuberosum* EST sequences from NCBI were used to identify 34 potential miRNA related to 6 different miRNA families. The psRNATarget server predicted 2633 potential target genes related to pre-miRNA. Most of the target genes were involved with translational and cleavage function. Later these potential target genes were annotated with geneontology (GO) terms via. agriGO ToolKit analysis server. All predicted GO terms were classified into 134 functional groups including biological processes, cellular component and molecular function. Out of which two distinct GO terms were related to defence response and response to stress during *P. infestans* infection. Back tracing of

such GO terms reveals that they were related to 5 distinct target genes and 34 miRNA. These five target genes were involved in translational and cleavage activity. Then, 34 miRNA were screened by constructing miRNA-miRNA relationship networks out of which predicted miRNA were supposed to be related to late blight disease of potato. This work can be further supported through experimental validation. Further in-depth experimental study can disclose the role of predicted miRNA during host pathogen interaction and disease development.

National / International Training Programme

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 Institute of the Council, State Agricultural Universities and State Government Departments, etc. & 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 June 22, 2015 to November 21, 2015. The Course comprised of two independent modules of three months duration each. One officer participated in both the modules. Module – I was organized during June 22, 2015 to August 22, 2015. Module-II was organized during September 01, 2015 to November 21, 2015. Three officers participated in Module – I and one officer participated in Module - II. The course covered under both the modules included Statistical Methods and Official Agricultural Statistics, Use of Computers in Agricultural Research, Sampling Techniques, Econometrics and Forecasting Techniques, Design of Experiments and Statistical Genetics.

Category	No. of Training Programmes	No. of Participants
CAFT	4	96
Resource Generation	8	143
Others	12	293
Total	24	532

Details of Training Programmes organised

S. No.	Title	Venue	Date	Sponsored by	No. of Participants
Centre of Advanced Faculty Training					
1.	Application of Computer Algorithms and Statistical Software Packages in Agriculture Course Director : Dr. Sangeeta Ahuja	ICAR-IASRI New Delhi	18 December 2015 to 07 January 2016	Education Division, ICAR, New Delhi	25
2.	Advances for Technological Enhancement in Agricultural Research Course Director : Dr. Arpan Bhowmik Co-Course Director : Dr. Cini Varghese	ICAR-IASRI New, Delhi	19 January to 08 February 2016	Education Division, ICAR, New Delhi	25
3.	Computational Tools and Techniques for Molecular Data Analysis in Agriculture Course Director : Dr. Dinesh Kumar Co-Course Director : Dr. Mir Asif Iquebal	ICAR-IASRI New, Delhi	11 February to 02 March 2016	Education Division, ICAR, New Delhi	23
4.	Recent Advances in Statistical Genetics and Genomics Course Director : Dr. Prabina Kumar Mehar Co-Course Director : Sh. Upendra Kumar Pradhan	ICAR-IASRI New, Delhi	11 February to 02 March 2016	Education Division, ICAR, New Delhi	23
Resource Generation					
5.	A refresher training programme on Integrated Sample Survey Methodology Coordinators : Dr. Hukum Chandra : Dr. Kaustav Aditya	ICAR-IASRI New Delhi	08-12 June 2015	Ministry of Agriculture Government of India	22
6.	Refresher training programme on Sample Survey and Sampling Design Course Director : Dr. Tauqueer Ahmad Co-Course Director : Dr. Ankur Biswas	ICAR-IASRI New Delhi	06-10 July 2015	Directorate of Economics and Statistics, Department of Planning, Government of Uttar Pradesh	18
7.	Training programme on Data Analysis and Interpretation Course Director : Dr. Rajender Parsad Co-Course Director : Dr. Arpan Bhowmik	IASRI, New Delhi New Delhi	10-22 August 2015	MoSPI, Govt. of India	40
8.	Training on Field data collection under the study Improving methods for estimating crop area, yield and production under mixed, repeated and continuous cropping	ICAR-IASRI New Delhi	31 August to 04 September 2015	FAO`	05
9.	Training programme on "Crop Cutting Experiments Technique" for the officials of Services Private Skymet Weather Services Private Ltd. Course Director: : Dr. Tauqueer Ahmad : Ms. Vandita Kumari	ICAR-IASRI New Delhi	14-19 September 2015	Skymet Weather Services Private Ltd., Noida	15
10.	International training programme on Use of Models in Crop Yield Estimation Course Director : Dr. Hukum Chandra Co-Course Director : Sh Raju Kumar	ICAR-IASRI New Delhi	02-06 November 2015	NSSTA, CSO* MOS&PI, GOI, New Delhi	08
11.	A refresher training programme on Small Area Estimation Techniques and Applications Course Director : Dr. Hukum Chandra Co-Course Director : Dr. Kaustav Aditya	ICAR-IASRI New Delhi	16-20 November 2015	NSSTA, CSO* MOS&PI, GOI, New Delhi	18

S. No.	Title	Venue	Date	Sponsored by	No. of Participants
12.	Training programme on Functions and Activities of IASRI for the participants of 69th regular term course-2015 on Official Statistics and Related Methodology of International Statistical Education Centre (ISEC) Kolkata conducted by National Statistical System Training Academy (NSSTA). Coordinator : Dr. Seema Jaggi	ICAR-IASRI New Delhi	31 December 2015	NSSTA, CSO MOS&PI, GOI, New Delhi	17
Other Training Programmes					
13.	Designing and Analysis of Experiments for the technical personnel of ICAR Coordinators : Dr. Susheel Sarkar : Dr. Sukanta Dash	ICAR-IASRI, New Delhi	20- 25 April 2015	Education Division of ICAR	16
14.	Training programmes for the MIS-FMS project with main focus on payroll Coordinators : Dr. Sangeeta Ahuja : Sh. SN Islam	ICAR-IASRI, New Delhi	15- 18 April 2015 11-16 May 2015 28-30 May 2015	IASRI, New Delhi	20 24 20
15.	Training programme for Payroll and HR module under MIS/FMS project Coordinator : Sh. SN Islam	ICAR-IASRI, New Delhi	22-24 June 2015	IASRI, New Delhi	18
16.	Training programme for graduate students on Statistical Analysis using Software Coordinators : Dr. Seema Jaggi : Dr. Eldho Varghese	ICAR-IASRI, New Delhi	01 June - 15 July 2015	IASRI, New Delhi	2
17.	Training programmes on Assets, Annual Account and Store under ICAR-ERP Coordinators : Dr. Mukesh Kumar : Dr. NS Rao	ICAR-IASRI New Delhi	13-15 July 2015	ICAR-IASRI New Delhi	21
18.	Training programme on Payroll and HR module Coordinators : Dr. Mukesh Kumar : Dr. Alka Arora	ICAR-IASRI New Delhi	18-21 August 2015	ICAR-IASRI New Delhi	24
19.	Training programme on Small Area Estimation Techniques. Course Director : Dr. Hukum Chandra Co-Course Director : Dr. Kaustav Aditya	ICAR-IASRI New Delhi	24-28 August 2015	ICAR-IASRI New Delhi	19
20.	Training programmes on Payroll and HR module Coordinators : Dr. Anshu Bharadwaj : Dr. Mukesh kumar	ICAR-IASRI New Delhi	01-04 September and 22-24 September 2015	ICAR-IASRI New Delhi	34
21.	Finance Module of MIS-FMS Coordinators : Dr. Mukesh Kumar : Dr. NS Rao	ICAR-IASRI New Delhi	05-07 October and 12-14 October 2015	ICAR-IASRI New Delhi	36
22.	Winter School on Bioinformatics and High Dimensional Genome Data Analysis Course Director : Dr. AR Rao Co-Course Director : Dr. PK Meher	ICAR-IASRI New Delhi	25 November to 15 December 2015	ICAR, New Delhi	20
23.	Training programme on Experimental Data Analysis for Ph.D. Students from various disciplines of P.G. School, IARI Coordinators : Dr. Seema Jaggi : Dr. Eldho Varghese	ICAR-IASRI New Delhi	07-11 December 2015	PG School New Delhi	20
24.	Training programme on Recent Advances in Next Generation Sequencing on Data Analysis under CAFT Coordinators : Dr. M Grover : Dr. DC Mishra	ICAR-IASRI New Delhi	08-18 January 2016	ICAR-IASRI, New Delhi	19

Faculty Members of PG School, ICAR-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)	1995
4.	Dr. Anil Rai, Principal Scientist	1995
5.	Dr. KN Singh, Principal Scientist	2011
6.	Dr. Rajender Parsad, Principal Scientist	1995
7.	Sh. S.D.Wahi, Principal Scientist	1987
8.	Dr. Lal Mohan Bhar, Principal Scientist	1998
9.	Dr. Tauqueer Ahmad, Principal Scientist	1998
10.	Dr. Amrit Kumar Paul, Principal Scientist	1998
11.	Dr. AR Rao, Principal Scientist	1998
12.	Dr. G K Jha, Principal Scientist, IARI	1999
13.	Dr. Cini Varghese, Principal Scientist	2000
14.	Dr. Himadri Ghosh, Principal Scientist	2004
15.	Dr. Prachi Misra Sahoo, Senior Scientist	2002
16.	Dr. Hukum Chandra, National Fellow	2003
17.	Dr. Anil Kumar, Principal Scientist	2010
18.	Dr. Amrender Kumar, Senior Scientist, IARI	2003
19.	Dr. Prawin Arya, Senior Scientist	2003
20.	Md. Wasi Alam, Scientist	2003
21.	Dr. Ranjit Kumar Paul, Scientist	2011
22.	Dr. Mir Asif Iqbal, Scientist	2011
23.	Dr. BN Mandal, Scientist	2011
24.	Dr. Susheel Kumar Sarkar, Scientist	2011
25.	Dr. Eldho Varghese, Scientist	2011
26.	Dr. Kaustav Aditya, Scientist	2012
27.	Dr. Bishal Gurung, Scientist	2013
28.	Dr. Sukanta Dash, Scientist	2013
29.	Dr. Arpan Bhowmik, Scientist	2014
30.	Dr. Ajit, Principal Scientist	2015
31.	Dr. Ankur Biswas, Scientist	2015

Faculty Members of PG School, ICAR-IARI in Computer Application

S. No.	Name	Year of Induction
1.	Dr. Anjani Kumar Choubey, Head (Computer Application)	2014
2.	Dr. Alka Arora, Senior Scientist	2001
3.	Dr. Sudeep, Senior Scientist	2002

S. No.	Name	Year of Induction
4.	Ms. Shashi Dahiya, Scientist	2001
5.	Md. Samir Farooqi, Scientist	2001
6.	Dr. KK Chaturvedi, Scientist	2002
7.	Ms. Anu Sharma, Scientist	2004
8.	Sh. SN Islam, Scientist	2004
9.	Dr. SB Lal, Scientist	2004
10.	Dr. Anshu Bhardwaj, Scientist	2004
11.	Dr. Sangeeta Ahuja, Scientist	2002
12.	Dr. Rajni Jain, Principal Scientist, NIAP	2007
13.	Sh. Pal Singh, Scientist	2010
14.	Dr. Mukesh Kumar, Senior Scientist	2014
15.	Dr. N. Srinivasa Rao, Senior Scientist	2014
16.	Dr. A.K. Mishra, Senior Scientist, IARI	2014

Faculty Members of PG School, ICAR-IARI in Bioinformatics

S. No.	Name	Year of Induction
1.	Dr. Anil Rai, Professor (Bioinformatics)	2010
2.	Dr. KC Bansal, Director, NBPGR	2010
3.	Dr. Seema Jaggi, Principal Scientist	2010
4.	Dr. Rajender Parsad, Principal Scientist	2010
5.	Dr. AR Rao, Principal Scientist	2010
6.	Dr. Sudeep, Senior Scientist	2010
7.	Dr. SB Lal, Scientist	2010
8.	Mohd. Samir Farooqi, Scientist	2010
9.	Ms. Anu Sharma, Scientist	2010
10.	Dr. TR Sharma, Director, NRCPB	2010
11.	Dr. T Mahapatra, Director, IARI	2010
12.	Dr. Kishore Gaikwad, Principal Scientist	2010
13.	Dr. T Napoleon, Senior Scientist	2010
14.	Dr. PK Singh, Senior Scientist	2010
15.	Dr. KV Bhat, Principal Scientist	2010
16.	Dr. SS Marla, Principal Scientist	2010
17.	Dr. Sunil Archak, Senior Scientist	2010
18.	Dr. DC Mishra, Scientist	2010
19.	Dr. Sarika, Scientist	2010
20.	Sh. Sanjeev Kumar, Scientist	2010
21.	Dr. AK Mishra, Senior Scientist	2010
22.	Dr. Mir Asif Iquebal, Scientist	2013
23.	Dr. Manendra Grover, Senior Scientist	2013
24.	Dr. UB Agandi, Senior Scientist	2014
25.	Dr. KK Chaturvedi, Scientist	

Research Fellowships

During 2015 - 16, 40 Ph.D. and 37 M.Sc. students received research fellowship. 31 Ph.D. students received ICAR-IASRI fellowship at the rate of Rs. 13,125/- p.m. in addition to Rs 10,000/- per annum as the contingent grant. 1 Ph.D. student received ICAR-SRF Scholarship @Rs.12,000/- p.m. in addition to Rs.10,000/- per annum as contingent grant. 5 Ph.D. students received Rajeev Gandhi Fellowship @ Rs.16,000/- P.M. 5 Ph.D. students received DST-Inspire scholarship @ Rs.18,000/-+30% H.R.A. p.m. in addition to Rs. 20,000/- per annum as contingent grant. 1 Ph.D. student received National Fellowship @ Rs.16,000- P.M. in addition to Rs.10,000/- P.A. as contingency grant.

12 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 ICAR-IASRI fellowship at the rate of Rs.7560/- p.m. in addition to Rs. 6000/- per annum as the contingent grant. 3 foreign students have not received the fellowship from the institute.

Strengthening of Post Graduate Programme

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

54th Convocation of Post Graduate School IARI

54th Convocation of Post Graduate School IARI was held during 1-5 February 2016. A total of 24 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:

- 3 Ph.D and 8 M.Sc. (Agricultural Statistics)
- 8 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 2014 - 15 in Agricultural Statistics

Trimester - III					
Code	Course Title	Credits		Instructors	
		L	P		
PGS 504	Basic Statistical Methods in Agriculture	2	1	Susheel Kumar Sarkar, BN Mandal, Sarika	
AS 503	Basic Sampling and Non-parametric Methods	2	1	AK Gupta, Anil Rai, Wasi Alam	
AS 563	Statistical Inference	4	1	KN Singh, LM Bhar	
AS 564	Design of Experiments	3	1	Seema Jaggi, VK Gupta, BN Mandal	
AS 566	Statistical Genetics	3	1	SD Wahi, Amrit Kumar Paul, Upendra Kumar Pradhan	
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	Wasi Alam, Bishal Gurung	
AS 691	Seminar	1	0	Kanchan Sinha	

Courses taught during the Academic Year 2015 - 16 in Agricultural Statistics

Trimester - I					
Code	Course Title	Credits		Instructors	
		L	P		
PGS 504	Basic Statistical Methods in Agriculture	2	1	Susheel Kumar Sarkar, Upendra Kumar Pradhan, AK Gupta	

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, Ranjit Kumar Paul, Eldho Varghese
AS 567	Applied Multivariate Analysis	2	1	AR Rao, Bishal Gurung
AS 568	Econometrics	2	1	GK Jha, Prawin Arya, Kanchan Sinha
AS 569	Planning of Surveys/Experiments	2	1	UC Sud, Prachi Misra Sahoo, BN Mandal
AS 572	Statistical Quality Control	2	0	Wasi Alam, Kanchan Sinha
AS 600	Advance Designed of Experiments	1	1	Rajender Parsad, Cini Varghese
AS 601	Advanced Sampling Techniques	1	1	Hukum Chandra, Prachi Misra Sahoo, Kaustav Adhitya
AS 602	Advanced Statistical Genetics	1	1	SD Wahi, AK Paul, Samrendra Das
AS 603	Regression analysis	1	1	LM Bhar, Ranjit Kumar Paul
AS 604	Linear Models	2	0	VK Gupta, Rajender Parsad
AS 606	Optimization Techniques	1	1	Amrender Kumar, BN Mandal
AS 691	Seminar	1	0	Eldho Varghese

Trimester - II

Code	Course Title	Credits		Instructors
		L	P	
PGS 504	Basic Statistical Methods in Agriculture	2	1	Eldho Varghese, Arpan Bhowmik, Ankur Biswas
AS 502	Basic Design of Experiments	2	1	Susheel Kumar Sarkar, Sukanta Dash, Anil Kumar
AS 551	Mathematical Methods in Statistics	4	0	Cini Varghese, Himadri Ghosh, Sukanta Dash, Samrendra Das
AS 562	Advanced Statistical Methods	2	1	Seema Jaggi, Ranjit Kumar Paul, Arpan Bhowmik
AS 565	Sampling Techniques	3	1	Anil Rai, Tauqeer Ahmed, Ankur Biswas
AS 570	Statistical Modelling	2	1	Ranjit Kumar Paul, Bishal Gurung, Wasi Alam
AS 573	Demography	2	0	AK Gupta, Prawin Arya
AS 605	Advanced Statistical Inference	1	1	KN Singh, Wasi Alam, LM Bhar
AS 607	Stochastic Process	3	0	Himadri Ghosh, Kanchan Sinha
AS 661	Advanced Designs for Single Factor Experiments	2	1	Cini Varghese, BN Mandal
AS 663	Advanced Theory of Sample Survey	2	1	Tauqueer Ahmed, Hukum Chandra
AS 691	Seminar	1	0	Bishal Gurung

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

Trimester - III				
Code	Course Title (L + P)	Credits		Instructors
		L	P	
CA 503	Statistical Computing in Agriculture	1	2	Rajender Parsad, Ranjit Kumar Paul, Sukanta Dash
CA 563	Operating System	2	1	N Srinivasa Rao, Sangeeta Ahuja

CA 568	Software Engineering	2	0	AK Choubey
CA 567	Computer Networks	2	1	SN Islam, Mukesh Kumar
CA 571	Modeling and Simulation	2	1	Anshu Bhardwaj, Amrit Kumar Paul
CA 691	Seminar	1	0	Alka Arora

Courses taught during the Academic Year 2015 - 16 in Computer Application

Trimester - I				
Code	Course Title (L + P)	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, Kanchan Sinha
CA 552	Computer Oriented Numerical Methods	2	1	Pal Singh, Upendra Kumar Pradhan
CA 560	Computer Organization and Architecture	3	0	N Srinivasa Rao, Anil Rai
CA 561/ BI 505	Principles of Computer Programming	2	1	SB Lal, KK Chaturvedi
CA 565	Compiler Construction	2	1	Sangeeta Ahuja, AK Mishra
CA 569	Web Technologies and Applications	2	1	Alka Arora
CA 570	Computer Graphics	2	1	Pal Singh
CA 575	Artificial Intelligence	2	1	Rajni Jain
CA 611	Design and Analysis of Algorithms	2	1	Sudeep, Mukesh Kumar
CA 621	Advances in Data Mining	2	1	Anshu Bharadwaj, D.C. Mishra, Sanjeev Kumar
CA 691	Seminar	1	0	N Srinivasa Rao
Trimester - II				
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, AK Mishra
CA 566/ BI 507	Data Base Management System	2	2	SB Lal, Mukesh Kumar, Soumen Paul
CA 572	GIS and Remote Sensing Techniques	2	1	Alka Arora, Anshu Bharadwaj, AP Ruhil
CA 577	Data Mining and Soft Computing	2	1	Alka Arora, Anshu Bharadwaj, AP Ruhil
CA 578	Information Security	2	1	Mukesh Kumar, Sudeep
CA 612	Fuzzy Sets and Rough Sets	2	1	Sudeep, Alka Arora
CA 691	Seminar	1	0	SN Islam

Courses taught during the Academic Year 2014-15 in Bioinformatics

Trimester - III				
Code	Course Title (L + P)	Credits		Instructors
		L	P	
BI 502	Protein Structure Analysis	2	1	Anil Rai, Sarika

BI 503	Computational Biology	2	1	AR Rao, DC Mishra
BI 504	Evolutionary Biology	2	1	Sunil Archak, AK Mishra
BI 621	Quantum Theory and Applications in Biology	2	1	Monendra Grover
BI 691	Seminar	1	0	MA Iquebal

Courses taught during the Academic Year 2015-16 in Bioinformatics

Trimester - I				
Code	Course Title (L + P)	Credits		Instructors
		L	P	
BI 501/ MBB 509/ GP 540	Introduction to Bioinformatics	2	1	AR Rao, KV Bhatt, Amole Kumar, U. Solanke
BI 505/ CA 561	Principles of Computer Programming	2	1	SB Lal, KK Chaturvedi
BI509/ BIO601	Nucleic Acids	2	1	BIO Faculty
BI 510/ MBB 501	Principles of Biotechnology	4	0	MBB Faculty
BI 511 / BIO 501	Basic Biochemistry	4	1	BIO Faculty
BI 512	Advanced Programming in Bioinformatics	2	2	UB Angadi, SB Lal
BI 601	Genome Assembly and Annotation	1	2	Sanjeev Kumar, DC Mishra
BI 602	Biomolecular Modelling and Simulation	2	1	UB Angadi, M Grover, Anil Rai
BI 622	Molecular Dynamics	2	1	SS Marla, Monendra Grover
BI 613	Parallel Programming and Algorithm Development	2	1	SB Lal, KK Chaturvedi
BI 691	Seminar	1	0	MA Iquebal
Trimester - II				
BI 506	Computational Genomics	3	1	MA Iquabal, DC Misra, Sarika
BI 507 / CA 566	Database Management System	2	2	SB Lal, Mukesh Kumar, Soumen Paul
BI 508	Computer Applications in Bioinformatics	2	1	SB Lal, KK Chaturvedi
BI 603	Machine Learning Techniques in Bioinformatics	2	1	Sanjeev Kumar, MA Iquebal
BI 604	Computational Techniques of Transcriptomics and Metabolomics	1	1	AR Rao, Samir Farooqi
BI 632	Peptide Design, Synthesis and Applications	2	1	Monender Grover, UB Angadi
BI 624	Genome Wide Association Study	2	1	KV Bhat, Sunil Archak, T Napoleon
BI 691	Seminar	1	0	Samir Farooqi

Board of Studies for Academic Year 2015-16

Agricultural Statistics

1.	Dr. Seema Jaggi, Professor (Agricultural Statistics)	Chairperson
2.	Dr. UC Sud, Director	Member (Ex-officio)
3.	Dr. Himadri Ghosh, Principal Scientist	Member
4.	Dr. Prachi Misra Sahoo, Senior Scientist	Member
5.	Dr. Eldho Varghese, Scientist	Member Secretary
6.	Sh. Pradip Basak, Student	Students' Representative

Computer Application

1.	Dr. Seema Jaggi, Professor (Computer Application)	Chairperson
2.	Dr. UC Sud, Director	Member (Ex-Officio)
3.	Dr. AK Choubey, Head, (Computer Application)	Member
4.	Dr. Sudeep, Senior Scientist	Member
5.	Dr. SB Lal, Scientist	Member Secretary
6.	Sh. Srikumar Biswas, Student	Students' Representative

Bioinformatics

1.	Dr. Anil Rai, Professor (Bioinformatics)	Chairman
2.	Dr. UC Sud, Director	Member Ex-officio
3.	Dr. KV Bhatt, Principal Scientist	Member
4.	Dr. Kishore Gaikwad, Principal Scientist	Member
5.	Dr. T Napoleon, Senior Scientist	Member
6.	Dr. Sanjeev Kumar, Scientist (Sr. Scale)	Member
7.	Dr. KK Chaturvedi, Scientist	Member Secretary
8.	Sh. Amit Kairi, Student	Students' Representative

Central Examination Committee for Academic Year 2015-16

Agricultural Statistics

1.	Dr. UC Sud, Director
2.	Dr. Seema Jaggi, Professor (Agricultural Statistics)
3.	Dr. Anil Rai, Head (CABin)
4.	Shri SD Wahi, Principal Scientist
5.	Dr. Girish Kumar Jha, Principal Scientist
6.	Dr. Cini Varghese, Principal Scientist

Computer Application

1.	Dr. UC Sud, Director
2.	Dr. Seema Jaggi, Professor (Computer Application)
3.	Dr. AK Choubey, Head (Computer Application)
4.	Dr. Alka Arora, Senior Scientist
5.	Dr. Srinivasa Rao, Senior Scientist
6.	Sh. KK Chaturvedi, Scientist

Bioinformatics

1.	Dr. UC Sud, Director
2.	Dr. Anil Rai, Professor (Bioinformatics)
3.	Dr. Rajender Parsad, Principal Scientist
4.	Dr. SS Marla, Principal Scientist
5.	Dr. KK Chaturvedi, Scientist
6.	Dr. M Grover, Senior Scientist