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Executive Summary

ICAR-Indian Agricultural Statistics Research Institute (ICAR-IASRI) is mainly responsible for conducting research and education in Agricultural Statistics and Informatics to bridge the gaps in the existing knowledge. The Institute has used the power of Statistics blended judiciously with Informatics and has contributed significantly in improving the quality of Agricultural Research. The Institute has also been providing education/ training in Agricultural Statistics and Informatics to develop trained manpower in the country. The research and education is used in improving the quality and meeting the challenges of agricultural research in newer emerging areas. A landmark for the institute this year was a study awarded by Food and Agriculture Organization (FAO) under the Global Strategy to Improve Agricultural and Rural Statistics on improving methods for estimating crop area, yield and production under mixed, repeated and continuous cropping. The networking services at IASRI have been further strengthened. The entire campus is Wi-Fi enabled with a high speed internet connection to allow the staff and students to access the internet no-matter wherever they are. ICAR Data Centre (Tier-III) has been established at the Institute to provide Unified Mail Messaging and Web Hosting solution in ICAR.

The Institute has made some outstanding and useful contributions to the research in Agricultural Statistics and Informatics. A number of research projects were undertaken in the Institute during this year. Research was carried out under 57 research projects (33 Institute funded, 22 externally funded, 1 National Professor Scheme and 1 Consultancy Project) in various thrust areas. Out of these 21 projects were in collaboration with other institutes,

11 projects were completed and 17 new projects were initiated.

Some salient research achievements are as follows:

- A method to generate minimally changed run sequences for fitting second order response surfaces was developed by rearranging the run orders of the central composite designs. The general expression for minimum number of changes in run sequences of these designs was obtained. A SAS macro for the generation of central composite design with minimum level changes in the run sequences was developed. A catalogue consisting of number of input factors, total number of runs, total number of changes in run sequences along with layout of designs for input factors upto 10 is also prepared.

- Universal optimality of block design with spatial indirect effect from neighbouring units under a general non-additive model has been established in the presence of interactions among the treatments applied in the adjacent plots as these effects contribute significantly to the response.

- A webpage of All India Coordinated Research Project on Vegetable Crops (www.iasri.res. in/aicrpvc) has been developed. Experiment creation module, Data upload and scrutiny module, Management module and Administrator module have been developed. β-version of the Information System was released. Database for updating attribute tables is being finalized. The line entries of various crops for Initial evaluation trials, Advanced varietal trial-I and Advanced varietal trial-II are being updated in the corresponding database tables.

- A general method for obtaining s^k factorial with minimum level changes in the run sequences has been developed. The general expression for factor wise number of level changes has been obtained. A SAS macro for the generation of s^k factorial with minimum level changes in the run sequences has been developed and made available at http://www.iasri.res.in/sscnars/sftsmcrs.aspx.

- Polycross nursery is a specific type of field design commonly used in the breeding of wind pollinated species where each genotype gets equal chance of being pollinated by any of the others. Series of polycross designs have been obtained for different experimental situations and an online solution WebPD has been developed for generation of these designs.

- A web application has also been developed for online generation of row-column designs for factorial experiments in two rows with unequal replication of treatment combinations for orthogonal estimation of main effects and two factor interactions.

- Forecasting agricultural commodity prices using time series data was undertaken to forecast prices of onion, wheat, mustard seeds, lentil and gram. The GARCH model was found to be a better model than ARIMA in forecasting spot price of gram and onion. For forecasting wheat, mustard and lentil prices, Vector Auto Regressive (VAR) model gave better results than ARIMA in most of the forecast days.

- Optimal one-step and two-step ahead forecast of Exponential Smooth Transition Autoregressive (ESTAR) family of nonlinear time-series model has been derived and applied to forecast oil sardine landings in Kerala.

- Monthly wholesale prices of onion crop for Mumbai, Nasik and Delhi markets have been analysed. Parametric and semiparametric multivariate GARCH model established the presence of volatility spillovers between onion market prices under consideration.

- Long memory property has been found to be highly significant in the squared return series (which is considered to be a good proxy of volatility) of gram in Delhi market. Accordingly, Fractionally Integrated Generalized Autoregressive Conditional Heteroscedastic (FIGARCH) model which allows for long memory behaviour and slow decay of the impact of volatility shock, revealed to be appropriate in modelling as well as forecasting the series.

- Small area estimation (SAE) has been used to provide estimates for those districts where there is no sample information under Improvement of Crop Statistics Scheme (ICS) and so direct estimates cannot be computed. Further, estimates generated by using SAE approach have smaller values of per cent coefficient of variation (CV) as compared to direct estimates. This clearly indicates that the SAE technique can be satisfactorily applied to produce reliable district level estimates of crop yield using Crop Cutting Experiments (CCE) supervised under ICS scheme.

- The SAE techniques for semicontinuous variables under a two part random effects model that allows for the presence of excess zeros as well as the skewed nature of the non-zero values of the response variable is studied. Empirical results suggest that the proposed method lead to efficient small area estimates for semicontinuous data of this type. A parametric bootstrap method is proposed to estimate the MSE of the proposed small area estimator. These bootstrap estimates of the MSE are compared to the true MSE in a simulation study.

- For skewed data, the commonly used small area methods, the model-based direct estimation (MBDE) and the synthetic type estimation (SYN) provide efficient estimates as compared to the linear mixed model based empirical best linear unbiased prediction. The MBDE is a direct estimator and unbiased in the presence of between area heterogeneity but can yield unstable estimates if sample sizes are too small and the synthetic type of empirical predictor only accounts for between area variability. An empirical best predictor (EBP) for small area means has been developed which addresses both of these issues simultaneously. The empirical results showed that the EBP for skewed data is efficient than the existing methods (MBDE and SYN).

- A quantitative assessment of harvest and post-harvest losses for 45 major agricultural crops / commodities in 120 districts of the country was made using stratified multistage random sampling design. A comparison of losses between 2013-14 *vis-à-vis* 2005-07 was made for various food grains, oilseeds, fruits and vegetables.

- For the situation when population level complete auxiliary information is available at the fsu level,

population level complete auxiliary information is available at the ssu level for all the fsu and population level auxiliary information is available only for the selected fsu, design weights under two stage sampling designs were calibrated using available auxiliary information at different stages. Further, the approximate variance and the Yates-Grundy form of estimate of variance of all the proposed calibration based product type estimators were also obtained.

- An attempt is being made to customize "Survey Solutions: CAPI (Computer Assisted Personal Interviewing) Software" developed by World Bank team in collaboration with Food and Agriculture Organization of United Nations, with the help of World Bank officials and configure an in-house server for the CAPI software so that the data from the field can be uploaded by the Field Investigators to IASRI server.

- Under the study on improving methods for estimating crop area, yield and production under mixed, repeated and continuous cropping by Food and Agriculture Organization (FAO) under the Global Strategy to Improve Agricultural and Rural Statistics program, two technical reports on "Synthesis of literature and framework" and "Gap analysis and proposed methodologies for estimation of crop area and crop yield under mixed and continuous cropping" were submitted to the FAO. The methodology for estimating crop area, yield and production under mixed, repeated and continuous cropping has been developed. Country schedule for obtaining information about the Agricultural Statistics System of the field testing countries and Work Plan for the field testing countries have been prepared and sent to two field testing countries i.e. Indonesia and Rwanda.

- The splice site sequence data were encoded using an approach based on the difference between the observed and estimated values of nucleotides. The observed values were taken based on occurrence and non-occurrence of nucleotides and the estimated values were computed on the basis of conditional dependencies between di-nucleotides at donor splice site motifs. Based on the proposed approach, a web application was developed to predict the donor splice sites in vertebrates and is available at http://cabgrid.res.in:8080/sspred/

- SAS codes for data generation as well as heritability estimation for different correlation structure of errors [AR(1) and AR(2)] in case of half sib and full sib models have been developed. Estimates of heritability and means square error (MSE) are obtained for heritabilities (0.1, 0.25 and 0.5), for different sample sizes and different correlation values. It has been observed that if correlation increase from -1 to 0 by 0.1 interval, the MSE decrease but if correlation increase from 0 to +1 by 0.1 interval, the MSE are increasing.

- An attempt has been made to derive the joint and conditional distributions of response variable and sire effects under correlated sire and error structures. The log likelihood function based on the observed data and the latent data has been derived theoretically and then, a theoretical expression for the Q-function which is the conditional expectation of the complete data likelihood function given the observed data and the current estimate has been derived.

- The raw micro-array data for rice and soybean under different abiotic stress conditions were pre-processed by using RMA algorithm implemented in R software. The probes which are expected to have some role in stress were identified by using a three stage filtering process from the pool of probes. Then the selected probe ids were matched to the respective gene id by using available database. Further, the modeling of transcriptional regulatory networks was done by directly taking micro-array values as gene expression values. The regulatory networks were constructed by using value of the regulatory strengths and the obtained results were validated by using published literature and available database. For time-series gene expression experiment, a feature (gene) selection criteria was developed by using support vector machine and mutual information based algorithms.

- Under National Agricultural Bioinformatics Grid (NABG) established in ICAR, a number of databases and tools have been developed and number of training programs/ workshops/ meetings of different domains were organized to sensitize and train researchers in the field of computational biology and agricultural bioinformatics.

- In the halophile proteins database available at http://webapp.cabgrid.res.in/protein/, various physicochemical properties have been listed, that are helpful in identifying the protein structure, bonding pattern and function of the

specific proteins.

- Artificial Neural Network approach has been used for breed identification with locus minimization resulting in reduction in cost of genotyping and is applied in breed identification server for goat available at http://nabg.iasri.res.in/bisgoat.

- The sugarbeet whole genome marker discovery and database SBMDb (http://webapp.cabgrid.res.in/sbmdb/) has been developed.

- FMD virus VP1 protein and integrin protein sequences of Bos, Gallus and Canis from PDB were retrieved and used for homology modelling. *silico* site directed mutation of the FMDV VP1 protein RGD domain amino acids to KGD resulted in loss of interaction between FMD VP1 protein and bos integrin. FMDV tropism in susceptible and resistant species and the importance of RGD domains for virus recognition and entry was deciphered through docking and interaction analysis *in silico.*

- A databank on "Resources Augmented and Knowledge Generated" has been developed and available at http://bioinformatics.iasri.res.in/NAIP4BSR/naipc4/. This covers the information on sub-projects, products, publications, patents, protocols developed etc., which could be of long term use to post-graduate students, researchers, research managers, regulatory bodies, policy administrators and agri-input industry.

- Anti Microbial Peptides (AMPs) are considered as alternative to chemical antibiotics. Artificial Neural Networks (ANNs) and Support Vector Machines (SVMs) have been applied to predict AMPs in cattle. SVMs with different kernels have exhibited high accuracy of prediction and were implemented on a web server available in public domain for classification/prediction of novel AMPs of cattle.

- An approach based on RF methodology was proposed (combined Random Forest) for the prediction of disease risk from imbalanced case-control data. The proposed approach was compared with the existing methods meant for imbalanced data, namely, Balanced Random Forest (BRF) and Weighted Random Forest (WRF) based on performance metrics, viz., sensitivity, specificity, classification accuracy, and precision. The proposed approach was illustrated using a case-control data set of Rheumatoid arthritis and found to perform better in terms of prediction accuracy over the existing BRF and WRF. Besides, SNPs associated with ulcerative colitis and rheumatoid arthritis diseases were identified at whole genome level by employing Least Absolute Shrinkage and Selection Operator (LASSO), a penalized regression technique.

- Identification of genes and transcription factors, which are co-expressed in multiple stress response, are important for understanding the underlying gene regulatory network. Meta-analysis of five abiotic stresses response in rice was performed by analyzing microarray samples. MCL clustering identified multiple modules that show high co-expression and further gene ontology enrichment analysis showed the stress specific modules and hub genes with high connectivity. Pathway analysis showed the involvement of genes in sucrose, carbohydrate, transport metabolism and Metabolism of terpenoids and polyketides.

- Tissue regulatory gene networks (TRGNs) with respect to salt and drought were reconstructed and investigated in rice under combined effect of salt and drought stress. It was suggested that the tissue regulatory network has a property of "small niche"; and there is substantial coordination between these niches mediated by common transcription factors. Pathway analysis of these subset of dynamic target genes were found to be involved with the processes such as stomatal closures, photosynthesis, root elongation and wax biosynthesis suggesting their probable role in providing stress tolerance in rice.

- Transcription factors (TF) knock-down approach has been used for in silico validation of developed network that mimics in-vitro knockdown experiment, which indicated that the constructed network had correctly identified the effected target genes governed by each of the TF's with an accuracy of 70%.

- Web based tool for modeling Gene Regulatory Network (GRN) facilitates pre-processing Next Generation Sequencing (NGS)/ microarray data, constructing GRN via different modeling formalisms and visualization of network. A pipeline for pre-processing NGS data with the available tools has been developed and five methods of modeling regulatory network have been integrated.

- MicroRNAs (miRNAs) are the key modulators of target gene regulation involved in different metabolism. Bread wheat (*Triticum aestivum*) is a hexaploid species with A, B, and D ancestral

genomes. Gene ontology (GO) analysis of the target genes showed enriched activity related to nitrogen, starch, sucrose, glucan and fructan biosynthesis process. Two novel miRNA's were verified by stem loop pulsed RT-PCR for their expression in root and leaf tissue under nitrogen starvation.

- Abiotic stress, especially during seedling and flowering stage, is one of the major factors responsible for huge yield losses in *Brassica juncea.* MicroRNA plays a key role in adaptive responses of the plants towards abiotic stress conditions through post transcriptional gene regulation. One of the miR-SNP (C/T) was found on the mature region of miR2926 which led to the distorted and unstable hairpin structure of miR2926 consequently there was complete loss of its function.

- Epigenetics refers to the changes in gene expression that do not involve changes in the DNA sequence. This concept implies that a new genetic state can be stably propagated through mitosis or meiosis independently of the inducible signal, yet can still revert to its original state. A web-based "Livestock Epigenetic Information System" has been developed (http://bioinformatics.iasri.res.in/ edil/) to analyse pigenetic information required for improvement in production traits and controlling diseases in livestock.

- A web based software (WP3) has been developed for carrying out phylogenetic analysis, simple sequence repeat (SSR) to primer design and expressed sequence tag (EST) to gene prediction. A separate library has been developed for connectivity to the ASHOKA supercomputing platform and the computations thereon.

- Protein structure comparison (PSC) is an important task for understanding the evolutionary relationships among proteins, predicting structure and function of proteins. Various technologies like Scoring algorithm, Software for protein structure comparison have been developed, each method optimizing its own scoring scheme. A web-based Software for protein structure comparison has also been developed for PSC for performing the protein structural analysis.

- Whole genome sequence data of Mangur fish (Clarias batrachus) were generated from Roche 454 and Ion Torrent sequencing platforms. The phylogenetic analysis of coding DNA sequences (CDS) and tRNA supports the monophyly of catfishes.

- For *multilabel functional classification of abiotic stress related proteins in Poaceae,* Post translational modification patterns such as Palmitoylation, KEN and D box, Calpain Cleavage sites, Polo like Kinase sites, Pupylation sites, S-Nitrosylation sites, Nitration Sites and Sumoylation were analysed. The physico-chemical properties of these proteins were also deduced and analyzed.

- Graph partitions obtained by spectral clusters shows significant improved result to decipher secondary structure segments and folding information than Markov CLustering (MCL). MATLAB codes for cluster analysis have been developed for further analysis and comparing 3D structures.

- Indian NARS Statistical Computing Portal (http://stat.iasri.res.in/sscnarsportal) has been strengthened by adding macros for customized analysis of data from split factorial (Main A$\times$B, Sub C) designs and strip-split plot designs. Design Resources Server (www.iasri.res.in/ design) was further strengthened by adding new link on response surface designs at http://www.iasri.res.in/design/Response%20Surface/RS_Home.html.

- Results Framework Document (RFD) is an instrument that helps prioritizing and measuring the performance of any department/organization. Results Framework Document Management System (RFD-MS) was initiated to manage RFD activities in ICAR. The RFD-MS facilitates institutes to prepare, submit and report RFDs targets and achievements online and provide access to officials authorized by the Institutes, respective SMDs and RFD coordination unit in ICAR. It also facilitates generation of consolidated reports. RFD-MS has been designed and developed in 3-tier architecture on the .NET platform. The system has a user interface for online data entry, updation and modification of various sections of RFD document. The interface for report and queries as per the requirement has been designed and developed. The consolidated reports of RFD with print option have been designed.

- Development of web based expert system on Tobacco using Agridaksh tool was initiated with Central Tobacco Research Institute, Rajahmundry to provide knowledge based system on various aspects of tobacco crop. The system aims to design and develop various modules on tobacco such as insect pests and

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diseases, abiotic stresses, varieties, soil types and nutrient disorders, weed management and world tobacco scenario. The customization, designing and development of tobacco expert system was done using the Agridaksh tool.

- ICAR-ERP system is available for access at http://icarerp.iasri.res.in. Following Modular approach, the system has been implemented in 108 ICAR institutions. Data digitization work was carried out in all ICAR institutions. Data was loaded in the system using scripts. More than 20000 users have been created in the system. Finance module is completely operational in all the institutes. Almost 3 lakh transactions have been recorded in different modules till March 2015.

- ICAR Data Centre (Tier-III) has been established at IASRI to provide Unified Mail Messaging and Web Hosting solution in ICAR. Domain name "icar.gov.in" has been registered and the Unified Communication and Web Hosting Services have been made operational. Digital certificates of servers were procured and installed SSL to provide the services of different applications through http://icar.gov.in domain. Coordination has been made with NIC to strengthen the existing NKN connectivity to newly created Data Centre (Dual link has been established). Unified messaging solution (email with chat features) has been implemented (https://mail.icar.gov.in). Email ids are being created for ICAR employees after verification of data from institutes. KRISHI Portal, Agroweb, NAIP and other application running from IASRI server (HYPM, NISAGENET) have been migrated into Data center environment.

- Developed a phenome data management system with several analysis modules meant for estimation of physical and biochemical traits of rice under moisture deficit and low temperature stress tolerance. Regression methodology was applied for estimation of leaf area and chlorophyll content of rice seedlings under pot culture conditions through image analysis. An online software "Leaf Area Estimator" has been developed and deployed on the production server for ready use by the experimental biologists.

- Dog Health Management Trainer (DHMT) was designed and developed to provide the detailed stepwise information to dog owners. DHMT serves as an expert for training of the dog owners who are beginners and are keen to know the scientifically correct methods of dog rearing.

- The software Expert System for Farm Power and Machinery Selection has been developed. DLL (Dynamic Link Libraries) and API (Application Programming Interface) have been developed for each module used in this software. It is a complete web based solution or web based expert system for farm power and machinery selection for rice-wheat crops.

The Institute organized the 68th Annual Conference of the Indian Society of Agricultural Statistics during January 29-31, 2015. During the Conference, a Workshop on "Methodology for Estimating Crop Area and Yield under Mixed and Continuous Cropping" was also organized. 9 students (6 Agricultural Statistics, 2 Computer Application and 1 Bioinformatics) received Appreciation Certificates for the excellent presentation of their papers in the respective sessions. The Institute has regularly organized the meetings of Research Advisory Committee (RAC), Institute Management Committee (IMC) and Institute Research Committee (IRC). Results Framework Document, 2014-15 was submitted to the Council.

Scientists of the Institute have published 128 research papers in National and International refereed Journals along with 24 popular articles/ short communications, 1 book, 9 book chapters, 4 papers in conference proceedings and 58 project reports/technical bulletins/ monograph/reference manuals/brochures. Besides this, 57 e-manuals/ e-resources/ macros were also developed.

During the year, 25 training programmes were organized in which 636 participants were imparted training

- Six 21 days training programme under Centre of Advanced Faculty Training on Forecast Modelling Analytics in Crops, Agricultural Web Applications Development using Content Management Tools, Recent Advances in Survey Design and Analysis of Survey Data using Statistical Software, Advances in Omics Data Analysis: Learning by Examples, Advanced Statistical Techniques in Horticulture Science Research and Recent Advances in Statistical Genetics were organized.

- Thirteen training programmes were conducted under National Agricultural Innovation Projects: Basic Training on Discovery Studio, High Performance Computing, Oracle Database 11g: Administration Workshop, Six Different modules

of SAS software: SAS Data Integration Studio, Fast Track, Data Flux Data Management Studio, Text Analytics Using SAS Text Miner, Managing SAS Analytical Models Using SAS Model Manager, Grid Computing (SAS Enterprise Scheduling with Platform Suite for SAS and SAS Content Categorization Studio: Building Models, Advance Training on Discovery Studio Software, Training for Post ICAR-ERP implementation, Knowledge Enhancement Session or MIS/FMS Solution by IBM and Post Go-Live Knowledge Enhancement Sessions for MIS/FMS Solution.

- Four Resource Generation training programmes were conducted on Data Analysis and Interpretation for ISS Probationers of XXXV Batch sponsored by CSO, Ministry of Statistics and Programme Implementation, Refresher Training Programme on Statistical Techniques sponsored by Livestock Department, Government of Chhattisgarh, International training programme on Importance of Statistical and Experimental Designs, Data Analysis and Biometrical Techniques in Agriculture Research sponsored by Ministry of Agriculture, Irrigation and livestock (MAIL), Afghanistan and International training programme on Applications of Remote Sensing and GIS Development in Agricultural Surveys sponsored by African-Asian Rural Development Organization.

- Two other training programmes sponsored by ICAR on Office Automation using Oracle ERP for Technical Personnels of ICAR were organized.

The activities relating to Post Graduate teaching programmes of the Institute were undertaken in collaboration with PG School, IARI. During the year, a total of 18 students {5 Ph.D. (Agricultural Statistics), 6 M.Sc. (Agricultural Statistics), 2 M.Sc. (Computer Application) and 5 M.Sc. (Bioinformatics)} completed their degrees. 32 new students {6 Ph.D. (Agricultural Statistics), 8 M.Sc. (Agricultural Statistics), 7 M.Sc. (Computer Application), 6 Ph.D. (Bioinformatics) and 5 M.Sc. (Bioinformatics)} were admitted. A Senior Certificate Course in Agricultural Statistics and Computing was also organized.

Dr. UC Sud visited Bangladesh to participate in the Workshop on Harmonization and Dissemination of Unified Agricultural Production Statistics in Bangladesh. Dr. Hukum Chandra Visited Italy to attend the collaborative training programme on Small Area Estimation under Generalized Linear Mixed Model at Department of Economics and Management, University of Pisa, Italy. He also visited Tsukuba, Japan to participate in Sixth Workshop on Forging Partnerships in Statistical Training in Asia and the Pacific: Networking for Agricultural and Rural Statistics, attended experts meeting on Skills Framework and Training Needs Assessment Tools for Agricultural and Rural Statistics and visited Chiba, Japan to attend the training programme at United Nations Statistical Institute for Asia and the Pacific on Assessing Training Needs of the Statistical Workforce in Agricultural Statistics. Sh. KK Chaturvedi attended training on Bioinformatics at Cornell University, Ithaca, USA sponsored by NAIP (ICAR). Dr. Sanjeev Panwar visited Addis Ababa, Ethiopia as a resource person in the training course on Advanced Experimental Designs, Data Analysis and Management for Breeding Trials. Dr. Susheel Kumar Sarkar visited Spain to attend training on Integrated Breeding Multi-Year Course (IB-MYC) Year 3 under Generation Challenge Programme - Integrated Breeding Platform (GCP-IBP) at Mediterranean Agronomic Institute of Zaragoza (IAMZ) in Zaragoza, Spain.

Scientists of the Institute have brought laurels to the Institute by receiving awards from different agencies. Dr. Seema Jaggi received the Bharat Ratna Dr. C. Subramaniam Award for Outstanding Teachers-2013 of ICAR for excellent teaching in the field of Social Sciences during the 86th ICAR Foundation Day and Award Ceremony held at NASC Complex, New Delhi on July 29, 2014. Dr. Hukum Chandra was awarded ICAR-National Fellow and also received Professor PV Sukhatme Gold Medal Award 2014 by the Indian Society of Agricultural Statistics during 68th Annual Conference of ISAS (29-31 January 2015) for his outstanding contribution in the field of Agricultural Statistics. Dr. Alka Arora received the Best Paper Award published in the journal of ISAS and Sh. KK Chaturvedi received Fellowship Award from Society for Scientific Development in Agriculture and Technology, Meerut.

ORGANOGRAM

RESEARCH ADVISORY COMMITTEE — **DIRECTOR** — INSTITUTE MANAGEMENT COMMITTEE
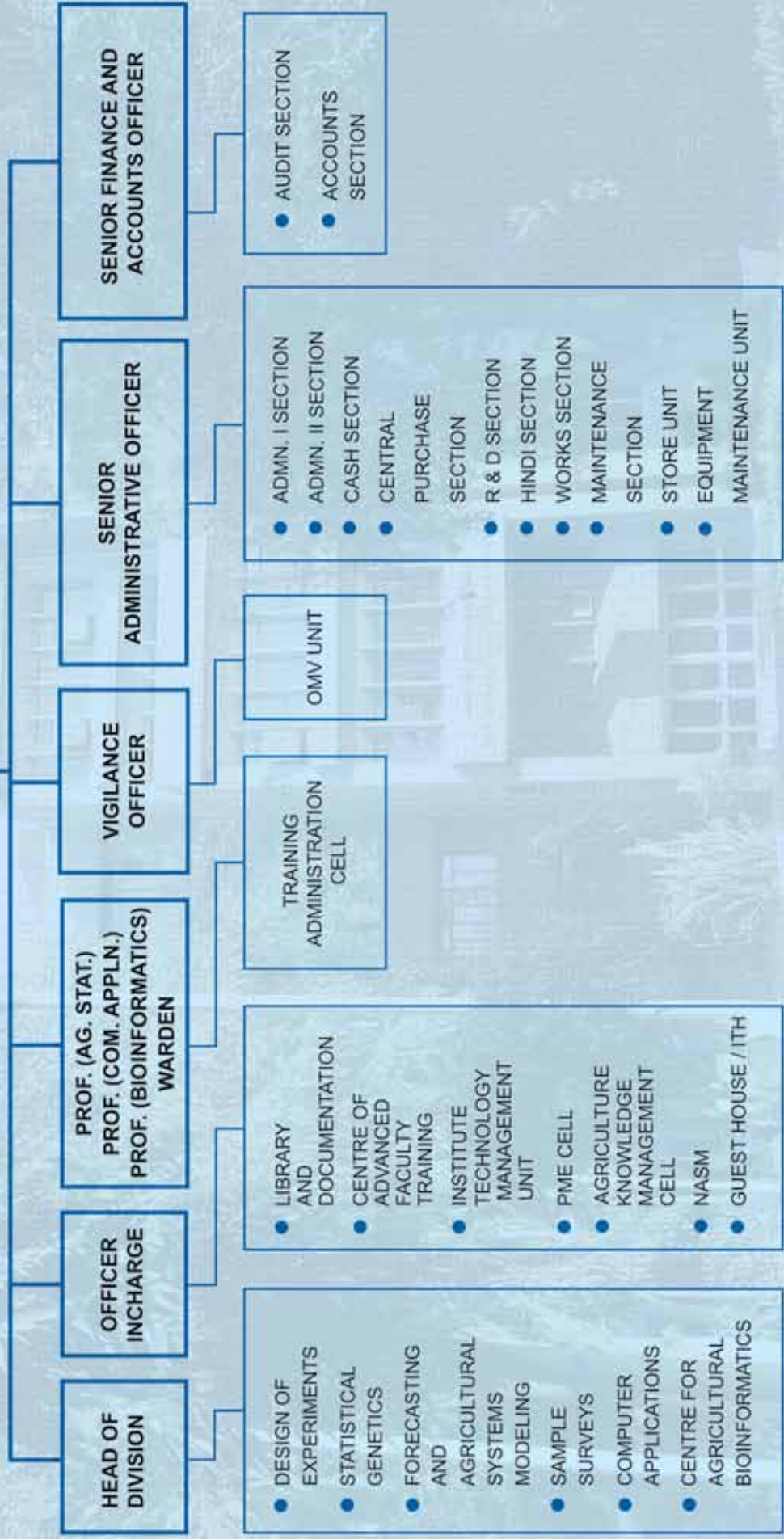
HEAD OF DIVISION

- DESIGN OF EXPERIMENTS
- STATISTICAL GENETICS
- FORECASTING AND AGRICULTURAL SYSTEMS MODELING
- SAMPLE SURVEYS
- COMPUTER APPLICATIONS
- CENTRE FOR AGRICULTURAL BIOINFORMATICS

OFFICER INCHARGE

- LIBRARY AND DOCUMENTATION
- CENTRE OF ADVANCED FACULTY TRAINING
- INSTITUTE TECHNOLOGY MANAGEMENT UNIT
- PME CELL
- AGRICULTURE KNOWLEDGE MANAGEMENT CELL
- NASM
- GUEST HOUSE / ITH

PROF. (AG. STAT.)
PROF. (COM. APPLN.)
PROF. (BIOINFORMATICS)
WARDEN

TRAINING ADMINISTRATION CELL

VIGILANCE OFFICER

OMV UNIT

SENIOR ADMINISTRATIVE OFFICER

- ADMN. I SECTION
- ADMN. II SECTION
- CASH SECTION
- CENTRAL PURCHASE SECTION
- R & D SECTION
- HINDI SECTION
- WORKS SECTION
- MAINTENANCE SECTION
- STORE UNIT
- EQUIPMENT MAINTENANCE UNIT

SENIOR FINANCE AND ACCOUNTS OFFICER

- AUDIT SECTION
- ACCOUNTS SECTION