CURRICULUM VITAE

Samarendra Das, Ph.D., ARS

Scientist
ICAR-Directorate of Foot and Mouth Disease
International Centre for Foot and Mouth Disease
(Indian Council of Agricultural Research)
Arugul, Bhubaneswar-752050, Odisha, India

Netaji Subhas ICAR-International Fellow
Indian Council of Agricultural Research (ICAR)
Krishi Bhawan, New Delhi-110001, India

Google scholar: **tfR9vO0AAAAJ**
ORCID: **0000-0002-0263-7027**

Phone: +91-0674-2601104 (O)
+91 7873836277 (R)
+91 9861345735 (M)
Fax: +91-5942-286307 (O)

Email id: samarendra.das@icar.gov.in
samarendra.das@louisville.edu
samarendra4849@gmail.com

Place of Birth: Amarsinghpur, Malapada, Jajpur, Odisha

Citizenship: India

Educational Background:

Institution and Location	Degree	Completion	Field of study
Orissa University of Agriculture and Technology, Bhubaneswar 755001, Odisha, India	B.Sc.	2009	Agriculture
Indian Agricultural Research Institute, New Delhi 110012, India	M.Sc.	2011	Agricultural Statistics
University of Louisville, Louisville, Ky 40292, USA	Ph.D.	2020	Bioinformatics

Ph. D. Details:

Dissertation Thesis Title: Statistical Approaches of Gene Set Analysis for High-throughput Genomic Studies

Year of Award: 2020
University: University of Louisville, Kentucky, USA
Funded by: Education Division, ICAR, New Delhi; Graduate Assistantship, James Brown Cancer Center, University of Louisville, USA; National Institutes of Health, USA

Thesis Supervisor: Shesh N. Rai, Ph. D.
Fellow, American Statistical Association
Elected Member, Delta Omega Honorary Society in Public Health
Director, Biostatistics and Bioinformatics Facility, JG Brown Cancer Center
Director, Biostatistics and Informatics, Center for Integrative Environmental Health Sciences
Wendell Cherry Chair in Clinical Trial Research
Professor, Department of Bioinformatics and Biostatistics
University: University of Louisville, Kentucky, USA

Employment Details:

Sl. No.	**Positions held**	**Name of the Institute**	**From**	**To**
1	Foundation Trainee	ICAR-National Academy of Agricultural Research Management, Hyderabad	January 2013	May 2013
2	Attachment Trainee	National Institute of Biomedical Genomics, Kalyani, West Bengal, India	June 2013	September 2013
3	Scientist	ICAR-Indian Agricultural Statistics Research Institute, New Delhi, India	October 2013	August 2017
4	Ph.D. Graduate Assistant	University of Louisville, Kentucky, USA	August 2017	May 2019
5	Ph.D. candidate	University of Louisville, Kentucky, USA	May 2019	December 2020
6	Student Assistant	James Graham Brown Cancer Center, Louisville, Ky, USA	November 2019	December 2020
7	Scientist (SS)	ICAR-Indian Agricultural Statistics Research Institute, New Delhi, India	2018	Present

2017-2020 deputation at University of Louisville, USA

Research Experience:

Scientist (SS), ICAR-Indian Agricultural Statistics Research Institute, New Delhi, India
(December 2020 – present)
Project 1: Development of Statistical Approach for Analysis of Zero-inflated and Over-dispersed Counts Data and Its Application in Single-cell Studies (PI)
Project 2: Development of (Co-PI)
Role:

- Responsible for proposal writing, funding acquisition, project administration, project co-ordination
- Experiments designing, statistical methodology, and tools development for high-throughput genomic studies including single-cell sequencing studies
- Software and Code development
- Manuscript drafting, correction, publication

Ph. D. Candidate, University of Louisville, USA
(August 2017 – December 2020)
Dissertation project: Statistical Approaches of Gene Set Analysis with Quantitative Trait Loci for High-Throughput Genomic Studies

- Responsible for experiments designing, statistical methodology and tools development for high-throughput genomic studies, big data analytics, data mining.
- Responsible for software development, data analysis, manuscript drafting and revision, research grant writing.

Mentor: Dr. Shesh N. Rai
Professor, Dept. of Bioinformatics and Biostatistics
University of Louisville, Ky, USA
Email id: shesh.rai@louisville.edu
Ph. 502/472-9120

Research Assistant, James Graham Brown Cancer Center
(November 2019 – December 2020)

- Responsible for assisting the supervisor on preparing the teaching materials, data analysis, grant writing, reviewing manuscripts, drafting manuscripts and other activities.
- Responsible for R codes and package development
- Supervised by: Shesh N. Rai, Ph.D.
  Director, Biostatistics and Bioinformatics facility, James Brown Cancer Center
  University of Louisville, Ky, USA

Scientist, ICAR-Indian Agricultural Statistics Research Institute, New Delhi, India
(January 2013 – August 2017)
Project 1: Modelling and construction of transcriptional regulatory networks using time-series gene expression data (AGENIASRISIL201401100030)
Role: Principal Investigator (05/2014 –01/2017)
Funded by Indian Council of Agricultural Research, New Delhi, India

Project 2: Development of gene selection approaches for classification of crop gene expression data. (AGENIASRISIL201503000067)
Role: Principal Investigator (10/2015 – 10/2018)
Funded by Indian Council of Agricultural Research, New Delhi, India

Project 3: Development of Rank based Stability Measures for Selecting Genotypes.

(AGENIASRISIL201502500062)
Role: Co-Principal Investigator (09/2015 – 08/2017)
Funded by Indian Council of Agricultural Research, New Delhi, India

- Responsible for research project writing, leading research projects as PI and Co-PI, project writing, manuscript drafting, reviewing manuscripts and project reports.
- Responsible for development of statistical approaches, models, and software for high dimensional gene expression data.
- Responsible for development of data mining techniques genomic data analysis.

Research Student, ICAR-Indian Agricultural Research Institute, New Delhi, India
(August 2009 – August 2012)

- Responsible for analyzing agricultural crop data, writing codes in SAS, R.
- Assisting supervisor for preparing teaching materials

Mentor(s): A. K. Paul, Ph.D., Principal Scientist
Anil Rai, Ph.D., Principal Scientist
ICAR-Indian Agricultural Research Institute, New Delhi, India

Awards and Fellowships:

Sl. No.	Name of Award	Awarding Agency	Year
1	ICAR Junior Research Fellowship (JRF)	Indian Council of Agricultural Research, New Delhi, India (2009 - 11)	2009
2	IARI Ph. D. Scholarship	Indian Agricultural Research Institute, New Delhi, India (2011 – 12)	2011
3	Nehru Memorial Gold Medal Award	Indian Agricultural Statistics Research Institute, New Delhi, India	2011
4	National Eligibility Test (NET)	Indian Council of Agricultural Research, New Delhi, India	2012
5	Agricultural Research Service	Indian Council of Agricultural Research, New Delhi, India	2012
6	Runner UP for MN Das Young Scientist Award	Society of Statistics, Computers, and Applications	2016
7	MN Das Memorial Young Scientist Appreciation Certificate	Society of Statistics, Computers, and Applications	2017
8	Netaji Subash-ICAR International Fellowship	Indian Council of Agricultural Research, New Delhi, India (2017 – 2020)	2017
9	Graduate Assistantship	University of Louisville, Kentucky, USA (2017 -2020)	2017
10	Financial Aid Award	Dept. Hepatobiology and Toxicology, University of Louisville, Kentucky, USA	2017
11	Best Paper Award (in Statistical Theory and Methodology),	The Indian Society of Agricultural Statistics, New Delhi, India	2018
12	Summer Internship	Ekstrom Library, University of Louisville, Kentucky, USA	2019

13	Graduate Student Assistant Award	James Graham Brown Cancer Center, Louisville, Ky, USA	2019
14	Student Assistantship	James Graham Brown Cancer Center, Louisville, Kentucky, USA (2019 -2020)	2019
15	Ph.D. dissertation completion award	Dept. Hepatobiology and Toxicology, University of Louisville, Kentucky, USA	2020
16	Graduate Dean's Citation Award	University of Louisville, Kentucky, USA (For outstanding contribution to Ph. D. dissertation)	2020

Professional Society Membership:

SN.	Membership	Society with address	Year
1	Life member	Society of Biotechnology and Bioinformatics, OUAT, Odisha, India	2015
2	Member	American Statistical Association, USA	2018
3	Member	ASA-Kentucky Chapter, University of Louisville, USA	2018
4	Life member	Indian Society of Agricultural Statistics, IASRI, New Delhi-12, India	2021

Research Interests: Computational Biology and Bioinformatics, Statistical Genetics and Genomics, Statistics

It is well known that, 21st century is the century of biology and further, data is considered as the gold for this century. Therefore, bioinformatics and computational biology may play a significant role in this era through contributing efficient approaches, algorithms and tools for biological data analysis. As a student of Bioinformatics and Computational biology, I have started working on development of statistical approaches, algorithms and tools for high throughput and high dimensional genomic data analysis. In my earlier posting, I worked as a Scientist in Indian Council of Agricultural Research, New Delhi, India, where, I formulated two research projects as a principal investigator and one as co- investigator. As part of the several core research teams, I have working experience to accomplish project goals like formulating research objectives, developing methodologies, algorithms and tools, project budgeting, reporting, etc. Most of my scientific works involved in the development of statistical approaches for gene selection, network biology, pathway analysis, etc. Apart from this, I was also involved in teaching of several courses to M.S. and Ph.D. students in the department of Agricultural Statistics, Computer Application and Agricultural Bioinformatics of Post Graduate (PG) School, Indian Agricultural Research Institute (IARI), New Delhi, India. As a faculty of PG school, I have a good academic experience as I extensively worked with other faculty members and graduate students. Currently, I am enrolled as a Ph.D. graduate student in Dept. of Interdisciplinary Studies, School of Interdisciplinary and Graduate Studies, University of Louisville, USA. Here, I have completed all my requisite course works with good academic grades having CGPA 3.8/4. Under the course works, I had a diverse academic exposure to courses offered by Biostatistics, Molecular Biology and Biochemistry, Computer Engineering and Computer Science and Biology departments. As part of the compulsory graduate research study, I along with the thesis advisor formulated the dissertation research work project. Here, my research focuses on the development of statistical approaches, algorithms and user-friendly tools for gene set analysis for varied form of genomic data. As it is dissertation research project, my role will be that of

Principal Investigator and will be responsible for overall project management, partnering and collaborating with other advisory committee members.

A. Contributions to Science

(1) Related to this work, I have recently engaged in development of statistical approaches for modeling of gene regulatory networks (GRNs) from high dimensional gene expression data. Further, these approaches for modelling gene-gene relationships in system biology studies. These networks allow us to carry out studies of different biological processes in a visual way. The noise and high dimensionality in the Gene Expression (GE) data have limited the applicability of the certain statistical techniques to model the underlying gene regulatory interactions. So, a project was undertaken to develop some statistical approaches to model and construct the GRNs under sparse biological conditions.

(a) **Das Samarendra**, Pandey P., Rai Anil and Mohapatra C. (2015). A computational systems biology approach to construct gene regulatory networks for salinity response in rice (Oryza sativa). Indian Journal of Agricultural Sciences. 85(12): 1546–52.

(b) **Das Samarendra**, Meher P.K., Pradhan U.P., Paul A.K. (2017). Inferring gene regulatory networks using Kendall's tau correlation coefficient and identification of salinity stress responsive genes in rice. Current Science 112(6):1257-63.

(c) **Das Samarendra**, Meher PK, Rai A, Bhar LM, Mandal BN (2017) Statistical Approaches for Gene Selection, Hub Gene Identification and Module Interaction in Gene Co-Expression Network Analysis: An Application to Aluminum Stress in Soybean (Glycine max L.). PLoS ONE 12(1): e0169605. doi:10.1371/journal.pone.0169605.

(d) **Das Samarendra** (2017). Modeling of Gene Regulatory Networks Using State Space Models. Curr Trends Biomedical Eng & Biosci 4(5): 555646. doi: 10.19080/CTBEB.2017.04.555646.

(2) Development of gene selection approaches for classification of crop gene expression data.

Related to this application, I was also involved in developing statistical approaches for gene selection from high dimensional gene expression data. Moreover, recent advances in genomic technologies enable the measurement of the activity levels of several thousands of genes or transcripts in a single experiment. DNA microarrays, with their ability to capture a substantial fraction of a cell state, are one of such powerful tools in genomics. Among these thousands of genes whose expression levels are measured, not all are required for classification, gene regulation modeling, modules detection, *etc*. The need is to select some genes or set of genes those are highly relevant with particular class, which is called informative genes. So, this project was undertaken to develop some statistical approaches to select biologically relevant genes from the high dimensional GE data.

Das, Samarendra, Rai, Anil, Mishra, D.C. and Rai, S.N. (2018). Statistical approach for selection of biologically informative genes. *Gene*, 655, 71-83. doi: 10.1016/j.gene.2018.02.044

Teaching:

2014 - 2017	Mathematical Methods in Statistics (AS 551) Bioinformatics (AS 571) Mathematical Foundations in Computer Application (CA 551)

	Advanced Statistical Genetics (AS 602) Statistical Methods (SSC: Module I) Statistical Genetics (SSC: Module II) Biological Network Modeling and Analysis (BI 614) Senior Certificate Course
2020 - 2022	Statistical Genetics (STAT 566) Biological Network Modeling and Analysis (BI 607) Advanced Statistical Genetics (STAT 603)

Faculty Development Program (FDP):

SN	Programmes	Duration	Role	#Participants
1	CAFT on “Recent Analytical Techniques in Statistical Genetics and Genomics”	January 17 - February 06, 2017 (21 days)	Coordinator	25
2	Winter School on "Advanced Statistical Techniques in Genetics and Genomics" during	March 02-22, 2017 (21 days)	Co-director	22
3	Workshop on “Statistical Genetics and Its Application in Agriculture”	March 18 – 20, 2020	Coordinator	35
4	Attachment training of Scientist (P)	April 06 –June 05, 2021	Mentor	1

Research Projects:

1. **ICAR-IASRI** research project entitled as “Modelling and construction of transcriptional regulatory networks using time-series gene expression data”; May 2014 – January 2017 (2.5 years). PI, Completed.
2. **ICAR-IASRI** research project entitled as “Gene Selection for Classification of Crop Gene Expression Data”; October 2014 – September 2018 (3 years). PI till August 2017, Completed.
3. **ICAR-IASRI** research project entitled as “Development of rank based stability measures for selecting genotypes”; September 2015 – August 2017 (2 years). Co-PI, Completed.
4. **Education Division,** ICAR funded research project entitled as “Statistical Approaches of Gene Set Analysis with Quantitative Trait Loci for High-throughput Genomic Studies”; August 2017 – December 2020 (3 years), PI, completed.
5. **SERB,** Department of Science and Technology funded research project entitled as “Statistical Approaches of Differential Gene Network Analysis for High-throughput Single-cell RNA-sequencing Studies”; Approved; Yet to Start, PI.
6. **ICAR-IASRI** research project entitled as “Development of Statistical Approaches for Analysis of Zero-inflated and Over-dispersed Counts Data and its Application in Single-cell Studies”; November 2021 – July, 2024 (2.5 years), PI.

7. **ICAR-IASRI** research project entitled as “Computational Prediction and Modeling of Nucleic Acid-binding Proteins in miRNA Biogenesis using Conditional Networks”; November 2021 – July, 2024 (2.5 years), Co-PI.

Software and Copyrights:

SN.	Name	Description	Copy right	Developer
1	dhga R package	Gene co-expression network and hub analysis	© 2017 Das et al CC BY 4.0	S Das
2	GSAQ R package	Gene set analysis with Quantitative Trait Loci (QTL)	© 2018 Das et al CC BY 4.0	S Das
3	BootMRMR R package	Biological informative gene selection from gene expression data	© 2018 Das et al CC BY 4.0	S Das
4	SwarnSeq R package	Single-cell RNA-seq data analysis	© 2021 Das et al CC BY 4.0	S Das
5	BSM R package	Relevant gene selection from gene expression data	© 2020 Das et al CC BY 4.0	S Das
6	GSQSeq R package	Gene set analysis with QTL for RNA-seq studies	© 2021 Das et al CC BY 4.0	S Das

Referred Publications: 21 (Google scholar id: tfR9vO0AAAAJ and ORCID id: 0000-0002-0263-7027)

1. Malhotra, A., **Das, S**. and Rai, S.N. (2022). Analysis of Single-Cell RNA-seq Data from Adenocarcinoma Cell Lines: A Stepwise Guide. *BioMedInformatics*. 2(1), 43-61. doi.org/10.3390/biomedinformatics2010003
2. **Das, S**., Rai, A., Merchant, M., Cave, M., and Rai, S.N. (2021). A Comprehensive Survey of Differential Expression Analysis Approaches in Single Cell RNA-sequencing Studies. *Genes*, 12(12), 1947. doi.org/10.3390/genes12121947. [IF: 4.096; NAAS: 10.1]
3. **Das, S**. and Rai, S.N. (2021). Statistical methods for single-cell RNA-sequencing data analysis. *MethodsX*, 8, 101580. doi.org/10.1016/j.mex.2021.101580
4. **Das**, **S**. and Rai, S.N. (2021). Statistical Approach for Gene Set Analysis with Quantitative Trait Loci for Crop Gene Expression Data. *Entropy* (Statistical Inference from High Dimensional Data II), *23*(8), 945; doi.org/10.3390/e23080945 [PMID: 34441085; PMCID: PMC8391627]. [IF: 2.524; NAAS: 8.524]
5. **Das**, **S**. and Rai, S.N. (2021). SwarnSeq: An Improved Statistical Approach for Differential Expression Analysis of Single-Cell RNA-Seq Data. *Genomics*, 113 (3), 1308-1324. doi.org/10.1016/j.ygeno.2021.02.014 [PMID: 33662531]. [IF: 6.25; NAAS: 12.25]
6. Sharma, N., Mishra, D.C., Farooqi, M.S., Budhlakoti, N., Chatturvedi, K.K., **Das, S.**, Rai, A., Kumar, A. (2021). Algorithm for selection of informative genes using gene expression data. *Int. J. Ag. Stat. Sci.*, 17(1), 2419-26. [NAAS:]
7. **Das**, **S**., McClain, C. J., and Rai, S.N. (2020). Fifteen Years of Gene Set Analysis for Genomic Studies: A Review of Statistical Approaches and Future Challenges. *Entropy* 22(4), 427; doi.org/10.3390/e22040427. [PMID: 33286201; PMCID: PMC7516904] [IF: 2.524; NAAS: 8.524]
8. **Das**, **S**. and Rai, S.N. (2020) Statistical Approach for Biologically Relevant Gene Selection from High-Throughput Gene Expression Data. *Entropy*, *22*(11), 1205.

doi.org/10.3390/e22111205. [PMID: 33286973; PMCID: PMC7712650] [IF: 2.524; NAAS: 8.524]
9. **Das S**, Chhuria S, Rouchka EC, Rai SN. (2020). A Computational Network Biology Approach to Understand Salinity Stress Response in Rice (*Oryza Sativa* L.). *Bioinform. Int.,* 1(1): 1003.
10. **Das**, **S**., Rai, A., Mishra, D.C. & Rai, S.N. (2018). Statistical Approach for Selection of Biologically Informative Genes. *Gene*, 655:71-83. doi: 10.1016/j.gene.2018.02.044. [PMID: 29458166] [IF: 3.688.524; NAAS: 9.688]
11. **Das**, **S**., Rai, A., Mishra, D.C. Rai, S.N. (2018). Statistical Approach for Gene Set Analysis with Trait Specific Quantitative Trait Loci. *Scientific Reports* 8, 2391. doi.org/10.1038/s41598-018-19736-w. [PMID: 29402907; PMCID: PMC5799309] [IF: 4.379; NAAS: 10.379]
12. Kumar, P., Bhar, L.M., Paul, A.K., Das, S., Roy, H.S. (2018). Development of Composite Stability Measure using Multi Criteria Decisions Making (MCDM) Techniques. *J. of the Ind. Soc. of Ag. Stat.* 72(2) 2018 121–127. [NAAS:]
13. **Das, S**., Meher P.K., Rai, A., Bhar, L.M., Mandal, B.N. (2017). Statistical Approaches for Gene Selection, Hub Gene Identification and Module Interaction in Gene Co-Expression Network Analysis: An Application to Aluminum Stress in Soybean (Glycine max L.). *PLoS ONE* 12(1): e0169605. doi:10.1371/journal.pone.0169605 [PMID: 28056073; PMCID: PMC5215982]. [IF: 3.24; NAAS: 9.24]
14. **Das, S**., Meher, P.K., Pradhan, U.P., Paul, A.K. (2017). Inferring gene regulatory networks using Kendall's tau correlation coefficient and identification of salinity stress responsive genes in rice. *Current Science,* 112(6):1257-63. [IF: 1.10; 7.10]
15. **Das, S.** (2017). Modeling of Gene Regulatory Networks Using State Space Models. *Curr Trends Biomedical Eng & Biosci.,* **4**(**5**): 555646. doi: 10.19080/CTBEB.2017.04.555646.
16. **Das, S**., Pandey P., Rai Anil and Mohapatra C. (2015). A computational systems biology approach to construct gene regulatory networks for salinity response in rice (*Oryza sativa*). *Indian Journal of Agricultural Sciences*. 85(12): 1546–52. [NAAS:6.20]
17. Das Samarendra, Paul A.K., Wahi S.D., Pradhan U.P. (2017). Comparative performance of imputation methods for different proportions of missing data in classification of crop genotypes. *J Indian Soc Agric Stat* 71(2), 147–153.
18. Behera S.K., Paul A.K., Wahi S.D. ,Iquebal M.A., Das S, Paul R.K., Alam W. and Kumar, A. (2014). Estimation of heritability of mastitis disease using moment estimators. *Int. J. Ag. Stat. Sci*., 10 (1), 243-247. [NAAS:]
19. Paul A.K., Paul R.K., Das S, Behera S.K and Dhandapani A (2015). Non-parametric stability measures for analysing non-normal data. *Indian Journal of Agricultural Sciences*, 85(8):1097-1101. [NAAS:]
20. Raman R.K., Paul A.K., Das S, Wahi, S.D. (2015). Empirical comparison of the performance of linear discriminant function under multivariate non-normal and normal data. *Int. J. Ag. Stat. Sci*. 11(2): 403-409. [NAAS:]
21. Das S, Paul A.K., Wahi S.D., Raman R.K. (2015). A comparative study of various classification techniques in multivariate skew-normal data. *J. of the Ind. Soc. of Ag. Stat*. 69(3), 271-280. [NAAS:]

Publication in press

1. Rai, S.N., **Das, S**., Pan, J. Bousamra, M. & Fu, X. (2021). Multigroup Prediction in Lung Cancer Patients and Comparative Controls using Signature of Volatile Organic Compounds in Breath Samples. *PLoS One.*

2. **Das, S**., Pradhan, U.K., Rai, S.N. (2022). Five Years of Gene Network Modeling and Construction in Single-cell RNA-sequencing Studies: Current Statistical Approaches and Outstanding Challenges. *Current Bioinformatics*

Publication under consideration

3. **Das, S.** and Rai, S.N. (2022). SwarnSeq R Shinny App and Bioconductor Package for Analysis of Single-Cell RNA-Seq Data. *Brief. Bioinformatics.*
4. **Das, S.,** Pradhan, U.K., Kumar, S., Rai, S.N. (2022). Differential Expression Analysis of Single-cell RNA-sequencing Data: Current Statistical Approaches and Outstanding Challenges. *PLoS Computational Biology.*

Book chapter:

5. **Das, S**. and Rai, S.N. (2021). Statistical Approach for Biologically Relevant Gene Selection from High-Throughput Gene Expression Data. *Statistical Inference from High Dimensional Data,* edited by Carlos Fernandez-Lozano, MDPI, pp. 35 -57.
6. **Das, S**., McClain, C.J. and Rai, S.N. (2021). Fifteen Years of Gene Set Analysis for High-Throughput Genomic Data: A Review of Statistical Approaches and Future Challenges. *Statistical Inference from High Dimensional Data,* edited by Carlos Fernandez-Lozano, MDPI, pp. 149 - 171.
7. **Das**, **S**. and Rai, S.N. (2021). A Statistical Perspective of Gene Set Analysis with Quantitative Trait Loci in Plant Breeding and Genetics. Soybean Breeding: Physiological, Molecular and Genetic Perspectives. *QTLian Breeding in Crop Plants: Present Progress and Future Perspectives*. Edited by Shabir Hussain Wani. Elsevier Publication (In press).
8. **Das, S.** and Maity, A. (2021). Utility of Network Biological Approaches to understand Aluminum stress in Soybean. *Soybean Breeding: Physiological, Molecular and Genetic Perspectives.* . Edited by Shabir Hussain Wani. Springer Publication (In press).

Reviewed Manuscripts from following Journals:

PLoS One
BMC Bioinformatics
Scientific Reports
Bioinformatics
ACM/IEEE Journal of Computational Biology
Current Science

Invited lectures/speaker

1. Delivered one invited lecture “Multivariate Data Analysis using R” in training programme on “Statistical Techniques for Data Analysis in Agriculture” on October 13, 2021 organized at IASRI, New Delhi.
2. Delivered one invited lecture “Bayesian Network Analysis” in training programme on “Statistics for Social Science Scholars” for ICAR-CIFE Students on March 23, 2021 organized at IASRI, New Delhi.
3. Delivered a talk on “Statistical approaches for gene selection and hub gene identification in gene co-expression network analysis” in Bioinformatics Journal Club, at Clinical and Translational Research Building, University of Louisville, USA on November 18, 2017.

4. Delivered a flash talk on “Statistical Approaches for Gene Set Analysis with Quantitative Trait Loci” in Bioinformatics session of the 2019 Southeast Regional IDeA Conference at Galt House Hotel, Louisville, Kentucky, USA on November 6, 2019.
5. Delivered a short talk on “Statistical Approaches for Gene Set Analysis” in the Data science session of the 2019 Southeast Regional IDeA Conference at Galt House Hotel, Louisville, Kentucky, USA on November 7, 2019.
6. Invited to participate in AgriSearch 2050 held on 18th May 2015 at NASC complex, New Delhi organized by ICAR and also made a presentation about the Role of Statistics and Informatics in Agricultural Research at 2050.
1. Delivered two Lectures on 2nd December, 2015 in the topic “Modeling of Gene Regulatory Networks” along with the practical in R in the Winter School on “Bioinformatics and High Dimensional Data Analysis” at ICAR-IASRI
2. Delivered two lectures on “Modelling of gene regulation” along with the practical in the CAFT program on “Recent Advances in Statistical genetics and genomics”
3. Delivered two lectures on “Statistical models in Gene expression genomics” along with the practical in the CAFT program on “Computational Tools and Techniques for Molecular Data Analysis in Agriculture”
4. Delivered one Lecture in Hindi Workshop on Statistical Techniques in Biometrics organized at ICAR-IASRI, New Delhi during 31 May-02 June, 2016.
5. Delivered two lectures on “Gene Co-Expression Network” along with the practical in the training program **Introduction to Bioinformatics** organized at ICAR-IASRI, New Delhi during 08-21 November, 2016 for technical personnel employed in ICAR.
6. Delivered two lectures on “Network Modeling and Analysis of Market Data in R” along with the practical in the CAFT program on **Advances in Statistical Modeling and Forecasting in Agriculture** organized at ICAR-IASRI, New Delhi during 23 December 2016- 12 January, 2017).
7. Delivered two lectures on “Basics of R” in the 21 days CAFT programme on **Advance Computational and Statistical Tools for Omics Data Analysis** organized at ICAR-IASRI, New Delhi during 01-21 December, 2016.
8. Delivered two lectures on “Biological Data Analysis” in the 21 days CAFT programme on **Advance Computational and Statistical Tools for Omics Data Analysis** organized at ICAR-IASRI, New Delhi during 01-21 December, 2016.
9. Delivered 12 lectures on the topics “Basics of R”, “Data analysis using R”, “Genetic Diversity Analysis”, “Gene Co-expression Network Analysis”, “Path Analysis” and “Feature Selection in Genomics” in the 21 days CAFT programme on **Recent Analytical Techniques in Statistical Genetics and Genomics** organized at ICAR-IASRI, New Delhi during 17 January -06 February, 2017.
10. Delivered 12 lectures on the topics “Basics of R”, “Data analysis using R”, “Genetic Diversity Analysis”, “Gene Co-expression Network Analysis”, “Path Analysis” and “Feature Selection in Genomics” in the 21 days winter school programme on **Advanced Statistical Techniques in Genetics and Genomics** organized at ICAR-IASRI, New Delhi during 02-22 March, 2017.
11. Delivered two lectures on “Genomic Data Analysis using R” in the 21 days CAFT programme on **Computational Approaches for Next Generation Sequencing (NGS)**

Data Analysis in Agriculture organized at ICAR-IASRI, New Delhi during 08-28 February, 2017.

12. Delivered two lectures on "Gene Selection and Gene Co-expression Network Analysis using R" in the 21 days CAFT programme on **Computational Approaches for Next Generation Sequencing (NGS) Data Analysis in Agriculture** organized at ICAR-IASRI, New Delhi during 08-28 February, 2017.

Selected National and International Conference Attended:

1. Attended 67th Annual conference of Indian society of agricultural statistics from 18-20 December, 2013 and presented paper entitled as "A system biology approach to construct gene regulatory networks for salinity response in rice"
2. Attended 68th Annual conference of Indian society of agricultural statistics from 25-27 January, 2015 and presented paper entitled as "Inferring gene regulatory networks using Kendall's tau correlation coefficient and identification of salinity stress responsive genes in rice"
3. Attended 6th World Congress on Biotechnology held during 05 – 07 October 2015 at Rohini, New Delhi, India and presented one research paper "Gene selection and co-expression modules detection common to various abiotic stress responses in Rice and Arabidopsis".
4. Attended National Seminar on Plant Genomics and Biotechnology: Challenges and opportunities in 21st Century held during 23-24 January 2016 at OUAT, Bhubaneswar and presented one research paper entitled as "Differential gene co-expression network analysis for identification of hub genes and gene modules associated with salinity stress response in rice" in the Young Scientist Forum.
5. Attended in the 18th Annual Conference of Society of Statistics, Computer and Applications held during 18 – 20 February 2016 at University of Jammu, Jammu and presented one research paper entitled as "Gene selection, module and hub gene detection for gene co-expression network analysis and application to Aluminium stress in Soybean" for MN Das memorial young scientist award.
6. Attended in the 19th Annual Conference of Society of Statistics, Computer and Applications held during 08 – 10 March 2017 at SKUAST-J, Jammu and presented one research paper entitled as "Gene set analysis with quantitative trait loci" for MN Das memorial young scientist award.
7. Attended and presented a poster entitled as "Identification of key genes for salinity stress response in Rice using NGS data" in Research in Louisville conference on October 12, 2018 held at Kosair Charities Clinical & Translational Research Building, 505 South Hancock, Louisville, Ky 40202, USA.
8. Attended and presented poster "Statistical approach for gene set analysis with trait specific quantitative trait loci" at in 2019 Southeast Regional IDeA Conference at Galt House Hotel, Louisville, Kentucky, USA on November 7, 2019.
9. Attended and presented poster "Identification of key genes for salinity stress response in Rice using NGS data" at 3rd annual Commonwealth Computational Summit held at University of Kentucky, Lexington, Kentucky, USA on October 15, 2019.
10. Attended and presented a paper "Hybrid Statistical Approach for Selection of Biologically Relevant Genes using Gene Expression Data" in the International Conference on "Recent Advances in Statistics and Data Science for Sustainable Development" of Indian Society for Probability and Statistics held during December 21-23, 2019 at Utkal University, Bhubaneswar, India.

11. Attended and presented a poster “SwarnSeq: An Improved Statistical Approach for Differential Expression Analysis of Single-Cell RNA-Seq Data” in the 4th Annual Commonwealth Computational Summit, University of Kentucky, USA on October 15, 2020.
12. Participated Graduate Student Regional Research Conference (GSRRC) held at University of Louisville, USA on February 27-28, 2020.
13. Participated in the 4th Annual Commonwealth Computational (virtual) Summit, University of Kentucky, USA on October 15, 2020.

Attended Training/Workshop (Outside India)

1. Attended short course by American Statistical Association on Data mining on October 13, 2018 at University of Kentucky, Lexington, KY, USA.
2. Attended “KBRIN 2019 Next Generation Sequencing and Bioinformatics Workshop” held on July 15 -19, 2019 at Bluegrass Community and Technical College in Lexington, Kentucky, USA in collaboration with University of Kentucky, Lexington, Ky, USA and sponsored by Kentucky Biomedical Research Infrastructure Network.
3. Attended the workshop on “Use of reference management software like Endnote in research article writing” on August 1, 2019 held at Kornhauser Library, Health Sciences Campus, UofL.
4. Attended Bioinformatics Core Workshop on High Throughput Sequence Analysis and Lessons Learned, Galt House Hotel, Louisville, Kentucky, USA on November 7, 2019.
5. Attended Data Science workshop, Galt House Hotel, Louisville, Kentucky, USA on November 8, 2019.
6. Attended and completed the (virtual) short course on “Introduction to RNA-seq analysis” organized by Basepairs on November 15, 2020.