Dr. Chiranjib Sarkar
Assistant Professor
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Department of Bioinformatics, University of North Bengal,
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Subject Specialization:

- Bioinformatics
- Gene regulatory network,
- Host-pathogen interaction study,

Areas of Research Interest:

- System Biology, Biological Network analysis, Machine learning and Artificial Intelligence.
- Structural Bioinformatics, Molecular Modelling and Docking.

Computational Skills:

- Programming languages: C, JAVA, R, Python, PERL, MySQL.
- Software: Accelrys Discovery Studio, CLC Bio, Cytoscape, SAS, SPSS.
- Web Designing: HTML, PHP, JSP

Academics and Education

- Qualified *ICAR-NET (Agricultural Statistics and Informatics)*, 2015
- *M.Sc. (Bioinformatics)* from ICAR-Indian Agricultural Research Institute, New Delhi. Sarkar, C. (2013). Understanding of protein structures of different *Pi54* alleles and their *in silico* interactions with Avr-Pi54 protein. M.Sc. Thesis, ICAR-Indian Agricultural Research Institute, New Delhi.
- Qualified *ICAR-AIEEA PG*, 2011.
- *B.Sc. (Agri) Hons.* from Bidhan Chandra Krishi Viswavidyalaya (Mohanpur, WB), (2007-2011).

- Ph.D. (Bioinformatics) from ICAR-Indian Agricultural Research Institute, New Delhi. Sarkar, C. (2022). A study on Gene Regulatory Network for Rice Blast Disease. Ph.D. Thesis, ICAR-Indian Agricultural Research Institute, New Delhi.

Research projects

Title of the Project	Funding Details	Duration	Remarks
An Ensemble approach for integration of gene regulatory network (GRN) and protein-protein interaction (PPI) network based on Machine learning technique.	1.5 Lakh by University research assistance.	2020-2021	*Completed*
Inferring dynamic Gene Regulatory Network (GRN) using Support Vector Machine (SVM).	0.75 Lakh by University research assistance.	2021-2022	*Ongoing*

Selective List of Publications:

Webtool:

Online Webtool for "Consensus Gene Regulatory Network Construction" (**http://cabgrid.res.in:8080/chiranjib/**).

Book/Chapter:

Iquebal, M. A., Jaiswal, S., Mukhopadhyay, C. S., Sarkar, C., Rai, A. and Kumar, D. (2015). Applications of bioinformatics in plant and agriculture, *PlantOmics: The Omics of Plant Science.* Springer India, Pages:756-789. DOI 10.1007/978-81-322-2172-2_27.

Journals:

Sarkar, C., Parsad, R., Mishra, D. C., and Rai, A. (2021). A Web Tool for Consensus Gene Regulatory Network Construction. *Frontiers in Genetics*, **12**, 745827.

Sarkar, C., Parsad, R., Mishra, D.C. and Rai, A (2020). An ensemble approach for gene regulatory network study in rice blast. *Journal of Crop and Weed* , **16** , 1-8.

Sarkar, C., Saklani, B.K., Singh, P.K., Asthana, R.K. and Sharma, T.R.(2019). Variation in the LRR region of Pi54 protein alters its interaction with the AvrPi54 protein revealed in silico analysis. *PloS one*, **14(11)**, e0224088.

Ray, S., Singh, P. K., Gupta D. K., Mahato, A. K., **Sarkar, C.**, Rathour, R., Singh, N. K. and Sharma, T. R. (2016). Analysis of Magnaporthe oryzae genome reveals a fungal effector, which is able to induce resistance response in transgenic rice line containing resistance gene, Pi54. *Frontiers in Plant Science*, **7**, 1140.

Conference Proceedings
Sarkar, C., Parsad, R. and Misra, D.C. (2018). An Ensemble Approach for Gene Regulatory Network Construction. *e-Proceedings Research Frontiers in Precision Agriculture*, 243-245, ISBN: 978-93-88237-13-0.