



*Chiranjib Sarkar*

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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 (Not completed 2014 to present).

## Research projects

<i>Title of the Project</i>	<i>Funding Details</i>	<i>Duration</i>	<i>Remarks</i>
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	<i>Completed</i>
Inferring dynamic Gene Regulatory Network (GRN) using Support Vector Machine (SVM).	0.75 Lakh by University research assistance.	2021-2022	<i>Ongoing</i>

## Selective List of Publications:

### 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 (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 by 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.