Dr. Dipanka Tanu Sarmah

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PERSONAL STATEMENT

As a highly motivated computational and systems biologist, I specialize in integrating mathematical modeling, machine learning, and multi-omics data analysis to decode complex biological systems. My work bridges mechanistic and data-driven frameworks, applying ODE-based and rule-based modeling, deep learning, spatiotemporal modeling, GWAS, and single-cell transcriptomic integration to uncover disease mechanisms and therapeutic targets.

I have extensive experience developing algorithms and computational pipelines for multi-omics datasets including transcriptomics, proteomics, phosphoproteomics, metabolomics, and single-cell data, aimed at identifying key regulatory mechanisms and therapeutic vulnerabilities across cancer, neurodegenerative, and infectious diseases.

My research outputs, published in high-impact journals such as Briefings in Bioinformatics, Bioinformatics, Gene, and Computational Biology & Chemistry, reflect a consistent record of innovation, interdisciplinary impact, and translational relevance in computational biology. In addition, I actively contribute to the scientific community as a peer reviewer for journals such as Computational and Structural Biotechnology Journal (CSBJ) and Cancer Genetics.

RESEARCH EXPERTISE

- **Mathematical & Computational Modeling:**
    - ODE-based, rule-based, and stochastic modeling of signaling and regulatory networks; spatiotemporal modeling of tumor–immune and neurodegenerative systems.
- **Machine & Deep Learning:**
    - Development and application of ML/DL frameworks for biomarker discovery, classification, and multi-omics feature integration (e.g., random forests, autoencoders, CNNs, GNNs).
- **Multi-Omics & NGS Analysis:**

    - Bulk and single-cell RNA-seq, ATAC-seq, proteomics, phosphoproteomics, and metabolomics; integration of omics layers for causal and regulatory inference.
  - **Network Systems Biology:**
    - Protein–protein interaction, gene co-expression, miRNA-mRNA, and drug–target networks; centrality, modularity, and rewiring analyses for target identification.
  - **Genome-Wide Studies:**
    - GWAS and eQTL integration to link genotype with multi-omics phenotypes.
  - **Functional Pathway Analysis:**
    - GO/KEGG/Reactome enrichment, transcriptional network inference, and pathway rewiring in disease progression.

TECHNICAL SKILLS

- **Programming & Modeling:**
  - MATLAB, R, Python, Julia, Mathematica, BioNetGen
- **Machine Learning / AI Frameworks:**
  - scikit-learn, TensorFlow, Keras, PyTorch
- **Omics & NGS Data Processing:**
  - Bulk and single-cell RNA-seq, ATAC-seq, and spatial transcriptomics; data preprocessing, normalization, differential expression, and integration pipelines
- **Network & Systems Tools:**
  - Cytoscape, Gephi, STRING, WGCNA, GENIE3
- **Visualization & Documentation:**
  - ggplot2, matplotlib, GraphPad, Adobe Illustrator, MS Office
- **Statistics & Big Data:**
  - Feature selection, dimensionality reduction, multivariate modeling, and survival analysis

WORK EXPERIENCE

Postdoctoral Researcher (June 2025 - Present)
Royal College of Surgeons in Ireland (RCSI), Dublin
PI: Dr. Niamh Connolly

Project: *Spatiotemporal transcriptome and proteome analysis of α-Synuclein pathology in Parkinson's disease to identify cell-type-specific vulnerability and tolerance mechanisms.*

Postdoctoral Researcher (Oct 2023 - May 2025)
University College Dublin (UCD), Ireland
PI: Prof. Walter Kolch, Prof. Boris Kholodenko, Asst.Prof. Oleksii Rukhlenko
Project: *Mathematical modeling and bioinformatics analysis of KRAS signaling in cancer systems biology.*

Senior Project Associate (Sept 2021-Sept 2023)
Translational Health Science and Technology Institute (THSTI), India
PI: Dr. Samrat Chatterjee
Project: *Autophagy as a molecular signature and therapeutic target in progressive diseases.*

Project Associate II (June 2020 -Aug 2021)
PI: Dr. Samrat Chatterjee
Project: *Disease progression modeling via protein perturbation networks.*

Junior Research Fellow (Nov 2015 - June 2020)
PI: Dr. Samrat Chatterjee
Project: *Improving the resolution of protein–protein interaction networks and studying autophagy in lung cancer.*

ACADEMIC PROFILE

Ph.D. in Mathematical Biology (Feb 2018 - May 2023)

- **Jadavpur University**, Kolkata, India
- **Supervisor:** Prof. Nandadulal Bairagi
- ***Thesis:*** *Protein perturbations in diseases with emphasis on autophagy process: Insights from mathematical modelling and network biology.*

M.Sc. in Mathematics (July 2013-July 2015)

- Gauhati University, Guwahati, India
- CGPA: 7.4/10
- Dissertation (4th Semestar)
  - **Supervisor:** Prof. Kanika Das
  - ***Thesis:*** *Invariance of Maxwell Equations Under Lorentz Transformation*

B.Sc. in Mathematics (July 2010 - March 2013)

- College: B. Borooah College, Guwahati, India
- Result: 56%

Higher Secondary (2010)

- Board: AHSEC
- College: Genius Academy, Assam
- Result: 70.6%

High School (2008)

- Board: SEBA
- School: Dhakuakhana H.S. School, Assam
- Result: 85.17%

PUBLICATIONS

Research/ Review Articles:

(*From Ph.D.)*

- **Sarmah, D. T.,** Kumar S., Paul A., Bairagi, N., & Chatterjee, S. (2023). A data-driven multilayer approach for identification of potential therapeutic targets in NASH. ***Physica A***. **[IF:3.1]**
- **Sarmah, D. T.,** Paul A., Berry U., Surjit M., Bairagi, N., & Chatterjee, S. (2023). BAG6 is a novel player in controlling nonalcoholic steatohepatitis: result from a comprehensive in-silico study. ***(preprint)***
- **Sarmah, D. T.,** Gujjar S., Mathapati S., Bairagi, N., & Chatterjee, S. (2023) Identification of critical autophagy-related proteins in diabetic retinopathy: A multi-dimensional computational study, **Gene [IF:2.4]**
- **Sarmah, D. T.,** Bairagi, N., & Chatterjee, S (2021). The interplay between DNA damage and autophagy in lung cancer: A mathematical study. ***Biosystems.*** **[IF:1.9]**
- **Sarmah, D. T.,** Bairagi, N., & Chatterjee, S. (2021). Tracing the footsteps of autophagy in computational biology. ***Briefings in Bioinformatics***. **[IF:7.7]**

(***From other projects***)

- Kumar, S., Agarwal, A., Sarmah, D. T., & Chatterjee, S. (2025). konnect2prot 2.0: Integrating advanced analytical tools for deeper understanding of protein properties in a functional protein-protein interaction network. ***Computational and Structural Biotechnology Journal*****. [IF:4.1]**
- Ansari, S., **Sarmah, D. T.,** Verma, R., Chandrasekar, K., Shalimar, Nayak, B., ... & Surjit, M. **(2025)**. Network controllability analysis reveals the antiviral potential of Etravirine against hepatitis E virus infection. Msystems, 10(9), [**IF:4.5]**

- Pandey, D., Kumar, S., **Sarmah, D. T***., & Chatterjee, S.* (**2025**). TCGAimmunosurv: An R package to identify genes associated with patient survival and immune cell state transitions using TCGA and single-cell RNA-seq data. ***Computational Biology and Chemistry*, [IF: 3.1]** [co-corresponding author]
- Kumar S., **Sarmah, D. T.,** Paul A., & Chatterjee, S. **(2024)**. Exploration of functional relations among differentially co-expressed genes identifies regulators in glioblastoma. ***Computational Biology and Chemistry*** **[IF: 3.1]**
- **Sarmah, D. T.,** Parveen R., Kundu J, & Chatterjee, S. **2023**. Latent tuberculosis and computational biology: A less-talked affair ***Progress in Biophysics and Molecular Biology*** **[IF: 4.5]**
- #Kumar, S., **# Sarmah, D. T.,** Asthana, S., & Chatterjee, S. (2023). konnect2prot: a web application to explore the protein properties in a functional protein–protein interaction network. ***Bioinformatics*** [#shared first authors] **[IF: 5.4]**
- Kumar, P., Soory, A., Mustafa, S. A., **Sarmah, D. T.,** Devvanshi, H., Chatterjee, S., ... & Srikanth, C. V. (**2022)**. Bidirectional regulation between AP-1 and SUMOylation pathway genes modulates inflammatory signaling during Salmonella infection. ***Journal of Cell Science*** **[IF:3.6]**
- Klionsky, D. J., Abdel-Aziz, A. K., Abdelfatah, S., Abdellatif, M., Abdoli, A., Abel, S., **Sarmah, D. T**., & Bartek, J. (**2021)**. Guidelines for the use and interpretation of assays for monitoring autophagy, ***Autophagy*** **[IF: 14.6]**
- Anand, R., Sarmah, D. T., & Chatterjee, S. (**2018)**. Extracting proteins is involved in disease progression using temporally connected networks. ***BMC Systems Biology***. [**IF: 2.048**]

Book Chapter:

- **# Sarmah, D. T., # Kumar, S., Chatterjee, S.,& Bairagi, N., (2023)** Dissecting big RNA-Seq cancer data using machine learning to find disease-associated genes and the causal mechanism. In Big Data Analytics in Chemoinformatics and Bioinformatics, Ed: S. C. Basak, R. Sujatha, **Elsevier.** [#shared first authors]
- **Sarmah, D.T** (2025) Decoding Disease with Network Biology. In Trends and Issues in Pure and Applied Sciences**,** Ed: DR. Nijara Goswami, DR. Ripa Kataki, B. Borooah college teachers' unit

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"konnect2prot" (Software Copyright: Diary No. 14303/2020-CO/SW)
Developed with Dr. S. Chatterjee, Dr. S. Asthana, Mr. D. T. Sarmah, et al.

CONFERENCES & PRESENTATIONS

- Speaker, *Advanced Drug Discovery and Development* (Nature & Shanghai Institute for Advanced Immunochemical Studies, 2024)
- Poster, *UCD Cancer Research Symposium*, Dublin (2024)

- Oral & Poster Award (3rd Prize), *Accelerating Biology 2023*, C-DAC Pune
- Best Poster Award, *Metabolic Associated Fatty Liver Disease Symposium*, THSTI (2022)
- Poster, *106th Indian Science Congress*, Punjab (2019)
- Oral & Poster, *Big Data & Computational Biology Conference*, Jamia Millia Islamia (2019)
- Oral, *Mathematical & Theoretical Biology*, Jadavpur University (2017)

PROFESSIONAL MEMBERSHIPS

- Indian Science Congress Association (ISCA)
- International Society for Computational Biology (ISCB)

PEER REVIEW ACTIVITY

Computational and Structural Biotechnology Journal (CSBJ)

Cancer Genetics