

Dipayan Sarkar

Siliguri, West Bengal, India

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Research Summary

Currently pursuing a PhD in bioinformatics and computational biology, focused on deep learning methods for biological sequence-based prediction and generative model development. Experience includes neural network training, transfer learning with pretrained protein language models, and analysis of large-scale biological datasets. Current work involves autoregressive generative modeling of biological sequences, with ongoing exploration of diffusion-based approaches for biological data.

Work Experience

University of North Bengal

PhD Research Scholar

Department of Bioinformatics

- Designed and implemented deep learning architectures for sequence-based protein-protein interaction prediction.
- Developed attention-based hybrid models integrating transfer learning from pretrained protein language models, trained and evaluated on large-scale biological sequence datasets.
- Developed and deployed web-based platforms for model inference and protein interaction network visualization.

Siliguri, India

2022–Present

Education

University of North Bengal

Ph.D. in Bioinformatics

Advisor: Dr. Chiranjib Sarkar

Focus: Deep learning-based frameworks for protein-protein interaction network prediction.

India

Expected March 2027

University of North Bengal

M.Sc. in Botany, 77.25% – First Class

Specialization: Biochemistry

India

2021

Ananda Chandra College, University of North Bengal

B.Sc. (Hons.) in Botany, 63.50% – First Class

India

2019

Haldibari High School (H.S.)

Higher Secondary (Class XII), 80.00% – First Class

WBCHSE | Subjects: Physics, Chemistry, Mathematics, Biology, English, Bengali

West Bengal

2016

Haldibari High School (H.S.)

Secondary (Class X), 91.58% – First Class

WBBSE | Subjects: Mathematics, Physical Science, Life Science, History, Geography, English, Bengali

West Bengal

2014

Publications

2025: Sarkar, D., & Sarkar, C. AttnSeq-PPI: Enhancing protein-protein interaction network prediction using transfer learning-driven hybrid attention. *Biochimica et Biophysica Acta (BBA)—Proteins and Proteomics*, 141102. doi:10.1016/j.bbapap.2025.141102

2022: Sarkar, C.; Sarkar, D.; Parsad, R.; Mishra, D. Package EGRNi. **CRAN**.
cran.r-project.org/package=EGRNi

Skills

Programming: Python (PyTorch, HuggingFace), R (CRAN package development), C (basic)

Deep Learning: Transformers, attention mechanisms, sequence modeling, transfer learning with pretrained language models

Generative AI: Autoregressive sequence generation, diffusion-based approaches, probabilistic sequence modeling for biological data

Scalable Training: GPU-based training, large-scale sequence datasets, parallel training on HPC environments

Bioinformatics: Biological sequence analysis, sequence-only protein–protein interaction prediction, generative modeling of biological sequences

Data & Viz: NumPy, Pandas, Matplotlib, Seaborn

Deployment: Docker, Flask, FastAPI, Linux server deployment, model-backed web applications

Software & Tools

AttnSeq-PPI: Deep learning-based protein–protein interaction prediction platform.
compbiosysnbu.in/attnseqppi/

ARACoFusion-PPI: Arabidopsis-specific PPI prediction and network analysis tool.
aracofusion.compbiosysnbu.in/

Awards & Certificates

2021: Qualified **CSIR-NET (JRF)** in Life Sciences — June 2021, **All India Rank: 216**

2022: Qualified **GATE** in Life Sciences (XL)

Grants & Computing Resources

2025: IndiaAI Compute Initiative — Awarded GPU cloud compute (NVIDIA L4) under the IndiaAI Mission for the project *Deep learning-based framework for protein-protein interaction network prediction* (Project ID: P1-S2025070964, Sep 2025 – Aug 2026). Funded under CSIR-UGC SRF Fellowship.

2025: Google TRC (TPU Research Cloud) Award — Granted free access to Google Cloud TPUs (v4, v5e, v6e) for machine learning research.