# Ashmita Dey

Jadavpur University, Kolkata, West Bengal, India ashmitadey19@outlook.com

### Summary

A dedicated Computer Science research scholar specializing in bioinformatics and computational biology, leveraging advanced computational techniques to address complex biological problems. Experienced in handling large-scale genomic, proteomic, and transcriptomic data, with a focus on designing and implementing innovative computational frameworks. Also, with extensive experience in analyzing single-cell omics datasets. Developed pathway-based clustering techniques for single-cell data analysis, contributing to a deeper understanding of cellular processes at the molecular level. Skilled in protein sequence structure analysis, particularly focused on transcription factors and tumor subclass classification, utilizing advanced computational methods for survival analysis. Committed to using computational tools to unravel complex biological phenomena and enhance our understanding of disease mechanisms. Skilled, in data analysis, machine learning, and statistical modeling, contributing to advancements in understanding biological systems. Collaborative and research-oriented, with a strong commitment to pushing the boundaries of interdisciplinary research at the intersection of computer science and life sciences.

### Skills

- **Programing Skills:** R (advance) and Python (advance), MATLAB (intermediate)
- Biostatistics: R, Python Excel
- **OS platform:** Windows and Linux
- **Genomics:** NGS data analysis (bulk seq, miRNAs), single-cell omics and integration, GSEA, pathway enrichment and ontology analysis, network analysis and survival analysis.
- Structural Biophysics: Sequence space study (Shannon entropy, direct coupling analysis, Expasy), Structure network, post transitional modification, intrinsically disorder protein, stability calculation (Foldx), quality assessment, liquid-liquid phase transition, protein modeling (I-TASSER, RaptorX)
- **Network Biology:** Protein-protein interaction network, pathway semantic similarity network, gene-miRNA network, gene-miRNA-TF network disease network, centrality calculation, co-expression network.
- Machine learning and Biostatistics: Skilled in using bioinformatics tools, clustering, classification and regression.
- Working Environment: RStudio, Anaconda, VS code

### **Professional Employment & Education History**

Degree	Duration	Institute	Projects	Place
Research Associate	2023-present	Indian Statistical Institute, Kolkata	Exploring the heterogeneity of systemic lupus patients based on autoantibodies distribution and multiomics approaches compared in two ethnic cohorts	West Bengal, India
Doctor of Philosophy	Thesis submitted	Jadavpur University	Computational and statistical methods to analyze multi-omics data	Kolkata, West Bengal, India
Research Fellow	2018-2023	Department of Science and Technology	Understanding the cell-to- cell heterogeneity in a multi-cellular organism through computational and analytical approaches	India
Project link person	2017-2018	Jadavpur University	Predicting Protein-Protein Interactions	Kolkata, West Bengal, India
Master of Technology	2015-2017	National Institute of Teacher's Training and Research - Dept of Computer Science and Engineering	Identifying miRNA- mRNA pairs associated with Multiple Breast Cancer Subtype	Kolkata, West Bengal, India
Bachelor of Technology	2011-2015	Haldia Institute of Technology	Cryptography and crypto analysis	Haldia, West Bengal, India

### **Academic & Professional Publication History**

Since 2018 I have published 7 peer reviewed journals and 4 conferences. I have an h-index of 5 and citation score of 75 as calculated using Google Scholar.

### **PUBLISHED**

- A.Dey, S. Sen, U. Maulik. 2022. Study of transcription factor druggabilty for prostate cancer using structure information, gene regulatory networks and protein moonlighting. Briefings in Bioinformatics, 23(1): 1-13, PMID: 34849560, DOI: 10.1093/bib/bbab465.
- S. Sen, A. Dey, S. Bandhyopadhyay, V. N. Uversky, U. Maulik. 2021. Understanding structural malleability of the SARS-CoV-2 proteins and relation to the comorbidities. Briefings in Bioinformatics, 22(6): 1-15, PMID: 34143202, DOI: 10.1093/bib/bbab232.
- **A.Dey**, S. Sen, U. Maulik. 2021. Unveiling COVID-19-associated organ-specific cell types and cell-specific pathway cascade. Briefings in Bioinformatics, 22(2): 914-923, PMID: 32968798, PMCID: PMC7543283, DOI: 10.1093/bib/bbaa214.
- **A.Dey**, S. Sen, Vladimir N Uversky, U. Maulik. 2021. Structural facets of POU2F1 in light of the functional annotations and sequence-structure patterns. Journal of Biomolecular Structure and Dynamics, 39(3): 1093-1105, PMID: 32081083, DOI: 10.1080/07391102.2020.1733092.
- S. Sen, A. Dey, U. Maulik. 2021. Studying the effect of alpha-synuclein and Parkinson's disease linked mutants on inter pathway connectivities. Scientific Reports, 11(16365): 1-14, PMID: 34381149, PMCID: PMC8358055, DOI: 10.1038/s41598-021-95889-5.
- J. P. Sarkar, I. Saha, A. Lancucki, N. Ghosh, M. Wlasnowolski, G. Bokota, A. Dey, P. Lipinski, D. Plewczynski. 2020. Identification of miRNA Biomarkers for Diverse Cancer Types using Statistical Learning Methods at the

- Whole Genome Scale. Frontiers in genetics, 11(982): 1-25, PMID: 33281862, PMCID: PMC7691578, DOI: 10.3389/fgene.2020.00982.
- S. Sen, A. Dey, S. Chowdhury, U. Maulik, K. Chattopadhyay. 2019. Understanding the evolutionary trend of intrinsically structural disorders in cancer relevant proteins as probed by Shannon entropy scoring and structure network analysis. BMC bioinformatics, 19(13): 231-242, PMID: 30717651, PMCID: PMC7394331, DOI: 10.1186/s12859-018-2552-0.

#### CONTRIBUTED PRESENTATIONS

- \* Presenting author
  - A. Dey\*, U. Maulik. 2022. Bioinformatics pipeline to unveil the heterogeneity of Glioblastoma Multiforme. Oral presentation: 2022 IEEE Calcutta Conference (CALCON), Kolkata, West Bengal, DOI: 10.1109/CALCON56258.2022.10060233.
  - A. Dey\*, U. Maulik. 2020. Identification of Cell-types based on the Pathway of Markers using Single-cell data. Oral presentation: 2020 IEEE Calcutta Conference (CALCON), Kolkata, West Bengal, DOI: 10.1109/CALCON49167.2020.9106539.
  - S. Sen\*, A. Dey, U. Maulik. 2018. Identifying potential hubs for kidney renal clear cell carcinoma from tf-mirna-gene regulatory networks. Oral presentation: 2018 IEEE Applied Signal Processing Conference (ASPCON), Kolkata, West Bengal, DOI: 10.1109/ASPCON.2018.8748806.
  - S. Karmakar, A. Dey\*, I. Saha. 2017. Use of quantum-inspired metaheuristics during last two decades. Oral presentation: 2017 7th International Conference on Communication Systems and Network Technologies (CSNT), Nagpur, Maharashtra, DOI: 10.1109/ASPCON.2018.8748806.
  - A. Dey\*, I. Saha, U. Maulik. 2017. A survey on multiple sequence alignment using metaheuristics. Oral presentation: 2017 7th International Conference on Communication Systems and Network Technologies (CSNT), Nagpur, Maharashtra, DOI: 10.1109/CSNT.2017.8418552.
  - S. Sen, **A.Dey**, U. Maulik. **Poster**: Unravelling the Dynamicity of POU2F1 based on Evolutionary Conservation and Structure Network Analysis Presented at Function COSI, ISMB/ECCB, Congress Center Basel, Switzerland.
  - A. Dey, R. Das, S. Sen\*, U. Maulik. Poster: moonPRED: A Deep Neural Network Based Tool to Predict Protein Moonlighting moonPred Presented at MLCSB COSI ISMB/ECCB, Congress Center Basel, Switzerland.
  - A. Dey\*, U. Maulik. Poster: Cell type-specific pathways associated with diffuse large b-cell lymphoma metastasis related to neuro-diseases Presented At 4th health sciences and innovation congress, Baku, Azerbaijan.
  - S. Sen, A. Dey\*, S. Chowdhury, U. Maulik, K. Chattopadhyay. Poster: Understanding the evolutionary trend of intrinsically structural disorders in cancer relevant proteins as probed by Shannon entropy scoring and structure network analysis Presented At 17th International Conference on Bioinformatics (InCoB 2018), New Delhi.

### Awards, Fellowships, & Grants

Year	Funding Sources	Achievements	Role
2023	Japan Society for the Promotion of Science	Best Team Presentation award	I had the privilege of being a member of Team A, where we collectively chose "Gender Inequality in Science society" as the topic for our presentation. Throughout the process, I worked closely with my teammates, engaging in collaborative brainstorming sessions, and actively refining the structure of our presentation.
2021	Innovation in Science Pursuit for Inspired Research implemented presented by Department of Science and Technology	Senior Research Fellow	In recognition of my research progress and publication records, the government of India upgraded my fellowship status and honored me with the position of Senior Research Fellow for the project "Understanding the cell-to-cell heterogeneity in a multi-cellular organism through computational and analytical approaches."
2020	IEEE Calcutta Conference (CALCON)	Best paper award	I had the honor of being the first author of the paper. The manuscript I presented was highly regarded by a panel of expert jurors who found it to be both informative and captivating. As a result, our article was selected as the best paper among the submissions.
2018-2020	Innovation in Science Pursuit for Inspired Research implemented presented by Department of Science and Technology	Junior Research Fellow	The government of India selected and awarded my project, "Understanding the cell-to-cell heterogeneity in a multi-cellular organism through computational and analytical approaches," with one of the prestigious fellowships in the country.
2017	Maulana Abul Kalam Azad University of Technology (MAKAUT), West Bengal	Gold medalist	I achieved the top rank among all colleges affiliated under MAKAUT during my master's degree

## **Non-University Affiliated Professional Activities**

### SERVICE AND OUTREACH

2023 The 14th HOPE Meeting with Nobel Laureates, participant

2018 IEEE CIS-Intel AI Academy one day Workshop, participant

2017 Regional Workshop on Quality and Sustainable, Volunteer

2016 1st National Innovation Talent Contest for Polytechnics, Volunteer

#### DEVELOPMENT

Human Genomics: Computational Methods and Applications, the course will cover recent advancements in the fields of Human Genomics with a wide coverage on computational studies, and introduction to real-life practical applications. The goal of lectures is to introduce participants to basic theoretical ideas of computational genomics with the special focus on algorithms, during this workshop, I have learned about the Biopython libraries and their application on bioinformatics. The lectures on omics help me to clear all the doubts regarding the covered area. From this workshop I have earned different implementation ideas to solve the bottleneck of the bioinformatic problems by utilizing computational methods. Finally, I am also able to build a strong network with the scientist those are contributed their excellent research in this field.

Seminar on Harnessing Big Data for Precision Medicine and Healthcare, Precision medicine is a type of health care that takesintoaccountindividual differences in genetic sandenvironmental exposures. Big data in biomedicine is expected to provide novel insights into health and disease states, which can be translated into personalized disease prevention and treatment plans, thanks to recent advancements in high-throughput omics profiling technologies, collections of large study cohorts, and the development of data mining algorithms. However, analyzing, integrating, storing, and interpreting petabytes of biomedical data generated by numerous measuring modalities is a huge issue. Experts are invited from different organizations to help us to solve the problems regarding patient privacy, coordination between participating medical centers and data analysis working groups, as well as differences in data sharing regulations, are also hot problems.

Seminar on Data Analytics Signal Processing with MATLAB, The workshop help me to understand the MATLAB which is a well-known programming and numeric computing platform. The workshop covers Creating, importing, and visualizing signals, preprocessing to improve data quality, extracting features in the time and frequency domains.

#### PEER REVIEW

Sadhana Published by the Indian Academy of Sciences IEEE 18th India Council International Conference (INDICON) Briefings in Bioinformatics BMC bioinformatics

#### PROFESSIONAL MEMBERSHIPS

JSPS HOPE Fellow International Society for Computational Biology Asia-Pacific Bioinformatics Network