

# Md. Jubayer Hossain

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## Research Statement

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My research focuses on developing reproducible bioinformatics pipelines for large-scale bulk and single-cell RNA-seq data to uncover molecular biomarkers, immunological signatures, and therapeutic targets in cancer and neurological diseases. By integrating multi-omics data analysis, machine learning, and biology, I aim to advance computational methods that bridge biological discovery and clinical translation.

## Education and Training

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### Master of Science in Microbiology

Jagannath University

Dhaka, Bangladesh

2019–2020

- Relevant Coursework: Genomics, Proteomics, Bioinformatics, Research Methodology and Scientific Writing

### Bachelor of Science in Microbiology

Jagannath University

Dhaka, Bangladesh

2016–2019

- Relevant Coursework: Biostatistics, Public Health and Hygiene, Bioinformatics I, Bioinformatics II

### Interdisciplinary Computational Biology

BRAC University

Dhaka, Bangladesh

January 2026

- Mastered high-resolution protein structure prediction and molecular visualization using AlphaFold2/3 and ChimeraX to investigate complex protein-ligand interactions
- Applied AI/ML frameworks and docking protocols to structural data from PDB and UniProt, culminating in an interdisciplinary project on predictive molecular modeling.

### AI in Public Health

Child Health Research Foundation (CHRF)

Dhaka, Bangladesh

Sep 2023

- Developed predictive models and data pipelines for disease surveillance, focusing on the calculation of typhoid incidence and vaccine impact in Bangladesh.
- Built LLM-based code generation and computer vision frameworks for medical image analysis while analyzing the ethical implications of algorithmic bias.

## Technical Skills

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- **Programming Languages:** Python, R, Julia, SQL, Bash, JavaScript
- **Bioinformatics:** bulk RNA-Seq, Single-Cell, Spatial Omics, and Multi-omics
- **Workflow Management & Reproducibility:** Nextflow, Docker, Git, GitHub
- **Computing Environments:** UNIX/Linux, HPC clusters, Cloud computing (AWS, Google Cloud)

## Research Experience

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### Visiting Scholar

Department of Public Health, Daffodil International University

Dhaka, Bangladesh

Sep 2025 – Present

- Investigated computational frameworks within public health genomics to facilitate large-scale biomarker discovery and clinical validation.
- Developed a specialized curriculum for AI-driven disease modeling, integrating neural network architectures into biomedical informatics.
- Synthesized heterogeneous digital health records with genomic datasets to evaluate predictive models for clinical outcomes.
- Led a multidisciplinary research initiative to translate raw sequencing data into evidence-based public health insights.

## Research Associate (Bioinformatics)

Bio-Bio-1:Bioinformatics Research Discussion Group

Dhaka, Bangladesh

2017 – 2019

- Analyzed genomic and transcriptomic datasets using computational tools in R and Python, with emphasis on high-throughput sequencing data.
- Designed and delivered training modules on sequence alignment algorithms, RNA-seq analysis pipelines, and data preprocessing workflows.
- Evaluated and implemented peer-reviewed bioinformatics methods for transcriptomic data, ensuring reproducibility and analytical rigor.
- Facilitated technical discussions on structural biology and next-generation sequencing (NGS) data interpretation.

## Data Enumerator

School of Allied Health, Curtin University

Perth, Australia

Oct 2022 – Nov 2022

- Collected and curated quantitative and qualitative data from 40 clinicians for a Delphi study on Patient Outcomes Measurement in Interprofessional Tuberculosis Care.
- Performed rigorous data validation and cleaning, achieving 100% dataset accuracy for downstream statistical analysis.

## Selected Publications

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1. Ahmed, M. Z., Billah, M. M., Ferdous, J., & **Hossain, M. J.\*** (2025). Pan-cancer analysis reveals immunological and prognostic significance of CCT5 in human tumors. *Scientific Reports*, 15, 14405. <https://doi.org/10.1038/s41598-025-88339-z>
2. Fariha, F. T. J., Fuad, M., Saha, C. S., Hossen, S., & **Hossain, M. J.\*** (2025). Comprehensive bioinformatics analysis reveals prognostic significance and immunological roles of WNT gene family in breast cancer. *Sci Rep* 15, 34490 (2025). <https://doi.org/10.1038/s41598-025-13315-6>
3. Bari, S.M., Fuad, M., **Hossain, M.J.** et al. A meta-analysis of public RNA-Seq data identifies conserved stress responses in rainbow trout. *BMC Genomics* 26, 999 (2025). <https://doi.org/10.1186/s12864-025-12127-2>
4. GBD 2023 Vaccine Coverage Collaborators (**Hossain, M. J.**, 2025). Global, regional, and national trends in routine childhood vaccination coverage from 1980 to 2023 with forecasts to 2030: A systematic analysis for the Global Burden of Disease Study 2023. *The Lancet*. [https://www.thelancet.com/journals/lancet/article/PIIS0140-6736\(25\)01037-2](https://www.thelancet.com/journals/lancet/article/PIIS0140-6736(25)01037-2)
5. GBD 2023 Headache Collaborators (**Hossain, M. J.**, 2025). Global, regional, and national burden of headache disorders, 1990–2023: a systematic analysis for the Global Burden of Disease Study 2023. *Lancet Neurology*. [https://www.thelancet.com/journals/laneur/article/PIIS1474-4422\(25\)00402-8/fulltext](https://www.thelancet.com/journals/laneur/article/PIIS1474-4422(25)00402-8/fulltext)

## Papers Under Review

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1. Islam, M. W., Rahman, M. M., Naznin, H., Hossain, M. S., Akter, T., Shatabde, Z. A., & **Hossain, M. J.\*** (2025). “Integrative bioinformatics analysis reveals COL13A1 and COL23A1 as potential diagnostic and prognostic biomarkers in thyroid cancer”. *Under Review*.
2. Islam, M. W., Fariha, F. T. J., Ahmed, M. Z., Ferdous, J., Lota, H. B., Hossain, M. S., Kundu, P., Shahjahan, M., & **Hossain, M. J.\*** (2025). “Bioinformatics-driven multi-omics profiling of CDK1 and CDK6 identifies prognostic and therapeutic roles in breast cancer”. *Under Review*.
3. Mabsurah, K., Yeanan, I. J., Sumaiya, M., Islam, T., Ahammad, K., Bhattacharjee, A., Ferdous, J., Billah, M. M., & **Hossain, M. J.\*** (2025). “Pan-cancer analysis identifies potential prognostic and immunological role of RAS-degrading WDR76 in human tumors”. *Under Review*.

## Working Papers

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1. **Hossain, M. J.**, Shahjahan, M., & Fuad, M. (2025). Fezf2-mediated cortical development: Multi-omics analysis. *Working Paper/GitHub*. <https://github.com/hossainlab/fezf2-multiomics>

2. **Hossain, M. J.**, Shahjahan, M., & Fuad, M. (2025). Single-cell meta-analysis of microglial activation in Alzheimer's disease. *Working Paper/GitHub*. <https://github.com/hossainlab/alzheimers-microglia-meta-analysis>
3. **Hossain, M. J.**, Shahjahan, M., & Fuad, M. (2025). Integrative spatial-scRNA-seq atlas of immunotherapy resistance mechanisms across cancer types. *Working Paper/GitHub*. <https://github.com/hossainlab/spatial-scRNA-immune-resistance>

## Selected Conference Presentations

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1. Ahmad, F., Fuad, M., Shahjahan, M., & **Hossain, M. J.** (2025). Identification of Subtype-Specific Prognostic Biomarkers in Esophageal Carcinoma through Integrated Bioinformatics Analysis. 9th BSM Annual Conference, University of Dhaka, Bangladesh. *GitHub*. [https://github.com/gsabioinfointernship/ESCA\\_Meta](https://github.com/gsabioinfointernship/ESCA_Meta)
2. Aditee, L. M., Fuad, M., Shahjahan, M., & **Hossain, M. J.** (2025). Network-Driven Bioinformatics Approach Uncovers Prognostic Signatures and Therapeutic Targets in Pancreatic Ductal Adenocarcinoma. 9th BSM Annual Conference, University of Dhaka, Bangladesh. *GitHub*. [https://github.com/gsabioinfointernship/PAAD\\_Meta](https://github.com/gsabioinfointernship/PAAD_Meta)
3. Ahamed, M. S., Fuad, M., Shahjahan, M., & **Hossain, M. J.** (2025). Bioinformatic Analysis of Transcriptomic Data Reveals Molecular Signatures Driving Colorectal Cancer. 9th BSM Annual Conference, University of Dhaka, Bangladesh. *GitHub*. [https://github.com/gsabioinfointernship/COADREAD\\_Meta](https://github.com/gsabioinfointernship/COADREAD_Meta)
4. Tabassum, R., Fuad, M., Shahjahan, M., & **Hossain, M. J.** (2025). Comparative Transcriptomic Meta-Analysis Reveals Shared and Distinct Transcriptional Networks and Pathway Crosstalk in Hepatocellular Carcinoma for Biomarker and Therapeutic Target Identification. 9th BSM Annual Conference, University of Dhaka, Bangladesh. *GitHub*. [https://github.com/gsabioinfointernship/LIHC\\_Meta](https://github.com/gsabioinfointernship/LIHC_Meta)

## Invited Talks

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1. **Computational Biology and Bioinformatics Research in Resource-Limited Settings: Strategies, Tools and Opportunities** (2025). Speaker, Jagannath University Higher Study and Research Society. In this talk, I delivered the strategies and techniques essential for mastering computational biology and bioinformatics research.
2. **Mastering Biomedical Data Management** (2024). Speaker, IFMSA Bangladesh, Dhaka, Bangladesh. In the era of big data and advanced technologies, the management of biomedical data presents both immense opportunities and significant challenges. In this talk, I explored the strategies and techniques essential for mastering biomedical data management.
3. **Undergraduate Research - Importance, Benefits, and Challenges** (2022). Speaker, CHIRAL Bangladesh, Dhaka, Bangladesh. This talk was designed to enhance the undergraduate research experience by focusing on critical communication skills for success in research and broad transferable professional skills.
4. **State the Art of Microbial Genome Analysis** (2022). Speaker, Jagannath University, Dhaka, Bangladesh. This talk was about the art of genomic data analysis. I explored genomic data analysis steps typically include data collection, quality check and cleaning, processing, modeling, visualization and reporting.

## Teaching Experience

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### Lead Organizer & Instructor

DeepBio Academy, Bioinformatics and Computational Biology

Dhaka, Bangladesh

June 2020 – Present

- Designed comprehensive bioinformatics curriculum specializing in Single-Cell RNA-seq (scRNA-seq) workflows and multi-omic data integration.
- Benchmarked computational tools for transcriptomics and genomics to ensure pipeline reproducibility and analytical rigor.
- Supervised a technical research team in processing high-throughput omics datasets to identify transcriptional drivers of disease.

- Mentored undergraduate students in the development of computational research portfolios, emphasizing open-science standards and version control.

## **Faculty (Bioinformatics)**

University of Dhaka (cBLAST)

*Dhaka, Bangladesh*

*Aug 2023 – Present*

- Instructed specialized modules in Biomedical Machine Learning, focusing on the application of Python-based neural networks to sequence analysis.
- Directed student research projects applying deep learning frameworks to identify regulatory elements in complex biological datasets.
- Facilitated technical practicums for 100+ trainees on scalable data science methodologies for high-throughput genomic data.
- Evaluated computational frameworks for performance, establishing rigorous criteria for the optimization of biological models.
- Bridge theoretical computational principles with experimental biology to foster collaborative research outputs.

## **Program Lead**

GSA Bioinformatics Internship

*Dhaka, Bangladesh*

*July 2025 – Dec 2025*

- Conducted a pan-cancer transcriptomics meta-analysis across four organ systems to identify conserved regulatory networks in tumorigenesis.
- Optimized high-throughput pipelines for Bulk and Single-Cell RNA-seq, implementing advanced batch-effect correction and normalization protocols.
- Mentored research interns in the utilization of High-Performance Computing (HPC) environments and R/Bioconductor analytical frameworks.
- Analyzed complex transcriptional networks using Gene Set Enrichment Analysis (GSEA) to uncover novel oncogenic drivers.
- Managed collaborative research workflows across three institutions, resulting in the generation of peer-reviewed conference abstracts.

## **Teaching Assistant**

Department of Microbiology, Jagannath University

*Dhaka, Bangladesh*

*Oct 2022 – Dec 2022*

- Assisted in the delivery of research methodology training, focusing on experimental design and statistical power in public health microbiology.
- Processed public health surveillance data to support departmental research on emerging epidemiological trends.
- Critiqued and refined student research proposals to ensure compliance with modern computational and microbiological standards.
- Communicated complex biological theories through technical presentations to diverse academic audiences.
- Implemented digital data-tracking systems to monitor research milestones and student performance metrics.

## **Leadership Experience**

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### **Founder, Bioinformatics Scientist & CEO**

DeepBio Limited

*Dhaka, Bangladesh*

*Jan 2025 – Present*

- Lead a team of 13 researchers executing scRNA-seq and bulk RNA-seq analysis pipelines for cancer genomics and transcriptomics projects.
- Develop and benchmark scalable bioinformatics workflows for biomarker discovery in cancer and neurodegenerative diseases.
- Build and maintain AI-integrated computational infrastructure for multi-omics data processing and interpretation.
- Develop and deliver a national training program in computational biology, upskilling undergraduate researchers across Bangladesh.

### **Founder & Capacity Building Director**

CHIRAL Bangladesh (Non-profit Research Institute)

*Dhaka, Bangladesh*

*June 2020 – Present*

- Founded and lead a research institute with dedicated divisions in Bioinformatics, Public Health, Geospatial Health, and AI-Healthcare.
- Published 20+ peer-reviewed articles in Q1/Q2 journals and 40+ conference papers in health informatics and computational biology.
- Supervised 15+ manuscripts through analytical development and peer-review preparation in global health and bioinformatics.

- Collaborated with Michigan State University on biomedical research capacity-building initiatives in South Asia.
- Trained 3,000+ early-career researchers in data science, research methodology, and computational biology workflows.

## Community Engagement

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### Nextflow Ambassador

Seqera

Barcelona, Spain

2025 – Present

- Advocated for the adoption of Nextflow-based DSL2 pipelines to ensure reproducibility and scalability in high-throughput single-cell and bulk RNA-seq workflows.
- Engineered technical tutorials and documentation for the deployment of portable scientific containers (Docker/Singularity) in cloud and HPC environments.
- Optimized community-driven bioinformatic workflows, focusing on the integration of standardized pipelines for large-scale transcriptomic data processing.
- Facilitated technical workshops on workflow orchestration, training researchers to manage complex multi-omic datasets with high analytical rigor.
- Collaborated with global health data scientists to implement best practices for version-controlled, open-source computational research.

### GBD Senior Collaborator

Institute for Health Metrics and Evaluation

Washington, USA

2025 – Present

- Contributed advanced statistical modeling and analytical validation to Global Burden of Disease (GBD) studies published in high-impact journals like The Lancet.
- Synthesized and audited complex epidemiological datasets from 190+ countries to strengthen the robustness of global health genomic evidence.
- Formulated predictive models for disease burden, utilizing large-scale data integration techniques to identify health trends across diverse populations.
- Evaluated the quality and consistency of multi-national health data, ensuring high-fidelity inputs for global health policy frameworks.
- Collaborated with international research cohorts to refine statistical methodologies for assessing neurological and metabolic disease prevalence.

## References

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