Md. Jubayer Hossain

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Research Statement

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

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

Specialized Training: AI in Public Health
Child Health Research Foundation (CHRF)

Dhaka, Bangladesh
2023

- Acquired Skills: Epidemiological Modeling, Disease Surveillance using AI, Time Series Analysis (LSTM, ARIMA), Medical Image Analysis (X-ray, MRI)

Research Experience

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.
- Formulated two research manuscripts (in preparation) analyzing genomic surveillance data and identifying novel molecular signatures in disease.
- 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

- Investigated emerging bioinformatics methodologies, focusing on the application of computational tools to genomic and transcriptomic datasets.
- Designed collaborative training modules in R and Python for data analysis, fostering foundational skills in computational biology for early-career researchers.
- Facilitated technical discussions on sequence alignment algorithms and structural biology, contributing to the group's research output.
- Developed learning content for high-throughput data processing, bridging the gap between theoretical biology and practical data science.
- Evaluated peer-reviewed literature for method validation, maintaining a rigorous standard for the group's computational research initiatives.

Research Intern

Dhaka, Bangladesh

International Center for Diarrhoeal Disease Research, Bangladesh (Part-time, Voluntary) *Feb 2022—Jun 2022*

- Designed and implemented a comprehensive search strategy across PubMed, Embase, and PsycINFO, screening 8,000+ articles to support a systematic review on intimate partner violence in South Asia.
- Streamlined the abstract screening process in Covidence, identifying 400+ potentially relevant studies.
- Conducted full-text screening of 120+ articles and extracted key variables for meta-analysis.
- Drafted a systematic review protocol based on PRISMA guidelines, ensuring methodological transparency and reproducibility.

Data Enumerator *Australia*

School of Allied Health, Curtin University (Part-time) *Oct 2022—Nov 2022*

- Collected both quantitative and qualitative data from 40 Bangladeshi doctors for a Delphi study on Patient Outcomes Measurement in Interprofessional Tuberculosis Care.
- Validated and cleaned all survey responses, achieving 100% accuracy in the final dataset.
- Enhanced the reliability of study outcomes by ensuring high-quality and complete data capture.

Selected Publications

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.*** (2025). Transcriptomic insights into heat and hypoxia stress in rainbow trout: A meta-analysis of public RNA-Seq data [Preprint]. *Research Square*. (Accepted by *BMC Genomics*) https://doi.org/10.21203/rs.3.rs-6710656/v1

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/

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

Papers Under Review

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 in Health Science Reports].

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 in Health Science Reports].

3. Mabsurah, K., Yeana, 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 in Discover Oncology].

Working Papers

1. **Fezf2-Mediated Cortical Development: Multi-Omics Analysis**. Integrative analysis of bulk and single-cell RNA-Seq data to elucidate Fezf2's role in cortical neurogenesis. *Tech:* Python, Seurat, Scanpy, DESeq2 *GitHub:* https://github.com/hossainlab/fezf2-multiomics

2. **Single-Cell Meta-Analysis of Microglial Activation in Alzheimer's Disease**. Meta-analysis of single-cell RNA-Seq datasets to identify microglial states and activation patterns in Alzheimer's disease. *Tech:* Python, Scanpy, R/Seurat, Harmony, scVI-tools *GitHub:* https://github.com/hossainlab/alzheimers-microglia-meta-analysis

3. **Integrative Spatial-scRNA-seq Atlas of Immunotherapy Resistance Mechanisms Across Cancer Types**. Comprehensive spatial transcriptomics and single-cell analysis to map tumor microenvironment and resistance mechanisms in immunotherapy. *Tech:* Python, Scanpy, Seurat, Squidpy, SpatialData, scVI-tools *GitHub:* https://github.com/hossainlab/spatial-scRNA-immune-resistance

Conferences

1. [+]**Hossain, M. J.**, Das, M. (2024). Diagnostic and Electrophysiological Features of Hirayama Disease in Young Adult Male: A Case Report. International Conference of Public Health, Institute of Epidemiology, Disease Control and Research (IEDCR), Dhaka, Bangladesh

2. Nayeem, M. U., Mrittika, M. A., [‡]**Hossain, M. J.**, Azad, A. K., Ferdous, J., Ahmed, S., Sanyal, S. K., Towhid, S. T. (2023). Quantitative Microbial Risk Assessment from Vancomycin-Resistant Enterococcus faecalis and Enterococcus faecium from a Specific Neighborhood in Dhaka City, Bangladesh. 36th Bangladesh Society of Microbiologists Annual Conference, Shahjalal University of Science and Technology (SUST), Sylhet, Bangladesh, January 2023.

Teaching Experience

Lead Organizer & Instructor
Dhaka, Bangladesh

DeepBio Academy, Bioinformatics and Computational Biology
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 studente in the development of computational research portfolios, emphasizing open-science standards and version control.
- Refined deep learning modules for biological applications, focusing on the interpretability of high-dimensional data reduction techniques.

Faculty (Bioinformatics)
Dhaka, Bangladesh

University of Dhaka (cBLAST)
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
Dhaka, Bangladesh

GSA Bioinformatics Internship
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

Dhaka, Bangladesh

Department of Microbiology, Jagannath University

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

Founder, Bioinformatician, and CEO

Dhaka, Bangladesh

DeepBio Limited

Jan 2025 – Present

- Conceptualized the computational infrastructure for a research-driven entity specializing in AI-integrated cancer genomics and transcriptomics.
- Orchestrated a multidisciplinary research cohort of 13 scientists, supervising the execution of high-throughput pipelines for single-cell (scRNA-seq) and bulk RNA-seq analysis.
- Benchmarked scalable bioinformatics workflows to accelerate biomarker discovery and translational research in neurodegenerative diseases.
- Formulated and implemented an international professional specialization program in computational biology, training scholars across four continents.
- Cultivated strategic research alliances with industry and academic partners to enhance regional capacity for large-scale multi-omics investigations.

Founder & Capacity Building Director

Dhaka, Bangladesh

CHIRAL Bangladesh

June 2020 – Present

- Established a non-profit research institute comprising four specialized divisions: Public Health, Bioinformatics, Geospatial Health, and AI-Healthcare.
- Catalyzed national capacity-building initiatives, educating over 3,000 Bangladeshi undergraduates in rigorous research methodology, data science, and scientific communication.
- Facilitated the transition of early-career Bangladeshi scholars into global research pipelines through mentored projects and computational workshops.
- Served as Principal Investigator for a publication portfolio of 20+ peer-reviewed articles (Q1/Q2) and 40+ conference papers in health informatics.
- Managed international research collaborations, including partnerships with Michigan State University, to bolster biomedical research capacity in South Asia.
- Evaluated the analytical rigor and peer-review preparation for 15+ manuscripts currently focused on global health and computational biology.

Community Engagement

Nextflow Ambassador

Barcelona, Spain

Seqera

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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Dr. Zeba Islam Seraj
UGC Professor
Department of Molecular Biology
and Biochemistry
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