H. M. A. Mohit Chowdhury

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Research Interests

Spatiotemporal modeling and time-series analysis, deep learning and computer vision, unsupervised learning and graph representation learning, 3D genome organization and Hi-C analysis, computational genomics, and multi-modal and generative AI for understanding chromatin organization and gene regulation. I am also interested in applying AI/ML and computational methods to broader research challenges in bioinformatics, health informatics, and other life sciences domains.

Education

Ph.D. in Computer Science and Engineering Expected May 2027 | GPA: 4.00

University of North Texas (UNT), Denton, TX

Dissertation: Deep Learning Algorithms for Multiscale 3D Genome Organization Analysis
Academic Advisor: Dr. Oluwatosin Oluwadare
Dissertation Committee: Dr. Serdar Bozdag, Dr. Mark V. Albert, Dr. Heng Fan
Prior Ph.D. Enrollment: University of Colorado Colorado Springs (UCCS), 2022 – 2025; transferred to UNT in Fall 2025

M.S. in Computer Science 2024 | GPA: 3.867

University of Colorado Colorado Springs (UCCS), Colorado Springs, CO

B.S. in Computer Science and Engineering 2017 | GPA: 3.71

Ahsanullah University of Science and Technology, Dhaka, Bangladesh

Research Experience

Graduate Research Assistant 2022 – Present

CompBio-AI Lab, University of North Texas (2025–Present); Bioinformatics, University of Colorado Colorado Springs (2022–2025) *Denton, TX; Colorado Springs, CO*

- Develop deep learning, computer vision, and graph representation learning methods for multiscale 3D genome organization analysis using Hi-C data, contributing to EmbedTAD (the first unsupervised TAD caller; *Communications Biology*, 2026), HiCInterpolate (spatiotemporal interpolation of Hi-C contact maps; bioRxiv, 2026), and HiCForecast (*Bioinformatics*, 2025).
- Design and implement machine learning pipelines for Hi-C contact matrix preprocessing, model development, training, and quantitative evaluation.
- Conducted a comparative evaluation of 22 chromatin loop callers and introduced BCC_{score} for task-specific benchmarking and tool selection (*BMC Bioinformatics*, 2024).
- Develop deployable and reproducible bioinformatics tools using Flask and Docker, including Robin and CNNSplice, to support computational workflows and accessibility for wet-lab and dry-lab researchers.

- Mentor NSF REU and UR2PHD undergraduate researchers on computational genomics projects, providing guidance in machine learning, scientific computing, and research methodology. One mentored REU project resulted in HiCForecast (*Bioinformatics*, 2025), on which I am second author.

Publications

Peer-Reviewed Journal Articles

- **Chowdhury, H. M. A. M.**, & Oluwadare, O. EmbedTAD: Using Graph Embedding and Unsupervised Learning to Identify TADs from High-Resolution Hi-C Data. *Communications Biology*, 9, 7 (2026). https://doi.org/10.1038/s42003-025-09224-z
- **Chowdhury, H. M. A. M.**, Fuller, M., & Oluwadare, O. Robin: An Advanced Tool for Comparative Loop Caller Result Analysis Leveraging Large Language Models. *NAR Genomics and Bioinformatics*, 8(1) (2026). https://doi.org/10.1093/nargab/lqag009
- Pinchuk, D., **Chowdhury, H. M. A. M.**, Pandeya, A., & Oluwadare, O. HiCForecast: Dynamic Network Optical Flow Estimation Algorithm for Spatiotemporal Hi-C Data Forecasting. *Bioinformatics*, 41(2) (2025). https://doi.org/10.1093/bioinformatics/btaf030
- Rohit, M., **Chowdhury, H. M. A. M.**, & Oluwadare, O. ScHiCAtt: Hi-C Super Resolution Using Attention Methods for Single Cell. *Computational and Structural Biotechnology Journal*, 27 (2024). https://doi.org/10.1016/j.csbj.2025.02.031
- **Chowdhury, H. M. A. M.**, Boult, T., & Oluwadare, O. Comparative Study on Chromatin Loop Callers Using Hi-C Data Reveals Their Effectiveness. *BMC Bioinformatics*, 25(1) (2024). https://doi.org/10.1186/s12859-024-05713-w
- Houchens, D., **Chowdhury, H. M. A. M.**, & Oluwadare, O. coiTAD: Detection of Topologically Associating Domains Based on Clustering of Circular Influence Features from Hi-C Data. *Genes*, 15(10) (2024). https://doi.org/10.3390/genes15101293
- Akpokiro, V., **Chowdhury, H. M. A. M.**, Olowofila, S., Nusrat, R., & Oluwadare, O. CNNSplice: Robust Models for Splice Site Prediction Using Convolutional Neural Networks. *Computational and Structural Biotechnology Journal*, 21 (2023). https://doi.org/10.1016/j.csbj.2023.05.031

Preprints and Working Papers

- **Chowdhury, H. M. A. M.**, & Oluwadare, O. HiCInterpolate: 4D Spatiotemporal Interpolation of Hi-C Data for Genome Architecture Analysis. *bioRxiv* (2026). https://doi.org/10.64898/2026.02.06.704438

Research Software & Tools

- **HiCInterpolate**: Deep learning framework for spatiotemporal interpolation of Hi-C contact maps, enabling intermediate genome architecture prediction from temporally sparse observations. https://github.com/OluwadareLab/HiCInterpolate
- **EmbedTAD**: Unsupervised TAD detection framework integrating graph embedding and density-based clustering for identifying topologically associating domains from high-resolution Hi-C data. https://github.com/OluwadareLab/EmbedTAD
- **Robin**: Containerized Flask-based web application integrating large language models for comparative analysis, interpretation, and visualization of chromatin loop caller results. https://github.com/OluwadareLab/Robin

- **HiCForecast**: Deep learning framework using dynamic network optical flow to predict future chromatin contact maps and model temporal changes in 3D genome organization. https://github.com/OluwadareLab/HiCForecast
- **ScHiCAtt**: Attention-based deep learning framework for enhancing the resolution of single-cell Hi-C contact maps. https://github.com/OluwadareLab/ScHiCAtt
- **Chromatin Loop Caller Benchmark**: Comparative benchmarking framework for evaluating 22 chromatin loop callers, introducing a task-specific BCC_{score} scoring metric to support systematic tool assessment and selection. https://github.com/OluwadareLab/Comprehensive_Loop-Caller_Benchmark
- **coiTAD**: Computational framework for identifying topologically associating domains from Hi-C data using clustering of circular influence features. https://github.com/OluwadareLab/coiTAD
- **CNNSplice**: Convolutional neural network models for splice-site prediction, with deployable inference workflows implemented using PyTorch, Flask, and Docker. https://github.com/OluwadareLab/CNNSplice

Research Presentations

Conference Talks

- EmbedTAD: Using Graph Embedding and Unsupervised Learning to Identify TADs from High-Resolution Hi-C Data. *MCBIOS 2026* and *Pikes Peak AI Summit 2025*.

Poster Presentations

- HiCInterpolate: 4D Spatiotemporal Interpolation of Hi-C Data for Genome Architecture Analysis. *ISMB 2026*.
- EmbedTAD: Using Graph Embedding and Unsupervised Learning to Identify TADs from High-Resolution Hi-C Data. *MCBIOS 2026* and *Pikes Peak AI Summit 2025*.
- Comparative Study on Chromatin Loop Callers Using Hi-C Data Reveals Their Effectiveness. *RECOMB 2024* and *MLRD Research Day 2024*.

Demonstrations & Tutorials

- Delivered hands-on training in Linux, Git, and Docker for undergraduate researchers participating in the NSF REU Summer Research Program, University of Colorado Colorado Springs, Summer 2023.

Teaching

- **Research-Based Instruction and Mentorship:** Mentored undergraduate researchers through the UR2PHD and NSF REU programs, providing hands-on instruction in computational biology, machine learning, scientific computing, Linux, Git, and Docker (see Academic Advising and Mentorship).
- **Courses Prepared to Teach:** Data Structures, Algorithms, Operating Systems, Software Engineering, Artificial Intelligence, Deep Learning, Computer Vision, and Computational Biology.
- **Curriculum Development Interests:** Interested in developing interdisciplinary courses in AI/ML for Life Sciences, Scientific Machine Learning, Computational Genomics, and Deep Learning for Biological Data, tailored to departmental needs and student backgrounds.

Academic Advising & Mentorship

- **UR2PHD Undergraduate Research Mentorship**, University of North Texas, Fall 2025–Spring 2026: Mentored undergraduate researchers in research methods, scientific literature review, and research communication; guided students in preparing and presenting their work at an undergraduate research showcase.
- **NSF REU Summer Research Mentorship**, University of Colorado Colorado Springs, Summer 2023: Provided research and technical mentorship, including hands-on instruction in Linux, Git, and Docker; served as Session Chair and Technical Assistant.
- **Laboratory Onboarding and Peer Mentorship**: Supported junior students with research environment setup, computational workflows, and peer review of code and technical writing.

Awards & Honors

- MCBIOS Travel Award, 2026
- College of Engineering (CENG) Anticipated Award, University of North Texas, 2025–2026 and 2026–2027
- Graduate School Travel Award, University of Colorado Colorado Springs, 2024
- Tuition Matching Grant, University of Colorado Colorado Springs, 2022–2023 and 2023–2024

Professional & Academic Service

- **Peer Reviewer:** *BMC Bioinformatics*, *BMC Genomics*, *Scientific Reports*, *Computational and Structural Biotechnology Journal*, *Genome Biology*, *BioData Mining*, IEEE International Conference on Bioinformatics and Biomedicine (BIBM), and *Analytical Letters*.
- **President**, Bangladeshi Student Association (BSA), University of Colorado Colorado Springs, 2024–2025.
- **Research Ethics Training:** Completed Responsible Conduct of Research (RCR-mini) training.

Industry Experience

- **Solution Developer**, Otto International, 2022: Managed AWS infrastructure and Terraform-based deployments for enterprise service bus (ESB) systems, implemented Jenkins CI/CD pipelines for cross-service releases and maintained production services built with Java and PostgreSQL.
- **Software Engineer (Remote, On-Demand)**, Asiatel(S) Pte Ltd. (transferred from Dovetail Technology), 2021–Present: Provided remote software development and maintenance support on an as-needed basis, subject to availability, for production applications built with C#, .NET Web API, and Microsoft SQL Server, supported Windows services hosted on IIS and AngularJS client integrations.
- **Software Engineer**, Dovetail Technology, 2020: Developed backend applications using C#, .NET Web API, and Microsoft SQL Server, implemented Windows services hosted on IIS and integrated AngularJS clients with backend systems.
- **Software Engineer**, IdeaScale Bangladesh, 2019–2020: Developed and maintained Java-based backend services using Spring and MySQL, containerized applications with Docker and modernized database access through migration to JPA and Querydsl.
- **Software Engineer**, Japan Marketing and Consultancy Ltd., 2019: Developed backend and frontend components for a healthcare directory platform using Node.js, Vue.js, and PostgreSQL.

- **Software Engineer**, Netweaver Software Ltd., 2017–2019: Led backend development for two e-commerce platforms using Java, Spring Boot, and MySQL, with frontend integration using SAP UI5 and JavaScript.

Technical Skills

- **Programming Languages**: Python, Java, C#, C, JavaScript, SQL
  Artificial Intelligence & Machine Learning: Machine Learning, Deep Learning, Computer Vision, Time-Series Analysis, Spatiotemporal Modeling, Convolutional Neural Networks, Attention Mechanisms, Graph Representation Learning, Graph Embedding, Clustering, Unsupervised Learning, Large Language Model (LLM) Integration, Model Evaluation, Performance Benchmarking
  Frameworks & Libraries: PyTorch, scikit-learn, RAPIDS (cuML, cuDF), NumPy, Pandas, Flask, Spring, Spring Boot, .NET, ASP.NET Web API, Node.js, Vue.js, AngularJS
  Cloud, Infrastructure & Development Tools: AWS (EC2, S3), Terraform, Docker, Jenkins, CI/CD, Git, Linux, IIS
  Computational Biology & Genomics: Bioinformatics, Computational Genomics, Hi-C Data Analysis, 3D Genome Organization, Chromatin Architecture, Single-Cell Genomics, DNA Sequence Analysis

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