H. M. A. MOHIT CHOWDHURY

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EDUCATION

Ph.D. in Computer Science and Engineering | **GPA: 4.00** — Expected May 2027
University of North Texas (UNT) — *Denton, TX*

- Research: Deep learning for multiscale 3D genome organization.

M.S. in Computer Science | **GPA: 3.867** — 2024
University of Colorado Colorado Springs (UCCS) — *Colorado Springs, CO*

RESEARCH EXPERIENCE

Graduate Research Assistant — 2022 – Present
CompBio-AI Lab, UNT (2025–Present); Bioinformatics, UCCS (2022–2025) — *Denton, TX; Colorado Springs, CO*

- Developed machine learning, deep learning, and computer vision methods for 3D genome analysis using Hi-C data, Python, and PyTorch. Key contributions include EmbedTAD (first unsupervised TAD caller; highest statistical scores among 7 callers across 5 noise levels), HiCInterpolate (4D intermediate Hi-C interpolation; leading PSNR, MS-SSIM, and HiCRep performance), HiCForecast (outperformed HiC4D across GenomeDISCO, PCC, SSIM, and PSNR), and a benchmark of 22 loop callers introducing the task-specific BCC_{score} metric.
- Built end-to-end ML pipelines for Hi-C preprocessing, model training, and evaluation. Deployed Flask and Docker-based tools (Robin, CNNSplice) for dry-lab and wet-lab collaborators.
- Published research in *Communications Biology*, *Bioinformatics*, *NAR Genomics and Bioinformatics*, *BMC Bioinformatics*, and *Computational and Structural Biotechnology Journal*.
- Mentored NSF REU, UR2PHD and new students in research methodology and reproducible ML workflows.

SELECTED PUBLICATIONS

- **Chowdhury** & Oluwadare. HiCInterpolate. *bioRxiv*, 2026. DOI
- **Chowdhury** & Oluwadare. EmbedTAD. *Communications Biology*, 2026. DOI
- **Chowdhury**, Fuller & Oluwadare. Robin. *NAR Genomics and Bioinformatics*, 2026. DOI
- Pinchuk, **Chowdhury**, Pandeya & Oluwadare. HiCForecast. *Bioinformatics*, 2025. DOI
- **Chowdhury**, Boult & Oluwadare. Loop-caller benchmark. *BMC Bioinformatics*, 2024. DOI
- **Additional Publications:** ScHiCAtt (*CSBJ*, 2024), coiTAD (*Genes*, 2024), CNNSplice (*CSBJ*, 2023). Google Scholar

TECHNICAL SKILLS

Languages: Python, Java, C#, C, JavaScript, SQL
ML / AI: Machine Learning, Deep Learning, Computer Vision, Time Series, Spatiotemporal Modeling, CNNs, Attention Mechanisms, Graph Embedding, Clustering, Unsupervised Learning, LLM Tooling, Model Evaluation, Benchmarking
Frameworks & Libraries: PyTorch, scikit-learn, RAPIDS (cuML, cuDF), NumPy, Pandas, Flask, Spring, Spring Boot, .NET, ASP.NET Web API, REST APIs, Node.js, Vue.js, AngularJS
Cloud & Developer Tools: AWS (EC2, S3), Terraform, Docker, Jenkins, CI/CD, Git, Linux, IIS
Domain Expertise: Bioinformatics, Computational Biology, Genomics, Hi-C Analysis, 3D Genome Organization, Single-Cell Genomics, Sequence Analysis

SELECTED RESEARCH PROJECTS

- **HiCInterpolate** | Python, PyTorch, Spatiotemporal DL — Developed a 4D deep learning method to interpolate intermediate Hi-C maps from two time points at 10Kb resolution; evaluated using PSNR, SSIM, GenomeDISCO, and HiCRep. GitHub

- **EmbedTAD** | Python, Graph Embedding, Unsupervised Learning — Developed the first unsupervised graph-embedding-based TAD caller; achieved the highest statistical scores among 7 callers across 5 noise levels. GitHub
- **HiCForecast** | Python, PyTorch, Optical Flow — Built a deep learning pipeline for future Hi-C map prediction, outperforming HiC4D across GenomeDISCO, PCC, SSIM, and PSNR on 4 datasets. GitHub
- **Robin** | Python, Flask, Docker, LLM — Built a deployable web application for chromatin loop-caller comparison and LLM-assisted analysis. GitHub
- **Loop-Caller Benchmark** | Python, Statistical Analysis — Benchmarked 22 chromatin loop callers and introduced the task-specific BCC_{score} metric. GitHub
- **ScHiCAtt** | Python, Attention Mechanisms, scHi-C — Developed attention-based methods for single-cell Hi-C enhancement. GitHub
- **CNNSplice** | Python, PyTorch, Flask, Docker — Built CNN-based splice-site predictors across 5 organisms, achieving up to $\sim$97% accuracy; deployed through Flask and Docker. GitHub
- **coiTAD** | MATLAB, Hi-C Analysis — Developed a TAD detection method using circular influence features from Hi-C contact maps. GitHub

Professional Experience

Solutions Developer 2022
Otto International

- Managed AWS and Terraform infrastructure for ESB deployments, implemented Jenkins CI/CD pipelines for cross-service releases, and maintained Java/PostgreSQL production services.

Software Engineer (Freelance/Remote) 2021 – Present
Asiatel(S) Pte Ltd (transferred from Dovetail Technology)

- Provide remote, on-demand software development and maintenance support for existing applications, completing requested tasks based on project needs and my availability.

Software Engineer 2020
Dovetail Technology

- Designed and deployed C#, .NET Web API, and MSSQL backends, developed Windows services on IIS, and integrated AngularJS clients into production workflows.

Software Engineer 2019 – 2020
IdeaScale Bangladesh

- Maintained Java/Spring/MySQL backends, containerized services with Docker, and migrated legacy SQL operations to JPA and Querydsl.

Software Engineer 2019
Japan Marketing and Consultancy Ltd

- Led backend development of a healthcare directory using Node.js, Vue.js, and PostgreSQL.

Software Engineer 2017 – 2019
Netweaver Software Limited

- Led backend development of two e-commerce platforms using Java, Spring Boot, MySQL, SAP UI5, and JavaScript.

Leadership & Professional Activities

- **Mentoring:** UR2PHD Mentor, UNT (Fall 2025 – Spring 2026); NSF REU Mentor and Linux, Git, and Docker Instructor, UCCS (Summer 2023). One mentored REU project resulted in a 2025 *Bioinformatics* publication.
- **Presentations:** Talks at MCBIOS 2026 and Pikes Peak AI Summit 2025, posters at ISMB 2026, MCBIOS 2026, RECOMB 2024, and MLRD 2024.
- **Awards:** MCBIOS 2026 Travel Award, UCCS Graduate School Travel Award (2024).
- **Peer Reviewer:** BMC Bioinformatics, BMC Genomics, Scientific Reports, CSBJ, Genome Biology, BioData Mining, IEEE BIBM, and Analytical Letters.