# Md Muhaiminul Islam Nafi

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#### OBJECTIVE

I am Md. Muhaiminul Islam Nafi. I am currently an undergrad student of Computer Science at BUET. I want to build a successful career using my technological knowledge and relevant skills. I want to contribute to the betterment of the place I am allowed to work for. I also want to hone my other skills like time management, fast adaptability, and creativity.

MOTIJHEEL GOVT. BOYS' HIGH SCHOOL 2015-2017

SSC — GPA: 5 00/5 00

NOTRE DAME COLLEGE DHAKA 2017-2019

HSC - GPA: 5.00/5.00

BANGLADESH UNIVERSITY OF ENGINEERING AND TECHNOLOGY 2020-present

B.Sc. in Computer Science and Engineering — CGPA: 3.96/4.00 (up to 7 terms)

#### SKILLS

**PROGRAMMING LANGUAGES** Python | Javascript | Typescript | C | c++ | Assembly (x86, MIPS) | Bash | Java | LaTeX

WEB DEVELOPMENT HTML | CSS | Express | React | Svelte | Django | Next.js | Figma | Docker | Spring Boot

Matplotlib | NumPy | Pandas | Scikit-learn | PyTorch MACHINE LEARNING

**TOOLS AND TECHNOLOGIES** Design Patterns | Git | Microservices architecture | Swagger API | Postman | MISP

> DATABASES MySQL | PostgreSQL | Oracle | Prisma ORM

WordPress CONTENT MANAGEMENT GAME DEVELOPMENT Pygame | Unity

#### **PUBLICATIONS**

# Prediction of protein-carbohydrate binding sites from protein primary sequence (Under review)

In this study, we propose StackCBEmbed, an ensemble machine learning model to effectively classify protein-carbohydrate binding interactions at the residue level. StackCBEmbed combines traditional sequence-based features along with features derived from a pretrained transformer-based protein language model. Link to the initial version of the manuscript: bioRxiv

# DeepBCTPred: Deep Learning-Based Prediction of Bladder Cancer Tissues from Endoscopic Images (Under review)

In this study, we designed a pipeline to generate new images and a novel genetic algorithm to effectively select images from them. Additionally, we combined handcrafted features with learned features.

### Predicting Protein-Carbohydrate Binding Sites: A Deep Learning Approach Integrating Protein Language Model Embeddings and **Structural Features** (Manuscript in preparation)

In this study, we created a novel deep learning architecture that integrates various dataset imbalance approaches with structural features.

## **AWARDS AND HONORS**

**BUET RISE GRANT** 

RISE Student Research Grant [No. S2024-01-004] (GRANT RECEIVE)

HONORABLE MENTIONS

MicroProcessor and MicroController project

Issued Sep 2015

## **PROJECTS**

#### ONCAMPUS

GITHUB LINK: BACKEND FRONTEND

Frontend: Framework: Next.js, Styling: Tailwind CSS, Component Library: Material Tailwind, Text Box: jodit-react, PDF Viewer: react-pdf, 360° Virtual Tour: react-photo-sphereviewer, Language: TypeScript

Backend: Framework: Node.js, Express, Architecture: Microservice Architecture, ORM: Prisma ORM, Security: Helmet, JWT, Authentication: Keycloak, NextAuth.js.

Database: PostgreSQL hosted on Supabase, File Storage: Edgestore, Google Calendar Integration: Google Cloud API.

Deployment: MS Azure Virtual Machines, Supabase, Docker (for Keycloak), SSL Certificate from Namecheap, API Documentation with Postman.

### MOOMARKET

GITHUB LINK: BACKEND & FRONTEND

Tech Stack: JavaScript (Node.js, Vanilla JS), Express, HTML, EJS, PostqreSQL, Git, GitHub, npm, Render.

**GITHUB LINK: BACKEND & FRONTEND** 

Tech Stack: JavaScript (Node.js, Vanilla JS), Express, HTML, EJS, Oracle DB, Git, GitHub, npm.

# CERTIFICATES

PERFECT ATTENDANCE CERTIFICATE Issued May 2020

NOTRE DAME COLLEGE DHAKA

CERTIFICATE IN NATIONAL SKILL STANDARD BASIC COURSE EXAMINATION, 2015

BANGLADESH TECHNICAL EDUCATION BOARD

#### INTERESTS

- · Watching movies
- · Reading novels
- Listening to music