

Nishat Anjum Bristy

Phone: +8801870215192

Email: nishatanjumbristy@gmail.com

Website: <https://nishatbristy007.github.io/nishatbristy/>

Research Interest

Computational Biology, Algorithms, Machine learning

Education

2016-2020 **Bachelors in Computer Science and Engineering**
Bangladesh University of Engineering and Technology
CGPA : 3.88/4.00, Position: 7/120

Publications

JOURNAL ARTICLES

2019 N. A. Moumi, B. Das, Z. T. Promi, **N. A. Bristy**, and M. S. Bayzid, "*Quartet-based inference of cell differentiation trees from chip-seq histone modification data*," PLoS one, vol. 14,no. 9, 2019 [<https://doi.org/10.1371/journal.pone.0221270>]

Research Experience

- 2017 - 2019 **Worked with Dr. Shamsuzzoha Bayzid on Quartet-based inference of cell differentiation trees from ChIP sequence histone modification data** (Computational biology, Phylogenetics)
- We leveraged the quartet-based phylogenetic tree estimation techniques to construct cell-type trees.
 - We estimated the quartets from ChIP sequence data and amalgamated the quartets to construct the cell-type trees.
 - We included both normal and cancerous cell types to expand the scope of our work.
 - We emphasized on the strength of the standard phylogenetic tree estimation approaches in replacing the traditional intricate *in vitro* methods which explains the relationships among different cell-types.
- 2019 - 2020 **Worked with Dr. Shamsuzzoha Bayzid on Species tree estimation from Triplet and Quartet trees included in gene trees** (Computational biology, Phylogenetics)
- We developed a highly accurate statistically consistent coalescent based method for estimating species trees from a collection of gene trees based on the number of triplets and quartets.
 - We modified the codebase of ASTRAL to support rooted triplets as well as unrooted quartets.
- 2019 **Working with Dr. Siavash Mirarab and Dr. Shamsuzzoha Bayzid on Alignment-free phylogenetic distance estimation under a no strand-bias model model** (Computational biology, Phylogenetics)
- We are working on estimating phylogenetic distances from unaligned sequences, under the 4 parameter time-reversible TK4 model, using a k-mer based approach.
 - We have developed a novel technique which is able to deal with mixed-strand data.
 - Our model is expected to overcome the limitations of the Jukes-Cantor model for unaligned sequences and show promising accuracy for larger distances.
 - This work is a collaboration with University of California, San Diego.
- May, 2021 **Working with Dr. Siavash Mirarab and Dr. Shamsuzzoha Bayzid on Accurate and hierarchical contamination detection using locality sensitive hashing** (Computational biology, Phylogenetics)

- We are trying to classify contaminant reads into different hierarchical taxonomic ranks using locality sensitive hashing.
- Our novelty is that we plan to bin the contaminant reads with a much smaller memory footprint.
- This work is based on a similar work, *CONSULT: Accurate contamination removal using locality-sensitive hashing*, and a collaboration with University of California, San Diego.

November,
2020

**Worked with Dr. Atif Hasan Rahman on
An RNN based method for the classification of HIV-1 genomes**

(Computational biology, Deep learning)

- We proposed an alignment-free subtyping method using Recurrent Neural Networks that operates on both time series analysis of the individual character and k-mer frequencies in HIV-1 sequences.
- With our character level time series analysis, a sliding window approach seemed to be the most accurate (95.54% training and 93.03% validation accuracy). This is because a sliding window gives the opportunity of increasing samples in the training dataset, as well as captures the co-occurrence of the contigs.

May, 2021

**Worked with Dr. Atif Hasan Rahman on
A deep learning based tool for sequence contamination detection**

(Computational biology, Deep learning)

We are leveraging the effectiveness of deep learning using a novel metagenomic binning approach, to model the co-occurrence of contigs belonging to the same genome.

May, 2020

**Working with Dr. Tanzima Hashem on 2 projects -
Detecting malnutrition and dehydration from facial images, and
A survey on different smartphone image analysis techniques for disease detection**

(Machine Learning, HCI)

- We are working on detecting malnutrition and dehydration from images of different body parts (face, eyes, lips, fingertips, etc.) that show significant variation in color and texture due to the disease.
- Our goal is to build an easily accessible machine learning based smartphone application, which will be able to detect dehydration and malnutrition levels.
- This work is a collaboration with [International Centre for Diarrhoeal Disease Research, Bangladesh](#).

Work Experience

February, 2021

Research Assistant

Department of CSE, BUET

November,
2020

Academic Co-ordinator

Bangladesh Mathematical Olympiad

Grants, honors & awards

2020

Winner of the first round of the **Sanger Institute Prize Competition, 2020**, arranged by Wellcome Sanger Institute

2019, 2020

University merit scholarship for academic excellence

2019,2020

Deans List Award

2011, 2013-14

National round champion at **Bangladesh Mathematical Olympiad** and **Bangladesh Physics Olympiad**

2013

Divisional champion at **National Creative Talent Hunt**, Bangladesh

2010

Received an award from the honorable president of Bangladesh, Zillur Rahman, for a **nation-wide essay competition**

Projects

2017

Website of a Bank management system with JSP, HTML, CSS (As part of the Database systems course)

2018-2019

Machine learning based Bank Credit Risk Prediction (A collaboration with [Bank Asia](#))

2019

TCP Reset Attack on video streaming (Computer security)

Selected Computer Literacy

Languages Python, C/C++, Java, Bash, Matlab, PHP, JavaScript, HTML/CSS, SQL
Libraries Keras, Tensorflow, NLTK, Pandas, NumPy
Frameworks Django

Leisure

Hobbies Reading, Sketching, Swimming, Learning languages
Languages Bangla, English, French, Arabic