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-occurance 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 self-sttention network, to model the co-occurance 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	**Accademic 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 accademic 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 colaboration 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