

Preonath Chondrow Dev

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Education

Master of Science in Biochemistry and Molecular Biology(With Thesis)

SHAHJALAL UNIVERSITY OF SCIENCE AND TECHNOLOGY(SUST)

2019-2021

Sylhet, Bangladesh

- CGPA: 3.57 out of 4.00
- **Thesis title:** Development of a disease detection tool from metagenomic sequence data utilizing k-mer frequency based algorithms: A gut microbiome study. [🔗](#)
 - Processed WGS microbial gut sequences (FastQC, BWA, and SAMtools) and built a database by encoding k-mers (SQLite3).
 - Developed and optimized a k-mer-based method for accurate prediction of categorized sequences (string matching algorithms and neural networks).
- **Thesis supervisor:** **Mohammad Uzzal Hossain**, Senior Scientific Officer - Bioinformatics Division, National Institute of Biotechnology, Dhaka

Bachelor of Science(Honours) in Biochemistry and Molecular Biology

SHAHJALAL UNIVERSITY OF SCIENCE AND TECHNOLOGY(SUST)

2015-2019

Sylhet, Bangladesh

- CGPA: 3.36 out of 4.00
- **Research Project:** Prediction of Missing DNA Methylation from Whole Genome Bisulfite Data Using KNN. [🔗](#)
 - Preprocessed the epigenomic dataset (Bash scripting) and developed model to impute missing CpG methylation values in DNA(k-Nearest Neighbors).
- **Advisor:** **Dr. Rashedul Islam**, PhD in Bioinformatics - University of British Columbia, Canada
- **Academic Advisor:** **Ayesha Tasnim**, Assistant Professor - Department of Computer Science & Engineering, SUST, Sylhet

Research Experiences

Child Health Research Foundation

RESEARCH OFFICER, BIOINFORMATICIAN - GENOMICS TEAM

Dhaka, Bangladesh

01 Aug 2022 - Present

- **CZI A Global Pediatric Cell Atlas of Nasal and Oral Mucosa.** [🔗](#)
 - Prepared single-cell libraries followed by cell isolation and capture, whole-transcriptome amplification by utilizing HoneyComb method.(1st in Bd)[🔗](#)
 - Analyzed single-cell RNA-seq data using Scanpy and Seurat on Terra, comparing data from sick and healthy samples, including:
 - Processing raw sequence, clustering and cell annotation, integration, identification of unique clusters (cells) and RSV & metagenomics analysis.
 - Performing SCTransform normalization, dimensionality reduction (PCA, UMAP), and Leiden clustering.
 - Annotating cell types using canonical markers and reference-based label transfer with prediction score filtering.
 - Subclustering major epithelial and immune populations (e.g., goblet, ciliated, B, T) to uncover lineage-specific heterogeneity.
 - Quantifying cell-type proportions across conditions using Kruskal-Wallis test, Dunn's post hoc, and Cohen's d.
 - Profiling viral tropism by measuring RSV transcript burden across annotated cell types.
- **Collaboration:** Ordovas-Montañes Lab - Boston Childrens Hospital, Harvard University, Massachusetts Institute of Technology (MIT) [🔗](#)
- **Training:** Received training on single-cell sequencing and analysis from the team members of Ordovas Montanes Lab, Boston Childrens Hospital. [🔗](#)
- **PCV effectiveness study via single-cell analysis of pregnant women.** [🔗](#)
 - Received training on: cell-cell communication, BCR background and 10x analysis, trajectory inference, differential abundance, multiomic scATAC.
 - Group Work and Presentation: Single-Cell Profiling of Ebola Virus Disease In Vivo Reveals Viral and Host Dynamics [🔗](#).
 - Trainer: Shalek Lab - MIT, Harvard Stem Cell Institute, and Faculty of Medicine - Mahidol University, Thailand [🔗](#)
 - PBMC isolation and single-cell sequencing.
- **Workshop:** Presented at the 2024 HCA Single-Cell Omics In-Person Computational and Experimental Design Workshop. [🔗](#)
- **Supported by:** Global Grand Challenges, Bill & Melinda Gates Foundation [🔗](#)
- **A computational framework to automatically interpret pediatric chest X-rays and diagnose pneumonia.**
 - Developed the model using CNN and PyTorch utilizing:
 - Convolutional layers, ReLU activation, batch normalization, max pooling, residual connections
 - Dropout, data augmentation, cross-entropy loss, adam optimizer, architectures: ResNet, VGG.
- **Funded by:** NIHR Global Health Research Unit on Respiratory Health [🔗](#)
- **Global Pneumococcal Sequencing Project.** [🔗](#)
 - Developed bash scripting to analyzing SPN WGS data of Illumina and Oxford Nanopore including:
 - Oxford Nanopore: Preprocessing (nanoq), assembly (Flye, Unicycler), polishing (Medaka), and assembly improvement (Pilon).
 - Illumina: Preprocessing (FastQC, Trimmomatic), mapping, taxonomy classification (Kraken2), serotyping (SeroBA), MLST(MLST, SRST2),
 - AMR detection (ResFinder), consensus sequence generation, gubbins recombination analysis, phylogenetic tree building and annotation
- **Training:** Received *Advanced Bioinformatics Training* by Wellcome Sanger Institute under GPS and JUNO projects in Bangalore, India. [🔗](#)
 - Nextflow workflow building on Docker for NGS analysis (FastQC, Trimmomatic, SPAdes, Kraken2, Prokka, QUAST, SeroBA, SRST2, Abriicate, Snippy)
- **Genomic epidemiology of Salmonella Paratyphi B isolates from Bangladesh.** [🔗](#)
 - Development of bioinformatics pipeline using bash scripting including:
 - Preprocessing, assembly, mapping, taxonomy classification, MLST, AMR detection, serotyping, variant calling,
 - Consensus sequence generation, gubbins recombination analysis, phylogenetic tree building and annotation (RAXML-NG & iTol)
- **Workshop:** *SeroCalculator Workshop* in Kigali, Rwanda. [🔗](#)
 - Learned the basic concept of sero- epidemiology, analyzed serological data and estimated sero-incidence of typhoid fever.

- Revealing the Disease complexity and Population Structure of Human Gut Microbiota from Diverse Cohort of Bangladesh Population.
 - Metagenomic analysis of 16S rRNA sequences. [🔗](#)
 - Data processing, feature table construction, taxonomic assignment, diversity analysis & visualization
 - Funded under “Establishment of National Gene Bank Project” (NIB), Ministry of Science and Technology, Bangladesh [🔗](#)

Teaching Experience

Child Health Research Foundation (CHRF)

TEACHING ASSISTANT, BUILDING SCIENTISTS FOR BANGLADESH

Dhaka, Bangladesh

2023-2024

- **Advanced Next Generation Sequencing** [🔗](#)
 - Linux OS, NGS Data Analysis: Quality checking, quality filter, genome assembly, genome annotation
 - Building consensus (CZID), sample sheet preparation for NextSeq2000, data uploading to NCBI and ENA
- **Next-Generation Pathogen Sequencing Training** [🔗](#)
 - Linux OS, bash scripting genome assembly, genome mapping, genome annotation, genome submission, MLST prediction
- **AI in Public Health** [🔗](#)
 - Data cleaning and preprocessing, data visualization, architecture of ML and DL libraries- Numpy, Pandas, Keras, TensorFlow
 - Dengue prediction in Puerto Rico using LSTM and ARIMA
 - Predicting pneumonia in X-rays using CNN
 - Advanced modeling techniques- PyCaret, GRU
- **Supported** by the Bill and Melinda Gates foundation, through the Democratizing Public Health Modeling Using AI-based Tools [🔗](#)

Bioinformatics Division, National Institute of Biotechnology (NIB)

INSTRUCTOR, BIOINFORMATICS DIVISION

Dhaka, Bangladesh

2021

- Delivered training on Bioinformatics for Biotechnology Research
 - Linux OS, bash scripting and biopython for NGS data analysis

Publications

- Malaker, A. R., Deb, P., Tanmoy, A. M., Kanon, N., Reaz, S., **Dev, P. C.**, Rahman, H., Tanvia, L., Rahman, A., Tanni, A. A., [other CHRF authors, BSHI authors], Tato, C., Nawshad, A. S. M. N. U., Imam, F., DeRisi, J. L., Saha, S. K., Hooda, Y., Saha, S. **Emerging Role of Human Parvovirus 4 in Pediatric Meningitis: A Multiyear Retrospective Observational Study.** (In process – to be submitted to *Lancet Microbe*)
- Debnath, J. P., Hossen, K., Sayed, S. B., Khandaker, M. S., **Dev, P. C.**, Sarker, S., Hossain, T. Identification of Potential Biomarkers for 2022 Mpox Virus Infection: A Transcriptomic Network Analysis and Machine Learning Approach. *Scientific Reports*. doi: **10.1038/s41598-024-80519-7**
- Islam, S., Kabiraj, R., Sarkar, H., **Dev, P. C.**, Tanni, A., Keya, D., Malaker, A. R., Tanmoy, A. M., Saha, S., Hooda, Y., Saha, S. Genome sequences of bacteriophages that infect *Salmonella Typhi* from Bangladesh. *Microbiology Resource Announcements*. 0:e00447-24. doi: **10.1128/mra.00447-24**
- Raju, R. S., Nahid, A. A., **Dev, P. C.**, Islam, R. VirusTaxo: Taxonomic classification of viruses from the genome sequence using k-mer enrichment. *Genomics*. 2022 Jul;114(4):110414. doi: **10.1016/j.ygeno.2022.110414**. Epub 2022 Jun 17. PMID: 35718090.
- Chowdhury, Z. M., Bhattacharjee, A., Ahammad, I., Hossain, M. U., Jaber, A. A., Rahman, A., **Dev, P. C.**, Salimullah, M., Keya, C. A. Exploration of *Streptococcus* core genome to reveal druggable targets and novel therapeutics against *S. pneumoniae*. *PLOS One*. 2022 Aug 18;17(8):e0272945. doi: **10.1371/journal.pone.0272945**. PMID: 35980906; PMCID: PMC9387852.

Conference Poster Presentations

- **Dev, P. C.**, Malaker, A. R., Keya, D. P., Tanmoy, A. M., Saha, S. K., Saha, S., Hooda, Y. Building a single-cell atlas of the nasopharyngeal mucosa to investigate RSV and SARS-CoV-2 infection. **2025 Human Cell Atlas General Meeting, Singapore**
- Keya, D. P., Malaker, A. R., **Dev, P. C.**, Walsh, J. L., Taliaferro, F., Tanvia, L., Tanmoy, A. M., Tang, Y., Juttukonda, L., Langan, E., Frischmann, A., Horwitz, B., Saha, S. K., Hooda, Y., Ordovas-Montañes, J., Saha, S. Harnessing single-cell genomics to understand pathophysiology of RSV infection in the nasal mucosa of children. **2025 Human Cell Atlas General Meeting, Singapore**
- Malaker, A. R., Keya, D. P., **Dev, P. C.**, Tanvia, L., Kanon, N., Hassan, S., Tanmoy, A. M., Islam, M. S., Shalek, A. K., Saha, S. K., Hooda, Y., Saha, S. Impact of PCV-10 vaccination on the immune cell population of pre-term infants in rural Bangladesh. **2025 Human Cell Atlas General Meeting, Singapore**
- **Dev, P. C.**, Malaker, A. R., Keya, D. P., Hooda, Y., Saha, S. Building a single-cell atlas of the nasopharyngeal mucosa to investigate SARS-CoV-2 infection. **2024 HCA Single-Cell Omics In-Person Computational and Experimental Design Workshop, Bangkok, Thailand**
- **Dev, P. C.**, Tanmoy, A. M., Rahman, A., Saha, S. K., Hooda, Y., Saha, S. Paratype v1.1: Recent updates to the genotyping tool for paratyphoid fever surveillance. **13th International Conference on Typhoid and Other Invasive Salmonellosis, Kigali, Rwanda**
- Rehman, A., **Dev, P. C.**, Hossain, M. M., Kazi, E., Goswami, S., Rehman, H., Hooda, Y., Tanmoy, A. M., Saha, S. K., Saha, S. Genomic epidemiology of *Salmonella enterica* serovar *Paratyphi B* isolates from Bangladesh. **13th International Conference on Typhoid and Other Invasive Salmonellosis, Kigali, Rwanda**

Accomplishment

- 2018-2024 **6th** out of 731, Position from Bangladesh: Handle: **Preonath_Shuvo_SUST, Rosalind** [🔗](#)
Rosalind is a platform for learning bioinformatics through problem solving and I solved these problems using Python.
- 2022-2023 **100+** Problem solved: Handle: **Preonath, Leetcode** [🔗](#)
Leetcode is a platform of algorithmic problems for competitive programming and I solved these problems using Python.
- 2023-2024 **220** out of 13558: Handle: **CHRFBD_datascience_team, DrivenData** [🔗](#)
DrivenData applies data science to health projects. My team predicted dengue spread using LSTM.
- 2017 **Accomplished Competitor: University Physics Competition**, [🔗](#)
This international competition challenges problem-solving with physics. My team worked on Solar Sailing to Mars.

Tanvir Hossain

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