# Preonath Chondrow Dev

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## Education

**Master of Science in Biochemistry and Molecular Biology(With Thesis)**                    *2019-2021*

SHAHJALAL UNIVERSITY OF SCIENCE AND TECHNOLOGY(SUST)                    *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, Bangladesh

**Bachelor of Science(Honours) in Biochemistry and Molecular Biology**                    *2015-2019*

SHAHJALAL UNIVERSITY OF SCIENCE AND TECHNOLOGY(SUST)                    *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).
  - **Academic Advisor:** Ayesha Tasnim, Asst. Professor, CSE, SUST, Sylhet, Bangladesh | **Advisor:** Dr. Rashedul Islam, Postdoctoral Fellow, Berkeley Lab, USA.

## Research Experiences

**Child Health Research Foundation**                    *Dhaka, Bangladesh*

RESEARCH OFFICER; BIOINFORMATICIAN - GENOMICS TEAM                    *2024-Present; 01 Aug 2022 - 2023*

- ***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:
    - Processed scRNA-seq data: SCTransform normalization, dimensionality reduction (PCA, UMAP), annotated cell types using canonical markers.
    - Performed label transfer with prediction score filtering, cluster refinement, and subclustering to uncover lineage-specific cellular heterogeneity.
    - Quantified cell type and subset frequencies across disease conditions; applied Kruskal–Wallis, Dunn's test, and Cohen's d effect size analysis.
    - Mapped RSV transcript burden across epithelial cell subsets to reveal location-specific viral entry, tropism, and infection response patterns.
  - ***Collaboration:*** Ordovas-Montañes Lab — Boston Children's Hospital, Harvard Medical School and the Broad Institute. ↗
  - ***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.** ↗
  - Isolated PBMCs, prepared single-cell libraries, and performed whole-transcriptome amplification using the HoneyComb method.
  - Generated PBMC scRNA-seq matrix using Terra BeenetPlus; applied Seurat SCTransform, PCA/UMAP, and used SingleR for coarse annotation.
  - Quantified cell-type frequencies and preterm–term variation via DE analysis, GO enrichment and Monocle3 trajectories: preterm versus term samples.
  - ***Workshop:*** Attended at the *2024 HCA Single-Cell Omics In-Person Computational and Experimental Design Workshop and 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 ↗
  - ***Supported by:*** Global Grand Challenges, Bill & Melinda Gates Foundation ↗
- **A computational framework to automatically interpret pediatric chest X-rays and diagnose pneumonia.**
  - Developed a contrast-enhanced Swin Transformer framework using PyTorch for accurate pneumonia classification from pediatric chest X-rays.
  - Employed modified Segment Anything Model to segment lung regions, enhancing disease localization and interpretability of model predictions.
  - ***Funded by:*** NIHR Global Health Research Unit on Respiratory Health ↗
- **Genomic epidemiology of Salmonella Paratyphi B isolates from Bangladesh.** ↗
  - Extracted genomic DNA and prepared libraries for whole-genome sequencing using Illumina (NextSeq 2000/iSeq 100) and Oxford Nanopore (MinION).
  - Developed hybrid pipeline using Bash scripting, integrating preprocessing, genome assembly, mapping, serotyping, MLST and AMR detection.
    - Included variant calling, consensus generation, recombination analysis, phylogenetic tree construction/annotation using RAxML-NG and iTOL.
    - Processed Nanopore reads: preprocessing (NanoQC), hybrid assembly (Flye, Unicycler), polishing (Medaka), and assembly improvement (Pilon).
  - **Workshop:** *Attended SeroCalculator Workshop* in Kigali, Rwanda; learned seroincidence simulation and antibody modeling for typhoid estimation. ↗
  - ***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, Abricate, Snippy...)
- **Whole Exome Sequencing and analysis services.**
  - Extracted genomic DNA from human samples, performed library preparation, and conducted whole-exome sequencing using Illumina NextSeq 2000
  - Developed Bash/Python pipeline for downstream analysis using GATK best practices and disease association detection including:
    - Performed QC, alignment, variant calling, CNV detection and variant annotation using ANNOVAR, VEP, and Franklin for clinical interpretation.
    - Integrated ClinVar, OncoKB, CIViC, VarSome to assign pathogenicity and associate variants with disease phenotypes and molecular mechanisms.
    - Applied constraint metrics and functional impact scores to prioritize rare variants with strong biological and clinically validated relevance.

**National Gene Bank, National Institute of Biotechnology(NIB)** *Dhaka, Bangladesh*
RESEARCH FELLOW *5 Sept 2021 - 30 June 2022*

- Revealing the Disease complexity and Population Structure of Human Gut Microbiota from Diverse Cohort of Bangladesh Population.↗
    - Performed metagenomic analysis of 16S rRNA: denoising (DADA2), feature table (q2-feature-table), and phylogenetic tree building (FastTree).
    - Conducted taxonomic assignment (q2-feature-classifier, SILVA), diversity analysis (q2-diversity), and visualized communities (Emperor).
    - Under "Establishment of National Gene Bank Project" (NIB), Ministry of Science and Technology, Bangladesh ↗

## Teaching Experience

**Child Health Research Foundation (CHRF)** *Dhaka, Bangladesh*
TEACHING ASSISTANT, BUILDING SCIENTISTS FOR 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.** ↗
    - Preprocessed data, performed visualization, and built ML/DL architectures using NumPy, Pandas, Keras, and TensorFlow.
    - Dengue prediction in Puerto Rico using LSTM and ARIMA; pneumonia detection in X-rays using CNN and 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)** *Dhaka, Bangladesh*
INSTRUCTOR, BIOINFORMATICS DIVISION *2021*

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

## Publications

- Hossen, K., Debnath, J. P., Khandaker, M. S., S. Majid, M. M. Islam, S. Arefin, **Dev, P. C.,**\* Sarker, S.,\* Hossain, T.\* *omicML: An Integrative Tool of Bioinformatics and Machine Learning Algorithms to Identify Transcriptomic Biomarkers*. *(In process)*
- Malaker, A. R., Deb, P., Tanmoy, A. M., Kanon, N., Reaz, S., **Dev, P. C.,** … A. A., 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)*
- 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, R. A., M., Tanmoy, A., 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., … **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**.

## 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.,*** *J. L. Walsh, F. Taliaferro, … B. Horwitz, S. K., Saha, Hooda, Y., J. Ordovas-Montanes, 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 Salmonelloses, Kigali, Rwanda.***
- Rehman, A., **Dev, P. C.,** Hossain, M. M., Kazi, E., … 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 Salmonelloses, 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 applied Python to solve these problems.

2022-2023  ***100+*** Problem solved: Handle: ***Preonath***, ***Leetcode***↗
Leetcode is a platform of algorithmic problems for competitive programming and applied Python to solve these problems.

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.

## References

**Dr. Tanvir Hossain**
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