Biplab Paul

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SUMMARY OF QUALIFICATION

- PhD level cell biologist with experience in bioinformatics.
- Expertise in developing computational pipelines to analyze a wide range of next generation sequencing data such RNA-Seq, Chip-Seq, single-cell RNA-Seq etc.
- Experience in R, Python and MatLab programming language.
- Comfortable with working in Unix, Linux, HPC computing platforms.
- Experience in using open source bioinformatic tools such as bowtie, hisat2, samtools, bedtools, deeptools, DESeq2, GO-Seq, Seurat, IGV etc.
- Wet laboratory experience in molecular biology, genetics, microscopy and RNA Biology.
- Strong communication and collaboration skills through collaborative work during PhD and Postdoc.

RELEVANT EXPERIENCE

Postdoctoral Fellow, **01/2020 – Present**
Massachusetts General Hospital, Harvard Medical School

- Analyzed bulk RNA-Seq, single-cell RNA-Seq (scRNA-Seq) and spatial transcriptomics (MERFISH) data generated from human liver tissue.
- Established wet laboratory methods for preparation of spatial transcriptomics sample from normal human liver using Multiplex Error Robust Fluorescence in situ hybridization (MERFISH).
- Adapted Matlab based pipeline for designing probe sets for MERFISH.

Visiting Research Scholar, University of California, Davis **09/2016 – 12/2019**

- Analyzed RNA-Seq data to identify mutation-specific effects on yeast transcriptomes, including custom analysis of NGS data to identify RNA processing defects using shell scripting, R and Python programming.
- Generated pipeline for analysis of Chip-Seq and RNA-Seq data from public database.
- Analyzed of gene expression by single molecule fluorescence in situ hybridization (smFISH).

EDUCATION

Ph.D. in Cell Biology, University of Alberta, Canada **05/2015 – 12/2019**
Thesis: Nuclear accumulation of polyadenylated non-coding RNA leads to a breakdown in nuclear RNA homeostasis.
Supervisor: Dr. Ben Montpetit

M.Sc. in Biochemistry, University of Regina, Canada **01/2009 – 04/2013**
Thesis: Role of β-galactofuranose and β-glucan in *Aspergillus nidulans* hyphal cell wall ultrastructure and physical properties.
Supervisor: Dr. Tanya Dahms

B.Sc. in Biotechnology and Genetic Engineering **09/2001 – 07/2006**

Khulna University, Bangladesh

SELECTED PUBLICATIONS

- LC Aguilar* **B Paul*,** T Reiter, L Gendron, AAN Rajan, R Montpetit, C Trahan, S Pechmann, M Oeffinger, and B Montpetit (2020) Altered rRNA processing disrupts nuclear RNA homeostasis via competition for the poly(A)-binding protein Nab2. Nucleic Acid Research. 48(20):1165-11694 (* denotes equal contribution).

- **Paul, B,** & Montpetit B. (2016) Altered RNA processing and export leads to retention of mRNAs near transcription sites, nuclear pore complexes, or within the nucleolus. Mol Biol Cell. 27:17, 2742-2756.