

CLIFF LUN

Cell: 347.654.4199 ▪ Email: cliffun@gmail.com Portfolio: <https://cliffun.github.io>

Skills

Technical: Python, R, Bash, SQL, git, Docker, HPC, Nextflow, Matlab

Bioinformatics: samtools, bedtools, bcftools, GATK/PLINK, SV callers, Peddy, Seurat, DESeq2, IGV

Neuroimaging: FSL, FreeSurfer, CONN, BrainVoyager, TrackVis, Mango, FreeView, DSI studio

Language: English, Cantonese, Mandarin, Spanish

Professional and Research Experience

Pacific Northwest Research Institute, Seattle, WA

November 2022 – Present

Bioinformatician, Carvalho Lab

- Drive analytics and data visualization for various rare disease projects related to SNVs and structural variations in MECP2 Duplication Syndrome, Primary Immunodeficiency Diseases (PIDD), and more
- Create and maintain pipeline for structural variation and complex rearrangement discovery in rare diseases
- Identified the missing variant on the alternate allele to explain phenotype of a patient with PIDD
- Develop expertise and train others on multiple genomic technologies (srGS, lrGS, OGM, aCGH, Hi-C, HPO)
- Design content to communicate research findings at scientific conferences
- Mentor undergraduate students to provide guidance and support on reaching professional goals

Icahn School of Medicine at Mount Sinai, New York City, NY

September 2018 – October 2022

Associate Researcher II, BioMedical Engineering and Imaging Institute

- Led analytics and data visualization for 15 NIH-sponsored neuroimaging projects spanning PTSD, anesthesia, environmental exposure, and trauma-driven vascular inflammation
- Implemented and improved image processing pipelines for the analysis, visualization, and archival of high-dimensional MRI data using CLI
- Drove efficiencies in analytics and reporting infrastructure through automation; write custom scripts in Python and Bash to accelerate data transformation
- Collected MR imaging and micro-CT imaging data across humans and rodents

Cancer Biotherapy Institute of Jiangsu, Xuzhou Medical University, Xuzhou, China July 2016 – August 2016

Research Assistant, Supervisor: Prof Yao Hong

- Determined the gene expression level of CCDC30 gene in cisplatin-induced HepG2 cell by qPCR and Western Blots assays
- Verified the interaction between HGFK1 and Met receptor in HepG2 cells by Co-immunoprecipitation assay
- Aggregated research data to generate insights about circle RNA as a driver of cancer development

Selected Publications

Christopher M. Grochowski, Jesse D. Bengtsson, Haowei Du, Mira Gandhi, **Ming Yin Lun**, et al. **Break-induced replication underlies formation of inverted triplications and generates unexpected diversity in haplotype structures**

bioRxiv 2023.10.02.560172; doi: <https://doi.org/10.1101/2023.10.02.560172>

Tang CY, Wang VX, **Lun MY**, Mincer JS, Ng JC, Brallier JW, et al. (2021) **Transient changes in white matter microstructure during general anesthesia**. PLoS ONE 16(3): e0247678. <https://doi.org/10.1371/journal.pone.0247678>

Education

Johns Hopkins University, Baltimore, Maryland

December 2023

Master of Science; Major in Bioinformatics

- GPA: 3.88 / 4.00

Georgetown University, Washington, D.C.

July 2018

Master of Science; Majors in Physiology and Biophysics

- GPA: 3.91 / 4.00

The University of Hong Kong, Hong Kong

June 2017

Bachelor of Science; Majors in Biochemistry and Molecular Biology & Biotechnology