

# CLIFF LUN

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## Skills

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

**Bioinformatics:** samtools, bedtools, bcftools, GATK, SV callers, Seurat, DESeq2, IGV, FASTQC, BAMQC, Peddy

**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, and more
- Create and maintain pipeline for structural variation discovery in rare disease across the whole genome
- 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 – Present

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

## Publications

Jian Zhang, Huizhong Li, Dazhi Gao, Baofu Zhang, Maojin Zheng, **Mingyin Lun**, Mengxue Wei, Rui Duan, Maomao Guo, Jiajun Hua, Qian Liu, Jin Bai, Hui Liu, Junnian Zheng & Hong Yao (2018) **A prognosis and impact factor analysis of DC-CIK cell therapy for patients with hepatocellular carcinoma undergoing postoperative TACE**, Cancer Biology & Therapy, DOI: 10.1080/15384047.2018.1433501

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

Prospective **Master of Science**; Major in Bioinformatics

- Current GPA: 4.00 / 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