

PROFESSIONAL EXPERIENCE

2023

Data Analyst Associate

Baylor College of Medicine

Houston, TX

- Partnered with team to develop and deploy automated NGS analysis pipeline on local servers with Docker, Python, R, and Bash.
- Worked with software engineers and clinical geneticists to fine-tune and prompt engineer several open-source LLMs for precision diagnosis of rare Mendelian genetic disorders. I applied inference optimization techniques such as mini-batching and output clipping to greatly reduce the runtime of model inference.
- Collaborated with lab members via GitHub to develop the Python back-end for a mentor-mentee matching tool using GPT-4 (via API) and RAG (FAISS) for leaders of clinical departments. We deployed the tool using Microsoft Azure and delivered a working product demo with a JS front-end for multiple clinical department heads.
- Lead bioinformatics team in analyzing collaborator data and delivering high-quality results in timely fashion. Regularly provided consulting and technical expertise to team and other group members to improve overall group efficiency.
- Fostered collaborative work environment by regularly leading weekly lab meetings and journal clubs. Implemented structured interview process including proficiency exam for incoming analysts, filling vacancies with effective candidates.

2022 | 2020

Graduate Research Assistant

UTHSC Houston Graduate School of Biomedical Sciences

Houston, TX

- Partnered with lab members to build a convolutional neural network with self-attention architecture in Python using Tensorflow/Keras for finding high-confidence transcription factor targets for viruses. Improved performance using a downsample-bootstrapping training method and 10-fold cross validation. Project was published in Cell Patterns and the code is publicly available on Github.
- Worked with team to run trajectory inference and pseudotime analysis using R packages Seurat and Slinghost on scRNAseq data to identify which transcription factor programs drive COVID-19 infection severity with the machine learning algorithms. Our work was published in Genes and the code is publicly available on Github.
- Fine-tuned ProteinBERT Transformer into a pan-virus MHC-epitope classification model for high throughput identification of vaccine targets for viruses
- Regularly lead group meetings and provided results to PI in timely manner. Helped foster a collaborative lab environment by helping to identify and solve problems encountered by all team members.

2020 | 2019

Research Assistant I

MD Anderson Cancer Center

Houston, TX

EDUCATION

2022 | 2020

M.S. in Quantitative Sciences

UTHSC Houston Graduate School of Biomedical Sciences

Houston, TX

2018 | 2015

UTHSC Houston McGovern School of Medicine

Houston, TX

2015 | 2011

B.S. in Biology, B.A. in Chemistry

Emory University

Atlanta, GA

AWARDS

2022

Best Quantitative Sciences Program Seminar Presentation

UTHSC Houston Graduate School of Biomedical Sciences

Houston, TX

2022

First Prize Poster Presentation

UTHSC Houston Graduate School of Biomedical Sciences

Houston, TX

2016

Rheumatology Research Foundation Research Award

UTHSC Houston McGovern School of Medicine

Houston, TX