I-SHU WANG

ishuwang9685@gmail.com; (412) 983-5473; https://www.linkedin.com/in/i-shu-wang-085a201b9/;https://wang9685.github.io/

EDUCATION

Carnegie Mellon University | Pittsburgh, PA | Aug 2022 – Dec 2023

Master of Science in Quantitative Biology And Bioinformatics - Advanced Study

Relevant Courses: Machine Learning, Algorithms & Advanced Data Structures, Fundamentals of Bioinformatics,

Bioinformatics Data Integration Practicum, *Deep Learning, Computational Medicine (*Fall Semester)

National Taiwan University | Taipei, Taiwan | Aug 2018 - Jun 2020

Master of Science in Biochemical Science & Technology

National Chung Cheng University | Chiayi, Taiwan | Aug 2014 - Jun 2018

Bachelor of Science in Biomedical Science; Certificate in Functional Genomics Program

EXPERIENCE

Carnegie Mellon University | Graduate Researcher | Pittsburgh, PA | Jan 2023 - Present

- · Analyzed extensive long-read RNA-seq data on a Linux platform to ascertain gene expression levels
- Constructed a pipeline using Snakemake to analyze alternative splicing events within sequencing data and employed parallel programming techniques to significantly reduce at least 75% processing time
- Collaborated closely with biologists to perform in-depth data analysis and developed an interactive web application interface for non-programmers to easily access and interpret data visualization figures

NGS High Throughput Genomics Core | Research Assistant | Taipei, Taiwan | Feb 2021 - Aug 2021

- Created diverse sequencing libraries and managed Illumina sequencers to acquire top-tier sequencing data
- Expertly demultiplexed sequencing data and employed Fastgc to assess the quality of data, ensuring data integrity
- Fostered effective communication with customers, adeptly addressing their requirements

National Taiwan University | Graduate Researcher | Taipei, Taiwan | Aug 2018 – Jun 2020

- Earned Excellence Award from Agricultural Chemical Society of Taiwan Annual Poster Competition Sessions
- Utilized BLAST and the NCBI database to engineer a plasmid for a gene knockout system

SKILLS

Computational skills: Python, Go Language, SQL, R, Linux, High Performance Computing, Cloud Computing **Bioinformatics Tools:** NCBI, BLAST, TCGA, Snakemake, Bioconductor, BioPython

Data Analysis: Numpy, Pandas, SciPy, Seaborn, plotly, ggplot, Matplotlib, Scikit-Learn, Pytorch, dash, Shiny

ACADEMIC PROJECTS

Carnegie Mellon University, Pittsburgh, PA

A python script for scanning open reading frame and extracting protein sequences | Oct 2022

 Created a Python script that perform a series of processes from examining whole genomics for bacteria, translating DNA sequences to protein sequences, to using BLAST to compare the protein sequences

Data analysis and visualization on oncology data | Dec 2022

Performed statistical analysis using Python and presented the results through effective visualization

Simulation of intercellular viral infection via cell-to-cell transmission | Dec 2022

• Contributed to the development of a dynamic simulation model in the Go programming language, enabling users to input critical parameters, including those related to drug or treatment strategies, derived from biological data

Construction of a Transcriptome Assembly and Annotation Pipeline | Apr 2023

- Integrated RNA data from related specie to annotate unannotated specie, enhancing accuracy of gene annotation
- The pipeline was scripted in shell scripting and developing on cloud-based high-performance computer

Analysis of differential gene expression and pathway enrichment in multiple cancers | Apr 2023

 Utilized RNA-seq data from TCGA and conducted differential gene expression analysis with DESeq2, revealing shared gene signatures across cancers. Employed Enrichr for pathway-based gene clustering

Frame-Level Speech Recognition | Sep 2023

• Designed MLP using PyTorch, aimed at achieving a high accuracy threshold of 90%. The entire model development and training process were processed on the Google Cloud Platform

Face Verification and recognition | Oct 2023

• Implemented a position-invariant models, based on CNN, that extracted feature representations invariant to facial position to recognize and verify faces in images, achieving robust pattern recognition