

# I-SHU WANG

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## EDUCATION

<b>Carnegie Mellon University</b>	Pittsburgh, PA
<i>Master of Science in Quantitative Biology And Bioinformatics - Advanced Study</i>	Dec 2023
Relevant Courses: Programming for Scientists, Data Analysis for Biological Sciences, Machine Learning, Algorithms & Advanced Data Structures, *Deep Learning (*Fall Semester)	
<b>National Taiwan University</b>	Taipei, Taiwan
<i>Master of Science in Biochemical Science &amp; Technology</i>	Jun 2020
<b>National Chung Cheng University</b>	Chiayi, Taiwan
<i>Bachelor of Science in Biomedical Science; Certificate in Functional Genomics Program</i>	Jun 2018

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## EXPERIENCE

<b>Carnegie Mellon University</b>	Pittsburgh, PA
<i>Graduate Researcher</i>	Present
<ul style="list-style-type: none"><li>Built a pipeline using Snakemake and parallel programming for analyzing alternative splicing on RNA-seq data</li><li>Conduct comprehensive data analysis to draw conclusive insights on expression levels from sequencing data</li><li>Developed an interactive web application to display the isoform categories for each gene</li></ul>	
<b>NGS High Throughput Genomics Core, Academia Sinica</b>	Taipei, Taiwan
<i>Research Assistant</i>	Aug 2021
<ul style="list-style-type: none"><li>Operated and maintained Illumina sequencers to get high quality sequencing data</li><li>Demultiplexed sequencing data and used Fastqc to examine quality of sequencing data</li><li>Proficiently prepared Next Generation Sequencing libraries employing diverse assays for both DNA and RNA samples</li></ul>	
<b>Department of Biochemical Science &amp; Technology, National Taiwan University</b>	Taipei, Taiwan
<i>Graduate Researcher</i>	Jun 2020
<ul style="list-style-type: none"><li>Earned <b>Excellence Award</b> from 2020 Agricultural Chemical Society of Taiwan Annual Poster Competition Sessions</li><li>Researched Basic Local Alignment Search Tool (BLAST) and NCBI to build plasmid for gene knockout system</li></ul>	
<b>National Taiwan University</b>	Taipei, Taiwan
<i>Teaching Assistant</i>	Jan 2019
<ul style="list-style-type: none"><li>Collaborated with a team of 4 to teach and train over 30 students to learn experiments</li><li>Designed project outline and moderated discussion for students' final projects</li></ul>	

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## SKILLS

**Computational skills:** Python, Go Language, SQL, R, Linux, High Performance Computing, git

**Bioinformatics Tools:** NCBI, BLAST, TCGA, Snakemake, Bioconductor, BioPython, alignment tools, annotation tools

**Data Analysis:** Numpy, Pandas, SciPy, Seaborn, Statsmodels, plotly, ggplot, Matplotlib, Scikit-Learn, dash, RShiny

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## ACADEMIC PROJECTS

<b>Carnegie Mellon University</b>	Pittsburgh, PA
<b>A python script for bacterial genome analysis</b>	Oct 2022
<ul style="list-style-type: none"><li>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 with database</li></ul>	
<b>Data analysis and visualization</b>	Dec 2022
<ul style="list-style-type: none"><li>Performed statistical analysis on cancer research using Python and presented the results through effective visualization</li></ul>	
<b>Simulation of intercellular viral infection via cell-to-cell transmission</b>	Dec 2022
<ul style="list-style-type: none"><li>Built a model for users to input parameters based on biological data to simulate viral spread in cells using Go language</li><li>Developed multiple unit test cases in Go language to ensure model accuracy and functionality</li></ul>	
<b>Construction of a Transcriptome Assembly and Annotation Pipeline</b>	Apr 2023
<ul style="list-style-type: none"><li>Used high-performance computer in cloud environment to analyze whole genome sequences of mammals</li><li>Integrated RNA data from related specie to annotate unannotated specie, enhancing accuracy of gene annotation</li></ul>	
<b>Analysis of differential gene expression and pathway enrichment in multiple cancers</b>	Apr 2023
<ul style="list-style-type: none"><li>Conducted analysis of differential gene expression to identify common gene signatures in multiple cancers using R programming language and TCGA database</li><li>Performed gene clustering for each cancer using Python to elucidate relationship between cancer and pathways</li></ul>	