

Shang-Hung Shih

Master student · Genomics and Machine Learning

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Education

National Taiwan University and Academia Sinica

Taipei, Taiwan

M.S. in Genome and Systems Biology Degree Program

Sep. 2018 - Expected Jul. 2020

- Working with Prof. Chien-Yu Chen who focus on Genomic AI.
- Related courses: Data Structures and Algorithms, Biomedical Data Mining, NGS, Bioinformatics and Genomic Medicine, etc.

Chung Shan Medical University

Taichung, Taiwan

B.S. in Biomedical Sciences

Sep. 2014 - Jul. 2018

- Joined a Bioinformatic research team of Prof. Yu-Fan Liu which focus on NGS application and analysis.
- Related courses: Linear Algebra, Java Programming, Bioinformatics, etc.

Professional Experience

Constructing Transcription Factor Binding Profiles using Deep Learning, NTU

Taipei, Taiwan

Personal Project at c4Lab

Dec. 2018 - Present

- Using the chromatin immunoprecipitation sequencing(ChIP-seq) data from the ENCODE to predict the transcription factor binding site. So far, I have constructed profiles of K562 and HepG2 two cell lines.
- Utilized Techniques: Linux, Python, Machine Learning

RSG(Regulator, Site, Gene) Network Team, NTU

Taipei, Taiwan

RSG Network Team Administrator

Oct. 2018 - Present

- Manage a team of 4 people to maintain the network which integrate over 4 gene regulation databases, and provide lab members with features generator service for machine learning.
- Utilized Techniques: Linux, Git, Python

Taiwan Biobank WGS Variant Calling, Taiwania and NTU

Taipei, Taiwan

Team member, WGS2RDD Team at c4Lab

Nov. 2018 - Dec. 2018

- Performed 498 WGS variant calling using Sentieon at Taiwania and additional analysis.
- Utilized Techniques: Linux

GVCFFiltering tool, NTU

Taipei, Taiwan

Final Project of NGS, Bioinformatics and Genomic Medicine

Nov. 2018 - Dec. 2018

- Developed a tunnable and faster tool for filtering vcf with Population gvcf(genome vcf) Allele Frequency.
- Performed Germline analysis and family segregation of Parkinson's disease.
- Utilized Techniques: Linux, Java

Prediction of Survival Rate in Patients with Cancer, Taiwan AI Academy

Taipei, Taiwan

Team member, Technical Leader Class, AI Executive Program

May. 2018 - Sep. 2018

- Used clinical data and molecular level data from TCGA to predict survival of patients with 28 types of cancer.
- Utilized Techniques: Linux, Git, Python, Machine Learning

Dockerized Somatic Mutation Analysis and Neo-antigen Prediction, CSMU

Taichung, Taiwan

Personal Project

Jul. 2016 - Nov. 2017

- Implemented dockerized somatic mutation analysis pipeline which is refer to GATK best practice.
- Performed somatic mutation analysis and neo-antigen prediction of 20 HCC and 200 OSCC patients.
- Utilized Techniques: Linux, Docker, multi-threading, Python, Perl

Skills

Java, Python, Perl, Git, Linux, Docker, Data Science