

Shang-Hung Shih (Albert)

Software Engineer · Full-Stack Web Development 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 - Jan. 2021

- Worked with Prof. Chien-Yu Chen who focus on Genomic AI applications.
- Related courses: Data Structures and Algorithms, Database Management System, 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 big data analysis.
- Related courses: Linear Algebra, Java Programming, Bioinformatics, etc.

Professional Experience

Software Engineer, Taiwan AILabs

Taipei, Taiwan

Typescript / ReactJS / Node.js / NestJS / Python(ML) / Redis / Neo4j / MongoDB / PostgreSQL / Docker / Kubernetes

Jan. 2020 - Present

- Maintained and refactored the AutoKB service of FedGPT.
- Designed and implemented the on-premise architecture of the GenDiseak gene analysis platform using k3s.
- Built variant detail page for clients to review and generate genetic reports.
- Redesign and implemented a pagination variant table viewer to achieve the goals of improving UI/UX and loading speed (from 6.5s to 1.5s, -76.9%).
- Built PubmedKB web app for entities relation visualization of NLP model result.
- Built proteomics data visualization for QCheck quality control web app.
- Developed signup system, variant table, DNA sequencing viewer, and pedigree editor for TAIgenomics web app for genetic analysis and diagnosis.
- Developed rule-based ACMG, ML-based v-score and inheritance pattern interpretation system for variant prioritization.
- Helped the algorithm team accelerate the processor build and deployment pipeline and reduced time by over 90%.

Software Engineer Intern, Taiwan AILabs

Taipei, Taiwan

Python / MySQL / SQLite / Docker

Mar. 2019 - Dec. 2019

- Designed and built a variant annotator with multi-processing and MySQL to solve the inefficiency of traditional annotation tools for matching 4 million variants to databases with 9 billion data, reduced the annotation time by 58%, and shortened the time for a whole genome sample from 2 hours to 50 minutes.

M.S. student and Server Administrator, NTU

Taipei, Taiwan

Python(CNN) / MySQL

Sep. 2018 - Dec. 2020

- Constructed transcription factor binding profiles using deep learning.
- Performed 1498 whole genome sequencing data analysis from Taiwan Biobank using Taiwania.

Side Projects and Honors

1st place in PIXNET 6th Hackathon Final: Travel Tech (Travel Charger)

Taipei, Taiwan

Python / Neo4j / Docker

Aug. 2019 - Sep. 2019

- Used Pixnet articles for correlation analysis and IG post data for sentiment analysis to provide personalized attraction recommendation and trip planning. I was mainly responsible for building relation graph for attraction recommendation.

Skills

Programming Language

TypeScript(ReactJS, Node.js, NestJS), Python

Others

SQL(MySQL, PostgreSQL, SQLite), NoSQL(MongoDB, Redis), GQL(Neo4j), Git, Linux, Docker, Kubernetes, k3s, Data Science