

# Shang-Hung Shih (Albert)

Software Engineer · Full-Stack Web Development and Machine Learning

☎ (+886) 910-024730 | ✉ shshih8497@gmail.com | 🏠 shanghungshih.github.io | 🌐 shanghungshih | 📺 shanghungshih

## 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*

Jan. 2020 - Present

*/ Qdrant / Docker / Kubernetes*

- 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.
- Redesigned 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, Qdrant), GraphQL(Neo4j), Git, Linux, Docker, Kubernetes, k3s, Data-Science