Bolong HE

☎ +86 18817456327
✉ ihebolong@gmail.com
🖥 www.hsoxo.com

Graduated from Simon Fraser University with a MSc in Applied Mathematics. I am currently a full stack engineer at PwC AC Shanghai. As a full stack engineer, I have profound experience in rapid prototyping, practical problems solving, and strong learning capabilities. Be curious and fresh about any software technology that solves problems and accomplishes goals.

Experience

February 2020 present	**Senior Technology Lead**, *PwC Shanghai Acceleration Center*, Shanghai, China. Designed and developed Status Connect System for PwC US Advisory. This application helps companies around the globe maintain strong connection with their employees for the COVID-19 related health status for better employee care and resource management.
February 2018 February 2020	**Python Software Engineer**, *3D Medicines Co., Ltd*, Shanghai, China. ∗ *3DMed Star Employee (Challenge the impossible)* Leader of the bioinformatics analysis framework, an automatic context generating system for genetic testing report (include a rule engine for genetic mutation annotations, a treatment recommendation system and a literature crawler for genetic mutation), and a clinical knowledge database.
February 2015 December 2017	**Teaching Assistant**, *Simon Fraser University*, Surrey, BC. Leading calculus and basic math workshop, leading differential equation tutorial, and helping students with their problems.

Education

2015-2017	**Master of Science in Mathematics**, *Simon Fraser University*, Surrey, BC. Project: Analysis of Firefighter Absences and Hiring Schedule Optimization at the Surrey Fire Department Coursework: continuous/discrete optimization, network flows, linear programming, numerical methods in continuous optimization, analytic number theory.
2010-2015	**Bachelor of Arts with Honours in Applied Mathematics**, *York University*, Toronto, ON. Coursework: combinatorics, cryptography, simulation and Monte Carlo methods, financial mathematics.

Project Experience (see next page for details)

2019	**Check-In Web App**, PwC US Advisory.
2019	**Clinical Knowledge Database and Treatment Recommendation System**, 3D Medicines Co., Ltd.
2018-2019	**BIW Bioinformatics Analysis Framework**, 3D Medicines Co., Ltd.
2018-2019	**Automatic Report Annotation Service**, 3D Medicines Co., Ltd.
Fall 2018	**Mutation Info Crawler and Analysis System**, 3D Medicines Co., Ltd.
Summer 2018	**Application of Drools BRMS**, 3D Medicines Co., Ltd.
Summer 2018	**Optimization of Amplicon Design for PCR**, 3D Medicines Co., Ltd.
Spring 2016	**Applications of Shortest Path Problem**, Simon Fraser University.
Spring 2015	**Compare Value at Risk Approaches On A Stock Portfolio** , York University.
Fall 2014	**Pricing American Option using Monte Carlo Method**, York University.

Computer Skills

Python, React, Gatsby, Vue, NodeJS, Golang, GraphQL, MySQL, Redis, MongoDB, CouchDB/PouchDB, Neo4j, Linux, Docker, LaTeX.

Project Experience (detail description)

2020   **Check-In Web App**, PWC US Advisory, (https://www.pwc.com/us/en/products/check-in.html).

I worked as a frontend tech lead in this project and responsible for the frontend architecture and implement frontend features. I designed the backend architecture with Koa framework as well. This project used Vue.js/Vuex at first and then move to React/Redux as the client required. The most interesting part of this project is I designed a json structure that could represent a user customized survey flow, and a visualized editor that can modify the customized survey in browser. Compare the existing survey apps online, we can include more complex logic and question flows, and we have more COVID-19 specific dashboard to view the survey data.

2019   **Clinical Knowledge Database and Treatment Recommendation System**, 3D Medicines Co., Ltd.

In this project, I a full stack developer responsible for a Vue.js based web user-interface, a Python based database service and a Python based treatment recommendation reasoner.

The key reason for a cancer patient doing a genetic test is to find out whether there are any treatments or drugs they can use. In practice, doctor is hard to give the patients precise treatment suggestions according to genetic test reports since the mutation for every patient can be different. In addition, this area is growing very fast now, many articles and clinical trials will be published every month. Therefore, a clinical knowledge database and a treatment recommendation system is required for a professional clinical medicine group. I designed this system along with a biologist for the purpose of maintaining the clinical knowledge and deducing the relevant treatments for the patients. Comparing with the software my company currently use, this new system borrows the idea from ontology and it can not only gives the treatment suggestions, but also give the full reason that why this treatment is recommended and the related references (e.g. articles, clinical trials, FDA labels, etc.).

2018-2019   **BIW Bioinformatics Analysis Framework**, 3D Medicines Co., Ltd.

In this project, I designed the framework architecture and implemented the program using Python.

The standard NGS bioinformatics analysis is a complex and time-consuming process in the genetic testing. The traditional SGE cluster is lack of computing and task scheduling systems and cannot utilize the computing resources well, which leads to waste of computing resources and low computational efficiency. I, along with the bioinformatics group in the company, designed and developed a distributed computing framework for parallel bioinformatics analysis based on SGE clusters using Python and MySQL. This project improve the calculation speed of the standard NGS bioinformatics analysis by 35% by optimizing the logic of computing task allocation. This project provides a state monitoring interface for cluster computing resources as well.

2018-2019   **Automatic Report Annotation Service**, 3D Medicines Co., Ltd.

The rule engine framework used in the project was designed and implemented to the company by myself. This project use Python (Flask, SQLAlchemy, Pandas) in conjunction with the MySQL database to build and develop a rule engine that business logic can be defined and visualized through a web interface. Compared to the predefined semantic modules by Drools, this rule engine is more in line with business needs, the rules are visualized clearer and the changes can be made by bioscientists more convenient. Compared with the accuracy of the manually completed mutation annotation statements, the accuracy is increased by 40%, and compare with hard coding the rules in program, the development efficiency is improved by 30%.

Fall 2018   **Mutation Information Crawler and Analysis System**, 3D Medicines Co., Ltd.

This project was designed and developed by myself.

I built a crawler based on Scrapy to crawl the Google Scholar and PubMed according to the genetic mutation information. The crawler crawls related literatures and papers and then does some fundamental NLP analysis. The crawler will filter out irrelevant contents and keep valid literature for further analysis by bioscientist. Compared with manual searches, the efficiency is increased by more than 80%.

Summer 2018   **Application of Drools BRMS**, 3D Medicines Co., Ltd.

This project used Java and Drools BRMS to separate the decision rules for drug recommendation in the genetic test report from the program code, and used the predefined semantic module of Drools to write the drug recommendation rule. This allows bioscientists and clinicians to review the medication recommendation rules and verify the rules enforce the required business rules. Besides, the maintenance of the rules can be carried out independently by the bioscientists as well, so that the efficiency and accuracy of maintenance work are both improved.

Summer 2018 **Optimization of Amplicon Design for PCR**, 3D Medicines Co., Ltd.

Amplicon design is critical important in DNA sequencing technology. Previously the amplicon designer uses exhaustive trial and error method, relying on the individual experience to compare the cost of different amplicon combinations. However, optimization of amplicon design has remained challenging due to the lack of a systematic method. As the magnitude of target DNA region and amplicon combination increases, the complexity of manual calculation and judgment will grow exponentially. In this study, we designed a mathematical model and use optimization algorithms to do the amplicon designing. We reduces the economic cost of the amplicon design by 60% and increases designing efficiency by at least 100% compared with the work done by even the top level experts. The mathematical model in project was designed by myself and implemented by Python and Gurobi®.