**Yujue Wang, M.S.**

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**Profile**

* 6+ years’ working experience in finance (programming and project managing).
* 3+ years’ working experience in bioinformatics, including website developing, single cell DNA whole genome sequencing (WGS) analyzing pipeline developing optimizing and implementing, and single nucleotide variations (SNVs) and short insertions and deletions (INDELs) from next generation sequencing data annotating and classifying.

**SKILLS**

reading riding

Python, R, HTML, CSS, JavaScript, SQL, Bash, C, Delphi, Java, Perl

Flask, jQuery

MySQL, SQLite

Mandarin Chinese (native speaker)

**PUBLICATIONS and WEBSITE DEVELOPMENTS**

Sun S\*, **Wang Y\***, Maslov AY, Dong X, Vijg J. SomaMutDB: a database of somatic mutations in normal human tissues. ***Nucleic Acids Res****.* 2022 Jan 7;50(D1): D1100-D1108. doi: 10.1093/nar/gkab914.

Dong X\*, Zhang L\*, **Wang Y**\*, Lee M., Maslov AY, Wang T, Gorbunova V, Vijg J. Identifying genome structural variations in single cells. In submission.

https://vijglab.einsteinmed.org/SomaMutDB/

<https://github.com/biosinodx/SCcaller>

<https://github.com/biosinodx/SCcaller3_PEA>

<https://www.vijglab.org/>

<https://srirajlab.com/>

https://yujuewangresume.net/

**WORK EXPERIENCE**

**Albert Einstein College of Medicine, Genetics Department,** *NY, USA.*Apr. 2019-present, **Research Technician.**

As a research technician, I help the postdocs, professors and labs with their projects.

* SomaMutDB is a website database that compiles all available somatic mutations data in healthy tissues including in-house data and publicly available data up to date. It provides multiple functions such as data visualization, data browsing, signature analyzing and data download. I designed the structure of the website system, programmed the front-end and the back-end. I implemented 6 mutation signature analyzing tools on the website. And I set up the MySQL database for it. The paper of this website database was published on Nucleic Acids Research. I am the co-first author.
* PEA (phasing, enhanced reference genome and assembly) method can identify genome structure variations (SVs) from single-cell WGS data. I designed and programmed the pipeline under the supervision of a postdoc. The paper of PEA method was submitted to *Nature Methods*. I am the co-first author.
* SCcaller can identify SNVs and INDELs from single cell sequencing data. I simplified the whole pipeline of SCcaller from 200 commands and almost 800 parameters per cell to just 1 command and 4 parameters per cell, reduced the IO by 92.8%. And I sped up the pipeline by 10 times with parallel running technic. I also fixed the bugs for the previous version in INDELs calling.
* I annotated and classify SNVs and INDELs identified from the WGS data in >1500 22q11.2 deletion syndrome patients into damaging LoF, damaging frameshift, damaging Missense, benign Missense, splice-disrupting, synonymous variants using multiple state-of-art algorithms, software, and public databases including VEP, Bystro, spliceAI, etc. under the supervision of a postdoc. I built an SQLite database for it. And I implemented multiple statistical tests including, for example, Fisher’s exact test, binomial test, variant-Set Test for Association using Annotation infoRmation (STAAR) based on the database. The paper of the project is on the way and I am the second author.
* I expanded the DNA mapping pipeline’s availability from only for the human genome to 7 different species for one lab. And I implemented the pipeline for 48 samples of 6 different species for the lab.
* I built and maintained the lab websites for two professors on the wowchemy and WIX platforms.
* I developed a job submission website for students and postdocs in Albert Einstein College of Medicine to facilitate their computational analyze.
* I am developing a structural variation calling method for one professor with Python (ongoing).

**Albert Einstein College of Medicine**, **Genetics Department,** *NY, USA.*Jul. 2018-Apr. 2019, **volunteer and waiting for my H1b visa approval.**

As a volunteer I helped postdocs to implement their analyzing pipelines on HPC. And I learned necessary knowledge (single-cell WGS sequencing, DNA mapping, variant calling, etc.) for optimizing the SNV caller for single-cell WGS data.

**China UnionPay Merchant Services Company, Ltd.**, Ufood Division, *Shanghai, China*. Dec. 2016-Nov. 2017, **Project Manager**.

Ufood provides solutions for restaurant management. As a project manager, I supervised 10 employees and managed the accounts of over 1000 different vendors. We designed applications for PC, tablet, and POS terminal, website for restaurant management, in addition to creating customized WeChat accounts for vendors and customers to facilitate reservations, ordering, and payments.

**China UnionPay Merchant Services Company, Ltd.**, MIS-POS (merchant integrated system – point of sale) Department, *Shanghai, China*. May 2012-Nov. 2016, **Programmer**.

I worked with senior personnel of international companies (Vanguard, McDonald's, Yum, NBA Play zone, Bestseller, ZARA, Decathlon, etc) to develop and implement their integrated payment system (IPS) for the Chinese market. IPS module is deployed on the computers of cashiers or vending machines to drive hardware and communicate with bank servers securely.

**EDUCATION**

**East China University of Science and Technology**, *Shanghai, China*, **M.S.**, Control Science and Engineering, Sep. 2007 - May 2012

**Tongji University**, *Shanghai, China,* **B.S.**, Electrical Engineering and Automation, Sep. 2003 – Jun. 2007

**AWARDS AND HONORS**

Employee of the Year in 2014 and 2015, China UnionPay Merchant Services Company, Ltd.