

Zicheng Su

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🎓 EDUCATION

The University of Queensland (UQ), Brisbane, Australia 2020 – Present

PhD student in Environmental Engineering, expected September 2024

Zhejiang University (ZJU), Hangzhou, China 2015 – 2019

B.S. in Agricultural Resources and Environmental Sciences, GPA: 3.75/4 Major GPA: 3.94/4

🧑‍💻 EXPERIENCE

The Institute of Urban Environment, Chinese Academy of Sciences (IUE CAS) 2020 – Present

Xiamen, China *Research Intern* Supervisor: Dr. Yue Zheng

Brief introduction: Working on projects about the quorum sensing systems in 8 types of *Methylobacterium* using skills of molecular biology

- Implemented purification and cultivation in 12L of liquid medium for each of the 8 types of *Methylobacterium*.
- DNA extraction and PCR on *Methylobacterium* to check the purity of liquid medium.
- Condense and extract the signal molecular from the liquid medium, then perform activity test using *Xanthomonas campestris* pv. *campestris* FE58.
- Knock out the gene for quorum sensing on *Methylobacterium* and investigate the consequences on strain Q8's growth without *rpfC* genes.

The University of Queensland July. 2020 – Present

Python, Perl, Linux Supervisor: Dr. Yue Zheng, Dr. Ji Lu, Dr. Min Zheng and Prof. Jianhua Guo

Brief introduction: 2 parts- (1) Assembled and reconstructed the genome of virus, bacteria or archaea of interest from environmental samples (2) Mapped the genes of interest from 400,000+ samples from all over the world to see the geographic distribution

- Performed pipeline of genome assembly (binning) on the metagenomic data of the wastewater samples, the steps including 1) Quality control on reads data; 2) Assembly; 3) Initial binning with 3 methods; 4) Reassemble-binning; 5) Refinement-binning; 6) Quality evaluation on genomes; 7) Classification.
- Annotated the functional proteins from the genomes of good-quality using KEGG.
- Searched for all the 16S rRNA sequences of all known acidophilic ammonia-oxidizers.
- Produced phylogenetic trees to evaluate the diversity and phylogenetic relationship of virus from samples.
- Screened for, retrieved, processed, and analyzed the sequences from 400,000+ raw amplicon datasets by International Nucleotide Sequence Database Collaboration.
- Investigated the geographic distribution of objects. Used web crawling (self programming) to fetch coordinates of 30,000+ detected samples, unified the format and then projected on map using Tableau.

⚙️ SKILLS

- Programming Languages: Python, Perl, Java
- Bioinformatics Softwares: Readqc, MetaSpades, Megahit, Maxbin2, Metabat2, Concoct, Krona, GTDB-tk, Checkm, MetaGeneMark, Linsi, Gblocks, RAxML, Figtree and so on.
- Research Fields: Bioinformatics, Microbiology, Analytical Chemistry for Environmental Sciences

♥️ HONORS AND AWARDS

National Scholarship for 4-year study abroad, Chinese Scholarship Council	2019
Top-up scholarship for living expense, The University of Queensland	2020
The First Prize of Jiande Scholarship for Academic Excellence, Zhejiang University	2019
The Second Prize of Academic Scholarship, Zhejiang University	2018

📄 MISCELLANEOUS

- Blog: <http://zichengsu.fun>
- Languages: English - Fluent, Mandarin - Native speaker, Cantonese - Native speaker