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 (CAS)   2020 – Mar. 2021

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   Jul. 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.
- Attonated the functional proteins from the genomes of good-quality using KEGG.
- Searched for all the 16S rRNA sequences of all known acidophillic 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

ℹ MISCELLANEOUS

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