YiFan Xiong

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Education

Fujian Agriculture and Forestry University | *Fuzhou, Fujian Province, CN* **Sep. 2019 - Jun. 2022**

- M.S. in Bioengineering. GPA: 3.33/4.0

Wuhan Institute of Bioengineering | *Wuhan, Hubei Province, CN* **Sep. 2015 - Jun. 2019**

- B.S. in Bioengineering. GPA: 3.56/4.0

Work experience

TsingHua University **Jul. 2024 - Present**

XGlab, Research Assistant, Supervisor: Prof. Xuegong Zhang

- Evaluate the biological meaning in different Large Language Models' gene embedding.
- Identify core TFs combinations in T cells reprogramming and cell development using the algorithm scDirect.

Suzhou Dynamic Biosystems Ltd. **Jun. 2023 - Jun. 2024**

Department of Bioinformatic, Bioinformatics Engineer

- Coding for Single-cell RNA-seq data analysis and virsulize. Independently developed R package cellPCT.
- Well-Paired-Seq platform single-cell data testing and troubleshooting.

Fuzhou Institue of Data Technology **Jul. 2022 - Jun. 2023**

Department of Digital Medicine, Bioinformatics Engineer

- Data collection, normalization and cell type annotation for hECA2.0 Sigle-cell database.
- Multi-Omics pipeline construction and NGS data analysis.

Research Experience

Undergraduate Research Assistant

Supervisor: Prof. Junlin Zhang & Prof. Zhongming Fang **Sep. 2016 - Jun. 2019**

Extraction and identification of anti-cancer bioactive peptides from traditional Chinese medicine

- Experiments including DNA extraction, PCR, vector construction, protein extraction, SDS-PAGE and cell culture, *et al*.

Functional verification of QinFeng tea by constructing Hyperuricemia animal models

- Construct mouse Hyperuricemia models using two protocols: a high-purine diet and the injection of uric acid metabolism enzymes inhibitors.
- Evaluate the models using quantitative analysis of uric acid and data processing.

Leaf transcriptome analysis of rice transgenic materials(Published)

- *OsAAP3* transgenic rice leaf tissue RNA-seq data analysis, from rawdata to DEG identification and gene functional enrichment analysis.
- Writting part of the paper and visualizing data.

Graduate Student Researcher

Plant Functional genomics lab | Supervisor: Prof. Shoukai Lin **Jun. 2019 - Jul. 2022**

Calcium-dependent protein kinase family in *Fragaria vesca* and their functions under biotic stresses(Published)

- Explore the evolutionary history and sequence pattern of FvCDPKs.
- Conduct transcriptome analysis of wild strawberry under different pathogen infections.

Reveal the role of *EjCDPK* members in response to freezing stress in *Eriobotrya japonica* fruitlets(Preprint)

- Identification of CDPK genes in loquat. Analysis gene sequence and protein motif patterns.

- Use weighted gene co-expression network analysis associated with physiological and biochemical traits to identify freezing stress response gene.
- Over-express the target gene in *Arabidopsis*, revealing that it can increase resistance to freezing stress.

Physiological and transcriptome analysis of *Eriobotrya japonica* fruitlets under freezing stress(Under review)

- Genome-wide identification of Loquat protein kinase using plant kinase HMM models.
- Determining expression patterns of freezing-stress-related protein kinases.

Publications

- **Yifan Xiong**, Shunquan Lin, Jincheng Wu, Shoukai Lin. Identification and Expression Analysis of CDPK Family in *Eriobotrya japonica*, reveals *EjCDPK25* in Response to Freezing Stress in Fruitlets. *bioRxiv*, 2024. https://doi.org/10.1101/2024.05.01.591999
- **Yifan Xiong**, Dahe Lin , Shiwei Ma, Chunhua Wang, Shoukai Lin. Genome-wide identification of the calcium-dependent protein kinase gene family in fragaria vesca and expression analysis under different biotic stresses. *European Journal of Plant Pathology*, 2022, 164(2):283-98. https://doi.org/10.1007/s10658-022-02560-4
- Wei Qilang, Zhenwei Yan, **Yifan Xiong**, and Zhongming Fang. Altered Expression of OsAAP3 Influences Rice Lesion Mimic and Leaf Senescence by Regulating Arginine Transport and Nitric Oxide Pathway. *International Journal of Molecular Sciences*, 2021, 22, no.4: 2181. https://doi.org/10.3390/ijms22042181

Bioinformatic Skills

- Programming languages: R, Python and shell
- NGS data analysis: scRNA-seq, bulk RNA-seq(miRNA, lncRNA, circRNA),WGS, WGBS, ATAC-seq
- Workflow Management: WDL, Snakemake
- Code Management and Version Control: Github and Gitlab
- Servers and Environment Manager: Conda, Docker, Slurm

Acdemic activates

The 10th National Symposium on Loquat | *Lanxi, Zhejiang province* **May. 2021**

- Submit an abstract on the topic of *Identification calcium sensors in loqut*

Academic poster competition for Graduate Student | *Fujian Agriculture and Forestry University* **May. 2022**

- Oral and poster presentation on the topic of my gradute thesis

Digital Medicine Algorithm Innovation Competition | *Fuzhou, Fujian province* **Aug. 2022**

- Organization assistant

The 2nd Symposium of Fujian Bioinformation Society | *Fuzhou, Fujian province* **Feb. 2023**

- Poster presentation

Honors & Awards

Scholarship for Undergraduates 3rd Place | *Wuhan Institute of Bioengineering* **Dec. 2015**

Annual Outstanding Undergraduates | *Wuhan Institute of Bioengineering* **Dec. 2016**

National English Competition for Undergraduates 3rd Place | *Wuhan Institute of Bioengineering* **May. 2017**

Scholarship for Undergraduates 2nd Place | *Wuhan Institute of Bioengineering* **Dec. 2017**

Scholarship for Undergraduates 1st Place | *Wuhan Institute of Bioengineering* **Dec. 2018**

Outstanding Graduates | *Wuhan Institute of Bioengineering* **Jun. 2019**

Scholarship for Graduates | *Fujian Agriculture and Forestry University* **Jun. 2020**

Academic Achievements Prize for Graduates | *Fujian Agriculture and Forestry University* **Jun. 2022**