

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 [cellIPT](#).
- [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>
- Jia Li, Xiaocheng Jia, Liyun Liu, Xianmei Cao, **Yifan Xiong**, Yaodong Yang, *et al.* Comparative biochemical and transcriptome analysis provides insights into the regulatory mechanism of striped leaf albinism in arecanut (*Areca catechu* L.). *Industrial Crops and Products*, 2020, 154:112734. <https://doi.org/10.1016/j.indcrop.2020.112734>

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

Academic activates

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

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

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 <i>Wuhan Institute of Bioengineering</i>	Dec. 2015
Annual Outstanding Undergraduates <i>Wuhan Institute of Bioengineering</i>	Dec. 2016
National English Competition for Undergraduates 3rd Place <i>Wuhan Institute of Bioengineering</i>	May. 2017
Scholarship for Undergraduates 2nd Place <i>Wuhan Institute of Bioengineering</i>	Dec. 2017
Scholarship for Undergraduates 1st Place <i>Wuhan Institute of Bioengineering</i>	Dec. 2018
Outstanding Graduates <i>Wuhan Institute of Bioengineering</i>	Jun. 2019
Scholarship for Graduates <i>Fujian Agriculture and Forestry University</i>	Jun. 2020
Academic Achievements Prize for Graduates <i>Fujian Agriculture and Forestry University</i>	Jun. 2022