XUE PAN

7520 N Clemens Way, Tucson, AZ 85743 •520-3587182 • xpan1@arizona.edu
•LinkedIn: www.linkedin.com/in/xue-pan-1095072a0
• GitHub: https://github.com/xpan1

PROFESSIONAL SUMMARY

Highly skilled Computational Biologist nearing completion of a PhD in Plant Sciences with extensive experience in bioinformatics, genomics, and transcriptomics. Specialized in the analysis of large-scale multi-omics data sets and Next Generation Sequencing (NGS) using advanced statistical and computational methods. Proficient in R, Python, etc. Seeking to apply my expertise in a challenging role focused on bioinformatics processing, pipeline development, and data visualization to contribute to innovative research.

EDUCATION

Doctor of Philosophy (Ph.D.) Candidate in School of Plant Sciences
University of Arizona, Tucson, AZ
Dissertation Title: "Identification of transcriptional programs in endosperm development"
Expected Graduation Date: August 2024

Master of Science (M.Sc.) in Crop Genetics and Breeding
China Agricultural University, Beijing, China
Thesis Title: "Genomic Selection using GWAS identified SNPs"
September 2015 - June 2017

Bachelor of Science (B.Sc.) in Seed Science and Engineering
Henan Agricultural University, Henan, China
August 2011 - July 2015

RESEARCH EXPERIENCE

-Lead Bioinformatics Analyst

- Developed and implemented computational algorithms for genomic data sets, emphasizing identification of key gene regulatory networks.
- Specialized in multi-omics data integration and analysis including RNA-seq, ATAC-seq, and ChIP-seq, applicable to single-cell analysis methods.
- Designed and analyzed high-throughput experiments in collaboration with experimental scientists, aligning with requirements for collaborative experimental design in research.
- Built workflows and pipelines to support Illumina NGS data generation, processing, and analysis, particularly Bulk RNA-seq.

-Molecular Experimental Scientists

- Designed and analyzed high-throughput experimental design, such as RNA-seq, Laser Captured Microdissection followed by RNA-seq (LCM-RNAseq), CRISPR-Cas9 system
- Familiar with molecular techniques: DNA and RNA Extraction, Polymerase Chain Reaction (PCR), Quantitative Real-Time PCR (qRT-PCR), Bimolecular Fluorescence Complementation (BiFC), Yeast Two-Hybrid Experiments, etc.

-Collaborative Research Scientist

- Collaborated with internal and external experimental groups to design and analyze multi-omic experiments, maximizing insights into biological processes.
- Worked on several manuscripts focused on genomics and computational biology, contributing to scientific knowledge in a team setting.

TEACHING EXPERIENCE

- **University of Arizona, School of Plant Sciences**
  Teaching Assistant – Plant and Animal Genetics (ACBS/PLS312)
  Three semesters
    - Facilitated and coordinated students' weekly lab projects.
    - Designed weekly lesson plans for present the main ideas of weekly lab projects (~30 students in lab section).
    - Graded lab write-ups and provided substantive constructive feedback.
    - Guided students to synthesize complex theoretical concepts from weekly lectures and apply them to weekly lab projects.

SKILLS

- **Bioinformatics**: Advanced in genomic and transcriptomic data analysis including time series RNA-seq, ATAC-seq, and ChIP-seq. Familiar with single-cell analysis methods and other multi-omics studies.
- **Programming Languages:** Proficient in R and Python, Bioconductor, Linux, HPC and cloud computing (AWS).
- **Statistical Analysis and Machine Learning:** Strong background in statistical methods, probabilistic modeling, and machine learning applications in biological data analysis.
- **Data Visualization:** Expertise in visualizing complex biological data using ggplot2, crucial for interpreting single-cell and spatial omics data.
- **Version Control Systems:** Experienced with Git and GitHub.
- **Pipeline and Web Application Development:** Experience with pipeline building tools such as Snakemake and R Shiny applications.

PUBLICATIONS AND MANUSCRIPTS

- Working on several manuscripts (MSs) focused on genomics and computational biology:

- MS1: Identification of cis-regulatory elements associated with maize endosperm development using temporal time series RNA-seq and ATAC-seq.
- MS2: Comparative time series transcriptome analysis associated in maize and sorghum endosperm development.

CONFERENCES AND PRESENTATIONS

- Attended conferences such as PAG and Maize Genetics Meetings, presenting and communicating my work with other professionals.

ADDITIONAL INFORMATION

- Strong critical thinking, problem-solving, and organizational skills.
- Willing to travel and work occasional evenings, weekends, and holidays as required.