SHANSHAN ZHANG

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EDUCATION

Ph.D. student in Statistics and Data Science, University of Arizona   Expected in 2024 Spring
Cumulative GPA: 3.94/4.00
The tentative title of the dissertation: Integrated Method for Community-Wide Microbial Source Tracking (IntMST) and Assessment of Variance Computation Methods for Causal Effect Estimation in Observational Studies.

M.S. in Statistics and Data Science, University of Arizona   2020
Ph.D., Science in Genetics, Fudan University, China   2009
B.S., Science in Agriculture, Zhejiang University, China   2004

SKILLS

STATISTICAL COURSES

- **Theory**: Theory of Probability, Theory of Statistics, Probability Math, Bayesian Statistical Theory and Applications
- **Methodology & Application**: Advanced Statistical Regression Analysis, Experiment Design, Analysis of Categorical Data, Statistical Consulting, Analysis of High Dimensional Data, Statistical Computing, Machine Learning, Statistical Methods in Bioinformatics, Applied Biostatistics, Bioinformatics and Functional Genomic Analysis
- **Computer languages**: Data Management and the SAS Programming Language, Fundamentals of Computing in Biosystems Analytics (Python, SQL, Linux, and HPC)

COMPUTER SKILLS

Statistical applications (R, SAS, Python, SQL); Biological-related software (e.g., Star, Tophat2, Cytoscape, Snapgene); Technical (e.g., MS Office, High Performance Computing, MS Office, R-markdown, Photoshop, Illustrator); Data analysis (e.g., Statistical modeling, Causal effects estimation, Machine learning, Next generation sequencing pipelines, Single-cell RNA-Seq analysis, Metagenomics data analysis).

PROFESSIONAL EXPERIENCE

School of Plant Sciences, University of Arizona   **Tucson, AZ**
Visiting Scholar   *2022 – Present*
- Provide statistical consulting services for experiment design and data analysis.
- Offer practical support for experiment implementation and manuscript writing.

School of Plant Sciences, University of Arizona   **Tucson, AZ**
Assistant Staff Scientist   *2014 – 2022*
Postdoctoral Research Associate I   *2009 – 2014*
- Managed multiple comprehensive projects in seed development of maize and Arabidopsis, including topics such as transcriptome profiling of early endosperm using laser-capture microdissection, gene imprinting identification, gene regulatory network investigation related to drought stress, and functional analysis of key transcriptional factors (e.g., *myb-related protein-1*, *Opaque-2*).
- Developed skills in laboratory management, handling new research projects, establishing laboratory platforms (e.g., laser-capture microdissection, dual-luciferase assay), operating and maintaining laboratory devices, training students, collaborating with colleagues, analyzing data, and manuscript writing;

- ▪ Developed diverse laboratory skills encompassing molecular biology, histology, biochemistry, genetics, anatomy, and bacteriology. Proficient in imaging and dissecting samples using various devices such as stereomicroscopes, fluorescence microscopes, confocal microscopes, laser-capture microdissection microscopes, vibratomes, and microtomes.

SELECTED PUBLICATIONS

1. Wu H, Li G, Zhan J, **Zhang S**, Beall BD, Yadegari R, Becraft PW (2022). Rearrangement with the nkd2 promoter contributed to allelic diversity of the r1 gene in maize (Zea mays). ***The Plant Journal***, 111(6), 1701-1716.
2. Ran D, **Zhang S**, Lytal N, An L (2020). scDoc: correcting drop-out events in single-cell RNA-seq data. ***Bioinformatics***, 36, 4233-4239.
3. **Zhang S**, Zhan J, Yadegari R (2018). Maize *opaque* mutants are no longer so opaque. ***Plant Reproduction***, 31, 319-326.
4. **Zhang S**, Wang D, Zhang H, Skaggs MI, Lloyd A, Ran D, An L, Schumaker KS, Drews GN, Yadegari R (2018). FERTILIZATION-INDEPENDENT SEED-Polycomb Repressive Complex 2 plays a dual role in regulating type I MADS-box genes in early endosperm development. ***Plant Physiol***, 177, 285-299.
5. **Zhang S**, Thakare D, Yadegari R (2018). Laser-Capture Microdissection of Maize Kernel Compartments for RNA-Seq-Based Expression Analysis. ***Methods Mol Biol***, 1676, 153-163.

ORAL PRESENTATIONS IN CONFERENCES, SEMINARS, AND WORKSHOPS

1. **Zhang S**, An L (2022). "*Causal effect estimation in observational studies*", Biosystems Engineering Graduate Seminar in the University of Arizona, Tucson, Arizona
2. **Zhang S**, and members in An L lab (2022). "*Introduction to R*", R workshop in the University of Arizona, Tucson, Arizona
3. **Zhang S**, Ran D, Ryu C-H, Drews GN, Wang X, Yadegari R (2017). "*Identification of gene networks regulating early endosperm in maize*", 24th Seed Institute conference, Los Angeles, California
4. **Zhang S**, Wang D, Zhang H, Lloyd A, Skaggs MI, An L, Drews GN, Schumaker KS, Yadegari R (2012). "*Polycomb Repressive Complex 2 regulates type I MADS box gene expression during endosperm development in Arabidopsis*", the annual meeting of the American society of plant biologists, Austin, Texas

SELECTED POSTER PRESENTATIONS IN CONFERENCES

1. Pan X, **Zhang S**, Spears CJ, Li G, Zhan J, Dannenhoffer JM, Drews GN, Yadegari R (2022). "*Transcriptional Networks of Endosperm Development in Maize*". Plant & Animal Genome Conference XXIX, San Diego, California
2. Ran D, **Zhang S**, An L (2018). "*Statistical Method for Gene Set Analysis of Single-cell RNA-seq Data*". ENAR Spring Meeting, Atlanta, Georgia
3. **Zhang S**, Wang D, Zhang H, Skaggs MI, Lloyd A, Ran D, An L, Schumaker KS, Drews GN, Yadegari R (2017). "*Differential spatiotemporal and epigenetic regulation of type I MADS-box gene expression by Polycomb Repressive Complex 2 during early endosperm development in Arabidopsis*". The 28th International Conference on Arabidopsis Research, St. Louis, Missouri