



Yue Wu

Postdoctoral Scholar, Genetics

 NIH Biosketch available Online

Bio

BIO

2016, BS, Nanjing University, China

2017-2022, Ph.D. University of Georgia, Advisor: Arthur Edison and Jonathan Arnold

2022-present, postdocs, Stanford University, Advisor: Michael Snyder

HONORS AND AWARDS

- Graduate school travel grant, UGA (2019)
- Outstanding graduate with honor, Nanjing University (2016)
- First-class People's Scholarship, Nanjing University (2014 – 2015)
- Silver Medal, iGEM (International Genetically Engineered Machine) competition (2014)

STANFORD ADVISORS

- Michael Snyder, Postdoctoral Faculty Sponsor

LINKS

- google scholar: <https://scholar.google.com/citations?user=QE1tszYAAAAJ&hl=en>
- github: <https://github.com/mikeaav>
- personal site that need update: <https://mikeaav.github.io>

Research & Scholarship

CURRENT RESEARCH AND SCHOLARLY INTERESTS

I built computational methods to integrate and model biological time series, including metabolic dynamics, longitudinal multi-omics data, and micro-sampling. I reduce dimensions, built clusters, and search for causal links.

1. Knowledge extraction from time-series metabolic systems. Recent developments in omics approaches provide a comprehensive view of the biological system at one time point. However, the understanding of the dynamic response to environmental perturbation is still limited in both data collection and computational analysis. I contributed to an NMR approach to collecting time-series metabolic data. I then designed the computational method to efficiently extract chemical information from the high-dimensional heavy dataset. This provides rich information regarding dynamic metabolic processes under different environments. I uncovered biological regulation in carbon metabolism and glycogen utilization from this high-dimensional time series, through modeling and time-series analysis. I built a new efficient workflow to understand metabolic dynamics and regulation, which can be expanded to other fermentation systems and the study of metabolic disease in humans.

2. Automation in phenotyping biological systems. New experimental approaches (e.g., microscopic devices) enable the recording of thousands of samples in a short time, which greatly promotes the phenotyping of plants, fungi, and human tissues. However, image annotation and information extraction are still manual intensive. I built multiple frameworks to classify phenotypes through ResNet in PyTorch, associate with genomic information, and uncover important structures through feature importance evaluation. I also built image segmentation programs through Detectron2 to annotate different symbiosis structures of Arbuscular mycorrhiza and worm population. Automation in phenotyping greatly

Publications

PUBLICATIONS

- **SAND: Automated Time-Domain Modeling of NMR Spectra Applied to Metabolite Quantification.** *Analytical chemistry*
Wu, Y., Sanati, O., Uchimiyu, M., Krishnamurthy, K., Wedell, J., Hoch, J. C., Edison, A. S., Delaglio, F.
2024
- **Characterizing the gene-environment interaction underlying natural morphological variation in *Neurospora crassa* conidiophores using high-throughput phenomics and transcriptomics** *G3-GENES GENOMES GENETICS*
Krach, E. K., Skaro, M., Wu, Y., Arnold, J.
2022; 12 (4)
- **Uncovering in vivo biochemical patterns from time-series metabolic dynamics.** *PloS one*
Wu, Y., Judge, M. T., Edison, A. S., Arnold, J.
2022; 17 (5): e0268394
- **Wild Isolates of *Neurospora crassa* Reveal Three Conidiophore Architectural Phenotypes** *MICROORGANISMS*
Krach, E. K., Wu, Y., Skaro, M., Mao, L., Arnold, J.
2020; 8 (11)
- **RTEExtract: time-series NMR spectra quantification based on 3D surface ridge tracking** *BIOINFORMATICS*
Wu, Y., Judge, M. T., Arnold, J., Bhandarkar, S. M., Edison, A. S.
2020; 36 (20): 5068-5075
- **Continuous in vivo Metabolism by NMR** *FRONTIERS IN MOLECULAR BIOSCIENCES*
Judge, M. T., Wu, Y., Tayyari, F., Haffori, A., Glushka, J., Ito, T., Arnold, J., Edison, A. S.
2019; 6: 26
- **Genome-Wide Analysis Reveals Ancestral Lack of Seventeen Different tRNAs and Clade-Specific Loss of tRNA-CNNs in Archaea** *FRONTIERS IN MICROBIOLOGY*
Wu, Y., Wu, P., Wang, B., Shao, Z.
2018; 9: 1245
- **Systematic analyses of glutamine and glutamate metabolisms across different cancer types** *CHINESE JOURNAL OF CANCER*
Tian, Y., Du, W., Cao, S., Wu, Y., Dong, N., Wang, Y., Xu, Y.
2017; 36: 88
- **Large-Scale Analyses of Angiosperm Nucleotide-Binding Site-Leucine-Rich Repeat Genes Reveal Three Anciently Diverged Classes with Distinct Evolutionary Patterns** *PLANT PHYSIOLOGY*
Shao, Z., Xue, J., Wu, P., Zhang, Y., Wu, Y., Hang, Y., Wang, B., Chen, J.
2016; 170 (4): 2095-2109
- **Identification of Arbuscular Mycorrhiza (AM)-Responsive microRNAs in Tomato** *FRONTIERS IN PLANT SCIENCE*
Wu, P., Wu, Y., Liu, C., Liu, L., Ma, F., Wu, X., Wu, M., Hang, Y., Chen, J., Shao, Z., Wang, B.
2016; 7: 429

PRESENTATIONS

- Automatic NMR spectral decomposition through computational fitting of time-domain signals - Network of Advanced NMR seminar (10/2021)

- Automatic NMR spectral decomposition through computational fitting of time-domain signals - MANA (October 2021)
- A new algorithm for time-series NMR spectra quantification by ridge tracking - MANA (November 2019)
- SAND: spectral automatic NMR deconvolution - IVAN (August 2022)