Ziye Wang

Undergraduate, Peking University, Beijing, China
zzi_yye@stu.pku.edu.cn

EDUCATION

Peking University, Beijing, China   Sept 2022 – Expected Jun 2026
B.S. in Bioinformatics, School of Life Sciences
B.S. in Mathematics and Applied Mathematics, School of Mathematical Sciences

*Cumulative GPA: 3.78/4.00 ** *

RESEARCH INTERESTS

Computational Evolutionary Biology, Computational and Statistical Genomics, Theoretical Population Genetics

PUBLICATIONS

1. **Wang, Z.**, & Zhang, C. (In press). An implementation of the Brownian motion model for Bayesian phylogenetic inference using continuous traits with missing states. *Paleobiology*.

2. Chen, W., **Wang, Z.**, & Champer, J. (2025). Stronger population suppression by gene drive targeting doublesex from dominant female-sterile resistance alleles. *bioRxiv*. doi:10.1101/2025.04.16.649134.
   Under revision at Nature Communications.

RESEARCH EXPERIENCE

Inferring mutation spectrum evolution with ancestral recombination graph   Jul 2025 – Current
Supervisor: **Prof. Rasmus Nielsen**, *UC Berkeley*
Collaborated with Dr. Yun Deng

- Developed a faster and less biased method for estimating mutation rate history by modeling mutations as a non-homogeneous Poisson process on the edges of an ancestral recombination graph (ARG), bypassing the need for precise mutation age imputation
- Demonstrated the superior accuracy and statistical power of this ARG-based framework over traditional SFS-based methods through `msprime` simulations
- Quantified the impact of hard-filtered singletons in the 1000 Genomes Project phased data, confirming the robustness of ARG inference against this data integrity issue
- Resolving the artifact of unexplained TpG-to-CpG mutation rate divergence between African and non-African populations predating the Out-of-Africa migration by applying a novel ARG-based polarization method for biallelic SNPs and performing joint inference of ARG across all populations to force a deep-time coalescence
- Investigating the temporal association between effective population size (N_e) and the ratio of non-synonymous to synonymous mutation rate (dN/dS) to verify the theoretical prediction that natural selection is more efficient in larger populations

Bayesian phylogenetic inference using continuous traits with missing states   Feb 2025 – Jun 2025
Supervisor: **Prof. Chi Zhang**, *Chinese Academy of Sciences*
Independent Researcher

- Implemented a Brownian motion model for continuous traits into widely-used Bayesian phylogenetics software `MrBayes`
- Adapted Felsenstein's pruning algorithm to support: (i) missing character states (ii) nonclock and relaxed clock models, (iii) evolutionary rate variation across tree branches, characters, and data partitions
- Performed simulations to quantify the advantage of using Brownian motion model with original data against using Mkv model with discretized data, measuring topological accuracy with the Mutual Clustering Information (MCI) metric
- Applied the model to mixed-character empirical datasets (pterosaur and ancient humans), performed tip dating analysis, and demonstrated that continuous traits can yield improved phylogenetic resolution

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*The official transcript from Peking University does not provide a GPA; this figure is based on a World Education Services (WES) course-by-course evaluation.

Spatio-temporal optimization of gene drive release strategies Jul 2024 – Jan 2025
Supervisor: **Prof. Jackson Champer**, *Peking University*
Independent Researcher

- Formulated a mathematical framework to define and quantify the "spread efficiency" of a gene drive release
- Developed and implemented a reaction-diffusion model in MATLAB to simulate the spatial population dynamics of four distinct gene drive systems (TARE, 2-locus TARE, TADE, and CifAB)
- Solved for the optimal, radially-symmetric release patterns by a numerical finite difference solver and performed global optimization using a gradient-descent based algorithm
- Discovered that the optimal release strategy exhibits distinct patterns based on the operational timeframe: a "blanket" release for rapid control, a non-intuitive "multiple-ring" release for intermediate times, and a "center" release for long-term efficiency

Modeling a gene drive for population suppression Jul 2023 – Dec 2023
Supervisor: **Prof. Jackson Champer**, *Peking University*
Collaborated with Weizhe Chen

- Developed a stochastic, individual-based model in SLiM to simulate the population dynamics of a CRISPR homing gene drive with dominant female-sterile resistance alleles
- Implemented and compared multiple gene drive systems in the model, including systems with recessive vs. dominant resistance alleles and with/without sterile homozygous drive males
- Designed and executed simulations to quantify the suppressive power of different drive strategies by measuring genetic load under a wide range of parameters, such as drive efficiency and fitness costs
- Demonstrated that generating dominant-sterile resistance alleles substantially improves population suppression compared to standard drives, even when the drive itself has imperfections like homozygous male sterility

TEACHING EXPERIENCE

Peer Tutor Sept 2023 – Current
School of Life Sciences, Peking University

- Tutored undergraduate students in core mathematical courses: Calculus (3 semesters), Probability and Statistics (1 semester), Linear Algebra (1 semester).
- Authored original teaching materials and led review sessions totaling 50+ hours; facilitated daily academic discussions and Q&A in course group chats.
- Recognized with the *Tingfang Scholarship* for outstanding contribution to peer education.

TECHNICAL SKILLS

Programming Languages:
Python, R, C, MATLAB, Shell

Population Genetics Software & Packages:
SLiM, msprime, tskit, Relate, SINGER, POLEGON, tsinfer, tsdate, threads

Phylogenetics Software & Packages:
MrBayes, RevBayes, Beast, TNT, ASTRAL, CASTER, ape, phytools, Tracer, FigTree

Bioinformatics & Developer Tools:
SAMtools, BCFtools, VEP, Snakemake, Git, Github, Conda, Unix/Linux Command Line, HPC Environments

SELECTED COURSES

Bioinformatics
Machine Learning Algorithms, Data Structure and Algorithm, Molecular Evolution and Phylogenetics, Statistical Analysis of Genomics Data, Mathematical Modeling in the Life Sciences

Mathematics & Statistics
Advanced Theory of Probability, Probability Theory (Honor), Applied Stochastic Processes, Mathematical Statistics, Biostatistics, Real Analysis, Linear Algebra, Abstract Algebra

PERSONAL INTERESTS

Piano (15 years), Guitar (beginner), "Random Walks" & Cycling, Billiards