Meng Yuan

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HIGHLIGHTS OF SKILLS

- Joint background in bioinformatics, data science and software engineering for collaborative research and reproducible data analytics
- 6+ years of experience designing, optimizing and maintaining reproducible bioinformatics pipelines for large-scale omics data (WGS, RNA-Seq) in HPC environments
- Proficient in Python, R, and Bash for statistical modelling, data analysis and visualization
- Strong foundation in software development (Git, documentation), with training in software engineering and machine learning
- Extensive experience in collaborative research and cross-disciplinary communication, with strong records of publications and conference presentations

Tools: Git, Slurm, Snakemake, NextFlow, Bioconda, FastQC, BWA, STAR, LASTZ, SAMTools, BCFTools, VCFTools, Picardtools, GATK, FreeBayes, PLINK, EIGENSOFT, GEMMA, IGV

Programming: R (Tidyverse, ggplot2, DESeq2, topGO), Python (Jupyter, NumPy, Pandas, Matplotlib, scikit-learn, TensorFlow), Bash, SQL

RELEVANT EXPERIENCE

Doctoral Researcher, *University of Toronto* *2019 - 2025*

- Developed pipelines for analyzing large-scale genomics datasets, utilizing HPC for raw reads processing, variant calling, expression analysis, eQTL mapping and population genomics
- Designed independent research projects integrating genomics and wet-lab experiments to test fundamental hypotheses in evolutionary genetics, collaborated with external institutions
- Created lab guidelines in computational genomics, collaborated efficiently with team members from different technical backgrounds and expertise
- Co-authored 5 peer-reviewed publications and efficiently presented at 5 conferences
- Managed sample preparation and optimized molecular lab protocols for DNA/RNA isolation

Lab and Tutorial Instructor, *University of Toronto* *2019 - 2025*

- Taught Python and R tutorials for data science and biostatistics courses over 3 iterations
- Instructed and evaluated students in hypothesis testing, statistical modelling, data visualization and research presentation over 3 iterations
- Mentored student research projects and taught molecular biology laboratory techniques

Mitacs Globalink Research Intern, *Simon Fraser University* *Summer 2018*

- Developed pipelines for transcriptomics and GO/KEGG enrichment analysis of conifer defense traits
- Identified 50+ candidate genes linked to wood quality improvements

Undergraduate Researcher, *Sichuan University* *2017 - 2018*

- Developed pipelines integrating NGS and Sanger sequencing for chloroplast genome assembly and annotation, contributed to journal publication

EDUCATION

Ph.D. in Evolutionary Genetics *2019 - 2025*
University of Toronto, Canada. Mitacs Graduate Fellowship, $15,000

Honours B.Sc. in Biology (major), **B.E. in Software Engineering** (minor) *2015 - 2019*
Sichuan University, China

Relevant Coursework: Machine Learning, Bayesian Statistics, Database Systems (SQL)

LEADERSHIP EXPERIENCE

Preprint Editorial Team, *Proceedings of the Royal Society B* *2020 - Present*

- Evaluated latest preprints on bioinformatics algorithms and applications (bioRxiv.org), made monthly suggestions for successful journal solicitation

Executive Committee, *Chinese Genomics online Meet-up* *2020*

- Invited speakers, hosted monthly online seminars on the advancements in genomics

Departmental Service, *U of T & Sichuan University* *2016 - 2023*

- Designed and organized public outreach activities and departmental workshops on science communication, led journal club discussions

PUBLICATIONS

First authored papers [Google scholar]:

1. *Cis*-regulation of gene expression between sexes and life stages in *Rumex hastatulus*. 2025. Under review at *Molecular Biology and Evolution*. *bioRxiv*. [Link] [Github]
   Gave talk at the 3rd Joint Congress on Evolutionary Biology (Montreal, Canada).
2. Testing for the genomic footprint of conflict between life stages in an angiosperm and moss. 2025. *Genome Biology and Evolution*. [Link] [Github]
   Gave talks at Plant and Animal Genome Conference 32 (San Diego, US), University of Lille (invited), and Evolution 2023 (Albuquerque, US).
3. Population genomics of parallel adaptation. 2020. *Mol Ecol*. [Link]

Other co-authored papers:

1. Widespread loss of Y expression in the absence of transcriptional dosage compensation in *Rumex hastatulus*. 2025. *bioRxiv*.
2. Phylogenomics resolves key relationships in *Rumex* and uncovers a dynamic history of independently evolving sex chromosomes. 2023. *Evolution Letters*.
3. Recombination landscape dimorphism and sex chromosome evolution in the dioecious plant *Rumex hastatulus*. 2022. *Philos Trans R Soc Lond B Biol Sci*.
4. The complete chloroplast genome of *Oenanthe javanica.* 2020. *Mitochondrial DNA Part B*.