Meng Yuan

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HIGHLIGHTS OF SKILLS

- Joint background in bioinformatics, software engineering and data science for collaborative research and reproducible data analytics
- 6+ years of experience testing, developing and maintaining bioinformatics pipelines for large-scale multi-omics analysis (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) and database management
- Extensive experience in collaborative research and cross-disciplinary communication, with strong records of publications and conference presentations

Tools: Git, Slurm, Snakemake, NextFlow, Bioconda, FastQC, Trimmomatic, fastp, BWA, STAR, LASTZ, SAMTools, BCFTools, VCFTools, BEDTools, Picardtools, GATK, FreeBayes, PLINK, EIGENSOFT, IGV, featureCounts, TensorQTL, Juicebox

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

RELEVANT EXPERIENCE

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

- Developed pipelines for analyzing large-scale genomics/transcriptomics data, utilizing HPC for variant calling, expression analysis, functional and population genomics
- Managed multiple independent projects, incorporating newest bioinformatic tools for evolutionary genetics research, skilled in data analysis, interpretation, and reporting
- Trained lab members in server use and bioinformatics, collaborated efficiently with multi-institutional teams from different technical backgrounds
- Co-authored 5 peer-reviewed publications and presented at 5 conferences
- Managed sequencing sample preparation and optimized molecular lab protocols

Lab and Tutorial Instructor, *University of Toronto* *Sept 2019 - Apr 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* *Jul - Oct 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* *Sept 2017 - Dec 2018*

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

EDUCATION

Ph.D. in Bioinformatics *Sept 2019 - Oct 2025*

University of Toronto, Canada. Mitacs Graduate Fellowship, $15,000

Honours B.Sc. in Biology, **B.E. in Software Engineering** (minor) *Sept 2015 - Jun 2019*

Sichuan University, China

Relevant Coursework: Software Development, Database System, Data Structure and Algorithms

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 latest advancements in genomics

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

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

PUBLICATIONS & PRESENTATIONS

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*.

Other co-authored papers:

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