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 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 best practices (Git, documentation, agile)
- Extensive experience in collaborative research and cross-disciplinary communication, with strong records of publications and conference presentations

Tools: Git, Slurm, Snakemake, NextFlow, Docker, FastQC, BWA, STAR, LASTZ, SAMTools, BCFTools, VCFTools, Picardtools, GATK, FreeBayes, PLINK, TensorQTL, Juicebox

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

RELEVANT EXPERIENCE

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

- Built pipelines for analyzing large-scale genomics/transcriptomics datasets, utilizing HPC for variant calling, expression analysis, population genomics and eQTL mapping
- Designed and led multiple independent projects integrating genomics, greenhouse and wet-lab experiments to test fundamental hypotheses in evolutionary genetics
- Trained junior team members in bioinformatics, 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), Data Structures & 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 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

Yuan M, Sacchi BM, Choudhury BI, Barrett SCH, Stinchcombe JR, Wright SI. 2025. *Cis*-regulation of gene expression between sexes and life stages in *Rumex hastatulus*. Under review at Molecular Biology and Evolution. bioRxiv. 2025:2025.06.16.659834.

Gave talk at the 3rd Joint Congress on Evolutionary Biology (Montreal, Canada). [Github Link]

Yuan M, Kollar LM, Sacchi BM, Carey SB, Choudhury BI, Jones T, Grimwood J, Barrett SCH, McDaniel SF, Wright SI, Stinchcombe JR. 2025. Testing for the genomic footprint of conflict between life stages in an angiosperm and moss species. Genome Biology and Evolution. 17(8):evaf138.

Gave talks at Plant and Animal Genome Conference 32 (San Diego, US), University of Lille (invited), and Evolution 2023 (Albuquerque, US). [Github Link]

Hibbins MS, Rifkin JL, Choudhury BI, Voznesenka O, Sacchi BM, **Yuan M**, Gong Y, Barrett SC, Wright SI. 2023. Phylogenomics resolves key relationships in *Rumex* and uncovers a dynamic history of independently evolving sex chromosomes. Evolution Letters. 9(2): 221-235.

Rifkin JL, Hnatovska S, **Yuan M**, Sacchi BM, Choudhury BI, Gong Y, Rastas P, Barrett SCH, Wright SI. 2022. Recombination landscape dimorphism and sex chromosome evolution in the dioecious plant *Rumex hastatulus*. Philos Trans R Soc Lond B Biol Sci. 377(1850):20210226.

Yuan M, Stinchcombe JR. 2020. Population genomics of parallel adaptation. Mol Ecol. 29(21): 4033-4036.

Zhang Z, Dong H, **Yuan M**, Yu Y. 2020. The complete chloroplast genome of *Oenanthe javanica.* Mitochondrial DNA Part B. 5(3):3151-3153.