

Meng Yuan

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HIGHLIGHTS OF SKILLS

- 5+ years of experience designing and optimizing reproducible bioinformatics workflows for NGS data in HPC environments
- Proficient in Python, R, and Bash for statistical modelling, pipeline development (Snakemake), and data visualization
- Strong foundation in software development (Git, documentation, agile), with training in machine learning, software engineering and database systems
- Extensive experience in collaborative research, cross-disciplinary communication, and mentoring in bioinformatics and data science

Tools: Git, Snakemake, Docker, Slurm, FastQC, BWA, STAR, LASTZ, GATK, FreeBayes, SAMTools/BCFTools, Picardtools, featureCount, PLINK, pixy, TensorQTL

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

RELEVANT EXPERIENCE

Doctoral Researcher, University of Toronto 2019 - Present

- Developed pipelines for analyzing large-scale NGS dataset (RNA-Seq, WGS), utilizing HPC for variant calling, expression analysis, population genomics and eQTL mapping
- Developed and led independent projects integrating genomics, greenhouse and wet-lab experiments
- Collaborated with multi-institutional teams; co-authored 4 peer-reviewed publications and presented at 4 international conferences
- Supervised students and trained staff in computational and experimental methods
- Managed sample preparation and optimized molecular lab protocols for DNA/RNA isolation

Lab and Tutorial Instructor, University of Toronto 2019 - Present

- Led Python and R programming tutorials for undergraduate data science and biostatistics courses over 3 iterations
- Instructed and evaluated students in hypothesis testing, statistical modelling, data visualization and 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 transcriptomic 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 (expected)

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, Database Systems (SQL), Data Structures & Algorithms, Bayesian Statistics

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.

Cisregulation of gene expression between sexes and life stages in *Rumex hastatulus*.

Under review for 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. 2024. Testing for the genomic footprint of conflict between life stages in an angiosperm and a moss species. Accepted at Genome Biology and Evolution. bioRxiv. 2024:2024.10.04.613734.

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.