

MATT GIBSON

Population genomics and evolution

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📍 Bloomington, IN, USA

🔗 <https://gibsonmatt.github.io/>

EXPERIENCE

Evolution and bioinformatics Ph.D. candidate

Population genomics of wild tomato

📅 Aug 2016 – Current

Indiana University

- Developed bioinformatic pipelines for processing and analyzing whole genome sequencing data
- Studied the genomic basis of climatic adaptations in plant populations, using whole genome sequencing and statistical genetic inference
- Completed coursework in evolution and machine learning

NIFA predoctoral fellow

Identifying candidate loci for stress tolerance in tomato

📅 May 2021 – Current

US Department of Agriculture

- Recipient of \$120,000 fellowship to research plant adaptation to climate variation and next-gen crop breeding using low-coverage whole genomes

Research assistant

Mating system inference methods in plants

📅 Aug 2013 – June 2016

University of Kansas

- Developed statistical inference methods for plant genomics applications

ACHIEVEMENTS

- Writer and recipient of over \$153,000 in research grant funding
- Published 9 peer-reviewed manuscripts in top field journals (4 first author)
- Peer reviewer for journals *Molecular Ecology*, *Molecular Biology and Evolution*, and *New Phytologist*

TECHNICAL SKILLS

- **Languages:** Python (advanced), R (advanced), C# (beginner), Stan (beginner), Node.js (beginner)
- **Workflow:** bash, zsh, LaTeX, slurm, torque, vim, tidyverse, markdown
- **Life Science:** bwa, STAR, STRUCTURE, samtools, bcftools, bedtools, ANGSD
- **Misc:** Microsoft Office suite, Adobe Illustrator

EDUCATION

Ph.D. Evolution and bioinformatics

Indiana University-Bloomington

📅 Aug 2016 – Current (Exp. May 2022)

"Population genomics of wild tomato"

B.S. Genetics, with honors

University of Kansas

📅 2011 – 2016

*"Connecting the breeding system to mating system in Macaronesian *Tolpis*"*

PROJECTS

Introgression and fruit color convergence in Galápagos tomato

- Led a project in which I performed novel field collections, reduced representation genome sequencing, and statistical genetic inference to describe a unique scenario of post-invasion fruit color convergence driven by introgression between two tomato species on the Galápagos islands.

Computational tool for detecting hemiplasy

- Contributed to the development of statistical software (HeIST) for predicting the risk of hemiplasy (false inference of convergent evolution) in phylogenetic data sets.

Landscape genomics in wild tomato

- Led a project in which I used high-fidelity genomic and climate data from >200 wild plant samples to understand the climatic drivers of adaptation and identify novel functional genes.

Mapping genes for flower color in genus *Jaltomata*

- Developed the bioinformatic pipeline for mapping the locations of genes controlling flower traits in the diverse plant genus *Jaltomata*

SOFTWARE

Hemiplasy Inference and Simulation Tool

🔗 <https://github.com/mhibbins/HeIST>

mvnselection

🔗 <https://gibsonmatt.shinyapps.io/mvnselection/>

prettymap

🔗 <https://gibsonmatt.shinyapps.io/prettymap/>