MATT GIBSON

Computational biologist

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SUMMARY

I am a computational biologist specializing in statistical inference from genomic datasets. In May 2022 I will receive a Ph.D. from Indiana University. I have published 9 research articles on population genetics and bioinformatics in top field journals such as *eLife* and *Molecular Ecology*. My research has focused on using genomes and computing to map genes shaping natural trait variation.

EXPERIENCE

Evolution and bioinformatics Ph.D. candidate

📅 Aug 2016 – Current

Indiana University

- Developed bioinformatic pipelines for 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 genetics and machine learning

NIFA predoctoral fellow

📅 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

📅 Aug 2013 – June 2016

University of Kansas

- Contributed to the development of statistical software for plant genomics applications

TECHNICAL SKILLS

- **Languages**: Python (advanced), R (advanced), bash (intermediate), C# (beginner), Stan (beginner), Node.js (beginner)
- **Bioinformatics**: RADseq assembly, samtools, bcftools, SNP calling in GATK, low-coverage genotyping in ANGSD, short read mapping/alignment, RNAseq analysis
- **Computing**: SLURM, torque, git, Unix tools
- **Statistics**: linear modeling/regression, mixed-effects models, GWAS, hidden Markov models, demographic modeling with maximum likelihood.

EDUCATION

Ph.D. Evolution and bioinformatics

Indiana University-Bloomington

📅 Aug 2016 – Current (Exp. May 2022)

B.S. Genetics, with honors

University of Kansas

📅 2011 – 2016

PROJECTS

Introgression and fruit color convergence in Galápagos tomato

- Led a project using reduced representation genome sequencing, HMM local ancestry inference, and admixture mapping to dissect the genetic basis of fruit color variation in Galápagos tomato.

Computational tool for detecting hemiplasy

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

Landscape genomics in wild tomato

- Led a project in which I used high-fidelity genomic and climate data with multivariate statistical models (RDA) to describe 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 for flower traits in the plant genus *Jaltomata*

SELECTED PUBLICATIONS

"Introgression shapes fruit color convergence in invasive Galápagos tomato". **Gibson, MJS.**, Torres, MdL., Brandvain, Y., & Moyle, LC. 2021. *eLife*. https://doi.org/10.7554/eLife.64165

"Regional differences in the abiotic environment contribute to genomic divergence within a wild tomato species". **Gibson, MJS.** & Moyle, LC. 2020. *Molecular Ecology*. https://doi.org/10.1111/mec.15477

"Determining the probability of hemiplasy in the presence of incomplete lineage sorting and introgression". Hibbins, MS., **Gibson, MJS.**, Hahn, MW. 2020. *eLife*. https://doi.org/10.7554/eLife.63753

"Genome-wide genotyping estimates mating system parameters and paternity in the island species Tolpis succulenta". **Gibson, MJS.**, Crawford, DJ., Holder, MT., Mort, ME., Kerbs, B., Menzes de Sequeira, M., Kelly, JK. 2020. *American Journal of Botany*. https://doi.org/10.1002/ajb2.1515

For a full list of publications refer to https://gibsonmatt.github.io/publications.html