

Michelle L. Gaynor, Ph.D.

NSF Postdoctoral Research Fellow in Biology

University of Michigan, Ecology and Evolutionary Biology

shellyleegaynor@gmail.com • Website: www.mlgaynor.com • Github: [mgaynor1](https://github.com/mgaynor1)**Summary**

I am a computation biologist with >9 years of experience in biodiversity informatics, statistics, mathematical model development, statistical genetics, next-generation sequencing, long-read sequencing, bioinformatics, predictive modeling, and software package development. For my dissertation, I integrated theory and organismal biology to understand the maintenance and persistence of mixed cytotype populations.

Education

2018 – 2024	Ph.D. in Botany	University of Florida, Gainesville, FL USA
2014 – 2018	B.S. in Biology	University of Central Florida, Orlando, FL. USA

Skills

- **Programing & Software Development:** R, C++, Python, Unix, Bash, Shiny, SQL, version control (git, GitHub), SLURM.
- **Statistical Modeling & Algorithms:** Model selection, maximum likelihood and machine learning, matrix-based population models, expected-maximization, numerical optimization, evidential based statistics, simulation-based model validation.
- **Bioinformatics:** Models for ploidal level prediction, sequence-based data analysis (QC, read mapping, variant calling, BLAST database queries), genome assembly (including microbial community long-read assemblies), population genomics, phylogenetics, API data management.
- **Writing & Documentation:** markdown/Rmarkdown (including pkgdown), LaTeX/Overleaf, Microsoft Office.

Professional Experience**General**

- **Scientific writing and communication:** My technical writing skills can be seen in my 11 publications (9 first or co-first authored), including several publications in high-impact journals including *Nature Communications* and *Systematic Biology*, with numerous manuscripts currently under review or in preparation. I have received **\$412,511** through fellowships (7) and research grants (28), including the NSF Graduate Research Fellowship and NSF Postdoctoral Research Fellowship in Biology.
- **Leadership and management:** Service to the Botanical Society of America including Early Career Advisory Committee for the society journals and as Student Representative of the Executive Board.
- **Undergraduate mentoring:** Supervisor for 10 undergraduate students at UF; these students have successfully obtained internal and external funding, presented research at conferences, and some will be primary or secondary authors on resulting publications.

Postdoctoral Research Fellow | University of Michigan | Ann Arbor, MI

2024 – 2027

- **Comparative phylogenetics:** I am currently working on developing new phylogenetic comparative methods that incorporate admixture proportions and gene-tree discordance to reconstruct ancestral niche dynamics. This method will then be used to understand the consequences of whole-genome duplication on species ecology by classifying niche dynamics among *Galax urceolata* (Diapensiaceae) mixed-cytotype populations and across the phylogeny of the order Ericales.

Graduate Research Assistant | University of Florida | Gainesville, FL

2018 – 2024

- **Theoretical modeling of mixed cytotype populations:** I designed a new matrix population model with demographic and environmental stochasticity to investigate coexistence of mixed cytotypes with on-going gene flow. I implemented this in an easy-to-use R package, AutoPop. I extended the above mathematical model and incorporated genotypes, mutation, and island-based migration for demographic inference.
- **Ploidal prediction based on sequence data:** I created statistical models to predict ploidal level based on site-based heterozygosity and implemented these models in an easy-to-use R package nQuack (written in C++ and R).
- **Population genetics of mixed-ploidy species:** Currently processing and analyzing mixed ploidy population genetic data for *Larrea tridentata* and *Galax urceolata*. With undergraduate researchers, we investigated the cytoecography of *G. urceolata* in relation to stomatal cell size, soil chemistry, soil fungal and bacterial community composition, and broad-scale climate.
- **Biodiversity informatics:** I have a strong background in biodiversity informatics through my research assistantship with iDigBio. This included creation and maintained of open access software, as well as curriculum (see more here: mgaynor1/BiodiversityResources).

Undergraduate Researcher | University of Central Florida | Orlando FL

2015 – 2018

- **Population genetics:** Designed and carried out study to test if genetic diversity of populations is maintained during restoration efforts. Analysis of genotypes included diversity, population structure, and clonality.
- **Meta-analysis:** Conducted a meta-analysis to assess how polyploidy affects the composition and abundance of secondary metabolites in non-cultivated species.

NSF-Funded REU | University of Missouri | Columbia, MO

2017

- **Population genomics:** Optimized a 96-well Urea DNA extraction method. Planted and maintained 360 varieties of *Brassica* (*B. napus*, *B. rapa*, and *B. oleracea*). Processed whole-genome resequencing data to investigate the potential diploid progenitors of *Brassica napus* (Perl and Python).

NSF-Funded iDigBio Researcher | University of Florida | Gainesville, FL

2017

- **Ecological niche modeling:** Identified whether ecological niche divergence existed among diploid, triploid, and autotetraploid *Galax urceolata*.

NSF-Funded REU | University of Colorado Boulder | Boulder, CO

2016

- **Community phylogenetics:** Investigated the influence of genome duplication on community structure of Brassicaceae and Rosaceae species across the United States and learned programming in Bash, Python, and R.

Select Software

My full publications can be found on [Google Scholar](https://scholar.google.com/) and additional software via [GitHub](https://github.com/). pkgdown or interactive markdowns linked when available.

- **nQuack:** An R package for predicting ploidy level from sequence data using site-based heterozygosity. Available on [GitHub](https://github.com/). Published in [Applications of Plant Science](#).
- **AutoPop:** R-based autopolyploid population and population genetic simulation. Available on [GitHub](https://github.com/). Published in [The American Naturalist](#).
- Maximum likelihood based ancestral reconstruction. Available on GitHub: [utremi](#) & [PaleoGenerate](#). Published in [Systematic Biology](#).
- **gatoRs:** Geographic and taxonomic occurrence R-based scrubbing. Available on [GitHub](https://github.com/). Published in [Applications in Plant Science](#).
- **Biology PhD Stipends:** Shiny app for Biology Ph.D. stipend benchmarking. Available on [GitHub](https://github.com/). Covered by [Nature](#).
- [ridigbio](#) contributor.