

# Paul Blischak, Ph.D.

Postdoctoral Research Fellow

1041 E. Lowell St. | Tucson, AZ 85721, USA | +1(330)703-3377 | [paul.blischak@gmail.com](mailto:paul.blischak@gmail.com)  
[pblischak.github.io](https://pblischak.github.io) | **LinkedIn:** [linkedin.com/in/paulblischak](https://linkedin.com/in/paulblischak) | **GitHub:** [github.com/pblischak](https://github.com/pblischak)

## Summary

---

Computational biologist with nine years of experience in statistical modeling, programming, software development, genomic data analysis, and scientific communication. My primary interest is in developing models and algorithms to decode complex genomes and providing tools that effectively translate this complexity into meaningful biological knowledge.

## Skills

---

- **Programming:** Python, R, C++, Unix, Bash.
- **Software Development:** version control (git, GitHub), make, Docker, continuous integration.
- **Statistical Modeling and Algorithms:** maximum likelihood and Bayesian inference, simulation-based model validation, deep/machine learning (TensorFlow), convolutional neural networks (Keras), empirical Bayes, expectation-maximization, numerical optimization.
- **Bioinformatics:** models for variant calling, high-throughput sequencing data analysis (QC, read mapping, GATK), genome annotation, population genomics, statistical phylogenomics.
- **Writing & Documentation:** markdown, reStructuredText, LaTeX, Jupyter notebooks, Rmarkdown, Microsoft Office.

## Education

---

**The Ohio State University** – Columbus, OH

Ph.D., Evolutionary Biology | Graduate Minor: Statistics | 2018

- Thesis title: Developing Computation Tools for Evolutionary Inferences in Polyploids.
- Awarded Distinguished University Fellowship (two full years of funding).

B.S., Mathematics | Minors: Statistics, Spanish | 2012

- Awarded Undergraduate Research Fellowship in mathematical biology.

## Professional Experience

---

NSF Postdoctoral Research Fellow | University of Arizona | Tucson, AZ

2018–current

- **Open-Source Software Development in Python:** Contributing code to the Python package *dadi* (available on [Bitbucket](https://bitbucket.org/pblischak/dadi)) to implement new models for population genomic and demographic inference.
- **Population Genomic Models for Inbred and Polyploid Species:** Deriving statistical models for demographic inference in species with non-equilibrium dynamics.
- **Population-Level, Whole-Genome Analyses for Crop Species:** Processing whole-genome resequencing data to better understand domestication and its impact on genetic variation.
- **Community-Driven Tool Development for Polyploid Genomics:** Leading an international, collaborative effort to build tools for polyploid genomics. Working to create a communal set of software packages, documentation, tutorials, and other publicly available resources on GitHub (called the “Ploidyverse”).

Graduate Research Fellow/Associate | The Ohio State University | Columbus, OH

2012–2018

- **Modeling Genotypes and Haplotypes in Polyploids:** Produced statistical models for genotype and haplotype inference in species with duplicated genomes and implemented the models in multiple programming languages (C++, Python, R).

- **Software Distribution and Documentation:** Maintained open-source software on GitHub with documentation written in markdown, Rmarkdown, and reStructuredText to facilitate the use of novel models and algorithms by other scientists.
- **Scientific Writing and Communication:** Wrote grants and fellowships that were successfully funded by the National Science Foundation and scientific societies. Published nine manuscripts, six as the primary author. Presented research at eight national and international conferences.
- **Wet-Lab Work:** Designed primers for sequencing targeted amplicons and conducted wet-lab work to extract and process DNA samples for high-throughput sequencing. Wrote Fluidigm2PURC software in Python to automatically process these data and to infer amplicon haplotypes.
- **Field Work:** Completed three field seasons to collect plant material in the western United States (MT, ID, OR, WA, UT, AZ, CA).

Undergraduate Research Fellow | The Ohio State University | Columbus, OH

2011–2012

- **Simulation-Based Analysis of Population Structure in Polyploid Species:** Designed and carried out a project investigating population structure in polyploids and learned programming in bash, Perl, and R. Presented research at an undergraduate research forum and a national meeting.

## Software and Relevant Publications

---

My full publication record can be found on [Google Scholar](#).

- **HyDe-CNN:** Hybridization detection with convolutional neural networks. Available on [GitHub](#). Preprint on [bioRxiv](#). [Python (TensorFlow)]
- **GMPi:** Raspberry Pi-based monitoring system for growth chambers. Available on [GitHub](#). Published in [Applications in Plant Sciences](#) (7:e11280). [Python]
- **EBG:** empirical Bayes genotyping of biallelic SNPs in polyploids. Available on [GitHub](#). Published in [Bioinformatics](#) (34:407–415; 2018). [C++]
- **Fluidigm2PURC:** automated processing and haplotype inference for targeted amplicons. Available on [GitHub](#). Published in [Applications in Plant Sciences](#) (6:e1156; 2018). [Python]
- **Ploidyverse:** community-driven tool development for polyploid genomics. Available on [GitHub](#). [Poster](#) from Plant and Animal Genome XXVII (San Diego, CA; 2019). [R]

## Select Presentations

---

- Assessing the impact of inbreeding on demographic estimates of domestication. Plant and Animal Genome XXVIII (2020). Paper in [Molecular Biology and Evolution](#) (37:2124–2136; 2020).
- Developing models for genotype uncertainty, inbreeding, and allelic inheritance in non-model polyploids. Evolution 2016. Austin, TX. [Slides](#) on [figshare](#).
- Estimating allele frequencies in non-model autopolyploids using high-throughput sequencing data. Botany 2015. Edmonton, Alberta, CA. [Slides](#) on [figshare](#).
- Detecting hybridization using phylogenetic invariants. Evolution 2017. Portland, OR. [Slides](#) on [figshare](#).

## Awards and Achievements

---

- 2018 | NSF Postdoctoral Research Fellowship in Biology | \$216,000.00
- 2017 | Osburn Award for Excellence in Research | \$1,500.00
- 2016 | NSF Doctoral Dissertation Improvement Grant | \$20,020.00
- 2014 | NSF Graduate Research Fellowship Program | Honorable Mention
- 2013–2015 | Three Graduate Student Research Grants | \$3765.00
- 2013 | National Institute for Mathematical and Biological Synthesis Visiting Graduate Student Fellowship