# ARIELLA GLADSTEIN, PH.D.

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**Expertise:** *Human population genetics, genomics, computational biology, bioinformatics, statistics*

## EDUCATION

**University of Arizona, Tucson, AZ**                                        *August 2018*
PhD in Ecology and Evolutionary Biology
Minor in Mathematics

**Beloit College, Beloit, WI**                                              *May 2011*
B.S. in Mathematical Biology & Russian, Cum Laude

Departmental Honors: Mathematical Biology

## RESEARCH EXPERIENCE

**Postdoctoral Fellowship**                                                 2018 - present
*Schrider Lab*                    *Department of Genetics, University of North Carolina, Chapel Hill*
Project: Inference of demographic history with deep learning

**Dissertation Research**                                                   2011 - 2018
*Hammer Lab*                          *Ecology and Evolutionary Biology, University of Arizona*
Dissertation: Inference of recent demographic history of population isolates using genome-wide high
density SNP arrays and whole genome sequences

**Functional Genomics Research Rotation**                                   Spring 2012
*Restifo Lab*                                        *Neuroscience, University of Arizona*

**Computational Genomics Research Rotation**                                Fall 2011
*Kececioglu Lab*                              *Computer Science, University of Arizona*

**Lab technician intern**                                                   Sp, Fall 2009
*Laboratory of Population Genetics*          *Russian Academy of Medical Sciences, Moscow, Russia*

## SKILLS

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|---|---|
| **Programming** | Python, Bash, R, Perl (including unit testing and profiling) |
| **Other Computer** | Linux command line, Git, HPC/HTC (with HTCondor, PBS, Slurm), cloud computing (OpenStack, AWS) |
| **Genomics** | PLINK, Bedtools, VCFtools, phasing, imputation, haplotype detection, population structure, genome simulation |
| **Data Science** | Numpy, Scikit-learn, Keras, Pandas, Spark, Tidyverse, Matplotlib, ggplot |
| **Reproducibility** | scripting, workflow development (Pegasus, Makeflow), containers (Singularity, Docker), Jupyter, Knitr |
| **Documentation** | LaTeX, Markdown, reStructuredText |
| **Language Skills** | English (native speaker), Russian (fluent), Spanish (basic) |

## AWARDS

Probabilistic Modeling in Genomics Grant (registration, meals, lodging)          *2018, 2019*

XSEDE Supplemental allocation (250,000 CPU hrs)                                   *2018, 2019*

XSEDE Startup allocation (100,000 CPU hrs, 6,500 GPU hrs, 5.5 Tb storage)              *2019*

| | |
|---|---|
| XSEDE Startup allocation (150,000 CPU hrs) | *2017* |
| Open Science Grid User School (travel, lodging, meals, cost of program) | *2017* |
| GPSC Travel Grant ($761) | *2015, 2016, 2017* |
| University of Arizona Galileo Circle Scholarship ($1,000) | *2015* |
| NIH Computational and Mathematical Modeling of Biological Systems Traineeship ($71,064) | *2013-2014* |
| NSF Integrative Graduate Education and Research Traineeship in Genomics ($97,083) | *2011-2013* |
| Society for Learning Unlimited Grant ($2,000) | *Fall 2009* |
| Study Abroad Enhancement Grant, Beloit College ($250) | *Spring 2009* |
| Beloit College Presidential Scholar ($60,000) | *2007-2011* |

## PUBLICATIONS

PopSim Consortium. 2019. A community-maintained standard library of population genetic models. *bioRxiv.* doi: `https://doi.org/10.1101/2019.12.20.885129`

Gladstein A.L. and Hammer M.F. 2019. Substructured population growth in the Ashkenazi Jews inferred with Approximate Bayesian Computation. *Molecular Biology and Evolution.* 36(6): 1162-1171. doi: `https://dx.doi.org/10.1093/molbev/msz047`

Gladstein A.L. et al. 2018. SimPrily: A Python framework to simplify high-throughput genomic simulations. SoftwareX, 7, 335-340. `https://doi.org/10.1016/j.softx.2018.09.003`

Gladstein A. and Hammer M.F. 2016. Population Genetics of the Ashkenazim. In: eLS. John Wiley & Sons, Ltd: Chichester. pp. 1-8. `https://doi.org/10.1002/9780470015902.a0020818.pub2`

Behar et al. 2013. No evidence from genome-wide data of a Khazar origin for the Ashkenazi Jews. *Human Biology.* 85.6:859-900. `https://doi.org/10.3378/027.085.0604`

Gladstein A.L. 2011. Split decomposition analysis groups Jewish populations together between European and Middle Eastern populations. *The Beloit Biologist.* 30:29-36.

## POSTERS AND PRESENTATIONS

**Invited Talks**

Inference of evolutionary history with Approximate Bayesian Computation. Open Science Grid All-Hands Meeting. 2018. Salt Lake City, Utah.

**Posters**

Gladstein A.L., Schrider R.D. Demographic model selection with deep learning. Probabilistic Modeling in Genomics. 2019. Aussois, France.

Gladstein A.L., Hammer M.F. Substructured population growth in the Ashkenazi Jews inferred with Approximate Bayesian Computation. Probabilistic Modeling in Genomics. 2018. Cold Spring Harbor, NY.

Gladstein A.L., et al. Efficient pipeline for whole genome simulation and summary statistic calculation with flexible demographic models. Meeting of the American Society for Human Genetics. 2017. Orlando, FL.

Gladstein A.L., et al. The effect of SNP array ascertainment bias on the distribution of runs of homozygosity lengths. Annual Meeting of the American Society for Human Genetics. 2015. Baltimore, MD.

## PROJECT MANAGEMENT

Managed team of 5, including computer scientists, software engineer, and mathematician, working on code development and high throughput computing for bioinformatics — *2017*

## WORKSHOPS AND HACKATHONS

SMBE satellite meeting on Speciation Genomics, Tjarno, Sweden (3 days) — *06/2019*

NCBI RNA-Seq in the Cloud hackathon, Chapel Hill, NC (3 days) — *03/2019*

Cyber Carpentry, Chapel Hill, NC (2 weeks) — *06/2018*

XSEDE HPC Workshop: Big Data, Tucson, AZ (2 days) — *02/2018*

Open Science Grid User School, Madison, WI (1 week) — *07/2017*

## COMMUNITY SERVICE AND OUTREACH

Helped with Cyber Carpentry workshop — *2019*

Poster presentation at UNC Women in Computing Research Symposium — *2019*

Helped with Research Bazaar workshop on R — *2018*

Teaching assistant for CyVerse Container Camp — *2018*

Active participant in the Research Bazaar — *2017, 2018*

Helped with Software Carpentry on Unix/Bash, Python, and Git — *2017*

Helped with the Tucson Womens Hackathon workshop on Git — *2017*

Judge for Graduate & Professional Student Council Travel Grants — *2012, 2016, 2017, 2018*

Judge for Tucson Magnet High School Science Fair — *2012, 2015*

Taught Population Genetics Module at the Kino School — *2013*

Arizona Assurance Mentor — *2012*

Judge for EEB Undergraduate Research Poster Session — *2012*

## TEACHING EXPERIENCE

**ECOL 320 Genetics** — Fall 2014, 2015, 2016
*Graduate Teaching Assistant* — *University of Arizona*

**ECOL 182L Intro to Ecology and Evolutionary Biology Lab** — Spring 2015
*Graduate Teaching Assistant* — *University of Arizona*

**BIOL 247 Biometrics** — Spring 2011
*Teaching Assistant* — *Beloit College*

## OTHER ACTIVITIES

**Circus Arts** — 2012 - present
*Aerial silks, aerial rope, lyra, flying trapeze, tightwire, handbalancing, contortion*

**Figure Skating** — 1998 - 2013
*Singles freestyle*