

# ARIELLA GLADSTEIN, PH.D.

(202) · 258 · 4408 ◇ [algladstein@gmail.com](mailto:algladstein@gmail.com) ◇ [github.com/agladstein](https://github.com/agladstein)

**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

---

### 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

L<sup>A</sup>T<sub>E</sub>X, Markdown, reStructuredText

### Language Skills

English (native speaker), Russian (fluent), Spanish (basic)

## AWARDS

---

XSEDE Supplemental allocation (250,000 CPU hrs)

*2018, 2020*

Probabilistic Modeling in Genomics Grant (registration, meals, lodging)

*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

---

<b>ECOL 320 Genetics</b> <i>Graduate Teaching Assistant</i>	Fall 2014, 2015, 2016 <i>University of Arizona</i>
<b>ECOL 182L Intro to Ecology and Evolutionary Biology Lab</b> <i>Graduate Teaching Assistant</i>	Spring 2015 <i>University of Arizona</i>
<b>BIOL 247 Biometrics</b> <i>Teaching Assistant</i>	Spring 2011 <i>Beloit College</i>

## OTHER ACTIVITIES

---

<b>Circus Arts</b> <i>Aerial silks, aerial rope, lyra, flying trapeze, tightwire, handbalancing, contortion</i>	2012 - present
<b>Figure Skating</b> <i>Singles freestyle</i>	1998 - 2013