

ARIELLA GLADSTEIN

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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

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^AT_EX, Markdown, reStructuredText

Language Skills

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

AWARDS

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

2019

XSEDE Supplemental allocation (200,000 CPU hrs)

2018

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

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., 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

NCBI RNA-Seq in the Cloud hackathon (3 days)	03/2019
Cyber Carpentry (2 weeks)	06/2018
XSEDE HPC Workshop: Big Data (2 days)	02/2018
Open Science Grid User School (1 week)	07/2017

COMMUNITY SERVICE AND OUTREACH

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

OTHER ACTIVITIES

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