

ARIELLA GLADSTEIN, PhD

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<https://ariella-gladstein.netlify.app> ◊ <https://github.com/agladstein> ◊ www.linkedin.com/in/ariella-gladstein

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, cloud computing

Genomics

PLINK, Bedtools, VCFtools, phasing, imputation, haplotype detection, population structure, genome simulation

Data Science

Numpy, Scikit-learn, Keras, Pandas, Spark, Tidyverse, Matplotlib, ggplot

Mathematical Skills

Probability theory, statistical inference, linear algebra

Reproducibility

scripting, workflow development (Pegasus, Makeflow, Snakemake), containers (Singularity, Docker), Jupyter, Knitr

Documentation

L^AT_EX, Markdown, reStructuredText

Language Skills

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

PUBLICATIONS

Adrión, J. R.*, Cole, C. B.*, Dukler, N.*, Galloway, J. G.*, Gladstein, A. L.*, Gower, G.*, Kyriazis, C.C.*, Ragsdale, A.P.*, Tsambos, G.*, ..., Gravel, S., Gutenkunst, R.N., Lohmeuller, K.E., Ralph, P.L., Schrider, D.R., Siepel, A., Kelleher, J., Kern, A.D. 2020. A community-maintained standard library of population genetic models. *eLife*. 9:e54967. doi: <https://doi.org/10.1101/2019.12.20.885129>

Bernstein M.N.*, Gladstein A., Latt K.Z. et al. Jupyter notebook-based tools for building structured datasets from the Sequence Read Archive [version 2; peer review: 2 approved]. *F1000Research* 2020. 9:376. doi: <https://doi.org/10.12688/f1000research.23180.2>

*First author

- 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 D.* 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

- Deep learning for demographic model choice. Human Evolutionary and Population Genomics Seminar. 2020. LANGE BIO, UGA-Cinvestav. Irapuato-Guanajuato, Mexico (virtual).
- Inference of evolutionary history with Approximate Bayesian Computation. Open Science Grid All-Hands Meeting. 2018. Salt Lake City, Utah.
- Code optimization for research scientists. Research Bazaar. 2018. Tucson, AZ.

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. UNC Women in Computing Research Symposium. 2019. Chapel Hill, NC.
- 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.

AWARDS

XSEDE Research allocation (250,000 CPU hrs)	2020
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)	2013-14
NSF Integrative Graduate Education and Research Traineeship in Genomics (\$97,083)	2011-13
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

PROJECT MANAGEMENT

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

[†]Presenter

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

Mentoring

Undergraduate interns in computer science, Tucson, AZ	2017
Arizona Assurance Mentor	2012

Teaching in community

Cyber Carpentry workshop, Chapel Hill, NC	2019
Research Bazaar workshop on R, Tucson, AZ	2018
CyVerse Container Camp, Tucson, AZ	2018
Software Carpentry on Unix/Bash, Python, and Git, Tucson, AZ	2017
Tucson Womens Hackathon workshop on Git, Tucson, AZ	2017
Population Genetics Module at the Kino School, Tucson, AZ	2013

Judge

Graduate & Professional Student Council Travel Grants, Tucson, AZ	2012, 2016, 2017, 2018
Tucson Magnet High School Science Fair, Tucson, AZ	2012, 2015
EEB Undergraduate Research Poster Session, Tucson, AZ	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>
RUSS 110, 115, 210, 215 Russian <i>Tutor</i>	2009-2011 <i>Beloit College</i>

STUDY ABROAD

Lomonosov Moscow State University <i>Biology Department</i>	Fall 2009 <i>Moscow, Russia</i>
Russian State University for the Humanities <i>Russian Studies</i>	Spring 2009 <i>Moscow, Russia</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