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

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, Snakemake), containers (Singularity, Docker), Jupyter, Knitr
Documentation	LaTeX, Markdown, reStructuredText
Language Skills	English (native speaker), Russian (fluent), Spanish (basic)

PUBLICATIONS

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 (https://doi.org/10.12688/f1000research.23180.2)

Adrion, 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`

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. LANGEBIO, 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*

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	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*

RUSS 110, 115, 210, 215 Russian   2009-2011
Tutor   *Beloit College*

STUDY ABROAD

Lomonosov Moscow State University   Fall 2009
Biology Department   *Moscow, Russia*

Russian State University for the Humanities   Spring 2009
Russian Studies   *Moscow, Russia*

OTHER ACTIVITIES

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

Figure Skating   1998 - 2013
Singles freestyle