

ARIELLA GLADSTEIN, PhD

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<https://github.com/agladstein> ♦ www.linkedin.com/in/ariella-gladstein

Expertise: *population genetics, genomics, computational biology, data science, machine learning, 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

EXPERIENCE

Research Scientist, Computational Biology

2021 - 2024

Ancestry team

Embark Veterinary, Remote

Developed dog breed ancestry and relative-matching products, enhancing computational efficiency while maintaining rigorous quality standards. Played a key role in improving pipeline automation from 40% to over 95% within one year and scaling processes from hundreds of thousands to millions of samples. Collaborated with a cross-functional team on a science initiative projected to save \$7.5 million annually. Served on the Diversity, Equity, Inclusion, and Belonging (DEIB) committee, co-authoring an Inclusive Norms document, designing and analyzing company-wide DEIB surveys, and contributing to various DEIB initiatives.

Postdoctoral Fellowship

2018 - 2020

Schrider Lab

Department of Genetics, University of North Carolina, Chapel Hill

Developed deep learning models for population genetics inference. Contributed to writing documentation and tutorials for the population genomics tskit software ecosystem. Actively participated in the PopSim Consortium, contributing to the development of the stdpopsim library.

Dissertation Research

2011 - 2018

Hammer Lab

Ecology and Evolutionary Biology, University of Arizona

Developed and applied computational methods for population genetics analysis, addressing ascertainment bias in identifying runs of homozygosity and demographic inference. Created and released software for high-throughput genomic simulations. Applied Approximate Bayesian Computation (ABC) to model the demographic history of Ashkenazi Jews.

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, R, Bash, unit testing, profiling, multiprocessing, Git

HPC/HTC & Cloud

Linux/Unix, SLURM, PBS, AWS, JupyterHub, Kubernetes

Genomics

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

Data Science

Numpy, Pandas, Scikit-learn, SciPy, Keras, Matplotlib, Seaborn, Plotly, ggplot

Reproducibility

Workflow development (Pegasus, Makeflow, Snakemake), containers (Singularity, Docker), virtual environments, Jupyter, Knitr

Documentation

L^AT_EX, Markdown, reStructuredText, JupyterBook, Confluence

Mathematical Skills

Probability theory, statistical inference, linear algebra

Language Skills

English (native speaker), Russian (fluent)

TEACHING EXPERIENCE

Introduction to using stdpopsim Workshop <i>Designed and presented interactive workshop on using stdpopsim, the standard library for reproducible, bug-free simulations of genetic datasets from published demographic histories.</i>	2020, <i>Virtual, PopSim Consortium</i>
NSF Cyber Carpentry Workshop <i>Assisted with 2-week workshop, where participants learned best practices for data-intensive computing, cloud infrastructure, and deep learning through hands-on projects.</i>	2019, <i>University of North Carolina, Chapel Hill</i>
Research Bazaar Workshop on R <i>Assisted with hands-on intro R workshop</i>	2018, <i>University of Arizona</i>
CyVerse Container Camp <i>Assisted with 3-day hands-on workshop on using containerized workflows for more reproducible science.</i>	2018, <i>University of Arizona</i>
Software Carpentry Workshop <i>Assisted with Software Carpentry hands-on workshop on basic Unix/Bash, Python, and Git</i>	2017, <i>University of Arizona</i>
Tucson Womens Hackathon workshop on Git <i>Assisted with hands-on workshop on basic Git</i>	2017, <i>University of Arizona</i>
ECOL 320 Genetics <i>Graduate Teaching Assistant</i>	2014 - 2016, <i>University of Arizona</i>
ECOL 182L Intro to Ecology and Evolutionary Biology Lab <i>Graduate Teaching Assistant</i>	2015, <i>University of Arizona</i>
Population Genetics Module <i>Developed and taught a 3-day module on population genetics to high schoolers.</i>	2013, <i>Kino School</i>
BIOL 247 Biometrics <i>Teaching Assistant</i>	2011, <i>Beloit College</i>
RUSS 110, 115, 210, 215 Russian <i>Tutor</i>	2009 - 2011, <i>Beloit College</i>

PUBLICATIONS

- Lauterbur, M. E., Cavassim, M. I. A., **Gladstein, A. L.**, ..., Wong, Y., Baumdicker, F., Cartwright, R. A., Gorjanc, G., Gutenkunst, R. N., Kelleher, J., Kern, A. D. Ragsdale, A. P., Ralph, P. L., Schrider, D. R., Gronau, I. 2023. Expanding the stdpopsim species catalog, and lessons learned for realistic genome simulations *eLife* 12:RP84874. <https://doi.org/10.7554/eLife.84874.3>
- Baumdicker, F.*, Bisschop, G.*, Goldstein, D.*, Gower, G.*, Ragsdale, A. P.*, Tsambos, G.*, Zhu, S.*, ..., **Gladstein, A. L.**, ..., Kelleher, J. 2022. Efficient ancestry and mutation simulation with msprime 1.0. *Genetics*. Volume 220, Issue 3. <https://doi.org/10.1093/genetics/iyab229>
- 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>
- 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>
- 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>

*First author

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.†, et al. A Novel Machine Learning Method for Classification of Village Dogs. Probabilistic Modeling in Genomics. 2023. Cold Spring Harbor, NY.

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

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

PROJECT MANAGEMENT

†Presenter

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

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

STUDY ABROAD

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

OTHER ACTIVITIES

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