

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 PhD in Ecology and Evolutionary Biology Minor in Mathematics	<i>August 2018</i>
Beloit College, Beloit, WI B.S. in Mathematical Biology & Russian, Cum Laude Departmental Honors: Mathematical Biology	<i>May 2011</i>

EXPERIENCE

Open Source Contributor <i>Tskit community</i> Contributed to writing documentation and tutorials for the population genomics tskit ecosystem.	2024 <i>Remote</i>
Research Scientist, Computational Biology <i>Ancestry team</i> 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.	2021 - 2024 <i>Embark Veterinary, Remote</i>
Postdoctoral Fellowship <i>Schrider Lab</i> Project: Inference of demographic history with deep learning	2018 - 2020 <i>Department of Genetics, University of North Carolina, Chapel Hill</i>
Dissertation Research <i>Hammer Lab</i> Dissertation: Inference of recent demographic history of population isolates using genome-wide high density SNP arrays and whole genome sequences	2011 - 2018 <i>Ecology and Evolutionary Biology, University of Arizona</i>
Functional Genomics Research Rotation <i>Restifo Lab</i>	Spring 2012 <i>Neuroscience, University of Arizona</i>
Computational Genomics Research Rotation <i>Kececioglu Lab</i>	Fall 2011 <i>Computer Science, University of Arizona</i>
Lab technician intern <i>Laboratory of Population Genetics</i>	Sp, Fall 2009 <i>Russian Academy of Medical Sciences, Moscow, Russia</i>

SKILLS

Programming	Python, R, Bash, (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, Pandas, Scikit-learn, SciPy, Keras, Matplotlib, Seaborn, Plotly, ggplot
Reproducibility	Workflow development (Pegasus, Makeflow, Snakemake), containers (Singularity, Docker), virtual environments, Jupyter, Knitr
Documentation	L ^A T _E X, Markdown, reStructuredText
Mathematical Skills	Probability theory, statistical inference, linear algebra
Language Skills	English (native speaker), Russian (fluent)

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>

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.[†], 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.

*First author

[†]Presenter

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
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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

Introduction to stdpopsim workshop, Virtual	2020
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

Biology Department

Fall 2009

Moscow, Russia

Russian State University for the Humanities

Russian Studies

Spring 2009

Moscow, Russia

OTHER ACTIVITIES

Circus Arts

Aerial silks, aerial rope, lyra, flying trapeze, tightwire, handbalancing, contortion

2012 - present

Figure Skating

Singles freestyle

1998 - 2013