ARIELLA GLADSTEIN, PhD

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`https://ariella-gladstein.netlify.app` ⋄ `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

Open Source Contributor 2024
Tskit community *Remote*
Contirbuted to writing documentation and tutorials for the population genomics tskit ecosytem.

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.

Postdoctoral Fellowship 2018 - 2020
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, 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	LaTeX, 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. 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.

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*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*

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	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