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

Open Source Contributor 2024 - present
Tskit community *Remote*
Contirbuted to writing and reviewing 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. 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	LaTeX, 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   2020, *Virtual, PopSim Consortium*
Designed and presented interactive workshop on using stdpopsim, the standard library for reproducible, bug-free simulations of genetic datasets from published demographic histories.

NSF Cyber Carpentry Workshop   2019, *University of North Carolina, Chapel Hill*
Assisted with 2-week workshop, where participants learned best practices for data-intensive computing, cloud infrastructure, and deep learning through hands-on projects.

Research Bazaar Workshop on R   2018, *University of Arizona*
Assisted with hands-on intro R workshop

CyVerse Container Camp   2018, *University of Arizona*
Assisted with 3-day hands-on workshop on using containerized workflows for more reproducible science.

Software Carpentry Workshop   2017, *University of Arizona*
Assisted with Software Carpentry hands-on workshop on basic Unix/Bash, Python, and Git

Tucson Womens Hackathon workshop on Git   2017, *University of Arizona*
Assisted with hands-on workshop on basic Git

ECOL 320 Genetics   2014 - 2016, *University of Arizona*
Graduate Teaching Assistant

ECOL 182L Intro to Ecology and Evolutionary Biology Lab   2015, *University of Arizona*
Graduate Teaching Assistant

Population Genetics Module   2013, *Kino School*
Developed and taught a 3-day module on population genetics to high schoolers.

BIOL 247 Biometrics   2011, *Beloit College*
Teaching Assistant

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

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`

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*First author

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.

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*

[†]Presenter

PROJECT MANAGEMENT

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

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
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