

ARIELLA GLADSTEIN, PhD

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<https://ariella-gladstein.netlify.app> ◊ <https://github.com/agladstein> ◊ www.linkedin.com/in/ariella-gladstein

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

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

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, utilizing high-throughput computing for simulations and high-performance GPUs, as well as a Kubernetes cluster, for model training. 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, utilizing over 11 million CPU hours in under six months to run large-scale simulations on the Open Science Grid and multiple HPC systems with a high-throughput workflow.

SKILLS

Programming

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

HPC/HTC & Cloud

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

Reproducibility

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

Genomics

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

Data Science

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

Documentation

L^AT_EX, Markdown, reStructuredText, JupyterBook, Confluence

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 <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>
BIOL 247 Biometrics <i>Teaching Assistant</i>	2011, <i>Beloit College</i>

AWARDS

XSEDE Research allocation (250,000 CPU hrs)	2020
XSEDE Supplemental allocation (250,000 CPU hrs)	2018, 2020
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
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

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 and Machine Learning, Tucson, AZ (2 days)	02/2018
Open Science Grid User School, Madison, WI (1 week)	07/2017

SELECT PUBLICATIONS, POSTERS, & TALKS

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- Gladstein A.L.***, et al. A Novel Machine Learning Method for Classification of Village Dogs. Probabilistic Modeling in Genomics. 2023. Cold Spring Harbor, NY. (Poster)
- Baumdicker, F.*, Bisschop, G.*, Goldstein, D.*, Gower, G.*, Ragsdale, A. P.*, Tsambos, G.*, Zhu, S.*, ..., **Gladstein, A. L.**, et al. 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.*, et al. 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.†**, Schrider R.D. Demographic model selection with deep learning. Probabilistic Modeling in Genomics. 2019. Aussois, France. (Poster)
- 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>
- Inference of evolutionary history with Approximate Bayesian Computation. Open Science Grid All-Hands Meeting. 2018. Salt Lake City, Utah. (Talk)
- Code optimization for research scientists. Research Bazaar. 2018. Tucson, AZ. (Talk)
- 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>

*Presenter

†First author