

Aaron J. Stern

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EDUCATION	Ph.D. Computational Biology	August 2015 - December 2020
	<i>UC Berkeley</i>	Advisor: Prof. Rasmus Nielsen
	My research has focused on using applied probability and statistics to analyze large-scale genomic datasets (e.g., DNA sequence variation, genome-wide association studies (aka GWAS), gene expression analyses) and draw insights on human evolution and complex traits. My projects/skills include:	
	<ul style="list-style-type: none">• Detecting natural selection using importance sampling of genealogies• Quantifying and disentangling selection on pleiotropically-related complex traits• Distinguishing genetic vs. environmental sources of complex trait differentiation• Modeling the impact of selection on functional variation on genetic epidemiological methods (e.g. GWAS, LD score regression)• Fine-mapping expression QTLs for FADS genes and fat metabolism	
	B.Sc. Engineering	2011 - 2015
	<i>Northwestern University</i>	
WORK EXPERIENCE	<i>Bioinformatics Scientist 2</i>	Feb 2021 - present
	GRAIL, Menlo Park, CA	
	Developing precision methods to detect residual disease in cancer patients.	
	<i>Computational Biology Fellow</i>	June 2017 - Sept 2017, March 2018 - July 2018
	AncestryDNA, San Francisco, CA	
	Developed methods and visualization tools to explore the recent demographic history of fine-scale human communities. I also worked on statistical methods for relationship and pedigree inference (Patent Pending #62/951,646).	
	<i>Research Intern</i>	Sept 2014 - June 2015
	Amaral Lab, Northwestern University	
	I developed statistical tools to model genetic variation in bacterial protein translation. I applied these methods to show a novel correlation between SD usage and species growth rate and doubling time.	
	<i>Research & Development Intern</i>	June 2014 - November 2014
	BigDataBio, LLC, Cambridge, MA	
	Deployed and wrote documentation for a visualization software pipeline to take .VCF and visualize the samples variants and their implications in disease.	
TEACHING EXPERIENCE	IB 249 <i>Statistical Genetics of Complex Traits</i>	Fall 2020
	UC Berkeley, Berkeley, CA	
	<ul style="list-style-type: none">• Co-authored syllabus and co-organized the course	

- Led discussion sections and held office hours. The course, taught by Adam Lucas, surveys the theory and practice (using R) of applied statistics, aimed at an audience of junior/senior statistics majors.
- Received Outstanding Graduate Student Instructor award (awarded to ~9% of GSIs)

Instructor, Python Bootcamp
Center for Computational Biology, UC Berkeley

2018, 2019, 2021

SKILLS

Programming languages: Proficient in Python (Pandas, NumPy, SciPy), UNIX, L^AT_EX; familiar with R, C/C++

Statistical/population genetics tools: Experienced with

- PLINK (association mapping/GWAS, population structure, data QC)
- h^2 estimation (LDSC, S-LDSC, SLDP)
- Fine-mapping (SuSIE)
- Population genetic simulators (e.g., ms, msprime, SLiM)
- Genealogy inference (Relate, ARGweaver)
- Demographic inference (e.g., IBDNe, fastSimCoal2)

Data: Experienced wrangling & producing insights from large-scale multi-omic data (e.g. 1000 Genomes, UK Biobank, GTEx, AncestryDNA genotypes & genealogies/pedigrees)

Selected courses: Statistical Learning Theory, Applied Probability, Applied Statistics, Theoretical Statistics, Information Theory, Real Analysis, Parallel Programming, Protein Structure & Function, Computational Biology, Population Genetics, Statistical Genetics of Complex Traits

PUBLICATIONS **Stern AJ**, Speidel L, Zaitlen NA, Nielsen R, “Disentangling selection on genetically-correlated complex traits using whole-genome genealogies”, *Am. J. Hum. Gen* (2020).

Stern AJ, Wilton PR, Nielsen R, “An approximate full-likelihood method for inferring selection and allele frequency trajectories using DNA sequence data”, *PLOS Genetics* (2019).

Stern AJ, Nielsen R, “Detecting Natural Selection,” *Handbook of Statistical Genetics, 4th Edition*, John Wiley & Sons (2019).

Prohaska A, Racimo F, Schork AJ, Sikora M, **Stern AJ***, Ilardo M*, *et al.*, “Human Disease Variation in Light of Population Genomics,” *Cell Reviews* (2019).

Corl A, Bi K, Luke C, Challa AS, **Stern AJ**, Sinervo B, Nielsen R, “Genetic change follows plasticity for cryptic coloration in a novel environment”, *Current Biology* (2018).

Ilardo M, Moltke I, Korneliussen T, Cheng J, **Stern AJ**, *et al.*, “Physiological and genetic adaptations to diving in Sea Nomads”, *Cell* (2018)

Hockenberry AJ, **Stern AJ**, Amaral LAN, Jewett M, “Bacterial growth rate demands shape variation,” *Molecular Biology & Evolution* (2017).

Gong B*, **Stern AJ***, Wang Y*, Zhou Y*, “Review of Statistical Analysis of Numerical Preclinical Radiobiological Data”, *ScienceOpen Research* (2016).

**PREPRINTS/
MANUSCRIPTS** **Zhang Y*,[‡], Stern AJ***, Nielsen R, “Evolution of local adaptations under genetic rescue is determined by polygenicity and mutational load”, *bioRxiv* (2020).

Cheng JY, **Stern AJ**, Racimo F, Nielsen R, “Ohana: detecting selection in multiple populations by modelling ancestral admixture components”, under review at *Molecular Biology & Evolution* (2019).

* indicates equal contribution

[‡] indicates mentored student

**PLATFORM
TALKS** “Disentangling selection on genetically-correlated complex traits using whole-genome genealogies,” American Society of Human Genetics (ASHG), October 29, 2020.
“Disentangling selection on genetically-correlated complex traits using whole-genome genealogies,” The Allied Genetics Conference (TAGC), April 27, 2020.
“An approximate full-likelihood method for detecting selection using ancestral recombination graphs,” Bay Area Population Genetics, November 4, 2017.
“An approximate full-likelihood method for detecting selection using ancestral recombination graphs” American Society of Human Genetics, October 19, 2017.

POSTERS **Rauchman C[‡], Stern AJ***, Nielsen R, “Selection biases LD-based heritability estimation,” Bay Area Population Genetics, November 9, 2019.
Stern AJ, Speidel L, Zaitlen NA, Nielsen R, “Disentangling selection on genetically-correlated traits using population genomic data,” American Society of Human Genetics, October 16, 2019.
Rauchman C[‡], Stern AJ*, Nielsen R, “Selection biases LD-based heritability estimation,” American Society of Human Genetics, October 16, 2019.
Song S, **Stern AJ**, *et al*, “Studying global variation of gene flow using geo-referenced genetic data,” American Society of Human Genetics, October 19, 2017.
Stern AJ, Nielsen R, “An approximate full-likelihood method for detecting selection using ancestral recombination graphs,” Society of Molecular Biology and Evolution, 2017.
Stern AJ, Hockenberry AJ, Amaral LAN, Rationally defining Shine-Dalgarno motifs in bacteria, Center for Computational Biology Retreat, November 21, 2015.

PATENTS Song S, Pei J, **Stern AJ**, Curtis RE, “Estimating family trees from DNA”, Patent Pending #62/951,646.

**GRANT-
WRITING** R01GM138634, “Enabling Precision Genomics Using Adaptive Variation”, Nielsen R & Hockemeyer D (2020),
• Co-authored Aims 1 & 2 and produced key preliminary results applying CLUES (Stern, *et al.* 2019) towards fine-mapping.

AWARDS Epstein Award Semi-Finalist, American Society of Human Genetics (\$750) 2020
Outstanding Graduate Student Instructor, Dept. of Statistics 2018
Center for Computational Biology Student Travel Grant (\$1630) 2017

**REFEREEING/
REVIEWING**

I have reviewed for the following journals:

- Genetics
- G3: Genes — Genomes — Genetics
- Evolution Letters
- Molecular Biology & Evolution

MENTORSHIP

- Zaid Ahmad (2020 – present) — undergrad at UC Berkeley in Math & Statistics. **Project:** *Inferring natural selection using ancient DNA.*
- Yulin Zhang (2019 – present) — undergrad at Sun Yat-sen University (Guangzhou, China) in Biology → incoming PhD student in Computational Biology at UC Berkeley. **Project:** *Evolution of local adaptations under genetic rescue is determined by polygenicity and mutational load.*
- Courtney Rauchman (2018 – present) — undergrad at UC Berkeley in Data Science & Genomics → data scientist at Amgen. She received a \$5,000 SURF award for our research. **Project:** *Confounding of LD score regression due to linked selection.*

SERVICE

Bay Area Population Genetics Meeting (Fall 2019)

Lead organizer

Bay Area Scientists in Schools (BASIS)

Sept 2015 - 2018

Team Leader

STEM enrichment for elementary school students in local Title I schools. I design and lead interactive scientific demonstrations relating to natural selection and speciation

Be A Scientist

Sept 2015 - 2017

Volunteer

STEM mentorship for 7th-graders in a local Title I public school. I guide a small group of students in designing, deploying, and interpreting their own scientific experiments