

# Aaron J. Stern

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- EDUCATION**
- Ph.D. Computational Biology** August 2015 - May 2021 (expected)  
*UC Berkeley*  
*Topic:* I am interested in theoretical population and statistical genetics, with a focus on modeling how natural selection shapes the genetic architecture of complex traits. Representative projects include:
- Estimating selection and allele frequency trajectories using ancestral recombination graphs (ARGs)
  - Quantifying and disentangling selection on genetically-correlated complex traits
  - Modeling genetic vs. environmental contributions to stratification in GWAS
- Advised by Prof. Rasmus Nielsen, Depts. of Statistics & Integrative Biology.  
Dissertation committee: Rasmus Nielsen, Yun Song, Priya Moorjani, Noah Zaitlen
- B.Sc. Engineering** 2011 - 2015  
*Northwestern University*  
Advised by Prof. Luis Amaral, Dept. of Chemical & Biological Engineering
- PREPRINTS/ MANUSCRIPTS**
- Stern AJ**, Speidel L, Zaitlen NA, Nielsen R, “Disentangling selection on genetically-correlated complex traits using whole-genome genealogies”, *bioRxiv* (2020), \*under review at\* Am. J. Hum. Gen.
- Zhang Y<sup>\*,‡</sup>**, **Stern AJ<sup>\*</sup>**, Nielsen R, “Evolution of local adaptations under genetic rescue is determined by polygenicity and mutational load”, in preparation.
- 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).
- PUBLICATIONS**
- 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<sup>\*</sup>**, Ilardo M<sup>\*</sup>, *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).

\* 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<sup>‡</sup>**, **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<sup>‡</sup>**, **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

Deans Scholar, School of Engineering, Northwestern University 2011 - 2015

## TEACHING EXPERIENCE

IB 249 *Statistical Genetics of Complex Traits* Fall 2020

UC Berkeley, Berkeley, CA

- Co-authored syllabus and co-organized the course

Stat 135 *Concepts of Statistics*  
UC Berkeley, Berkeley, CA

Fall 2018

- 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

## WORK EXPERIENCE

*Computational Biology Fellow* 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.

*Research Intern*  
Amaral Lab, Northwestern University

Sept 2014 - June 2015

I studied variation in the Shine-Dalgarno (SD) sequence, a short translational motif widespread in bacteria yet uncharacterized for all but a small number of species. I developed statistical methods for quantifying SD usage. I applied these methods to show a novel correlation between SD usage and species growth rate and doubling time.

*Research & Development Intern*  
BigDataBio, LLC, Cambridge, MA

June 2014 - November 2014

Deployed and wrote documentation for a visualization software pipeline to take .VCF and visualize the samples variants and their implications in disease.

## REFEREEING/ REVIEWING

I have reviewed for the following journals:

- Genetics
- G3: Genes — Genomes — Genetics
- Evolution Letters

## SKILLS

*Programming languages:* Python, UNIX, L<sup>A</sup>T<sub>E</sub>X

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

## 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 sci-entific 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

UC Berkeley Center for Computational Biology

Sept 2015 - present

*Volunteer*

- Organized guest faculty speaker series (2016-17) with equal gender representation
- Organized student research symposium (2016)
- Organized student research lunchtime seminars (2017-18)
- Volunteered for Berkeley Connect (career & mentorship group) as panelist and industry visit chaperone