

# Aaron J. Stern

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|------------------------|--|
| EDUCATION              | <b>Ph.D. Computational Biology</b> 2015 - present<br><i>UC Berkeley</i><br><i>Topic:</i> 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: <ul style="list-style-type: none"><li>• Estimating selection and allele frequency trajectories using ancestral recombination graphs (ARGs)</li><li>• Quantifying and disentangling selection on genetically-correlated complex traits</li><li>• Modeling genetic vs. environmental contributions to stratification in GWAS</li></ul><br>Advised by Prof. Rasmus Nielsen, Depts. of Statistics & Integrative Biology.<br>Dissertation committee: Rasmus Nielsen, Yun Song, Priya Moorjani, Noah Zaitlen |
|                        | <b>B.Sc. Engineering</b> 2011 - 2015<br><i>Northwestern University</i><br>Advised by Prof. Luis Amaral, Dept. of Chemical & Biological Engineering   |
| TEACHING<br>EXPERIENCE | Stat 135 <i>Concepts of Statistics</i> Fall 2018<br>UC Berkeley, Berkeley, CA<br><br>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.<br><br>Received Outstanding Graduate Student Instructor award (awarded to ~9% of GSIs)   |
|                        | <i>Instructor</i> , Python Bootcamp 2018 - 2019<br>Center for Computational Biology, UC Berkeley   |
| WORK<br>EXPERIENCE     | <i>Computational Biology Fellow</i> June 2017 - Sept 2017, March 2018 - July 2018<br>AncestryDNA, San Francisco, CA<br>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.  |
|                        | <i>Research Intern</i> Sept 2014 - June 2015<br>Amaral Lab, Northwestern University<br>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.

## 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

Yulin Zhang (2019 – present) — senior at Sun Yat-sen University in Guangzhou, China. **Project:** *Evolution of local adaptations under genetic rescue is determined by polygenicity and mutational load.*

Courtney Rauchman (2018 – present) — is in her fourth year of undergraduate studies at UC Berkeley, majoring in Data Science. 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

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

## PREPRINTS/ MANUSCRIPTS

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

**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 (in press).

Prohaska A<sup>†</sup>, Racimo F<sup>†</sup>, Schork AJ<sup>†</sup>, 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).

\* indicates equal contribution

‡ indicates mentored student

## INVITED TALKS

“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.

## ABSTRACTS

**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.

## AWARDS

Charles J. 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