

# Aaron J. Stern

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EDUCATION	<b>Ph.D. Computational Biology</b> 2015 - present <i>UC Berkeley</i> <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> <i>Advised by Prof. Rasmus Nielsen, Depts. of Statistics &amp; Integrative Biology.</i> <i>Dissertation committee: Rasmus Nielsen, Yun Song, Priya Moorjani, Noah Zaitlen</i>
	<b>B.Sc. Engineering</b> 2011 - 2015 <i>Northwestern University</i> <i>Advised by Prof. Luis Amaral, Dept. of Chemical &amp; Biological Engineering</i>
TEACHING EXPERIENCE	Stat 135 <i>Concepts of Statistics</i> Fall 2018 UC Berkeley, Berkeley, CA  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)
	<i>Instructor, Python Bootcamp</i> 2018 - 2019 Center for Computational Biology, UC Berkeley
WORK EXPERIENCE	<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.
	<i>Research Intern</i> Sept 2014 - June 2015 Amaral Lab, Northwestern University 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

Outstanding Graduate Student Instructor, Dept. of Statistics

2018

Center for Computational Biology Student Travel Grant (\$1630)  
Deans Scholar, School of Engineering, Northwestern University

2017  
2011 - 2015