

## Aaron J. Stern

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<b>EDUCATION</b>	<b>Ph.D. Computational Biology</b> 2015 - present <i>UC Berkeley</i> Advised by Prof. Rasmus Nielsen, Depts. of Statistics & Integrative Biology. Dissertation committee: Rasmus Nielsen, Yun S. Song, Priya Moorjani, Ian J. Wang
	<b>B.Sc. Engineering</b> 2011 - 2015 <i>Northwestern University</i> Advised by Prof. Luis Amaral, Dept. of Chemical & Biological Engineering
<b>TEACHING EXPERIENCE</b>	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)
	<b>WORK EXPERIENCE</b>  <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.  <i>Research &amp; 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.
<b>SKILLS</b>	<i>Programming languages:</i> Python, UNIX, L <sup>A</sup> T <sub>E</sub> X <i>Selected courses:</i> Statistical Learning Theory, Applied Probability, Applied Statistics, Theoretical Statistics, Targeted Learning, Information Theory, Real Analysis, Parallel Programming, Protein Structure & Function, Population Genetics
<b>COMMUNITY SERVICE</b>	Bay Area Scientists in Schools (BASIS) Sept 2015 - present <i>Team Leader</i>

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 - present  
*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

Summerbridge SF 2008 - 2011  
*Volunteer tutor*

Mentored and tutored lower-income middle school students in mathematics through a tuition-free academic enrichment program.

**PUBLICATIONS** Stern AJ, Nielsen R, “An approximate full-likelihood method for inferring selection and allele frequency trajectories using DNA sequence data”, submitted to *PLOS Genetics*.

Stern AJ, Nielsen R, “Detecting Natural Selection,” *Handbook of Statistical Genetics, 4th Edition*, John Wiley & Sons 2018 (in press).

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

## INVITED TALKS

Stern AJ, Nielsen R, “An approximate full-likelihood method for detecting selection using ancestral recombination graphs,” Bay Area Population Genetics, November 4, 2017.

Stern AJ, Nielsen R, “An approximate full-likelihood method for detecting selection using ancestral recombination graphs” American Society of Human Genetics, October 19, 2017.

## ABSTRACTS

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)	2017
Deans Scholar, School of Engineering, Northwestern University	2011 - 2015