

# Kristin M. Lee

New York, NY

☎ (414) 630 - 5594

✉ [kmlee90@gmail.com](mailto:kmlee90@gmail.com)

in LinkedIn: [kristinmleeph](#)

GitHub: [kristinmlee](#)

## Professional Experience

- 2018–present **Postdoctoral researcher**, *Columbia University*.
- Analyzing large genomic datasets across many species to study the evolution of color vision.
- 2013–2018 **Graduate student researcher**, *University of California, Davis*.
- Developed novel statistical models to understand population genetic and genomic data.
  - Built publicly-available statistical inference pipelines in R.
  - Collaborated with other researchers, across disciplines and universities, to analyze and explore their data.
  - Presented at invited international conferences and seminars; received recognition for best student talks.
- 2017–2018 **R programming instructor**, *STEMinist Data Science Bootcamp, UC Berkeley and UC Davis*.
- Co-created and taught multiple, intensive R programming workshops for undergraduate and graduate students.
  - Designed lecture material and hands-on exercises including final-day challenge projects at multiple skill levels.

## Education

- 2013–2018 **University of California, Davis**, *Population Biology*, PhD.
- Dissertation title: Detecting signatures of convergent adaptation in population genomic data
- 2008–2013 **University of Wisconsin – Madison**, *Biology and Mathematics*, BS.

## Selected Projects

### DMC **Distinguishing Modes of Convergence**.

- Created a model-based, composite likelihood approach to detect signals of convergent adaptation and discern between the processes that generate this pattern in population genetic data.
- Wrote a highly-flexible statistical inference pipeline in R used by other scientists in the field.
- Simulated data to test robustness of methods and perform parametric bootstrapping for model comparison and obtain confidence intervals for parameter estimation.
- Published work in GENETICS, where it was showcased as one of the best articles published in 2017.

### MyAdIDAS **DMC Modified for Young Adaptive Introgression Distinguished from Allele Standing**.

- Collaborated with other researchers to extend my inference framework for their data scenario.
- Published work in Science, a top academic journal selective for cutting-edge research.

### runDMC **Genome-wide scan version of DMC**.

- Extended and modified previous framework to efficiently run on large, multi-population genomic datasets.
- Created visualization to easily recognize important patterns on this large scale.

## Leadership

- 2019–present **Career Development Subcommittee member**, *Genetics Society of America (GSA)*.
- Developing content for early-career scientists by building relationships with professionals across sectors.
- 2016–2018 **After School Coding Club instructor**, *Martin Luther King Jr. K-8, Sacramento, CA*.
- Taught weekly coding activities to middle schoolers to teach fundamentals and generate excitement for STEM.

## Relevant Courses

- Statistics Probability Theory, Statistical Computing, Statistical Methods for Bioscience I and II, Statistical Rethinking: A Bayesian Course with Examples in R and Stan, Stochastic Methods
- Comp. Sci. Introduction to Programming, Introduction to Data Structures, Introduction to Bioinformatics

## Technical Skills: R, SQL, Java, MATLAB, LaTeX

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## Awards

- 2014 – 2018 **Graduate Research Fellowship**, *National Science Foundation*, (\$150,000).
- 2016 **Fitch Award Finalist**, *Society for Molecular Biology and Evolution*, (\$2,000).
- 2016 **Hamilton Award Finalist**, *Society for the Study of Evolution*, (\$500).
- 2013 **Population Biology Graduate Group Fellowship**, *UC Davis*, (\$30,000).
- 2013 **Hilldale Undergraduate Research Fellowship**, *UW Madison*, (\$4,000).
- 2012 **Zoology Undergraduate Research Grant**, *UW Madison*, (\$1,500).

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## Publications

1. **Lee KM**, Coop G, 2019. Population genomics perspectives on convergence. *Philosophical Transactions B* (in press; out June 11, 2019). [Link to preprint on bioRxiv](#).
2. Oziolor EM, Reid NM, Yair S, **Lee KM**, VerPloeg S, Bruns PC, Shaw JR, Whitehead A, Matson CW, 2019. Adaptive introgression enables evolutionary rescue from extreme environmental pollution. *Science*, 364(6439), 455-457. [Link](#).
3. **Lee KM**, Coop G, 2017. Distinguishing among modes of convergent adaptation using population genomic data. *GENETICS*, 207: 1591-1619. [Link](#).
4. Lee CE, Remfert JL, Opgenorth T, **Lee KM**, Stanford E, Connolly JW, Kim J, Tomke S, 2017. Evolutionary responses to crude oil from the Deepwater Horizon oil spill by the copepod *Eurytemora affinis*. *Evolutionary Applications*, 10: 813-828. [Link](#).

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## Presentations

### Invited Seminars

- 2018 Temple University Institute for Genomics and Evolutionary Medicine, *Philadelphia, PA*.
- 2018 Stanford University Center for Computational, Evolutionary and Human Genomics, *Palo Alto, CA*.
- 2017 Duke University Population Biology, *Durham, NC*.
- 2016 UC Berkeley Center for Theoretical Evolutionary Genomics, *Berkeley, CA*.

### Invited Conference Oral Presentations

- 2017 Society of Systematic Biologists (Evolution meeting), *Portland, OR*.
- 2016 Society for the Molecular Biology and Evolution, *Gold Coast, Queensland, Australia*.
- 2016 Society for Study of Evolution (Evolution meeting), *Austin, TX*.

### Contributed Conference Oral Presentations and Seminars

- 2018 Columbia University Evolution Supergroup, *New York, NY*.
- 2018 Genetics Society of America (Population, Evolutionary and Quantitative Genetics), *Madison, WI*.
- 2017 Society for the Molecular Biology and Evolution, *Austin, TX*.
- 2016 Bay Area Population Genomics, *Berkeley, CA*.
- 2015 UC Davis Center for Population Biology, *Davis, CA*.
- 2015 Society for the Molecular Biology and Evolution, *Vienna, Austria*.
- 2013 UW-Madison Undergraduate Research Symposium, *Madison, WI*.