

JAZLYN MOONEY

University of California, Los Angeles
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EDUCATION

University of California Los Angeles
Ph.D. in Genetics and Genomics
Advisor: Kirk Lohmueller

2015-June 2020 (Expected)

University of New Mexico
BS with Honors Anthropology and Biology (Summa Cum Laude)
Honors Thesis: "Inferring Evolutionary History from Ancestry Informative Markers (AIMs)"
Advisor: Jeffrey Long

2010-2014

RESEARCH INTERESTS

I am interested in using bioinformatics to analyze next-generation sequence data to study patterns of human genetic diversity across the world. Additionally, I am interested in exploring how we can implement population genetics to better understand the evolutionary origins of disease in human populations.

RESEARCH EXPERIENCE

DNA Science Intern at Ancestry.com
Mentor: David Turissini

June 2019-August 2019

DNA Science summer intern with the Population Genetics team at Ancestry.com in San Francisco.
Project title: Generating Hierarchical Population Labels Informed by Genetics

University of California Los Angeles Genetics and Genomics Department
Advisor: Kirk Lohmueller

2015-Present

1. My first project focused on determining the impact of recent demography on genetic diversity in admixed population isolates. I analyzed whole genome sequence data from Costa Rican and Colombian isolates and compared them to the Finnish population. Additionally, I determined the amount of genetic diversity in each group by using population-genetic summary statistics, tested mechanisms that generate long runs of homozygosity, and analyzed the distribution of deleterious variation in the genome. Finally, I explored the relationship between pedigree inbreeding coefficients, ancestry, long runs of homozygosity, and fitness.
2. My second project is focused on conservation genomics and testing the impact of long-term small effective population size in Ethiopian Wolves. I inferred the demographic history of Ethiopian Wolves using approximate Bayesian computation. I surveyed genetic diversity in the Ethiopian Wolf relative to other wolves and breed dogs. Lastly, I have run a selection scan to determine whether there are genes under positive selection to aid adaptation to high altitude.
3. My third project involved using dogs as a model organism for examining the link between complex disease and weakly deleterious recessive variants. I did this by associating the burden of long runs of homozygosity and identity-by-descent segments with a number of different phenotypes. I also examined biases in the Online Mendelian Inheritance in Animals database, which contains a list of Mendelian disease causal variants and the breed in which they were discovered. Finally, I tested whether long runs of homozygosity can be used to detect inbreeding depression in a population.

University of New Mexico Evolutionary Anthropology Department**2012-2014****Undergraduate Research Assistant****Advisor: Jeffrey Long**

My research was focused on both data processing and analysis. My data processing projects involved developing and writing a protocol for downloading and working with sequence data from the UCSC Genome Browser. I also made a pipeline to assemble genomes and produce comparative phylogenetic trees as the final output.

For the data analytics portion of my research, I filtered HapMap genome data for target African and Non-African ancestry informative markers, AIMs. I then constructed haplotypes containing the target AIMs and their flanking SNPs. I calculated the homozygosity for each haplotype and used this information to identify potential archaic introgression in Non-African populations.

University of Chicago - Pritzker School of Medicine Experience in Research (PSOMER)**2013****Undergraduate Research Assistant****Advisor: Michael Maitland**

My research project focused on using genetic haplotypes to explore patient reactivity to Sunitinib and Sorafenib, drugs used to treat advanced cancer. Specifically, I looked in African American males for SNPs that were correlated with improved treatment outcome. I presented my research and poster at an internal conference at the end of the eight weeks.

University of New Mexico - Research in Molecular Biology**2013****Undergraduate Research Assistant****Advisors: Donald Natvig and Coenraad Adema**

This research integrated both benchwork and computational work. First, I processed DNA and RNA sequences from both plants and animals using basic purification techniques that are required for collecting sequence data. These techniques included enzymatic manipulation, hybridization, molecular cloning, primer construction, and gel electrophoresis. After sequencing, I read and analyzed the raw sequence data in Sequencher and sent the novel sequence data to GenBank.

TEACHING EXPERIENCE**University of California Los Angeles****Fall 2019**

Teaching Assistant for Population Genetics

University of California Los Angeles**Fall 2017**

Computational Instructor for Advanced Human Genetics

University of California Los Angeles**Fall 2016**

Teaching Assistant for Genetics Course

SKILLS

Programming Languages: Python, R, C++, MySQL

Operating Systems & General Applications: LINUX/UNIX, MS Windows, MS Office Suite

Computing Clusters & Software: AWS, Slurm, SGE

Bioinformatics Tools (selected): Next generation sequencing analyses (GATK, VCFTools, BCFTools, PLINK, SHAPEIT, Beagle), Phylogenetics (Sequencher, MEGA, FigTree, Geneious, Phylip), Data processing and visualization (tidyverse), Simulation software (ms, SLiM)

AWARDS AND HONORS

Stanford CEHG Fellow (\$13500 stipend & \$1500 travel fees)

2020-2021

SACNAS Scientific/STEM Symposia Session Workshop (Organized session)

2019

UCLA Dissertation Year Fellowship (\$21000 annual stipend & tuition and fees)

2019

Selected as a Platform Session moderator for the American Society of Human Genetics annual meeting

2018

Graduate Programs in Bioscience (GPB) Fellowship Incentive Program/Shine Fellowship (\$3000 annual)

2016-Present

National Science Foundation (NSF) Graduate Research Fellowship (GRFP) (\$34000 annual stipend & \$12000 fees)

2015-Present

Presidential Scholarship at University of New Mexico

2010-2014

New Mexico Lottery Success ABQ Scholarship

2010-2014

Undergrad Minority Scholarship

2013

Honors Award/Anthropology Scholarship

2013

Miscellaneous Scholarships

2012

Enterprise Rent-a-Car Diversity Scholarship

2011

Dean's List at University of New Mexico

2010-2014

CONFERENCES AND PRESENTATIONS

Mooney JA*, Huber CD, Service S, Sul JH, Marsden CD, Zhang Z, et al. Understanding the hidden complexity of Latin American population isolates.

2017 American Society of Human Genetics (ASHG) **Poster**

2018 American Society of Human Genetics (ASHG) **Poster** (Reviewer's Choice Abstract)

2018 Bay Area Population Genomics (BAPG) **Talk**

2018 Population Evolutionary and Quantitative Genomics (PEQG) **Poster**

2018 Informatics Center for Neurogenetics and Neurogenomics (ICNN) Symposium **Talk**

2018 UCLA Quantitative and Computational Biology Retreat **Talk**

2018 UCLA Human Genetics Retreat (Leena Peltonen Award Finalist) **Talk**

Mooney JA*, Yohannes A, Lohmueller KE. The impact of identity-by-descent on fitness and disease in domesticated and natural *Canid* populations. (*in preparation*)

2019 UCLA Human Genetics Retreat (Leena Peltonen Award Finalist) **Talk**

2020 Society for Molecular Biology and Evolution (SMBE) **Talk**

PUBLICATIONS

Mooney JA, Huber CD, Service S, Sul JH, Marsden CD, Zhang Z, et al. Understanding the hidden complexity of Latin American population isolates. *Am J Hum Genet.* 2018;103(5):707–26. <https://doi.org/10.1016/j.ajhg.2018.09.013>.

Mooney JA, Marsden CD, Randall DA, Yohannes A, Wayne RK, Lohmueller KE. Inferring the demographic history and examining genetic diversity in a critically endangered canid: the Ethiopian wolf. (*in preparation*)

Mooney JA, Yohannes A, Lohmueller KE. The impact of identity-by-descent on fitness and disease in domesticated and natural *Canid* populations. (*in preparation*)

EXPERIENCE AND PROFESSIONAL ACTIVITIES

Student Advisory Committee Member for Graduate Programs in Bioscience (GPB) at UCLA

2018-Present

Organizing Committee, UCLA QCBio Annual Career Panel and Networking Event

2017

SACNAS Member at UCLA

2015-2017

Member of the Association for Multi-Ethnic Bioscientists' Advancement at UCLA

2015-Present

Founder and Chair of the Association for Multi-Ethnic Bioscientists' Advancement at UCLA

2015-2018

Primate Enrichment at Rio Grande Zoo in New Mexico

2010-2015