

JAZLYN MOONEY

University of Southern California
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APPOINTMENTS

University of Southern California
Gabilan Assistant Professor in Quantitative and Computational Biology **2022-Present**

EDUCATION

Stanford University of California
Postdoc in Biology **2020- January 2022**
 Advisor: Noah Rosenberg

University of California Los Angeles
Ph.D. in Genetics and Genomics **2015-September 2020**
 Advisor: Kirk Lohmueller

University of New Mexico
BS with Honors Anthropology and Biology (Summa Cum Laude) **2010-May 2014**
 Honors Thesis: "Inferring Evolutionary History from Ancestry Informative Markers (AIMs)"
 Advisor: Jeffrey Long

AWARDS AND HONORS

USC Women in Science and Engineering Gabilan Assistant Professorship **2022**
 UCLA Human Genetics Leena Peltonen Award winner **2019**
 Platform Session moderator for the American Society of Human Genetics annual meeting **2018**
 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**
 Enterprise Rent-a-Car Diversity Scholarship **2011**
 Dean's List at University of New Mexico **2010-2014**

TEACHING EXPERIENCE

University of Southern California **Spring 2024-**
 Instructor for QBIO115g Ethics in Biology, Medicine, and Statistics
University of Southern California **Spring 2023**
 Co-Instructor for QBIO105 Introduction to Quantitative Biology Seminar
University of Southern California **Fall 2022-**
 Co-Instructor for QBIO475 Statistical and Evolutionary Genetics
San Francisco State University **Fall 2020**
 Instructor for BIOL 870 Biology Colloquium
University of California Los Angeles **Fall 2020**
 Co-instructor for HUMGEN 19: How Genetics has Contributed to Racial Injustice in America and the World
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 Genetics

ADDITIONAL LECTURES

"Introduction to Eugenics role in Genetics", FALL 2022, PM 534 Statistical Genetics, Prof. Charleston Chiang, University of Southern California
 "History of Heredity", SPRING 2022, BIOS 232 Introduction to Genetics, Ethics, and Society, Profs. Roshni Patel and Rachel Ungar, Stanford University
 "Introduction to Eugenics role in Genetics", FALL 2023, PM 534 Statistical Genetics, Prof. Charleston Chiang, University of Southern California
 "Conservation Genomics in Ethiopian Wolves", SPRING 2023, QBIO 105 Introduction to Quantitative Biology, Profs. Remo Rohs &

Jazlyn Mooney, University of Southern California
 "Conservation Genomics in Ethiopian Wolves", SPRING 2023, BIOL 360 Genetics, Prof. Eduardo Amorim, California State University Northridge
 "Tracing our Genealogical Ancestors", SPRING 2024, BISC 321 Science, Technology, and Society, Prof. Grayson Jagers, University of Southern California
 "Introduction to Eugenics role in Genetics", FALL 2024, PM 534 Statistical Genetics, Profs. Charleston Chiang & Arun Durvasula, University of Southern California

ADDITIONAL TEACHING TRAINING

Stanford University Scientific Teaching Workshop Series for aspiring faculty (2020-2021). Series led by Profs. Kimberly Tanner and Jeff Schinske that focused on scientific pedagogy through research-based strategies for student engagement, assessments, and retention in life science classes.

SERVICE TO THE DEPARTMENT

Member of Graduate Committee Jalen Langie (Epidemiology)	2024
Member of Qualifying Committee Teagan Biatto (MEB)	2024
Co-organizer Center for Ecological and Evolutionary Dynamics (CEED) Seminar Series	2023-
Member of Qualifying Exam and Graduate Committee Bryan Dinh (CBB)	2023-
Member of Qualifying Exam and Graduate Committee Daniel Olivares-Cordero (MEB)	2023-
Member of Qualifying Exam and Graduate Committee Jenna Dilworth (MEB)	2023-
Member of Master's Committee Caroline Solis (CSUN-EEB)	2023
Member of Qualifying Exam and Graduate Committee Joseph Hale (MCB)	2022-
Member of Qualifying Exam and Graduate Committee Ilan Goldstein (MCB)	2022-
Member of Qualifying Exam and Graduate Committee Dallace Francis (CBB)	2022-
Faculty founder of Women and other Minoritized Genders in Computational Biology	2022-
Member of CBB graduate admissions committee	2021-

SERVICE TO THE FIELD

Member of the Genetics Society of America Nominating Committee	2024
Co-organizer SACNAS Scientific/STEM Symposia Session Workshop " <i>Introduction to Data Analysis in R using the Tidyverse</i> "	2022
Co-organizer of SBE 2021 symposium " <i>Population genetics of identity-by-descent and runs of homozygosity: causes, consequences, and utility</i> " with Zachary Szpiech	2021
Co-organizer SACNAS Scientific/STEM Symposia Session Workshop " <i>Beyond Excel: Data Visualization with RStudio to Improve Your Posters, Presentations, and Publications</i> "	2019
Student Advisory Committee Member for Graduate Programs in Bioscience (GPB) at UCLA	2018-2020
Organizing Committee, UCLA QCBio Annual Career Panel and Networking Event	2017
American Society of Human Genetics Member	2015-2023
Member of the Association for Multi-Ethnic Bioscientists' Advancement at UCLA	2015-2020
Founder and Chair of the Association for Multi-Ethnic Bioscientists' Advancement at UCLA	2015-2020
Primate Enrichment at Rio Grande Zoo in New Mexico	2010-2015

INVITED SEMINARS

Seminar for Department of Ecology and Evolution, UCD, Davis, CA	2025
Seminar for Genetics and Genomics Academy, NC State, Raleigh, NC	2025
Seminar for The Center for Behavior Evolution and Culture, UCLA, Los Angeles, CA	2024
Seminar for Precision health and genomics: Indigenous Mentoring and Ethics (PRIME), CU Anschutz, Denver Colorado	2024
Seminar for the Department of Biology, CSUN, Los Angeles, CA	2024
Seminar for Opportunities in Research (MORE), Cal State East LA, Los Angeles, CA	2024
Seminar for the Department of Ecology and Evolutionary Biology, UCI, Irvine, California	2023
Seminar for the Department of Evolution, Ecology, and Organismal Biology, UCR, Riverside, CA	2023
Seminar for the San Diego Wildlife Alliance, Escondido, CA (<i>virtual</i>)	2023
Seminar for the Center of Ecological and Evolutionary Dynamics (CEED), USC, Los Angeles, CA	2023
Seminar for the Natural History Museum Los Angeles County, Los Angeles, CA	2022
Seminar for Introduction to Genetics, Ethics, and Society, Stanford University, Stanford, CA	2022
Seminar for the USC Computational Biology Symposium, USC, Los Angeles, CA	2022
Seminar for the Molecular Biology Interdepartmental Doctoral Program, UCLA, Los Angeles, CA	2022

Seminar for The Center for Theoretical and Evolutionary Genetics, UC Berkeley, Berkeley, CA (virtual)	2022
Seminar for the Department of Ecology and Evolutionary Biology, U of A, Tucson, AZ	2022
Seminar for the Department of Ecology and Evolutionary Biology, MSU, Lansing, MI (virtual)	2022
Seminar for the Department of Biology, SDSU, San Diego, CA	2022
Seminar for Department of Biology, PSU, State College, PA	2021
Seminar for the Department of Genetics, UGA, Athens, GA (virtual)	2021
Seminar for the Department of Quantitative and Computational Biology, USC, Los Angeles, CA	2021
Seminar for the Molecular Biology Interdepartmental Doctoral Program, UCLA, Los Angeles, CA	2021
Seminar for the Department of Biology Colloquium, CSU Dominguez Hills, Carson, CA (virtual)	2021

CONFERENCE PRESENTATIONS

- The Eugenics Movement and Scientific Racism—Past, Present, and Future
2024 TAGC *Invited Panelist*
- Population genetics in Wild and Captive Populations of Conservation Concern: Challenges and Opportunities
2024 Keynote Conservation Genomic Paris
- Considerations for Inferring Demography and Detecting Selection in Understudied Species in the Genomics Era
2024 Keynote Speaker for SMBE 2024 session on New computational approaches to estimate past demographic events and natural selection
- Armstrong EE, **Mooney JA**. Reference Bias Differentially Impacts Estimates of Genetic Load and Diversity: A Case Study in Canidae
2024 Plant and Animal Genomics (PAG) XXXI
2023 California Islands Symposia X
- Armstrong EE, **Mooney JA**, Solari KA, Kim BY, Barsh GS, Grant VB, Greenbaum G, Kaelin CB, Panchenko K, Pickrell JK, Rosenberg N., et al. *Unraveling the Genomic Diversity and Evolutionary History of Captive Tigers in the United States*.
2023 Evolution
- Mooney JA**, Marsden CD, Yohannes A, Wayne RK, Lohmueller KE. *Long-term small population size, deleterious variation, and altitude adaptation in the Ethiopian wolf, a severely endangered canid*.
2023 Plant and Animal Genomics (PAG) XXX *Invited Presentation*
- Mooney JA**, Agranat-Tamir L, Pritchard JK, Rosenberg NA. *On the number of genealogical ancestors tracing to the source groups of an admixed population*.
2022 American Society of Human Genetics (ASHG)
2022 USC Computational Biology Symposium
2022 Computational Genomics Summer Institute (CGSI) Symposium
- Mooney JA**, Yohannes A, Lohmueller KE. *The impact of identity by descent on fitness and disease in dogs*.
2021 Society for Molecular Biology and Evolution (SMBE)
2020 Society for Molecular Biology and Evolution (SMBE)
- Mooney JA**, Huber CD, Service S, Sul JH, Marsden CD, Zhang Z, Sabatti C, Ruiz-Linares A, Bedoya G, Fears SC, Kremeyer B, et al. *Understanding the hidden complexity of Latin American population isolates*.
2018 Bay Area Population Genomics (BAPG)
2018 Informatics Center for Neurogenetics and Neurogenomics (ICNN) Symposium

EDITORIAL ACTIVITIES

Guest Editor for BMC Biology: Conservation genomics collection

INVITED REVIEWER FOR

Science, Proceedings of the National Academy of Sciences, Cell Genomics, American Journal of Human Genetics, American Journal of Biological Anthropology, Molecular Biology and Evolution, Genome Biology and Evolution, PLoS Genetics, Frontiers in Genetics, eLife, Evolution Letters, Evolutionary Applications, Heredity

MANUSCRIPTS IN PREPARATION

Updated 11/25/24

Carey, SB, Sacks, BN, Quinn, N, Harkess, A, Armstrong, EE, **Mooney, JA** (expected submission January 2025). A Coyote Reference Genome.

Senior authors Armstrong and Mooney generated the data for the reference genome. I also conducted phylogenetic analyses of PRDM9.

Akopyan, M, Genchev, M, Armstrong, EE, **Mooney, JA**. Divergent reference genomes compromise the reconstruction of demographic histories, selection scans, and population genetic summary statistics

Corresponding author. I supervised postdoctoral fellow Maria Akopyan and QBIO undergraduate Matthew Genchev. I guided analyses, processed data, developed code, and drafted the manuscript. Submitted Cell.

Sherman, C, **Mooney, JA**, Claw, K (expected submission February 2025). The Lasting Impact of Eugenics on Indigenous Genomics.

Co-corresponding author. Came up with topic and co-wrote the Perspective which will be submitted to Genetics.

PREPRINTS

Amorim, CEG, Di, C, Lin, M, Marsden, C, Del Carpio, CA, Mah, JC, Robinson, JA, Kim, BY, **Mooney, JA**, Cornejo OE, Lohmueller, KE. Evolutionary consequences of domestication on the selective effects of new amino acid changing mutations in canids. [Preprint]. 2024 November 15. DOI: 10.1101/2024.11.13.623529

I generated the data used for major analyses and contributed to writing the manuscript. Under review at PNAS.

Ferrari, T, Feng, S, Zhang, X., **Mooney, JA**. Towards Simulation Optimization: An Examination of the Impact of Scaling on Coalescent and Forward Simulations. [Preprint]. 2024 April 29. DOI: 10.1101/2024.04.27.591463

Co-corresponding author. I supervised QBIO lab trainee Tessa Ferrari, guided analyses, developed code, and drafted the manuscript. In revision at Genome Biology and Evolution.

Sweetalana, **Nataneli, S**, **Huang, S**, **Mooney, JA**, Szpiech, ZA. Genotypic and phenotypic consequences of domestication in dogs. [Preprint]. 2024 May 05. DOI: 10.1101/2024.05.01.592072

Co-corresponding author. I guided analyses, developed code, and drafted the manuscript. In revision at Molecular Ecology.

PEER REVIEWED PUBLICATIONS

Kreger, J, **Mooney, JA**, Shibata, D, MacLean, AL. Developmental hematopoietic stem cell variation explains clonal hematopoiesis later in life. [Preprint]. 2024 March 05. DOI: 10.1101/2024.03.02.583106

I helped guide analyses, drafted the manuscript, and helped with revision. Accepted at Nature Communications.

Armstrong EE, **Li, C**, Campana, MG, **Ferrari, T**, Kelley, JL, Petrov, DA, Solari, KA, **Mooney, JA**. Recommendations for Population and Individual Diagnostic SNP Selection in Non-Model Species. [Preprint]. 2024 July 06. DOI: 10.1101/2024.07.03.601943

Corresponding author. I supervised QBIO lab trainees Chenyang (Julie) Li and Tessa Ferrari, guided analyses, developed code, and drafted the manuscript. Accepted at Molecular Ecology Resources.

Armstrong EE, **Mooney JA**, Solari KA, Kim BY, Barsh GS, Grant VB, Greenbaum G, Kaelin CB, Panchenko K, Pickrell JK, Rosenberg NA, Ryder OA, Yokoyama T, Ramakrishnan U, Petrov DA, and Hadly EA. Unraveling the genomic diversity and admixture history of captive tigers in the United States. Proc. Natl. Acad. Sci. 121, e2402924121 (2024). doi: 10.1073/pnas.2402924121. Epub 2024 Sep 19. PMID: 39298482.

Co-first and Co-corresponding author. I worked with Ellie Armstrong (co-first author) on this project. I did many of the analyses and drafted the manuscript. I worked on the submission, correspondence with editor, revisions, and revisions of the manuscript.

^This paper was the September 2024 cover article for PNAS and highlighted by Science, NY Times, Stanford Media, and Dornsife Media.

Agranat-Tamir L, **Mooney JA**, Rosenberg NA. Counting the genetic ancestors from source populations in members of an admixed population. Genetics. 2024 Apr 3;226(4):iyae011. doi: 10.1093/genetics/iyae011. PMID: 38289724; PMCID: PMC10990421.

My primary work was on the foundation for this paper, the results from my publication on genealogical ancestors were used as the base to compute genetic ancestors. I read and provided feedback on the manuscript. This manuscript has been resubmitted to Genetics.

Armstrong EE, Bissell KL, Fatima HS, Heikkinen MA, Jessup A, Junaid MO, Lee DH, Lieb EC, Liem JT, Martin EM, Moreno M, Otgonbayar K, Romans BW, Royar K, Adler MB, Needle DB, Harkess A, Kelley JL, **Mooney JA**, Mychajliw AM. Chromosome-level assembly of the gray fox (*Urocyon cinereoargenteus*) confirms the basal loss of PRDM9 in Canidae. G3 (Bethesda). 2024 Apr

3;14(4):jkae034. doi: 10.1093/g3journal/jkae034. PMID: 38366575; PMCID: PMC10989890.

I am co-last and co-corresponding for the first gray fox reference genome paper. I helped shape the paper and analyses. I provided essential data for PRDM9 analyses.

Mooney JA, Agranat-Tamir L, Pritchard JK, Rosenberg NA. On the number of genealogical ancestors tracing to the source groups of an admixed population. *Genetics*. 2023 Jul 6;224(3). doi: 10.1093/genetics/iyad079. PubMed PMID: 37410594; PubMed Central PMCID: PMC10324943.

First author. I developed code, conducted analyses, and wrote the manuscript.

^This paper was the July 2023 cover article for GENETICS and highlighted by Axiom, The Daily Trojan, Stanford Media, and Dornsife Media in an article and YouTube video.

Mooney JA, Marsden CD, Yohannes A, Wayne RK, Lohmueller KE. Long-term Small Population Size, Deleterious Variation, and Altitude Adaptation in the Ethiopian Wolf, a Severely Endangered Canid. *Mol Biol Evol*. 2023 Jan 4;40(1) PubMed Central PMCID: PMC9847632.

First author and co-corresponding. I developed code, conducted analyses, advised undergraduate trainee Abigail Yohannes, and wrote the manuscript.

Mooney JA, Yohannes A, Lohmueller KE. The impact of identity by descent on fitness and disease in dogs. *Proc Natl Acad Sci U S A*. 2021 Apr 20;118(16) PubMed Central PMCID: PMC8072400.

First author. I developed code, conducted analyses, advised undergraduate Abigail Yohannes, and wrote manuscript.

Sura SA, Smith LL, Ambrose MR, Amorim CEG, Beichman AC, Gomez ACR, Juhn M, Kandlikar GS, Miller JS, **Mooney JA**, Mummah RO, Lohmueller KE, Lloyd-Smith JO. Ten simple rules for giving an effective academic job talk. *PLoS Comput Biol*. 2019 Jul;15(7):e1007163. doi: 10.1371/journal.pcbi.1007163. eCollection 2019 Jul. PubMed PMID: 31344032; PubMed Central PMCID: PMC6657819.

Assisted with figures and reading the manuscript.

Mooney JA, Huber CD, Service S, Sul JH, Marsden CD, Zhang Z, Sabatti C, Ruiz-Linares A, Bedoya G, Freimer N, Lohmueller KE. Understanding the Hidden Complexity of Latin American Population Isolates. *Am J Hum Genet*. 2018 Nov 1;103(5):707-726. PubMed Central PMCID:PMC6218714.

First author. I developed code, conducted all but one analysis, and wrote the manuscript.

RESEARCH SUPERVISION

Mahija Mogalipuvvu, Quantitative Biology Undergraduate student, USC	2024-
Sydney Bruce, Quantitative Biology Undergraduate student, USC	2024-
Peyton Hall, Quantitative Biology Undergraduate student, USC	2024-
Matthew Genchev, Quantitative Biology Undergraduate student, USC	2023-
Maria Akopyan, Quantitative Biology Postdoctoral Fellow, USC Future Position: NSF PRFB at UC Riverside starting January 1, 2025	2023-2024
Shirin Nataneli, Computational Biology and Bioinformatics Graduate Student, USC	2022-
Tessa Ferrari, Quantitative Biology undergraduate student, USC Current position Research Technician I in Mooney Lab at USC	2022-
Chenyang (Julie) Li, Quantitative Biology Undergraduate student, USC Current position: Graduate student Emory PBEE	2022-2024
Tina Lasisi, Quantitative Biology Postdoctoral Fellow, USC Current position: Assistant Professor University of Michigan Department of Anthropology	2022- 2023
Anika Shrivastava, Quantitative Biology Undergraduate student, USC	2022-
Mengdi Chai, Quantitative Biology Undergraduate student, USC Current position: Harvard Master of Science in Computational Biology and Quantitative Genetics	2022- 2023
Abigail Yohannes, Political Science Undergraduate student, UCLA Current position: North Carolina A&T Master of Science in Data Science and Engineering	2019- 2020

PRIOR SUCCESSFUL EXTERNAL RESEARCH FUNDING

National Science Foundation (NSF) Postdoctoral Research Fellow in Biology (PRFB)	2021-2022
Stanford Propel Postdoctoral Scholars (decline for NSF PRFB)	2021
Stanford Center for Computational, Evolutionary, and Human Genetics (CEHG)	2020-2021
UCLA Dissertation Year Fellowship	2019
Graduate Programs in Bioscience Fellowship Incentive Program/Shine Fellowship	2016
National Science Foundation Graduate Research Fellowship	2015

EXTERNAL GRANTS AND FUNDING

NIH R35 ESI-Maximizing Investigators' Research Award (MIRA) Title: Population Genomics Across Global Populations: Flexible Methods for Inference and Detecting Rare Recessive Variation Amount: 2,056,520 Role: PI	2024 Submitted
NSF CAREER Title: Advanced Computational Methods and Population Genomics for Conservation: Assessing Genetic Diversity, Extinction Risk, and Reference Genome Bias Amount: 1,170,326 Role: PI	2024 Submitted
HHMI Freeman Hrabowski Title: Unifying population genetics and comparative genomics for demographic inference and quantifying rare recessive variation Role: PI	2024 Submitted
NSF CAREER Title: Advanced Computational Methods and Population Genomics for Conservation: Assessing Genetic Diversity, Extinction Risk, and Reference Genome Bias Amount: 1,170,326 Role: PI	2023 Not Funded
NIH R25 Genome Research Experiences to Attract Talented Undergraduates into Genomic Fields to Enhance Diversity (GREAT) Title: Enabling research experience in bioinformatics data science to attract underrepresented undergraduates into genomics Amount: 1,836,782 Role: co-PI	2023 Not Funded
President's Sustainability Research Award (PSRA) Title: Integrating threat distributions with susceptibility distributions to improve conservation outcomes for pollinators Amount: 250,000 Role: co-PI	2023 Not Funded
NIH R35 ESI-Maximizing Investigators' Research Award (MIRA) Title: Unifying population genetics and comparative genomics for demographic inference and quantifying rare recessive variation Amount: 2,044,300 Role: PI	2022 Not Funded
NIH R25 Genome Research Experiences to Attract Talented Undergraduates into Genomic Fields to Enhance Diversity (GREAT) Title: Enabling research experience in bioinformatics data science to attract underrepresented undergraduates into genomics Amount: 1,836,555 Role: co-PI	2022 Not Funded
HHMI Freeman Hrabowski Title: Unifying population genetics and comparative genomics for demographic inference and quantifying rare recessive variation Role: PI	2022 Not Funded