Maya Lemmon-Kishi

Computational Biologist

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Education

University of California, Berkeley
Berkeley, California

Ph.D. Candidate in Computational Biology *Aug. 2019 - Exp. Dec 2025*

- Advised by Rasmus Nielsen
- Proposed Thesis: "Phylogeny-based Approaches for the Expanded Analysis of Ancient Environmental DNA"

University of Pittsburgh
Pittsburgh, Pennsylvania

B.S. in Computer Science, *magna cum laude* *Aug. 2014 - Dec. 2018*

Research Experience

Graduate Researcher and NSF GRFP Fellow
Berkeley, California

Rasmus Nielsen Lab *May 2020 - Present*

- Building a phylogenetics-based method in C to date ancient environmental DNA (eDNA) samples from epochs that extend beyond the capabilities of traditional dating techniques, such as carbon-14 dating
- Extending the use of the phylogenetics-based molecular dating method to calibrate the molecular clock across various taxonomy using dated ancient environmental DNA samples
- Designing an algorithm in C to estimate long phylogenetically compatible haplotypes for species with poor reference databases from short read NGS eDNA to study these species with population genetic techniques
- Mentor undergraduate students on computational projects related to environmental DNA
- Set up a server (Ubuntu 20.04) and maintaining a second inherited server as the system administrator for 10+ users

Undergraduate Researcher - PittSmartLiving
Pittsburgh, Pennsylvania

Advanced Data Management Technologies Lab *Sept. 2018 - May 2019*

- Developed a Flask interactive web application to visualize public transportation connectivity of various U.S. cities
- Produced a Flask web application for researchers to quickly summarize navigate passenger density data

Undergraduate Researcher
Pittsburgh, Pennsylvania

Kostka Lab, University of Pittsburgh *Jan. 2018 - Dec. 2018*

- Implemented an automated Nextflow pipeline of a commonly used single-cell Drop-Seq method to increase productivity in the lab
- Analyzed single cell kidney data in R to determine validity of the Nextflow pipeline through comparison with published results

Undergraduate Researcher and Student Leader (Pittsburgh iGEM)
Pittsburgh, Pennsylvania

Department of Bioengineering, University of Pittsburgh *Apr. 2016 - May 2017*

- Lead an interdisciplinary team to design a lead and thallium biosensor using biological components
- Developed a Simulink model to predict long-term lead blood level concentration in children depending on lead water levels to demonstrate the importance of early lead detection
- Managed and planned all cloning and transformation related experiments with *E. coli*

Undergraduate Researcher
Pittsburgh, Pennsylvania

Banerjee Lab, University of Pittsburgh *Jan. 2016 - May 2016*

- Developed a spheroid analysis macro to analyze pancreatic organoids with ImageJ processing
- Analyzed islet organoids using qPCR to determine which organiods produced insulin in various hydrogel environments
- Cell culture of fibroblasts and human umbilical vein endothelial cells to create iselt organoids for use in experiments

Fellowships

NSF Graduate Research Fellow, University of California, Berkeley *2021 - Present*

Berkeley Connect Fellowship, University of California, Berkeley *Aug. 2022 - May 2023*

Publications

Candiello, J., Grandhi, T.S.P., Goh, S.K., Vaidya, V., **Lemmon-Kishi, M.**, Eliato K.R., Ros, R., Kumta, P., Rege, K., Banerjee, I. 3D Heterogeneous Islet Organoid Generation from Human Embryonic Stem Cells Using a Novel Engineered Hydrogel Platform. *Biomaterials*. 2018. 177: 27-39.

Honors & Awards

Student Service and Leadership Award, Center for Computational Biology Retreat 2024 *2024*
SACNAS Travel Scholarship, 2023 SACNAS NDiSTEM Conference *2023*
2nd Place, SheInnovates Hackathon *2018*
Most Creative Hack, SheInnovates Hackathon *2018*
Nomination for Best Environmental Project, iGEM 2016 *2016*
Gold Medal, iGEM 2016 *2016*

Skills

Programming	C, Python, R
Bioinformatics	RAxML, mafft, IQTree, BWA, samtools, ape
Tools	Git, Nextflow, Bash, Snakemake, Conda, LaTeX, ggplot, ggtree
Pipelines	Taxonomic Classification, Alignment, NGS Processing

Industry Experience

Data Engineering Intern
West Sacramento, California
COMPUTATIONAL LIFE SCIENCE, BAYER CROP SCIENCE *May 2019 - Aug. 2019*

- Worked with key members of the Biologics team to develop an internal R Shiny tool to improve data management and to assess the data landscape of experimental data in the biologics discovery pipeline
- Streamlined data upload and developed long term storage strategy for the laboratory analysis pipeline

Genotyping Development Scientist Intern
Chesterfield, Missouri
BAYER CROP SCIENCE (FORMERLY MONSANTO) *Apr. 2018 - Aug. 2018*

- Completed a cross functional project to create a method in R for processing SNP data to quantify differences in recombination rates across germplasm to improve inbred line specific genetic maps used in breeding programs
- Developed an algorithm in R to impute genetic information for haploid induced maize from non-destructive tissue sampling maintaining seed viability as part of the double haploid breeding pipeline
- Identified discordance due to breeding errors in genetic cross data and built tools to identify these individuals for the quality control process

University Service

UCB Computational Biology Building Bridges to Graduate School Program
Berkeley, California
ORGANIZER AND REPRESENTATIVE *Oct. 2022 - Present*

- Built partnerships with Berkeley undergraduate programs and several California State University (CSU) Departments to introduce the field computational biology
- Obtained funding to host workshops on pathways and preparation for a STEM PhD
- Presented graduate research to an audience of undergraduates from a variety of majors

Center for Computational Biology Industry Speaker Seminar Series
Berkeley, California
STUDENT ORGANIZER *Jan. 2024 - Jan. 2025*

- Invite speakers from local biotech to talk about their industry career in computational biology
- Organize and host dinner with speakers and several members of the Berkeley computational biology community
- Restructured the seminar to interfere less with speaker's schedule, increasing our acceptance to 100%

Center for Computational Biology Peer Mentoring Program
Berkeley, California
CO-FOUNDER *Jan. 2021 - June 2023*

- Founded and obtained funding for a peer mentoring program that pairs junior students in the Computational Biology PhD program with senior students to build community and support networks during the first two years of graduate school
- Developed workshops on various topics that are continued to be used

Center for Computational Biology DEI Committee
Berkeley, California
GRADUATE STUDENT REPRESENTATIVE *June 2020 - June 2022*

- Reformed the admissions process with a formalized rubric and procedure to increase equity
- Developed an action plan for the Center for Computational Biology that highlights changes in mentoring, faculty, admissions, and outreach to increase diversity, inclusivity, and equity
- Wrote the first climate survey for the Center for Computational Biology graduate program and incorporated the findings in the action plan

Teaching Experience

Berkeley Connect Teaching Fellow *Berkeley, California*

CENTER FOR COMPUTATIONAL BIOLOGY, UNIVERSITY OF CALIFORNIA, BERKELEY *Aug. 2022 - May 2023*

- Designed and taught a curriculum to introduce a variety of topics and skills for computational biology for 80 students from a variety of academic backgrounds

Python Bioinformatics Bootcamp Lecturer *Berkeley, California*

CENTER FOR COMPUTATIONAL BIOLOGY, UNIVERSITY OF CALIFORNIA, BERKELEY *June 2021, Jan. 2022, June 2022*

- Taught students (both academic and industry, ranging from undergraduates to faculty) fundamental programming skills such as logic, control flow, and data structures in Python
- Updated the curriculum to incorporate more biologically relevant examples and problems

Python Bioinformatics Bootcamp Teaching Assistant *Berkeley, California*

CENTER FOR COMPUTATIONAL BIOLOGY, UNIVERSITY OF CALIFORNIA, BERKELEY *Jan. 2021, June 2021, Jan. 2022*

- Supported the lecturer by answering questions and helped students work through practice problems

Undergraduate Teaching Assistant - Cell and Molecular Biology *Pittsburgh, Pennsylvania*

DEPARTMENT OF BIOENGINEERING, UNIVERSITY OF PITTSBURGH *Aug. 2017 - Apr. 2018*

- Taught weekly recitation of Cellular Biology to bioengineering students
- Wrote and graded weekly quizzes and presentations

Mentorship

Undergraduate Mentor *Berkeley, California*

UNIVERSITY OF CALIFORNIA, BERKELEY

- Robin Rheem: Advised Robin through re-implementation of haplotype estimation project from C into Rust for increased computational efficiency and subsequent analysis to validate method (Dec 2024. - Present)
- Chris Dong: Mentored Chris on a project to incorporate environmental variables in population structure analysis of environmental DNA and developed his skills in computational tools (Sept. 2021 - May 2022)

Center for Computational Biology Peer Mentor *Berkeley, California*

CENTER FOR COMPUTATIONAL BIOLOGY, UNIVERSITY OF CALIFORNIA, BERKELEY *Aug. 2021 - Present*

- Mentored three pre-qualifying exam computational biology students through their first two years and participated in program workshops

Berkeley Connect Teaching Fellow *Berkeley, California*

CENTER FOR COMPUTATIONAL BIOLOGY, UNIVERSITY OF CALIFORNIA, BERKELEY *Aug. 2022 - May 2023*

- Mentored around 80 students over two semesters from various backgrounds and experience interested in computational biology
- Topics discussed included how to find research opportunities on campus, email professors, apply to internships, apply to graduate school, improve learning skills, and have a career in computational biology

iGEM Summer Research Fellowship Supervisor (Pittsburgh iGEM) *Pittsburgh, Pennsylvania*

DEPARTMENT OF BIOENGINEERING, UNIVERSITY OF PITTSBURGH *May 2017 - Oct. 2017*

- Developed laboratory management skills supervising the team on day to day planning and experiments

Presentations

ORAL

Lemmon-Kishi, M. and Nielsen, R. Decoding Time: A Phylogenetic Framework for Molecular Dating of Sedimentary Ancient DNA. Veridical Data Science for Biology. Berkeley, California. July 11th, 2025.

Lemmon-Kishi, M. and Nielsen, R. Decoding Time: A Phylogenetic Framework for Molecular Dating of Sedimentary Ancient DNA. sedaDNA Scientific Society Conference. Tromso, Norway. June 23-25, 2025.

Lemmon-Kishi, M. and Nielsen, R. Decoding Time: A Phylogenetic Framework for Molecular Dating of Sedimentary Ancient DNA. Center for Ancient Environmental Genomics Symposium. Fredensborg, Denmark. April 3-4, 2025.

Lemmon-Kishi, M. and Catamura, C. Ancient Biodiversity to Personalized Medicine: The Power of Computational Biology. Biology Colloquium Series. Stanislaus State. Stanislaus, California. March 7, 2025.

Lemmon-Kishi, M. and Nielsen, R. What's the Rate: Molecular Clock Calibration Using Sedimentary Ancient DNA. SMBE 2024: Molecular Evolution Through Metagenomics Symposium. Puerto Vallarta, Mexico. July 7-11, 2024.

Lemmon-Kishi, M. Building Tools to Explore Ancient Biodiversity: A Journey into Computational Biology. Center for Compuational and Applied Mathematics Seminar. CSU Fullerton. Fullerton, California. February 21, 2024.

Lemmon-Kishi, M. and Nielsen, R. ratePlacer: An Efficient Molecular Dating Method for Ancient sedDNA Samples. Center for Computational Biology Retreat. Los Gatos, California. November 3-5, 2023.

Lemmon-Kishi, M. and Nielsen, R. Haplotype Estimation for Environmental DNA. Center for Computational Biology Retreat. Los Gatos, California. November 4-6, 2022.

Lemmon-Kishi, M. and Nielsen, R. A Penalized Likelihood Approach to Estimating Haplotypes from Environmental DNA. Evolution 2022. Cleveland, Ohio. June 24-28, 2022.

Lemmon-Kishi, M. and Nielsen, R. Estimating haplotypes for environmental DNA. Evolution 2021. Virtual. June 21-25, 2021.

Lemmon-Kishi, M. and Nielsen, R. A Computationally Efficient Method to Estimate Phylogenetically Compatible Haplotypes from eDNA. 2021 NHGRI Research Training and Career Development. Virtual. April 19–21, 2021.

Lemmon-Kishi, M., Chu, C., Peddada, V., et. al. Hot Metal Switch: Synthetic in vitro gene circuit for the detection of metal ions. iGEM Jamboree 2017. Boston, Massachusetts. October 27-31, 2016.

Poster

Lemmon-Kishi, M. and Nielsen, R. Molecular Clock Calibration with Sedimentary Ancient DNA. Bay Area Population Genetics. Berkeley, California. November 8, 2024.

Lemmon-Kishi, M. and Nielsen, R. Molecular Clock Calibration with Sedimentary Ancient DNA. Center for Computational Biology Retreat. Los Gatos, California. October 25-27, 2024.

Lemmon-Kishi, M. and Nielsen, R. ratePlacer: An Efficient Molecular Dating Method for Ancient sedDNA Samples. Bay Area Population Genetics. Stanford, California. December 2, 2023.

Lemmon-Kishi, M. and Nielsen, R. ratePlacer: An Efficient Molecular Dating Method for Ancient sedDNA Samples. sedDNA Meeting. Potsdam, Germany. June 6-9, 2023.

Lemmon-Kishi, M. and Nielsen, R. A Penalized Likelihood Approach to Estimating Haplotypes from Environmental DNA. Biology of Genomes. Cold Spring Harbor Laboratories, New York. May 10-14, 2022.

Lemmon-Kishi, M. and Nielsen, R. A Penalized Likelihood Approach to Estimating Haplotypes from Environmental DNA. Center for Computational Biology Retreat. Berkeley, California. October 21-22, 2021.

Lemmon-Kishi, M. and Nielsen, R. A Computationally Efficient Method to Estimate Phylogenetically Compatible Haplotypes from eDNA. Center for Computational Biology Retreat. Virtual. March 3-5, 2021.

Lemmon-Kishi, M., Chu, C., Peddada, V., et. al. Thallium and Lead Detection Using Cell-Free Circuitry. Biomedical Engineering Society Conference 2016. Minneapolis, MN. October 8, 2016.