# Maya Lemmon-Kishi

#### **COMPUTATIONAL BIOLOGIST**

### Education\_

### **University of California, Berkeley**

Berkeley, California

Ph.D. Candidate in Computational Biology

Aug. 2019 - Exp. Aug 2025

- Advised by Rasmus Nielsen
- Proposed Thesis: "Beyond Occupancy: Methods and Applications to Expand the Use of Environmental DNA"

### **University of Pittsburgh**

Pittsburgh, Pennsylvania

Aug. 2014 - Dec. 2018

 ${\it B.S. IN Computer Science}, magna~cum~laude$ 

- Program Honors in Computer Science
- Minors in Bioengineering and Chemistry

# 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
- Curating a taxonomically diverse and comprehensive organelle genome database containing whole genome alignments and phylogenetic trees for ancient eDNA workflows
- Set up a server (Ubuntu 20.04) and maintaining a second inherited server as the system administrator for 10+ users

#### **Graduate Rotation Student**

Berkeley, California

VARIOUS LABS

Sept. 2019 - May 2020

- Implemented a RNA-seq pipeline to generate custom reference genomes to analyze the genomic signature of sunflower domestication
- Developed a method to calculate population genetic summary statistics from environmental DNA in Python to observe population structure without invasive tissue sampling
- Explored methods to detect non-Brownian phylogenetic signal of leaf chemical composition data for co-evolution of herbivory defense

## **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
- Gold medalist and nominated for Best Environmental Project at the iGEM Jamboree 2016

### **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

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# **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

# Leadership Experience

# UCB Computational Biology Building Bridges to Graduate School Training Program

Berkeley, California

ORGANIZER AND REPRESENTATIVE

Oct. 2022 - Present

- Built partnerships with Berkeley undergraduate programs that aim to serve underrepresented students in STEM
- Organized a small group mentoring workshop for Berkeley undergraduate students affiliated with our on-campus partner programs
- Presented materials that cover topics, such as: components of a PhD program, preparation for PhD programs, various research training opportunities, and introduction to research in Computational Biology

# **Center for Computational Biology Peer Mentoring Program**

Berkeley, California

CO-FOUNDER

Jan. 2021 - June 2023

- Founded 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
- Organized and obtained funding for workshops and panels on topics such as the qualifying exam and "Personalizing Your Graduate Training for Future Career Goals"

# **Center for Computational Biology DEI Committee**

Berkelev, 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

# **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

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# Mentorship

### **Center for Computational Biology Peer Mentor**

Berkeley, California

CENTER FOR COMPUTATIONAL BIOLOGY, UNIVERSITY OF CALIFORNIA, BERKELEY

Aug. 2021 - Present

• Mentored two 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.

### **Undergraduate Mentor**

Berkeley, California

University of California, Berkeley

Sept. 2021 - May 2022

• 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.

### **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

# **Fellowships**

2021 -Present

NSF Graduate Research Fellow, University of California, Berkeley

Berkeley, California

Aug. 2022 -May 2023

**Berkeley Connect Research Fellowship**, University of California, Berkeley

Berkeley, California

## **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. (2018) "3D Heterogeneous Islet Organoid Generation from Human Embryonic Stem Cells Using a Novel Engineered Hydrogel Platform." *Biomaterials*. 177: 27-39.

# **Presentations**

#### ORAL

**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 Computational and Applied Mathematics Seminar. CSU Fullerton. Fullerton, California. Feb. 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. 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.

# Honors & Awards \_\_\_\_\_

2023	SACNAS Travel Scholarship, 2023 SACNAS NDISTEM Conference	Portland, Oregon
2018	<b>2nd Place</b> , SheInnovates Hackathon	Pittsburgh, Pennsylvania
2018	Most Creative Hack, SheInnovates Hackathon	Pittsburgh, Pennsylvania
2016	Nomination for Best Environmental Project, iGEM 2016	Boston, Massachusetts
2016	Gold Medal, iGEM 2016	Boston, Massachusetts