# Maya Lemmon-Kishi

Computational Biologist

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## Education

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

Ph.D. in Computational Biology — *Aug. 2019 - Exp. May 2025*

- Advised by Rasmus Nielsen
- Proposed Thesis: "Beyond Occupancy: Methods and Applications to Expand the Use of Environmental DNA"
- Coursework: Population Genetics, Phylogenetics, Parallel Computing, Intro to Advanced Probability and Statistics

### University of Pittsburgh
*Pittsburgh, Pennsylvania*

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

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

## Research Experience

### Graduate Researcher
*Berkeley, California*

Nielsen Lab — *May 2020 - Present*

- Awarded NSF GRFP Fellowship to develop methods for population genetic analyses of environmental DNA (eDNA)
- Developing a Python tool to analyze eDNA with population genetic summary statistics to be used as a way to estimate genetic health and connectivity of species without invasive tissue sampling
- Designing an algorithm in C to estimate long phylogenetically compatible haplotypes for species with poor reference databases from short read NGS eDNA so that we can study these species with population genetic techniques; presented at Evolution and Biology of Genomes
- Building a phylogenetics-based method in C to date ancient eDNA samples from epochs that extend beyond the capabilities of traditional dating techniques, such as carbon-14 dating
- Maintaining an inherited server and set up a second server (Ubuntu 20.04) 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 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; demoed at the Rail-Volution 2018 Mobility Showcase
- 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; published in *Biomaterials*
- 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

## 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 develop an internal R Shiny tool to improve the data management and assess the data landscape for 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 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

## Mentorship

### Undergraduate Mentor
*Berkeley, California*

University of California, Berkeley
*Sept 2021 - 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.

### 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

## Leadership Experience

### Center for Computational Biology Peer Mentoring Program
*Berkeley, California*

Co-founder and organizer
*Jan. 2021 - Present*

- 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 years of graduate school
- Organize and obtain 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
*Berkeley, California*

Graduate Student Representative
*Jun. 2020 - Present*

- 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 not only in the program but with general impact on the field of computational biology.
- Wrote the first climate survey for the Center for Computational Biology graduate program and incorporated the findings in the action plan.

## Fellowships

2021 - Present **NSF Graduate Research Fellow**, 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. 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.

**Lemmon-Kishi, M.**, Chu, C., Ni Chochlian, A. Synthetic Biology and iGEM. TECBio and DiSCoBio. University of Pittsburgh. Pittsburgh, PA. 2016

### Poster

**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.

**Lemmon-Kishi, M.**, Ni Chochlian, A. Hot Metal Switch at H2Oh!. Carneige Science Center. Pittsburgh, PA. 2016

## Teaching Experience

**Berkeley Connect Teaching Fellow** — *Berkeley, California*

Center for Computational Biology, University of California, Berkeley — *Aug. 2022 - present*

- Design curriculum to introduce and teach skills for computational biology
- Mentoring students from various backgrounds and experience interested in computational biology

**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

**Undergraduate Teaching Assistant - General Chemistry** — *Pittsburgh, Pennsylvania*

Department of Chemistry, University of Pittsburgh — *Aug. 2015-May 2016*

- Held additional offices hours for general chemistry students

## Honors & Awards

### Academic

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| 2017 - 2018 | **Dean's List**, Dietrich School of Arts and Sciences | *Pittsburgh, Pennsylvania* |
| 2015 - 2016 | **Dean's List**, Swanson School of Engineering | *Pittsburgh, Pennsylvania* |
| 2014 | **Term List**, Swanson School of Engineering | *Pittsburgh, Pennsylvania* |

### Extracurricular

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|---|---|---|
| 2018 | **2nd Place**, 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* |

## Skills

**Programming** C, Python, R
**Operating Systems** Linux/Unix, Windows
**Tools** Git, Bash, Conda, Snakemake, LaTeX