

# JINGYOU RAO

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## RESEARCH OVERVIEW

I develop experimental and computational methods to map protein sequence–function relationships, combining deep mutational scanning (DMS), combinatorial mutagenesis, and statistical modeling. My research uses human olfactory receptors to study epistasis and functional diversification, and extends to membrane proteins such as CFTR to investigate genotype-dependent drug responses.

## EDUCATION

**University of California, Los Angeles** Sep. 2021 – Dec. 2025

PhD in Computer Science (Subfield: Computational Biology)

Thesis Title: Statistical and Computational Methods to Uncover the Genetic Architecture of Protein Function

**University of California, Los Angeles** Sep. 2018 – Jun. 2021

Bachelor of Science in Computer Science

Bachelor of Science in Computational and Systems Biology (Concentration: Biological Data Science)

summa cum laude

## RESEARCH EXPERIENCE

**Coyote-Maestas Lab (Department of Bioengineering and Therapeutic Sciences, UCSF)**

Postdoctoral Researcher

Dec. 2025 – Present

Visiting Scholar

Jun. 2024 – Dec. 2025

- Develop scalable cloning and screening strategies for DMS, including high-order combinatorial libraries to map protein sequence–function relationships.
- Lead experimental and computational studies of human olfactory receptors to characterize fitness landscapes, epistasis, evolutionary diversification, and ligand–receptor relationships.
- Investigate pharmacologic modulation and genotype–drug interactions in CFTR and other clinically relevant membrane proteins using quantitative cell-based assays.
- Integrate molecular biology, next-generation sequencing, and computational analysis to connect genetic variation with protein function and therapeutic response.

**Pimentel Lab (David Geffen School of Medicine, UCLA)**

Jul. 2021 – Sep. 2025

Graduate Student Researcher

- Developed Bayesian hierarchical models to estimate variant effects and quantify uncertainty in DMS experiments.
- Developed residue-level summaries to interpret functional variation across DMS experiments.
- Modeled relationships among molecular phenotypes of a single protein using DMS data.

## JOURNAL PUBLICATIONS

1. Accurate variant effect estimation in FACS-based deep mutational scanning data with Lilace  
Jerome Freudenberg, [Jingyou Rao](#), Matthew K. Howard, Christian Macdonald, Noah Greenwald, Willow Coyote-Maestas & Harold Pimentel; *Genome Biology* 2026. <https://doi.org/10.1186/s13059-026-03934-1>
2. Rosace-AA: Enhancing Interpretation of Deep Mutational Scanning Data with Amino Acid Substitution and Position-Specific Insights  
[Jingyou Rao](#), Mingsen Wang, Matthew K. Howard, Christian Macdonald, James S. Fraser, Willow Coyote-Maestas & Harold Pimentel; *Bioinformatics Advances* 2025. <https://doi.org/10.1093/bioadv/vbaf218>
3. dotears: Scalable, consistent DAG estimation using observational and interventional data  
Albert Xue, [Jingyou Rao](#), Sriram Sankararaman, Harold Pimentel; *iScience* 2025.

<https://doi.org/10.1016/j.isci.2024.111673>

4. Mapping kinase domain resistance mechanisms for the MET receptor tyrosine kinase via deep mutational scanning  
Gabiella O. Estevam, Edmond M. Linossi, Jingyou Rao, Christian B. Macdonald, Ashraya Ravikumar, Karson M. Chrispens, John A. Capra, Willow Coyote-Maestas, Harold Pimentel, Eric A. Collisson, Natalia Jura, James S. Fraser; *eLife* 2024. <https://doi.org/10.7554/eLife.101882>
5. Rosace: a robust deep mutational scanning analysis framework employing position and mean-variance shrinkage  
Jingyou Rao, Ruiqi Xin, Christian Macdonald, Matthew K. Howard, Gabiella O. Estevam, Sook Wah Yee, Mingsen Wang, James S. Fraser, Willow Coyote-Maestas & Harold Pimentel; *Genome Biology* 2024. <https://doi.org/10.1186/s13059-024-03279-7>

## PREPRINTS

1. Cosmos: A Position-Resolution Causal Model for Direct and Indirect Effects in Protein Functions  
Jingyou Rao, Mingsen Wang, Matthew K. Howard, Willow Coyote-Maestas & Harold Pimentel; *bioRxiv* 2025. <https://doi.org/10.1101/2025.08.01.667517>

## ORAL PRESENTATIONS

1. Flash talk: Mapping the Protein Epistasis Landscape by Deep Mutational Scanning  
Biophysics Society Annual Meetings, Feb. 2026. San Francisco, CA, USA.
2. Research: Statistical and Computational Tools to Decode Genetic Architecture of Protein Functions  
Computational Genomics Research Institute, Jul. 2025. Los Angeles, CA, USA.
3. Research: Modeling Growth-based Deep Mutational Scanning Counts with Rosace  
Variant Effect Seminar Series by Atlas of Variant Effects, Aug. 2024. Virtual.  
Recording: <https://youtu.be/Nt5juj-CgxM>
4. Workshop: What is in a variant score?  
Mutational Scanning Symposium, May 2024. Boston, MA, USA.  
Recording: <https://youtu.be/A5qd-oyk7EY>
5. Research: Computational Approaches for Inferring Gene Regulation in *in situ* Perturbation Screens  
CSHL Biological Data Science Conference, Nov. 2022. Long Island, NY, USA.

## POSTER PRESENTATIONS

1. Mapping the Protein Epistasis Landscape by Deep Mutational Scanning  
Jingyou Rao, Matthew K. Howard, Claudia Llinas del Torrent, Ira Irklienko, Catherine H. Shin, Aashish Manglik, Willow Coyote-Maestas; Probabilistic Modeling in Genomics, Mar. 2026. Berkeley, CA, USA.
2. Modeling Relationships in Multi-Phenotype DMS Using Graph Theory and Ensemble View.  
Jingyou Rao, Mingsen Wang, Matthew Howard, Ever O'Donnell, Willow Coyote-Maestas, Harold Pimentel; Mutational Scanning Symposium, May 2025. Barcelona, Spain.
3. Decomposing the Position and Amino-Acid Substitution Effect in Deep Mutational Scanning  
Jingyou Rao, Mingsen Wang, Chris Macdonald, Matthew Howard, James Fraser, Willow Coyote-Maestas, Harold Pimentel; Mutational Scanning Symposium, May 2024. Boston, MA, USA.
4. Quantifying Uncertainty in Estimation of Isoform Expression Heritability  
Jingyou Rao, Nicholas Mancuso, Harold Pimentel; CSHL Genome Informatics, Nov. 2021. Virtual.

## COMMUNITY SERVICE

**Atlas of Variant Effects Alliance**

Dec. 2024 – Present

Member of Variant Effect Seminar Series Committee (<https://www.varianteffect.org/seminar-series>)

- Coordinate seminar programming (30+ seminars to date) and create promotional content.

Member of Data Coordination and Dissemination Workstream (<https://ave-dcd.github.io/>)

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## MENTORING EXPERIENCE

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1. Joanna Rhim. Undergraduate student in Computational and Systems Biology, UCLA. (2024–Present)
  - UCLA Bruins-In-Genomics (B.I.G.) Summer program 2025 (<https://qcb.ucla.edu/big-summer/>)
  - Project: simulating functional effects of double-mutant sequences through quantification of epistatic interactions and hotspot enrichment via Tranception
2. Joanna Jiang. Master's student in Biostatistics, UCLA. (2024–2025)
  - Project: modeling protein position correlation in DMS using Gaussian process
  - Now a PhD student in Statistics at UC Davis
3. Ruiqi (Riley) Xin. Undergraduate student, UCLA. (2022–2024)
  - Project: software and website development for Rosace
  - Co-author on Rao et al. Genome Biology 2024
  - Now a PhD student in Bioinformatics at University of Chicago
4. Jianping Ye. Undergraduate student, UCLA. (2021–2022)
  - Project: review of computational methods for pooled CRISPR screens
  - Now a PhD student in Mathematics at University of Maryland

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## TEACHING EXPERIENCE

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1. Teaching Assistant, UCLA (Winter 2022)  
CSC121/C221 Probabilistic Models in Computational Genomics

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## SOFTWARE

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1. Cosmos: a position-resolution causal model for direct and indirect effects in protein functions. Sole software developer.  
<https://github.com/pimentellab/cosmos>
2. Rosace-AA: extension of Rosace to decompose position and amino acid substitution effects. Sole software developer.  
<https://github.com/pimentellab/rosace-aa>
3. Rosace: statistical inference for growth-based deep mutational scanning (DMS) screens. Sole software developer.  
<https://github.com/pimentellab/rosace>