

JINGYOU (ROSE) RAO

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EDUCATION

University of California, Los Angeles Sep. 2021 – Current

PhD Candidate in Computer Science (Subfield: Computational Biology)

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)

Latin Honors: Summa Cum Laude Cumulative GPA: 3.978

RESEARCH

Pimentel Lab (David Geffen School of Medicine, UCLA) Jul. 2021 – Current

Graduate Student Researcher

- Developed Bayesian hierarchical models to infer the functional effects of protein mutations with reliable uncertainty estimate for deep mutational scanning (DMS) experiments
- Extracted residue-level summary statistics for insights and interpretation across multiple DMS experiments
- Ongoing: Exploring relationships between different molecular phenotypes of a single protein
- Ongoing: Building framework of Bayesian active learning for protein epistasis experiment design with DMS

Coyote-Maestas lab (Department of Bioengineering and Therapeutic Sciences, UCSF) Jun. 2024 – Current

Visiting Scholar

- Developing new protocols for systematically generating combination of multiple mutations in proteins
- Comparing different vector fluorescence systems for protein functional readouts

JOURNAL PUBLICATIONS

1. Rosace: a robust deep mutational scanning analysis framework employing position and mean-variance shrinkage
Jingyou Rao, Ruiqi Xin, Christian Macdonald, Matthew K. Howard, Gabriella O. Estevam, Sook Wah Yee, Mingsen Wang, James S. Fraser, Willow Coyote-Maestas & Harold Pimentel; *Genome Biology* 2024.

ORAL PRESENTATION

1. Research: Modeling Growth-based Deep Mutational Scanning Counts with Rosace
Variant Effect Seminar Series by Atlas of Variant Effects, August 2024. Virtual.
Recording: <https://youtu.be/Nt5juj-CgxM>
2. Workshop: What is in a variant score?
Mutational Scanning Symposium, May 2024. Boston, MA, USA.
Recording: <https://youtu.be/A5qd-oyk7EY>
3. Research: Computational Approaches for Inferring Gene Regulation in *in situ* Perturbation Screens
CSHL Biological Data Science Conference, Nov 2022. Long Island, NY, USA.

SOFTWARE

1. ROSACE: statistical inference of growth-based deep mutational scanning (DMS) screens
A Bayesian hierarchical model that employs position and mean-variance shrinkage with Stan
<https://github.com/pimentellab/rosace>

SKILLS & ACTIVITIES

Language: Chinese (native), English (working proficiency), French (elementary), Spanish (elementary)

Interests: Backpacking, Mountaineering, Ballet, Scuba diving, Ashtanga yoga