

Zachary Sailer

GRADUATE STUDENT · COMPUTATIONAL EVOLUTIONARY BIOLOGIST · SOFTWARE DEVELOPER

Harms Lab · Department of Chemistry & Biochemistry · University of Oregon

✉ zsailer@uoregon.edu | [zsailer](#) | [@zrsailer](#)

Research Interests

I am seeking to understand how protein sequence space shapes protein evolution. How does the distribution of function in sequence space determine evolutionary trajectories? What is the role of epistasis in these spaces? How do the statistical properties of sequence space scale with increasing space size? To answer these questions, I am developing new techniques and software to extract key features of sequence spaces, and then using these tools to study evolutionary trajectories through this space.

Education

PH.D. CANDIDATE IN CHEMISTRY AND BIOCHEMISTRY

UNIVERSITY OF OREGON

Eugene, OR

Sep. 2013 - Present

B.S. IN PHYSICS

CALIFORNIA POLYTECHNIC STATE UNIVERSITY

San Luis Obispo, CA

Sep. 2009 - Jun. 2013

Research Positions

GRADUATE RESEARCH STUDENT MICHAEL J HARMS, PHD

UNIVERSITY OF OREGON

Eugene, OR

Sep. 2013 - Present

CORE DEVELOPER BRIAN GRANGER, PHD

IPYTHON-JUPYTER TEAM

San Luis Obispo, CA

Dec. 2012 - Sep. 2013

UNDERGRADUATE RESEARCH STUDENT JONATHAN FERNLER, PHD

CAL POLY SAN LUIS OBISPO

San Luis Obispo, CA

Jun. 2011 - Jul. 2013

Publications

SAILER ZS*, HARMS MJ

“Molecular ensembles make evolution unpredictable”

PNAS

2017

SAILER ZS*, HARMS MJ

“High-order epistasis shapes evolutionary trajectories”

PLOS Computational Biology

2017

SAILER ZS*, HARMS MJ

“Detecting high-order epistasis in nonlinear genotype-phenotype maps”

Genetics

2017

Presentations

Invited Talk · “How Jupyter makes experimental and computational collaborations easy”

JUPYTERCON

NYC, NY

Aug. 2017

Invited Talk · “High-order epistasis makes evolution unpredictable”

SOCIETY OF MOLECULAR BIOLOGY AND EVOLUTION

Austin, TX

Jul. 2017

Poster · “High-order Interactions Create Long-Term Memory in Protein Evolution.”

GIBBS SOCIETY FOR BIOTHERMODYNAMICS

Carbondale, IL

Oct. 2016

Poster · “Long-term memory in Molecular Evolution Shapes Evolutionary Outcomes.”

PROTEIN FOLDING CONSORTIUM

St. Louis, MO

May 2016

Poster · “High-order Epistasis in Genotype-Phenotype Maps Shapes Evolutionary Outcomes”

GIBBS SOCIETY FOR BIOTHERMODYNAMICS

Carbondale, IL

Oct. 2015

Poster · “Long-term memory in molecular evolution shapes evolutionary outcomes.”

PROTEIN FOLDING CONSORTIUM

Berkeley, CA

May 2015

Speaker · “Dielectric Spectroscopy in Liquid Crystals”

AMERICAN PHYSICS SOCIETY, CALIFORNIA-NEVADA SECTION

San Luis Obispo, CA

Nov. 2012

Open Source Software

CONTRIBUTOR JUPYTER NOTEBOOKS

Web application that allows you to create and share documents that contain live code, equations, visualizations and explanatory text.

<https://github.com/jupyter/notebook>

CONTRIBUTOR IPYTHON

Command shell for interactive computing in Python that offers introspection, rich media, shell syntax, tab completion, and history.

<https://github.com/ipython/ipython>

CONTRIBUTOR LATTICEPROTEINS

2d lattice protein simulator written in Python.

<https://github.com/jbloomlab/latticeproteins>

OWNER EPISTASIS

Python API for estimating statistical high-order epistasis in large genotype-phenotype maps.

<https://github.com/harmslab/epistasis>

OWNER GPMP

Python API for analyzing, manipulating, and simulating large genotype-phenotype map data.

<https://github.com/harmslab/gpmap>

OWNER PHYLOGENETICS

Python API for managing phylogenetic projects

<https://github.com/zsailer/phylogenetics>

OWNER PHYLOPANDAS

Pandas DataFrames for Phylogenetics

<https://github.com/zsailer/phylopandas>

OWNER PYASR

Ancestral Sequence Reconstruction in Python

<https://github.com/zsailer/pyasr>

Honors & Awards

ART ROSEN MEMORIAL SCHOLAR

TOP STUDENT IN QUANTUM LABORATORY

San Luis Obispo, CA

May 2012

Teaching

WORKING ON GITHUB AS A TEAM

Guest lecture introducing bioinformatics graduate students how to contribute to open source projects on Github. (20 students)

July 2017

REPRODUCIBILITY AND OPEN SCIENCE POWERED BY JUPYTER

Guest lecture introducing bioinformatics graduate students to the Jupyter Notebook and how it can be used for reproducible research. (20 students)

July 2017

COLLABORATING ON CODE

Guest lecture introducing bioinformatics graduate students to clone, sharing, and collaborating on code using Git and Github (20 students).

July 2016

GENERAL CHEMISTRY LABORATORY

Introduce undergraduates to general chemistry laboratory techniques (40 students).

2013-2014

Mentoring

THOMAS BAILEY Biochemistry Graduate Student

Winter 2017

ABRAHAM RICKETT Biochemistry Undergraduate student

Winter 2015 - Spring 2017

SOFIE CHRISTIE Academy for Science and Engineering High School Intern

Summer 2015