Zachary **Sailer**

GRADUATE STUDENT · COMPUTATIONAL EVOLUTIONARY BIOLOGIST · SOFTWARE DEVELOPER

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

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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   *Eugene, OR*

UNIVERSITY OF OREGON   *Sep. 2013 - Present*

B.S. IN PHYSICS   *San Luis Obispo, CA*

CALIFORNIA POLYTECHNIC STATE UNIVERSITY   *Sep. 2009 - Jun. 2013*

Research Positions

PHD CANDIDATE MICHAEL J HARMS   *Eugene, OR*

UNIVERSITY OF OREGON   *Sep. 2013 - Present*

CORE DEVELOPER BRIAN GRANGER   *San Luis Obispo, CA*

IPYTHON-JUPYTER TEAM   *Dec. 2012 - Sep. 2013*

UNDERGRADUATE RESEARCH ASSISTANT JONATHAN FERNLER   *San Luis Obispo, CA*

CAL POLY SLO   *Jun. 2011 - Jul. 2013*

Publications

SAILER ZS*, HARMS MJ   *PLOS Computational Biology*

"High-order epistasis shapes evolutionary trajectories"   *May 2017*

SAILER ZS*, HARMS MJ   *Genetics*

"Detecting high-order epistasis in nonlinear genotype-phenotype maps"   *March 2017*

Honors & Awards

TRAVEL AWARD   *Austin, TX*

SCIPY CONFERENCE 2017   *June 2017*

ART ROSEN MEMORIAL SCHOLAR   *San Luis Obispo, CA*

TOP STUDENT IN QUANTUM LABORATORY   *May 2012*

Presentations

Accepted Speaker · "How Jupyter makes computational and experimental collaborations easy."   *New York City, NY*

JUPYTERCON 2017   *August 2017*

Accepted Speaker · "High-order epistasis is inevitable in molecular systems."   *Austin, TX*

SOCIETY OF MOLECULAR BIOLOGY AND EVOLUTION MEETING   *July 2017*

Poster · "High-order Interactions Create Long-Term Memory in Protein Evolution."   *Carbondale, IL*

GIBBS SOCIETY FOR BIOTHERMODYNAMICS   *Oct. 2016*

Poster · "Long-term memory in Molecular Evolution Shapes Evolutionary Outcomes."   *St. Louis, MO*

PROTEIN FOLDING CONSORTIUM   *May 2016*

Poster · "High-order Epistasis in Genotype-Phenotype Maps Shapes Evolutionary Outcomes"   *Carbondale, IL*

GIBBS SOCIETY FOR BIOTHERMODYNAMICS   *Oct. 2015*

Poster · "Long-term memory in molecular evolution shapes evolutionary outcomes.""   *Berkeley, CA*

PROTEIN FOLDING CONSORTIUM   *May 2015*

Speaker · "Dielectric Spectroscopy in Liquid Crystals"   *San Luis Obispo, CA*
AMERICAN PHYSICS SOCIETY, CALFORNIA-NEVADA SECTION   *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.
github.com/jupyter/notebook

CONTRIBUTOR IPYTHON
Command shell for interactive computing in Python that offers introspection, rich media, shell syntax, tab completion, and history.
github.com/ipython/ipython

CONTRIBUTOR LATTICEPROTEINS
2d lattice protein simulator written in Python.
github.com/zsailer/latticeproteins

OWNER EPISTASIS
Python API for estimating statistical high-order epistasis in large genotype-phenotype maps.
github.com/harmslab/epistasis

OWNER GPMAP
Python API for analyzing, manipulating, and simulating large genotype-phenotype map data.
github.com/harmslab/gpmap

OWNER PHYLOGENETICS
Python API for managing phylogenetic projects, constructing phylogenetic trees, and reconstructing ancestral sequences.
github.com/zsailer/phylogenetics

Teaching

CH410/510: COMPUTATIONAL BIOINFORMATICS   *March-June 2017*
Introduced graduate students to scientific computation, simulation, regression, and statistics in Python.
Students were exposed popular open source software tools/packages like Jupyter Notebooks, Pandas,
Scikit-learn, Numpy, Scipy, and Matplotlib. (30 students)

COLLABORATING ON CODE   *July 2016*
Guest lecture introducing bioinformatics graduate students to clone, sharing, and collaborating on code
using Git and Github (20 students).

CH210: GENERAL CHEMISTRY LABORATORY   *2013-2014*
Introduce undergraduates to general chemistry laboratory techniques (40 students).

Mentoring

THOMAS BAILEY Biochemistry Graduate Student   *Winter 2017*
ABRAHAM RICKETT Biochemistry Undergraduate student   *Winter 2015 - Present*
SOFIE CHRISTIE Academy for Science and Engineering High School Intern   *Summer 2015*