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

Graduate Research Assistant 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   *Proceedings of the National Academy of*
                                                                 Sciences of the United States of America

"Molecular ensembles make evolution unpredictable"   *2017*

Sailer ZS*, Harms MJ   *PLOS Computational Biology*

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

Sailer ZS*, Harms MJ   *Genetics*

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

Honors & Awards

Art Rosen Memorial Scholar   *San Luis Obispo, CA*

Top student in Quantum Laboratory   *May 2012*

Presentations

Invited Talk · "How Jupyter makes experimental and computational collaborations easy"   *NYC, NY*

JupyterCon   *Aug. 2017*

Invited Talk · "High-order epistasis makes evolution unpredictable"   *Austin, TX*

Society of Molecular Biology and Evolution   *Jul. 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, CALIFORNIA-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.
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 GPMAP
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

Teaching

WORKING ON GITHUB AS A TEAM   *July 2017*
Guest lecture introducing bioinformatics graduate students how to contribute to open source projects
on Github. (20 students)

REPRODUCIBILITY AND OPEN SCIENCE POWERED BY JUPYTER   *July 2017*
Guest lecture introducing bioinformatics graduate students to the Jupyter Notebook and how it can be
used for reproducible research. (20 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).

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*