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 physicist, turned software developer, turned evolutionary biologist. I currently study protein evolution – particularly the mechanisms that shape how proteins evolve. My research is motivated by the broad question: *how does a protein's genotype-phenotype map shape its evolution?*. Specifically, I have written a lot about epistasis and how it shapes evolutionary trajectories in protein genotype-phenotype maps. I am also passionate about open and reproducible science. Adjacent to my research, I work hard to develop software that makes reproducibility simple.

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 STUDENT MICHAEL J HARMS, PHD   *Eugene, OR*
UNIVERSITY OF OREGON   *Sep. 2013 - Present*

CORE DEVELOPER BRIAN GRANGER, PHD   *San Luis Obispo, CA*
IPYTHON-JUPYTER TEAM   *Dec. 2012 - Sep. 2013*

UNDERGRADUATE RESEARCH STUDENT JONATHAN FERNLER, PHD   *San Luis Obispo, CA*
CAL POLY SAN LUIS OBISPO   *Jun. 2011 - Jul. 2013*

Publications

SAILER ZS*, HARMS MJ   *PNAS*
"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*

SAILER ZS*, SUMMERS RL, SHAFIK SH, JOULE A, MARTIN RE, AND HARMS MJ   *In Prep*
"Predicting evolutionary trajectories towards chloroquine resistance in a plasmodium falciparum
genotype-phenotype map."   *2018*

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*

Invited Talk · "Dielectric Spectroscopy in Liquid Crystals"   *San Luis Obispo, CA*
AMERICAN PHYSICS SOCIETY, CALFERNIA-NEVADA SECTION   *Nov. 2012*

Highlighted 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

CONTRIBUTOR BIOPYTHON

Python tools for computational molecular biology

https://github.com/biopython/biopython

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 PHYLOPANDAS

Pandas DataFrames for Phylogenetics

https://github.com/zsailer/phylopandas

OWNER PHYLOGENETICS

Python API for managing phylogenetic projects

https://github.com/zsailer/phylogenetics

OWNER PYASR

Ancestral Sequence Reconstruction in Python

https://github.com/zsailer/pyasr

Honors & Awards

TRAVEL AWARD	*Austin, TX*
SCIPY 2017	*July 2017*
TRAVEL AWARD	*New York City, NY*
JUPYTERCON 2017	*August 2017*
ART ROSEN MEMORIAL SCHOLAR	*San Luis Obispo, CA*
TOP STUDENT IN QUANTUM LABORATORY	*May 2012*

Teaching

WORKING ON GITHUB AS A TEAM	*September 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)

SCIENTIFIC PYTHON COURSE (TA)	*March-June 2017*

Introduce graduate students to scientific computing, basic machine-learning, and image processing in Python. (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 (TA) *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 - Spring 2017*
SOFIE CHRISTIE Academy for Science and Engineering High School Intern *Summer 2015*