

GRADUATE STUDENT · COMPUTATIONAL EVOLUTIONARY BIOLOGIST · SOFTWARE DEVELOPER

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

☑ zsailer@uoregon.edu | ☑ zsailer | У @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

Eugene, OR

University of Oregon **B.S. IN PHYSICS**

Sep. 2013 - Presen

CALIFORNIA POLYTECHNIC STATE UNIVERSITY

San Luis Obispo, CA

Research Positions

GRADUATE RESEARCH ASSISTANT MICHAEL J HARMS

Eugene, OR

University of Oregon

3cp. 2013 - 1 1c3c11

CORE DEVELOPER BRIAN GRANGER

San Luis Obispo, CA

IPYTHON-JUPYTER TEAM

Dec. 2012 - Sep. 2013

UNDERGRADUATE RESEARCH ASSISTANT JONATHAN FERNIER

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"

In Review

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

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

Carbondale, IL

GIBBS SOCIETY FOR BIOTHERMODYNAMICS

UCL. 2016

 $\textit{Poster} ~\cdot~ \text{``Long-term memory in Molecular Evolution Shapes Evolutionary Outcomes.''}$

St. Louis, MO

PROTEIN FOLDING CONSORTIUM

May 2016

 $\textbf{\textit{Poster}} ~\cdot~ \text{``High-order Epistasis in Genotype-Phenotype Maps Shapes Evolutionary Outcomes''}$

Carbondale, IL

GIBBS SOCIETY FOR BIOTHERMODYNAMICS

Poster • "Long-term memory in molecular evolution shapes evolutionary outcomes.""

Berkeley, CA May 2015

PROTEIN FOLDING CONSORTIUM

Speaker · "Dielectric Spectroscopy in Liquid Crystals"

San Luis Obispo, CA

AMERICAN PHYSICS SOCIETY, CALFORNIA-NEVADA SECTION

1000. 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, constructing phylogenetic trees, and reconstructing ancestral sequences.

https://github.com/zsailer/phylogenetics

Teaching_

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

ABRAHAM RICKETT Biochemistry Undergraduate student

SOFIE CHRISTIE Academy for Science and Engineering High School Intern

Winter 2017

Winter 2015 - Present

Summer 201