GRADUATE STUDENT · COMPUTATIONAL EVOLUTIONARY BIOLOGIST · SOFTWARE DEVELOPER

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

Research Interests_

I am physicist, turned software developer, turned evolutionary biologist. Having worked in the biological sciences throughout by graduate career, I have been acutely aware that they lag behind in software. I would like to push to field into the modern software world by leveraging and developing tools like Jupyter, XX, and XX.

Education ___

Ph.D. IN CHEMISTRY AND BIOCHEMISTRY

Eugene, OR

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

Sep. 2013 - June 2018

CALIFORNIA POLYTECHNIC STATE UNIVERSITY

San Luis Obispo, CA

Research Positions

GRADUATE RESEARCH STUDENT MICHAEL J HARMS, PHD

Eugene, OR

University of Oregon

Sep. 2013 - Presei

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"

Genetics

SAILER ZS*, HARMS MJ
"Detecting high-order epistasis in nonlinear genotype-phenotype maps"

2017

Causa 76* Hanna Mil

In Prep

SAILER ZS*, HARMS MJ

2018

"Epistasis as uncertainty."

In Prep

SAILER ZS*, SUMMERS RL, SHAFIK SH, JOULE A, MARTIN RE, AND HARMS MJ "Predicting evolutionary trajectories towards chloroquine resistance in a plasmodium falciparum

genotype-phenotype map."

2018

Presentations_

Invited Talk · "Resurrecting ancient proteins in Python."

Austin, TX

SciPy

Invited Talk · "How Jupyter makes experimental and computational collaborations easy"

NYC. NY

JupyterCon

Aug. 2017

Invited Talk • "High-order epistasis makes evolution unpredictable" Society of Molecular Biology and Evolution

Austin, TX

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

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

May 2016

GIBBS SOCIETY FOR BIOTHERMODYNAMICS

PROTEIN FOLDING CONSORTIUM

Carbondale, IL

PROTEIN FOLDING CONSORTIUM

Invited Talk · "Dielectric Spectroscopy in Liquid Crystals"

AMERICAN PHYSICS SOCIETY, CALFORNIA-NEVADA SECTION

May 2015

San Luis Obispo, CA

Nov 201

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/biopythor

CONTRIBUTOR NETWORKX

Python package for complex networks.

https://github.com/networkx/networkx

OWNER NX_ALTAIR

NetworkX graphs in Altair.

https://github.com/zsailer/nx_altair

OWNER PANDAS_FLAVOR

The easy way to write your own flavor of Pandas.

https://github.com/zsailer/pandas_flavor

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 PHYLOVEGA

Declarative tree visualizations in Python powered by Vega

https://github.com/zsailer/phylovega

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

SCHOLARSHIP RECIPIENT

Austin, TX

SCIPY 2017

New York City, NY

TRAVEL AWARD

JUPYTERCON 2017

August 2017

DECEMBER 17, 2019 ZACHARY SAILER · CV

SCHOLARSHIP RECIPIENT

Austin, TX

SCIPY 2017

ART ROSEN MEMORIAL SCHOLAR San Luis Obispo, CA

TOP STUDENT IN QUANTUM LABORATORY

May 2012

Teaching

REPRODUCIBILITY AND OPEN SCIENCE POWERED BY JUPYTER

June 20

Guest lecture introducing bioinformatics graduate students to Jupyter Lab, Binder, and RISE for reproducible research. (20 students)

Working on Github as a team September 201.

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 20:

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 201

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

LEANDER GOLDBACH INTERNATIONAL MASTERS STUDENT

May 2018 - August 2018

adas

DOUG SCHUETT SUMMER PROGRAM FOR UNDERGRADUATE RESEARCH (SPUR) STUDENT

Summer 2018

adas

THOMAS BAILEY BIOCHEMISTRY GRADUATE STUDENT

Winter 2017

adas

ABRAHAM RICKETT BIOCHEMISTRY UNDERGRADUATE STUDENT

Winter 2015 - Spring 2017

adas

SOFIE CHRISTIE ACADEMY FOR SCIENCE AND ENGINEERING HIGH SCHOOL INTERN

Summer 201

adas