

Education

- Expected 2022 **Ph.D Bioengineering**, *University of Virginia*, Charlottesville, VA.
Advisor: Phil Bourne
- 2014 **B.S. Bioinformatics**, *University of California, Santa Cruz*, Santa Cruz, CA.
Thesis: *Correcting Frameshift Mutations in Transcriptomics Data*
Advisors: Mark Blaxter (Edinburgh), Dietlind Gerloff

Research Experience

- Jan 2018– **PhD student**, *Univeristy of Virginia*, Charlottesville, VA.
Work with Phil Bourne, collaborate w/ Anna Panchenko (NIH/NCBI)
Applying 3D Convolutional Neural Networks to predict protein-protein interactions.
- Sep 2015– **Predoctoral Fellow**, *National Institutes of Health*, Bethesda, MD.
Worked with Phil Bourne and Michael Grigg (NIH/NIAID)
Knocked out *T. gondii* surface proteins with CRISPR/Cas9 to understand function, evolution
- Sep 2015– **Graduate Student Intern**, *Harvard Medical School*, Boston, MA.
May 2016 Worked under Debora Marks and Chris Sander
Helped develop a python framework for coevolutionary sequence analysis
Added coevolutionary restraints into *Phenix* to improve low-resolution X-ray structures
- Jan-Aug 2015 **Postbac Fellow**, *National Center for Biotechnology Information*, Bethesda, MD.
Worked under Alexey Shaytan in Anna Panchenko's group
Wrote HistoneDB 2.0 Django webserver to classify histone sequences by variant with HMMs
- Apr-Dec 2014 **Student Assistant**, *Lawrence Berkeley National Labs*, Berkeley, CA.
- Sum 2010-11 Worked under Nigel Moriarty in Paul Adam's Lab
Validated and modelled glycoproteins by ligand fitting and built 2D carbohydrate builder
- Sep-Dec 2013 **Undergraduate Researcher**, *The University of Edinburgh*, Edinburgh, UK.
Worked under Martin Jones in Mark Blaxter's Lab for UCSC Senior Thesis
Wrote HSP-Tiler to fix frameshift mutations in RNAseq data using python, BLAST, HMMs
- May-Aug 2013 **Amgen Scholar**, *Washington University in St. Louis*, St. Louis, MO.
Worked under Garland Marshall
Wrote python script to add subsituents to drugs and screened with OpenEye docking
- Sep 2010– **Undergraduate Researcher**, *University of California, Santa Cruz*, Santa Cruz, CA.
May 2013 Worked under Dietlind Gerloff
Created webserver to study evolution of Malarial surface proteins and release homology models

Publications

Published

Thomas A. Hopf, ..., **Eli J. Draizen**, ..., Chris Sander, and Debora S. Marks. The EVcouplings Python framework for coevolutionary sequence analysis. *Bioinformatics*, 2018.

Cameron Mura, **Eli J. Draizen**, and Philip E. Bourne. Structural biology meets data science—does anything change? *Current Opinion in Structural Biology*, 2018.

Nigel W. Moriarty, **Eli J. Draizen**, and Paul D. Adams. A restraints editor for generation and customisation of geometry restraints. *Acta Cryst. D*, 73(2):123–130, Feb 2017.

Lei Xie, **Eli J. Draizen**, and Philip E. Bourne. Harnessing big data for systems pharmacology. *Annu Rev Pharmacol Toxicol.*, 57(1):245–262, 2017.

Eli J. Draizen, ..., David Landsman, and Anna R. Panchenko. HistoneDB 2.0: a histone

database with variants – an integrated resource to explore histones and their variants. *Database*, 2016:baw014, 2016.

In Preparation

Nigel W. Moriarty, **Eli J. Draizen**, and Paul D. Adams. CarboLoad: Modelling, validation, and prediction of carbohydrates in phenix.

Eli J. Draizen, D. Steve Hall, Felecia D. Kemp, Jonathan Magasin, and Dietlind L. Gerloff. Plasmodium 6-Cys model database.

Eli J. Draizen, Edward Y. Liaw, Jonathan Magasin, D. Steve Hall, Felecia D. Kemp, and Dietlind L. Gerloff. Tracking the evolutionary link between distant Apicomplexan surface protein families by their distinct disulfide patterns.

Invited Talks

- July 6, 2018 **ISMB-ISCB Student Council Symposium**, *Deep Learning Approaches to Predict Protein-Protein Interactions*, Chicago, IL.
- July 21, 2017 **ISMB-ISCB Student Council Symposium**, *Determining the functions of the Apicomplexan SRS/6-Cys protein family: A Structural and Evolutionary Understanding of Pathogen Invasion*, Prague, CZ.
- May 14, 2015 **ICSB RSG-DC Student Research Symposium**, *Classification of Histone Variants*, College Park, MD.

Poster Presentations

- 2018 **ISMB-ISCB Student Council Symposium**, *Deep Learning Approaches to Predict Protein-Protein Interactions*, Chicago, IL.
Eli J. Draizen, Alexander Goncarencu, Cameron Mura, Anna R. Panchenko, Philip E. Bourne
- 2018 **NIH Graduate Student Research Symposium**, *Identifying Structural Motifs involved in Protein-Protein Interactions using Deep Neural Networks*, Bethesda, MD.
Eli J. Draizen, Alexander Goncarencu, Anna R. Panchenko, Philip E. Bourne
- 2017 **ISMB-ISCB Student Council Symposium**, *Determining the functions of the Apicomplexan SRS/6-Cys protein family: A Structural and Evolutionary Understanding of Pathogen Invasion*, Prague, CZ.
Eli J. Draizen, Beth Gregg, Philippe Youkharibache, Dietlind L. Gerloff, Michael E. Grigg, Philip E Bourne
- 2016 **International Workshop on Bioinformatics and Systems Biology**, *Predicting circadian gene expression in *Nuerospora crassa**, Tokyo, JP.
Alan Pacheco, Yuqing Zhang, **Eli Draizen**, Matthew Sachs, Deborah Bel-Pedersen, James Galagan
- 2013 **Amgen Scholars Closing Symposium**, *Developing Epigenetic Therapeutics for the Eradication of Latent HIV*, Washington Univ. in St. Louis, St. Louis, MO.
Eli J. Draizen, Matthew K. Nguyen, Isaac B. Henson, Chris M. W. Ho, Garland R. Marshall
- 2012 **Research Review Day**, *The Evolutionary Link Between Coccidian SRS Proteins and the Malarial '6-Cys'-DomainFamily: New Clues from Modelled Structures*, Santa Cruz, CA.
Dietlind L Gerloff, Edward Liaw, **Eli Draizen**, David S Hall, Felicia Kemp, Richard Carter
- 2011 **Undergraduate Research Symposium**, *Bioinformatics Data Preparation Enables Effective Searches For Malarial Antigen Homologs*, Santa Cruz, CA.
Eli Draizen, Felicia Kemp, Edward Liaw, and Dietlind L. Gerloff

Outreach

- July 6, 2018 **14th Annual ISCB Student Council Symposium**, *Co-Chair*, Chicago, IL.
July 12, 2017 **ISCB RSG-DC Summer Workshop**, *Organizer*, College Park, MD.
2012-2014 **Programming for Biologists (BME160)**, *Grader/Tutor*, Santa Cruz, CA.

Skills

Languages Python, R, Perl, C/C++, Cython, Boost.Python, SQL, Javascript, Java, PHP, Obj-C
Packages PyTorch, Tensorflow, Scikit-Learn, pandas, numpy, matplotlib, Flask, Django, Biopython
Structure PyMol, Chimera, MODELLER, Phenix, CNS, HADDOCK, OpenEye, AutoDock, VMD
Sequence HMMER, HHpred, Blast, EVcouplings
Databases NCBI, PDB, Pfam, SIFTS, EupathDB

Relevant Coursework (* Graduate)

Comp. Sci. Data Structures, Algorithms, Database Systems, Machine Learning
Math/Stats Vector Calculus, Discrete Math, Linear Algebra, Differential Equations, Probability Theory, Classical/Bayesian Inference, Linear Statistical Modeling, Statistical Analysis of Network Data*
Science General Chemistry, Organic Chemistry, Biochemistry, Genetics, Cell Biology, Intro Physics: Mechanics/E&M, Advanced Macromolecular Structure/Function*, Enzyme Mechanisms*
Bioinformatics Comp Bio Tools, Bioinformatics Models/Algorithms*, Computational Genomics*, Computational Systems Biology*, Dynamics and Evolution of Biological Networks*

References

Phil Bourne

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- peb6a@virgnia.edu

Anna Panchenko

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- 301-435-5891

Dietlind Gerloff

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Mark Blaxter

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Garland Marshall

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