Eli Draizen

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Education

Expected 2022	**Ph.D Biomedical Engineering**, *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**, *University of Virginia*, Charlottesville, VA. Work with Phil Bourne & Cameron Mura Predict protein-protein interactions with 3D Convolutional Neural Networks Developing new protein clustering methods with Variational Autoencoders
Sep 2015– Aug 2018	**Predoctoral Fellow**, *National Institutes of Health*, Bethesda, MD. Worked with Phil Bourne & Michael Grigg (NIAID), Knocked out *T. gondii* surface proteins with CRISPR/Cas9 to understand function, evolution
Sep 2015– May 2016	**Graduate Student Intern**, *Harvard Medical School*, Boston, MA. Worked under Debora Marks & 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 Sum 2010-11	**Student Assistant**, *Lawrence Berkeley National Labs*, Berkeley, CA. 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– May 2013	**Undergraduate Researcher**, *University of California, Santa Cruz*, Santa Cruz, CA. Worked under Dietlind Gerloff Predicted structures of Malarial surface proteins with MODELLER and HMMER Created a public webserver to share structures

Publications

Published

Daniele Parisi*, Gabriel J. Olguín-Orellana*, **Eli J. Draizen*** Draizen, ..., and R. Gonzalo Parra. Nurturing tomorrow's leaders: The iscb student council symposia in 2018. *F1000Research*, 2019.

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.

Preprints

Menuka Jaiswal, Saad Saleem, Yonghyeon Kweon, **Eli J Draizen**, Stella Veretnik, Cameron Mura, and Philip E. Bourne. Deep learning of protein structural classes: Any evidence for an 'urfold'?, 2020.

Sean Mullane, Ruoyan Chen, Sri Vaishnavi Vemulapalli, Eli J. Draizen, Ke Wang, Cameron Mura, and Philip E. Bourne. Machine learning for classification of protein helix capping motifs, 2019.

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 15, 2020 **ISMB**-**3DSig**, *Deep Learning of Protein Structural Classes: Any Evidence for an 'Urfold'?*, Virtual, https://doi.org/10.5281/zenodo.3909755.

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

2020 **ISMB**-**3DSig**, *A Data-engineering Pipeline for Deep Learning in Structural Bioinformatics*, Virtual, https://doi.org/10.5281/zenodo.3914449.
Eli J. Draizen, Cameron Mura, Philip E. Bourne

2019 **7th CAPRI**, *Template-based protein interaction and binding affinity predictions for deep learning*, Hinxton, UK, https://doi.org/10.5281/zenodo.2641017.
Eli J. Draizen, Zheng Zhao, Cameron Mura, Philip E. Bourne

2018 **ISMB**-**ISCB Student Council Symposium**, *Deep Learning Approaches to Predict Protein-Protein Interactions*, Chicago, IL.
Eli J. Draizen, Alexander Goncearenco, 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 Goncearenco, 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, SQL, Javascript, Java, PHP, Obj-C
Frameworks	PyTorch, Keras, Tensorflow, Scikit-Learn, pandas, numpy, matplotlib, Seaborn
Web	Flask, Django, SQLAlchemy, Bootstrap, Jekyll, D3
Cloud/HPC	AWS, Mesos, Slurm, SGE, LSF, Toil, boto, Snakemake, CWL
Structure	HADDOCK, CNS, PyMol, MODELLER, APBS, Phenix, Chimera, AutoDock, VMD
Sequence	HMMER, HHpred, Blast, Biopython, EVcouplings, MUSCLE, UCLUST, FastTree, RAxML
Databases	CATH, EPPIC, ECOD, SCOPe, NCBI, PDB, Pfam, SIFTS, EupathDB

Relevant Coursework (* Graduate)

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