Jeremiah Gaiser

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PROFILE

I am a doctoral student in the University of Montana's Biochemistry program. My research interests are in development of machine learning approaches to drug discovery and toxicology prediction. I graduated in May of 2020 from the University of Montana with a Bachelors of Science in Computational Biochemistry and minors in Math and Computer Science. As an undergraduate researcher, I developed a foundation in genetic sequencing and annotation methods in genomics research. Before my undergraduate education, I worked as a professional web developer.

EDUCATION

THE UNIVERSITY OF MONTANA, Missoula, MT **May 2020**

- Bachelors of Science in Computational Biochemistry, GPA 3.63. Minors in Computer Science and Mathematics

- Selected as Outstanding Graduating Computational Biochemistry Senior.

WORK AND RESEARCH EXPERIENCE

UNIVERSITY OF MONTANA, Missoula, MT

Undergraduate researcher (Wheeler Lab / Grimes Lab) **June 2017-present**

- Deep learning models for drug discovery
    - Advisor: Travis Wheeler (University of Montana)
    - Context: Joint European Disruptive Initiative Covid-19 drug discovery contest, collaborative with Amit Roy (RML) and Vishwesh Venkatraman (Norwegian University of Science and Technology)
    - Focus: latent-space representation of ligands and proteins as foundation for binding affinity prediction
    - Technology: PyTorch, cluster compute.

- Developed model for annotating protein-coding DNA sequence
    - Advisor: Travis Wheeler
    - probabilistic model for sequence alignment of amino acid to codon, based on codon neighborhood
    - Implemented in C programming language and integrated into fork of HMMER codebase

- Investigation of annotation of conserved, non-coding elements across eukaryotic genomes
    - Advisors: Martin Frith (University of Tokyo), Travis Wheeler (University of Montana)
    - Used large volumes of genome-scale metadata (Uniprot, Dfam, fRNAdb) and sequence alignment tools (HMMER, LAST) to estimate conservation in non-coding sequences in eukaryotic genomes.
    - Project initiated during summer internship at the University of Tokyo

- Cytoscape Network Browser (http://cytoscape.cs.umt.edu/)
    - Advisors: Mark Grimes (University of Montana), Travis Wheeler (University of Montana)
    - Developed graphical user interface for visually navigating protein interaction networks
    - Built and implemented application architecture using several different technologies, including cytoscape and its API, R, python, and front-end web technologies and frameworks such as HTML, CSS, javascript, cytoscape.js, jquery, and react.js.
    - Exercised communication and teamwork with co-developer
    - Manuscript: http://stke.sciencemag.org/content/11/531/eaaq1087.abstract

PRIME INCORPORATED, Bozeman, MT

Web Developer **May 2015 - August 2016**

- Development of websites and applications for small to medium sized businesses
    - Used frontend and backend technologies including HTML, javascript, css, jquery, PHP, and content-management systems including Expression Engine and CraftCMS.
    - Worked with team of developers, designers, and managers
    - Communicated with clients via email, phone, and in person to discuss projects

RELEVANT COURSEWORK

Genomics	Genetics and Evolution	Organic Chemistry
Biochemistry (including lab)	Machine Learning	Design/Analysis of Algorithms
Nucleic Acids	Data Analysis	Cellular and Molecular Biology