David Foutch | Computational Biologist | 3008 Nottingham Cir Mt. Juliet, TN 37122 | Email: dfoutch@analysisandinformatics.org | 865-208-3646 | Personal website | GitHub | LinkedIn

SKILLS:

- *Graph Theory & Network Analysis:* Extensive experience in leveraging graph theoretical concepts such as betweenness, closeness, degree, and eigenvector centrality to analyze biological networks and identify critical biological features.
- *Bioinformatics & Computational Biology:* Proficient in using bioinformatics tools and computational approaches, including PyMOL plugin development, AutoDock, PyRx, and graph neural networks (GNNs), to advance research in protein function, drug discovery, and molecular interactions.
- *Statistical Analysis & Data Extraction:* Strong background in statistical analysis, including the use of SQL for extracting and analyzing clinical phenotypes from electronic health records. Experienced in conducting research to inform drug repurposing and addiction studies.
- *Web Application Development:* Skilled in designing and deploying CI/CD pipeline-driven web applications using Flask, Dash, and AWS Amplify. Capable of developing applications that enable comprehensive analysis of biological networks and data visualization.
- *Programming Languages:* Proficient in Python, SQL, Bash, and MATLAB, with hands-on experience in using libraries such as Pandas, NumPy, Matplotlib, NetworkX, Plotly, and py3Dmol for data analysis and visualization.
- *Automation & Scripting:* Experienced in automating tasks such as the retrieval and analysis of PDB crystal structures and implementing scripts for complex data processing and analysis in research projects.
- *Scientific Communication:* Demonstrated ability to convey complex scientific concepts through presentations and publications, with a strong track record of contributing to peer-reviewed journals.

WORK EXPERIENCE:

Blind Lab at Vanderbilt University Medical Center | May 2023 to present | Collaborator

- Leveraged graph theory, bioinformatics, and statistical analysis to uncover physical mechanisms linking docked ligand binding energy and functional regulation in LRH1. *In publication.*
- Developed an easy-to-install PyMOL plugin designed for visualizing graph theoretical properties of protein structure networks including betweenness, closeness, degree, and eigenvector centrality, facilitating the identification of allosteric communication pathways, functional “hot spots”, and regions crucial to biological function. *In preparation.*
- Designed and deployed a CI/CD pipeline-driven web application leveraging GitHub for version control and AWS Amplify for hosting. The application, built with Python's NetworkX, Plotly, py3Dmol, and Dash, provides comprehensive analysis of network properties in primary, secondary, and tertiary protein structures, enabling deeper insights into protein function and interactions.

- Leading a graph-theoretical initiative to characterize the chemical and graph theoretical properties of allosteric binding sites using AutoDock's and PyRx with a curated library of small-molecules, advancing computational drug discovery.
- Currently designing a project leveraging graph neural networks (GNNs) and protein structure networks to evaluate p53 protein structures and quantify potential conformational rearrangements associated with loss-of-function and rescue mutations.

Center for Precision Medicine at Vanderbilt University Medical Center | May 2021 to May 2023 | Statistical Analyst

- Extracted clinical phenotypes from electronic health record data using SQL, sourced from the Vanderbilt Institute for Clinical and Translational Research, to inform research on prenatal opioid addiction and Alzheimer's drug repurposing.
- Developed and launched a clinical informatics web application using Flask, Neo4j, and D3.js to investigate relationships between standardized medical codes (ICD-9, ICD-10, CUI, CPT) for more efficient exploration and analysis of potential drug repurposing opportunities.

Nexus Information Systems | July 2020 to May 2021 | Independent Consultant

- Automated retrieval and analysis of 130+ PDB crystal structures which informed the identification of essential contact interactions in RORγ. *In publication.*
- Delivered presentations on MRI physics, convolutional neural networks applied to fMRI analysis, and preliminary work on fMRI analysis using MATLAB's Statistical Parametric Mapping.

EDUCATION:

- University of Tennessee Knoxville | Aug 2015 to May 2020 | MS in Genome Science and Technology
  - MS Thesis: *"Network Analysis of Protein Structure Networks Upon Ligand Binding"*
  - Published as *"Protein conformational switch discerned via network centrality properties"* in Computational and Structural Biotechnology Journal | 2021 | https://doi.org/10.1016/j.csbj.2021.06.004
- Southern Illinois University Carbondale | Aug 2013 to May 2015 | ABT in Plant Systems Biology
- Southern Illinois University Carbondale | Aug 2008 to May 2013 | BS in Mathematics & BA in Experimental Psychology

PUBLICATIONS:

- **Foutch D** and Blind R.D. *"NetPy: Protein Structure Network Analysis,"* in preparation
- Haratipour H, **Foutch D**, and Blind R.D *"Heuristic of rigid docking scores,"* 2024.
- Pham B, Cheng Z, Lopez D, Lindsay RJ, **Foutch D**, Majors RT, Shen T. *"Statistical analysis of protein-ligand Interaction patterns,"* 2022.
- **Foutch D**, Pham B, Shen T. *"Protein conformational switch discerned,"* 2021.