Eli McPherson
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Bioinformatician | Machine Learning & High-Performance Computing

Summary

Bioinformatician with ten years of computational biology and in-lab biological development experience specializing in protein discovery and mapping. Passionate about tinkering and tuning code to balance computing resource utilization with appropriate hardware specifications for robust, accurate, scalable deliverables. In my current role as a bioinformatics consultant, I advise multiple clients on the technical direction of their drug discovery projects, architect machine learning algorithms to analyze multi-omics (e.g. RNASeq, protein abundance, enzyme activity) data pipelines, and use those pipelines to make protein property predictions.

Education

Master of Science in Biomedical Engineering – Boston University, 2024
Bachelor of Science in Chemical and Biological Engineering – Colorado State University, 2017

Skills

Programming Languages: Python, MATLAB, R
Machine Learning & AI tools: PyTorch, TensorFlow, scikit-learn, OR-Tools, Ray
Bioinformatics tools: PyMOL, HMMER, BLAST, KEGG, GO, STRING, HISAT2, STAR, MultiQC, Nextflow, nf-core
Cloud & infrastructure: Git, Docker, SQL, HPC workflows, AWS, Azure,
In-Lab Biological Automation Instrumentation: Hamilton STAR, Opentrons, Echo, Biostack, Synergy H1, JESS
Laboratory & Experimental Techniques: DNA Extraction, Chromatography, Assay Development, Strain Design, Directed Evolution, ELISA, Fluorescence/Luminescence Assays, High Throughput Lab Automation, Drug Discovery
Workplace Collaboration and Leadership: SOP generation and validation, verbal and written presentation of results, overseeing teams of 2-40 people, translating between cross-functional teams, project management, high-throughput automation integration

Experience

Senior Engineer | AI/ML Bioinformatician | Boston, MA | August 2024 – Present
- Propose, design, and implement bioinformatics drug target identification pipeline using PDB, GO, and STRING.
- Independently research viable methods of cell line and disease characterization for optimal client use cases. In one notable instance, identified RNAseq as the most financially viable assay methodology for client needs, and implemented large scRNAseq and bulkRNAseq dataset analysis using Nextflow, as well as associated preprocessing and differential expression analysis.
- Proposed, designed, and implemented automated neural net architecture (LLM and MLP) tuning, training, and production analysis repositories for a client using Ray, PyTorch, and Scikit-learn on GPUs, cutting down client's generation of predictive algorithms from large biological datasets from weeks to minutes/hours and maximizing recommended biomolecule feature organisms for customers by 1000%.

Student Researcher | Khalil Lab, Boston University | Boston, MA | September 2023 – August 2024
- Developed custom Python modules integrating ML algorithms for luminescence detection in DIY bioreactors (eVOLVER), resulting in successfully defended MS thesis, and robust characterization of this methodology's specific limiting factors.
- Independently led experimental design for this project and collaborated closely with Khalil lab members to integrate findings into lab's eVOLVER platform.

Senior Research Associate | Resonance Medicine | Boston, MA | January 2023 – March 2023
- Scaled a directed evolution platform from manual bench-based assays to a semi-automated, high-throughput workflow that reduced hands-on experimental time by 75%, directly resulting in improved experimental precision and associated reductions in cost for company's drug discovery pipeline.

Research Associate I/II | Joyn Bio | Boston, MA | September 2020 – October 2022
- Independently proposed and implemented an automated high-throughput robotics workflow for liquid handlers, achieving a 400% improvement in experimental throughput and 90% reduction in manual intervention.
- Developed and implemented quantitative immuno assay protocols for detection of toxic molecules in host bacterial organisms. Independently conducted and validated in vitro data analysis and communicated verbal and written results to cross-functional teams (Strain Design, Bioengineering, Leadership).
- Acted as primary liaison with external collaborator to translate results of in vitro immuno assay protocols to in vivo assay protocols, resulting in improved product efficacy validation.
- Wrote, reviewed, and validated SOP protocols for integration of laboratory automation in close collaboration with interdisciplinary teams, resulting in fundamental changes to the company's assay procedure.

Research Assistant | Colorado State University | Fort Collins, CO | August 2014 – December 2017

-   Developed novel protocols for loading guest molecules into computationally designed protein hosts, and established chemical conjugation workflows to stabilize protein crystals, resulting in two publications.

Other Experience

Founder & CEO, Paper Crane Coffee Roasters (Nov 2022 – Present)
-   Entrepreneurial leadership experience managing operations, partnerships with local Boston, MA businesses, and product quality.

Peace Corps Volunteer – Ethiopia (Jan 2018 – Mar 2020)
-   Provided community health education initiatives.

United States Marine Corps – Sergeant (Aug 2006 – Jul 2010)
-   Leadership and team coordination of 40 Marines, and mission operations management. Deployed to Iraq.

Publications

McPherson, E. (2024). Luminescence detection in eVOLVER for autonomous bioreactor control.

Huber, T. R., **McPherson, E. C.,** Keating, C. E., & Snow, C. D. (2018). Installing Guest Molecules at Specific Sites within Scaffold Protein Crystals. Bioconjugate Chemistry, 29(1), 17–22. https://doi.org/10.1021/acs.bioconjchem.7b00668

Huber, T. R., Hartje, L. F., **McPherson, E. C.,** Kowalski, A. E., & Snow, C. D. (2017). Programmed Assembly of Host–Guest Protein Crystals. Small (Weinheim an Der Bergstrasse, Germany), 13(7), np-n/a. https://doi.org/10.1002/smll.201602703