



# PATRICK FINNERTY

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 [github.com/patimus-prime](https://github.com/patimus-prime)  [gitlab.com/patimus-prime](https://gitlab.com/patimus-prime)

## Summary

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Chemist — Chemical Engineering — Bioinformatics

- 3+ years of experience in pharmaceutical R&D, bioinformatics, and data analysis/visualization
- Proficient in experimental design, testing, and characterization of biological samples; skilled in technical document writing and evaluation for regulatory compliance
- Experienced in data analysis from various assays and experimental conditions, including UV-Vis spectroscopy, mass spectrometry, viscosity/rheometry, HPLC, and bioassays
- Managed vendor relationship and served as a subject matter expert for flow imaging microscopy instrument

## Education

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**Universitat Autònoma de Barcelona**

**September 2020 – September 2021**

*M.Sc. Bioinformatics (Thesis: Analysis of Hemoprotein Binding Sites )*

*Barcelona, Spain*

**University of Arizona**

**2014 – 2018**

*B.Sc. Chemical Engineering*

*Tucson, AZ*

*B.Sc. Molecular and Cellular Biology*

*B.A. Biochemistry*

## Professional Experience

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**Eli Lilly, Bioproduct Research & Development**

**June 2018 – September 2020**

*Scientist – Formulation Chemist*

*Indianapolis, Indiana*

- Designed and executed experiments to characterize antibody formulations, assess susceptibility to degradation, and determine optimal formulations. Extensive experimental design and testing: dozens to 100s of samples, numerous assays evaluating stability/activity at multiple timepoints and temperatures. Chemicals selected from GRAS list: buffer systems, excipients, osmotic agents, and stabilizers/surfactants
- Authored and evaluated technical documents such as process development and validation reports, SOPs, and lab notebooks to ensure FDA regulatory compliance and support GMP activities; approx. 150 documents written or reviewed during 2 year tenure
- Analyzed data from approx. 20 different assays and variable experimental conditions, and built predictive models, data dashboards with Excel and PowerBI. Assessed results from UV-Vis spectroscopy, mass spectrometry, viscosity/rheometry, HPLC, bioassays, particle count, pH, and more. Maintained data integrity and experimental reproducibility via LIMS system.
- Developed SOP, served as subject matter expert (SME), and managed vendor relationship for flow imaging microscopy instrument. Method development for the instrument involved ensuring reproducibility of subvisible particle count/images at 2-100µm range. Vendor coordination: resolved problems related to instrument performance, quality of results, scientific validity

## Technical Skills

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**Lab Techniques**

HPLC, pH, flow imaging microscopy/particle analysis, HIAC particle counter, UV-Vis spectrophotometry, IR spectroscopy, gas chromatography, osmometry, rheometry, bacterial and mammalian cell culture, centrifugation, aseptic technique/fume hood/biosafety cabinet

**Data Analysis**

Excel, PowerBI, Python, R

**Statistics**

PCA/MDS, ANOVA, SVM, GNB, linear/logistic regression, clustering and multi-class classification, time-series analysis, signal processing, detrending

**Data Visualization**

Streamlit, Dash, Quarto, matplotlib, seaborn; Rmarkdown, xaringan, ggplot2, plotly

*Research & Projects below!*

## Research & Projects

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### Rare Genetic Disease Investigation 🔗

Oct 2022 – Present

*Python, Nextflow, Kubernetes, Google Cloud, Azure, gnomAD*

- Investigating population prevalence of a rare genetic disorder, variant annotation of 3500 mutant proteins
- Implement Nextflow pipeline that ingests protein sequence data and distributes jobs to Kubernetes cluster to generate cheminformatic data, protein structures via OpenFold/AlphaFold; model protein interactions with ligands and chaperone proteins at relevant pH conditions, i.e. 6 to 7.4., simulate interaction energies via DiffDock
- Conduct statistical analysis of interaction energy results to determine if there are significant differences between approx. 160 predicted deleterious variants and wildtype proteins

### Full Stack App Development 🔗

May 2022 – Present

*JavaScript/Typescript, Next.js, React, Python, Streamlit*

- Developed website that presents portfolio work, prototype notebooks, and apps, linked from this resume: 🍷
- Front-end development: Designed and developed the user interface and user experience (UI/UX) of the website, using React and Mantine components, totaling 20+ pages/customized components, ensuring a visually appealing and responsive design that is optimized for various screen sizes and devices and highly maintainable
- Back-end development: core website is developed with Nextjs framework, React, Javascript, ESL 6; data-intensive apps are implemented with Python, Streamlit, embedded as iframes; website and apps are connected to databases by clients for SQL and GraphQL
- CI/CD and version control: Static site updated and deployed to Vercel upon Git update; Streamlit embeddings are managed via Git, Poetry, Hugging Face

### Machine Learning and Statistical Analysis Projects 🔗

March 2022 – Present

*Python, PyTorch, Sci-kit, XGBoost, Statsmodels, Imbalanced-learn, Jupyter*

- Identified 100 prime candidates from 6,000 samples of high-throughput screening data; detrended spectrophotometer absorbance data, ANOVA, compared candidates to baseline expression level 🔗
- Predicted classification of protein target of 500,000 small molecules given SMILES codes: generated QSAR data with RDKit/Mordred, handled imbalanced dataset, conducted feature engineering, hyper-parameter tuning 🔗
- Analyzed high-dimensional RNASeq TCGA data (20,000 genes x 1000 tumor samples): gene expression analysis; merged with clinical data, successfully predicted negative cancer status 🔗

### Master's Thesis: Analysis of Hemoprotein Binding Sites 🔗

April 2021 – September 2021

*Python, R, R Markdown, UCSF Chimera*

*Barcelona, Spain*

- Designed and programmed robust pipeline to simulate/extract structural data from 100 proteins sourced from RCSB PDB; Python used to generate data from simulation software, R to organize and visualize data
- Implemented high-throughput functionality for 8+ features for Chimera molecular visualization software
- Wrangled and integrated data from 9 heterogeneous datasets; visualized and analyzed data, and automated reporting

## Professional Affiliations and Interests

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**Society of Hispanic Professional Engineers**

**2016 – 2023**

**American Institute of Chemical Engineers**

**2016 – 2023**

**Interests:** Cooking, reading, achieving fluency in Spanish, salsa dancing, learning piano, learning to surf, skateboarding