

Jared Croyle

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Passionate data engineer combining genomics expertise with scalable pipelines to drive actionable insights.

Education

University of California, Berkeley, B.S. in Molecular Environmental Biology & Minor in Data Science May 2025

Relevant Coursework: Machine Learning, Data Analytics, Computational Structures, Practical Genomics, General Genetics

Technical Skills

Languages & Tools: Python, R, SQL, BASH, HTML5/CSS3, Git, GitHub, Linux, MacOS, VSCode, Excel

Data Engineering: Apache Spark, Databricks, Delta Lake, Azure, Jupyter Notebooks, Pandas, NumPy

ML & Data Analysis: Scikit-learn, SciPy, Matplotlib, Seaborn, OpenCV, Feature Engineering, Clustering

Experience

Genomic Data Engineering Intern, Evolab at UC Berkeley – Berkeley, CA February 2024 – May 2025

- Developed and productionized scalable Python/BASH pipelines to ingest and transform 10K+ semi-structured genomic records, supporting biodiversity modeling and adaptive trait analysis.
- Automated ETL workflows for data integration using open-source tools and custom scripts, improving throughput by 30%.
- Built modular components for statistical validation of predictive models, visualized results using Matplotlib to support reporting for scientific and engineering stakeholders.

Genomic Data Intern, Evolutionary Genomics Lab at UC Berkeley – Berkeley, CA September 2024 – December 2024

- Designed structured metadata systems using Excel and SQL for 500+ genomic samples to ensure data integrity, reproducibility, and scalability in downstream analytics pipelines.
- Streamlined QC and cataloging pipelines, supporting long-term genomic research access.

Bioinformatics Fellow (NSF-REU), Stajich Lab at UC Riverside – Riverside, CA June 2023 – August 2023

- Developed reproducible pipelines (AMPTk, DADA2, Python) to process 7M+ metabarcode reads, generating 10K+ high-confidence ASVs and contributing to the discovery of 3 novel fungal species and 2 peer-reviewed publications.
- Applied clustering algorithms and phylogenetic analysis to microbial communities, uncovering statistical patterns to predict ecological interactions.

Veterinary Assistant and X-ray Technician, West Riverside Veterinary Hospital – Riverside, CA June 2021– May 2023

- Supported diagnostics and medical data analysis to optimize patient care and identify trends in clinical outcomes.

Projects

Genomic Variant Classifier Pipeline, <https://github.com/jaredcroyle/clinvar-variant-classifier>

- Built a production-style ML pipeline using XGBoost and SHAP to classify ClinVar genomic variants, with automated evaluation, HTML reporting, and SHAP-based interpretability.

Leadership & Service

General Member, Epsilon Eta, University of California, Berkeley January 2024 – May 2025

- Mentored undergraduate students in biology and contributed to community outreach focused on environmental justice.

Science Education Ambassador, The Aquarium of the Pacific – Long Beach, CA May 2018 – August 2019

- Supported international biodiversity monitoring and translated research into educational content for 10K+ visitors.

Awards and Publications

- Kelly, K., Liu, X., **Croyle, J.**, and Stajich, J.E. (2025). *Climate impact on the biocrust mycobiome*.
- **Croyle, J.**, Kelly, K., Liu, X., and Stajich, J. E.. *Draft genome sequence of endophytic fungus Coniochaeta sp.* (In Prep)
- Nona Award – Most impactful open-source bioinformatics platform, Nonaworks Hackathon (2024)
- Innovation Award – Most innovative project in synthetic biology software, Nonaworks Hackathon (2024)