Jared Croyle

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AI/ML engineer specializing in distributed training systems, simulation modeling, and computational genomics.
I build high-performance workflows that turn complex biological and quantitative data into interpretable, actionable systems.

Education

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

Coursework: Data Structures & Algorithms, Machine Learning, Probability & Statistics, Data Science, Computational Genomics

Experience

AI Engineer Fellow, HandshakeAI – Remote — September 2025 – Present

- Built distributed reinforcement learning pipelines powering adaptive personalization in real time
- Implemented continuous feedback systems that improved robustness and reduced inference latency
- Collaborated across engineering teams to ship production ML services and backend microservices

Data Science Intern, Evolab at UC Berkeley – Berkeley, CA — February 2024 – May 2025

- Engineered Spark pipelines for multi-terabyte datasets, reducing compute latency by 30%
- Developed probabilistic forecasting models with real-time simulation under uncertainty
- Contributed to scalable ML architecture used for experimental data analysis across the lab

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

- Built Python-based classifiers for 7M+ biological signal measurements
- Optimized Monte Carlo simulation workflows, cutting runtime by 40%
- Combined wet-lab and computational pipelines to support microbial genomics research

Projects

FastAPI Genetic Sequence Classifier – github.com/jaredcroyle/FastAPI-ML-Classifier

- PyTorch-powered DNA sequence classifier with REST endpoints built using FastAPI.
- Dockerized for full reproduction, modular model management, and deploy-ready architecture.

Trunkline: Full-Stack Predictive ML Pipeline – github.com/jaredcroyle/Trunkline-SynBioML

- Full-stack ML platform integrating ingestion, forecasting, RL-style optimization, and experiment tracking.
- Designed for scientific workflows needing automation, monitoring, and scalable orchestration.

Technical Skills

Languages & Systems: Python, C++, TypeScript, R, SQL, Bash, Linux/MacOS
Machine Learning: PyTorch, deep learning, reinforcement learning, statistical modeling
Distributed Systems: Spark, Kafka, Docker, Kubernetes, CI/CD pipelines
Engineering: API design (FastAPI), testing (PyTest), Git/GitHub workflows
Data/Modeling: Simulation & forecasting, ETL/ELT pipelines, large-scale data processing

Leadership & Service

Mentor, Epsilon Eta Professional Sustainability Fraternity, University of California, Berkeley — January 2024 – May 2025

- Mentored students in analytical reasoning, research skills, and scientific communication.

Awards and Publications

- **Nona & Innovation Award** – Most impactful and innovative bioinformatics software, Nonaworks Hackathon (2024)
- Kelly, K., Liu, X., **Croyle, J**., and Stajich, J.E. (2025). *Climate impact on the biocrust mycobiome.*