Jared Croyle

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General Resume for jaredcroyle.com

Education

University of California, Berkeley – *B.S. in* Molecular Environmental Biology & Data Science   May 2025
Relevant Coursework: Machine Learning, Data Analytics, Practical Genomics, General Genetics, The Human Genome, Evolution, Computational Structures, Probability and Statistics, Linear Algebra and Differential Equations

Technical Skills

Languages: Python, R, SQL, HTML5, CSS3, BASH

Data Engineering: Apache Spark, Databricks, Delta Lake, Jupyter Notebooks

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

Tools & Platforms: Git, GitHub, Linux, MacOS, VSCode, Excel, Word, Powerpoint

Molecular Biology & Bioinformatics: NGS Library Preparation, PCR, DNA Extraction, DNA Amplification & Purification, Microbial Culturing, Demographic Modeling, Comparative Genomics, Phylogenomics, Metagenomics, Metabarcoding Analysis

Experience

Bioinformatics and Data Engineering Intern, Evolab at UC Berkeley – Berkeley, CA   February 2024 – May 2025
  • Designed and optimized Python/BASH pipelines to process large-scale semi-structured genomic data (~10,000 sequences) for biodiversity and species adaptation research.
  • Automated data ingestion, transformation, and statistical validation of species divergence models using custom scripts and open-source libraries. Visualized insights using Matplotlib, enhancing collaboration between biologists and engineers.

Genomic Data Intern, Evolutionary Genomics Lab at UC Berkeley – Berkeley, CA   September 2024 – December 2024
  • Created and maintained structured metadata systems for 500+ insect DNA samples using Excel and SQL-based tools.
  • Streamlined data QC workflows and scalable cataloging for museum-wide genomic digitization.

Bioinformatics Research Fellow (NSF-REU), Stajich Lab at UC Riverside – Riverside, CA   June 2023 – August 2023
  • Engineered reproducible pipelines using AMPtk and DADA2 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.
  • Utilized clustering algorithms and phylogenetic analysis to identify significant microbial groups, leveraging patterns to predict ecological interactions and furthering our understanding of fungal biodiversity.

Veterinary Assistant and X-ray Technician, West Riverside Veterinary Hospital – Riverside, CA   June 2021– May 2023
  • Supported diagnostic imaging and treatment data to optimize patient care and identify trends in clinical outcomes.

Additional Experience

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.

Student Eco-Ambassador, The Aquarium of the Pacific – Long Beach, CA   May 2018 – August 2019
  • Supported international field research projects by assisting with water quality data collection and wildlife biodiversity monitoring - synthesized findings into educational materials for public engagement.

Awards and Publications

  • Kelly, K., Liu, X., **Croyle, J**., and Stajich, J.E. (2025). *Culture dependent and independent survey reveals a strong influence of climate on the biocrust mycobiome.*

  • **Croyle, J**., Kelly, K., Liu, X., and Stajich, J. E.. *Draft genome sequence of endophytic fungus Coniochaeta sp. isolated from the Mojave Desert.* (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)