

# Eric Au

[ericdotau@gmail.com](mailto:ericdotau@gmail.com) | <https://edotau.github.io/>  
(408) -786-4934 | San Francisco, CA

## EDUCATION

San Jose State University

Bachelor of Science in Applied & Computational Mathematics

- **Undergraduate Research:** A Gap-Oriented Genetic Algorithm for aligning multiple protein sequences based on computational biology concepts and principles.
- **Relevant Coursework:** Bioinformatics Numerical Analysis, Scientific Computing, Mathematical Modeling, Statistics, Data Structures and Algorithms, Differential Equations and Dynamical Systems

## COMPUTATIONAL SKILLS

- **Programing Languages:** Go(Lang), Bash/Linux, Python, HTML/CSS/JS/TS, C/C++, Mysql/Postgres, R
- **Cluster & Cloud Computing:** AWS/CDK, Google Cloud, Dask, Kubernetes, Slurm
- **APIs & Frameworks:** Apache, Docker, Django, Prefect, REST API, React, Terraform, TensorFlow

## MOLECULAR BIOLOGY

- **NGS Library Preparation & High-throughput Sequencing:** Illumina, Oxford Nanopore Technologies, Pacific Bioscience, RNA-Seq, ATAC-Seq, Whole Genome, Hi-C, Target Enrichment
- **Liquid Handling and Automation:** Agilent Bravo, Hamilton STAR, Tecan Microplate Readers
- **Quality Control & Quantification:** DNA/RNA extraction, Nanodrop, qPCR, Qubit, Tape Station

## EXPERIENCE

Mammoth Biosciences, Inc.

Software Engineer, Full Stack

Mar 2022 – Present

- Develops full stack applications and infrastructure to advance CRISPR gene-editing diagnostics platform
- Improves cloud infrastructure for submitting cloud batch jobs by optimizing cost and resource allocation
- Computational support with scientific analysis for experiments to enable cross functional team efforts

Berkeley Lights, Inc.

Software Engineer, Bioinformatics

Jun 2021 – Mar 2022

- Built scalable automation testing infrastructure for continuous integration and deployment using cloud compute engines, storage buckets, and data warehouses and improved cutting-edge bioinformatics software
- Developed computing pipelines for scRNA-SEQ and enhanced T-Cell-Receptor discovery analysis toolbox
- Engineer high quality genomic software to optimize data wrangling features on R&D Life Sciences products

Invitae Corporation

Research Associate

Jan 2021 – Apr 2021

- Designed and established validation strategies for library prep and sequencing of SARS-CoV-2 samples as public health surveillance that identified the novel strain variant CAL.20C as well as other variants
- Supported clinical sample management and developed scaling assays with laboratory automation, data analysis, software and leaded end-to-end pipeline development for exploratory projects

Duke University

Research Analyst, Molecular Genetics and Microbiology

Jul 2018 – Dec 2020

- Programed a framework which computed Illumina, Pacific Biosciences, Oxford Nanopore sequencing that produced a full 22 chromosome genome assembly that identified candidate genes and genomic changes
- Developed graph data structure that incorporated genome diversity within populations which captured detailed and accurate variant analyses of haplotype-resolved genes and/or genomic regions
- Identified allele specific enhancers from regions of open chromatin that overlap differentially expressed genes to pinpoint biological discovery of functional enhancers in the developing brain

## Stanford University

Life Science Research Professional, Genetics

Oct 2013 – Jul 2018

- Managed RNA-Seq analysis on responses to physical activity from a cohort and produced a comprehensive molecular map that accelerated the development of therapeutics and exercise recommendations
- Designed DNA/RNA isolation assays at production scale which optimized workflow and reduced cost

Senior Lab Technician, Developmental Biology

- Responsible for replenishing stock supplies, facilitated stickleback fish feeding & health monitoring to increase efficiency and quality of all laboratory experiments

## PUBLICATIONS

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- Mangan RJ, Alsina FC, Mosti F, Sotelo-Fonseca JE, Snellings DA, **Au EH**, Carvalho J, Sathyan L, Johnson GD, Reddy TE, Silver DL, Lowe CB. Adaptive sequence divergence forged new neurodevelopmental enhancers in humans. DOI: [10.1016/j.cell.2022.10.016](https://doi.org/10.1016/j.cell.2022.10.016). **Cell Press** 2022.
- Wucherpennig JI, Howes TR, Au JN, **Au EH**, Roberts Kingman GA, Brady SD, Herbert AL, Reimchen TE, Bell MA, Lowe CB, Dalziel AC, Kingsley DM. Evolution of stickleback spines through independent cis-regulatory changes at HOXDB. DOI: [10.1038/s41559-022-01855-3](https://doi.org/10.1038/s41559-022-01855-3). **Nature Ecol. Evol.** 2022.