

Eric Au

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(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, Google Cloud, Dask, Kubernetes, Slurm, Sun Grid Engine (SGE)
- 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:** Beckman Coulter Biomek, Agilent Bravo
- **Quality Control & Quantification:** Nanodrop, Qubit, Tape Station, qPCR, DNA/RNA extraction

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

Jul 2017 – 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

Oct 2013 – Jul 2017

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

PUBLICATIONS

- 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. (2022). Adaptive sequence divergence forged new neurodevelopmental enhancers in humans. **Cell**. 2022.
- Wucherpennig, JI, TR Howes, Au JN, **Au EH**, Kingman GAR, Brady SD, Herbert AL, Reimchen TE, Bell MA, Lowe CB, Dalziel AC, and Kingsley DM. Evolution of stickleback spines through independent cis-regulatory changes at HOXDB. **Nature Ecol. Evol.** 2022.