Eric Au

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

EXPERIENCE

Mammoth Biosciences, Inc.

Software Engineer, Full-Stack   Mar 2022 – Present

- Manages cloud infrastructure using CDK and Terraform to deploy load balancers, batch jobs, and serverless AWS Lambda functions to ensure consistency and efficiency across our platforms
- Develops full-stack applications incorporating Django, MySQL, and JavaScript React to answer complex questions at the intersection of computer science and biomedical research, leveraging problem-solving skills to create innovative solutions that improved the accuracy and efficiency of the CRISPR diagnostics platform
- Leads development of Kubernetes cluster in AWS Cloud (EKS) to scale Jupyter Hub Notebooks, optimizing compute cost and making the software accessible to users

Berkeley Lights, Inc.

Software Engineer, Bioinformatics   Jun 2021 – Mar 2022

- Designed architecture of testing processes and automation infrastructure to scale continuous integration and deployment of software applications, which positively impacted cross-functional teams
- Supported clinical sample management and developed computing pipelines for scaling assays in laboratory automation and leaded end-to-end pipeline development for exploratory research and development projects
- Formulated library prep and sequencing strategies for SARS-CoV-2 samples as part of public health surveillance, which led to the identification of the novel strain variant CAL.20C

Duke University

Research Analyst, Molecular Genetics and Microbiology   Jul 2018 – Dec 2020

- Created a graph data structure that includes population genome diversity and allows for accurate variant analysis of haplotype-resolved genes and genomic regions
- Programmed frameworks to compute Illumina, Pacific Biosciences, and Oxford Nanopore sequencing to assemble a full 22-chromosome genome, which leads to identified candidate genes and genomic changes
- Identified allele-specific enhancers from regions of open chromatin that overlap differentially expressed genes to pinpoint the 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 the production scale which optimized workflow and reduced cost

Senior Lab Technician, Developmental Biology

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

COMPUTATIONAL SKILLS

- **Programming Languages:** Go, Bash/Linux, Python, HTML/CSS/JS/TS, C/C++, MySQL/ Postgre, R
- **Cluster & Cloud Computing:** Amazon Web Services, Google Cloud Platform, Dask, Kubernetes, Slurm
- **APIs & Frameworks:** Apache, Boto3, Docker, Django, Prefect, React, Terraform, TensorFlow

EDUCATION

San Jose State University　　　　　**Bachelor of Science in Applied & Computational Mathematics**
- **Relevant Coursework:** Bioinformatics Numerical Analysis, Scientific Computing, Mathematical Modeling, Statistics, Data Structures and Algorithms, Differential Equations and Dynamical Systems

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. Adaptive sequence divergence forged new neurodevelopmental enhancers in humans. DOI: 10.1016/j.cell.2022.10.016. **Cell Press 2022**.
- Wucherpfennig 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. **Nature Ecol. Evol. 2022.**