

Eric Au

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EXPERIENCE

Mammoth Biosciences, Inc.

Software Engineer, Full-Stack

Mar 2022 – Present

- Manages cloud infrastructure using Cloud Formation and Terraform stacks to deploy load balancers, batch jobs, and serverless AWS Lambda functions to ensure consistency and efficiency across our platforms
- Leads development of cost-optimized Kubernetes cluster in AWS Cloud (EKS) to scale Jupyter Hub Notebooks to streamline and enhance accessibility for end-users
- Develops full-stack applications, leveraging Django, MySQL, and ReactJS that innovate creative solutions to improve the accuracy and efficiency of the CRISPR diagnostics platform and drive business value
- Communicates effectively to explain technical concepts in a concise manor, as well as proactively listen and collaborate with others to foster an environment of open communication and teamwork

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
- Displayed exceptional time management skills, prioritizing tasks effectively, managing multiple projects simultaneously, and consistently delivering high-quality work on or ahead of schedule

Duke University

Research Analyst, Molecular Genetics and Microbiology

Jul 2018 – Dec 2020

- Implemented a computational graph framework and incorporated bioinformatic algorithms, which leveraged problem-solving skills at the intersection of computer science and biomedical research
- 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

Senior Research Associate, Developmental Biology

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
- Responsible for replenishing stock supplies, and facilitated stickleback fish feeding & health monitoring, which increased 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:** Docker, Django, Flask, Prefect, NodeJS, ReactJS, Redux, Terraform
- **Business Solutions:** Adobe Illustrator, Confluence, Google Docs, Github, Jira, Lucid, Microsoft Office

EDUCATION

San Jose State University

Bachelor of Science in Applied & Computational Mathematics

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

PUBLICATIONS

- Au EH, Fauci, C, Luo Y, Mangan RJ, Snellings DA, Shoben CR, Weaver S, Simpson S, Lowe CB. Genomics: Uniting high performance and readability for genomics with Go. <https://doi.org/10.1093/bioinformatics/btad516>. **Bioinformatics** 2023.
- 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. <https://doi.org/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 HOXD8. <https://doi.org/10.1038/s41559-022-01855-3>. **Nature Ecol. Evol.** 2022.