

Eric Au

ericdotau@gmail.com | <https://edotau.github.io/>

(408)-786-4934 | New York, NY

EXPERIENCE

Mammoth Biosciences, Inc.

Software Engineer, Full-Stack

Mar 2022 – Present

- Develops full-stack applications, leveraging Django, MySQL, and ReactJS to create solutions that improve the accuracy of the CRISPR diagnostics platform and drive business value
- 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
- Orchestrate migration of applications and databases from legacy into structured dev/test/prod environments, enhancing operational efficiency, reducing deployment risks, & accelerating product delivery

Berkeley Lights, Inc.

Software Engineer, Bioinformatics

June 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
- Transformed bioinformatic solutions into revenue-generating production-grade software
- Lead library prep and sequencing strategies for SARS-CoV-2 samples as part of public health surveillance, which pinpointed the identification of the novel strain variant CAL.20C

Duke University

Data Scientist, R&D

Jul 2018 – Dec 2020

- Engineered robust RESTful API applications for streamlined retrieval of public genetic data, providing essential tools for bioinformaticians to conduct comprehensive analyses
- Optimized data processing workflows through the seamless integration of advanced job submission pipelines, facilitating the assembly of a complete Telomere to Telomere 22-chromosome genome
- Designed and deployed a state-of-the-art computational graph framework, incorporating tailored bioinformatic algorithms, showcasing adeptness in melding computer science techniques with intricate challenges in biomedical research

Stanford University

Senior Research Associate, Bioinformatics

Oct 2013 – Jul 2018

- Supported clinical sample management and developed computing pipelines for scaling assays in laboratory automation and led end-to-end pipeline development for exploratory research and development projects
- Communicates effectively to explain technical concepts in a concise manner, as well as proactively listen and collaborate with others to foster an environment of open communication and teamwork
- Displayed exceptional time management skills, prioritizing tasks effectively, managing multiple projects simultaneously, and consistently delivering high-quality work on or ahead of schedule

COMPUTATIONAL SKILLS

- **Programming Languages:** Go, Bash/Linux, Python, NodeJS, ReactJS, HTML/CSS/JS, C/C++, PHP
- **Cloud Computing:** Amazon Web Services (AWS), Google Cloud Platform (GCP)
- **APIs & Frameworks:** Dask, Docker, Django, Flask, Kubernetes, Luigi, Prefect, Redux, Slurm, Terraform
- **Database:** MySQL, Postgre

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**.
- 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 HOXD8. <https://doi.org/10.1038/s41559-022-01855-3>. **Nature Ecol. Evol. 2022**.