

Lawrence Du

Machine Learning • Biotechnology

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2911 McKinley Dr. Santa Clara, CA 95051

Skills

Techniques

Neural networks (CNNs, GANs, GraphNN, Transformers), Louvain/Leiden, k -fold cross-validation, SVMs, PCA, decision trees

Tools

Tensorflow, Pytorch, Jax, Numpy, Numba, Pandas, Sklearn, Conda, Flask, AWS, Google Cloud, Jenkins, Terraform, Docker, Metaflow, Kubernetes

Languages

Python, SQL, C#, Java, Dart, Bash, C/C++, Matlab, Some Mandarin and Spanish

Experience

* Senior Machine Learning Platform Engineer* • [Freenome](#)

Aug 2022 - Present (San Francisco, CA)

- Developed cloud based research tooling for classifying cancer disease risk using Kubernetes, Terraform, Docker, and Google Cloud.

Software Engineer - Machine Learning Engineering • [23andMe](#)

Apr 2020 - Aug 2022 (Sunnyvale, CA)

- Built a large-scale feature engineering ETL pipeline for imputed SNPs (~10 million samples x ~1 million SNPs) using AWS Batch, Metaflow, AWS Glue, and AWS Athena used to feed downstream GWAS and Polygenic Risk Score (PRS) ML models.
- Improved PRS model AUCs and auPRCs through model stacking.

Data Scientist - Ancestry Product • [23andMe](#)

Nov 2018 - Apr 2020 (Sunnyvale, CA)

- Developed Recent Ancestor Locations (RAL) - a high precision, high recall country matching algorithm which serves >10 million customers worldwide.
- Deployed RAL using MLflow and AWS Fargate
- Improved graph-based techniques for unsupervised identification of populations by identity-by-descent (IBD) relationships.

Bioinformatician IV • [Scripps Research](#)

May 2018 - Oct 2018 (San Diego, CA)

- Developed a classifier for organ transplant rejection using RNA data.
- Wrote pipelines for Nanopore long-read sequencers using CWL.

Independent Consultant • [Juno Diagnostics](#)

Sept 2017 - Feb 2018 (San Diego, CA)

- Developed patent – [US20210020314A1 - Deep learning-based methods, devices, and systems for prenatal testing](#) along with a Tensorflow based classifier for detecting prenatal genetic abnormalities from high throughput sequencing data.

Data Science Fellow • [Insight](#)

Jan 2017 - Apr 2017 (Remote Session - San Diego, CA)

- Wrote [DeepPixelMonster](#) - a Deep Convolutional Generative Adversarial Network (DCGAN) for creating pixel art (deployed as Flask App on AWS EC2).

PhD Student Biology • UC San Diego • [Scott A. Rifkin Lab](#)

Aug 2010 - May 2017 (La Jolla, CA)

- Wrote [DeepNuc](#) - a CNN model for classifying over 500,000 transcriptional start site (TSS) flanking sequences from humans, mice, fruit flies, and nematodes as well as for over 60,000 microRNA target sequences.
- Researched the role of RNA expression noise during animal development by imaging single molecule RNA expression data in >5,000 embryos and analyzing data using self-written MATLAB tools for image segmentation, fluorescence quantification, and image deconvolution.

Education

Ph.D Biology UC San Diego, 2010 - 2017

B.A. Biological Sciences *Genetics and Development, Magna Cum Laude* Cornell University, 2006 - 2010

Activities and interests

Hobbies

Running, painting, [3D modeling](#), developing a [VR game](#), and [my tech blog](#)

**Extracurricular
Activities**

UCSD GSA Lobby Corps • [BioEASI Art and Science Board](#) • Genetics Training Program Grant • Hughes Scholar (2009)
• [Cornell Undergraduate Research Board \(Vice President\)](#) • Friends of Farmworkers