

# Lawrence Du

Machine Learning • Data Science • Molecular Biology

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## Skills

### Techniques

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

### Tools

Tensorflow, Linux, Pandas, NumPy, Numba, Sklearn, Matplotlib, Flask, AWS (EC2, S3, CloudFormation, Batch, Step Functions), Conda, LaTeX, Jenkins, Metaflow, Unity Game Engine

### Programming

Python, C#, SQL, Java, Dart, Bash, MATLAB/Octave, HTML/CSS, C/C++, Perl

### Languages

Mandarin Chinese and some Spanish

## Experience

### Software Engineer II - Machine Learning Engineering • 23andMe

Apr 2020 - Present (Sunnyvale, CA)

- Wrote and optimized a large scale compute backend + pipeline for processing 200 million+ genotyping marker statistics to support improved machine learning models and Genome Wide Association Studies.
- Built out cloud infrastructure for aforementioned pipeline using Cloudformation, AWS Batch, AWS Stepfunctions, and Metaflow.

### Data Scientist - Ancestry Product • 23andMe

Nov 2018 - Apr 2020 (Sunnyvale, CA)

- Developed (and now maintain) current version of machine-learning based country matching algorithm which reaches >10 million customers worldwide.
- Adapted new Recent Ancestor Locations to run as a microservice on AWS backed hardware using MLflow for model artifact tracking.
- Improved graph-based techniques for unsupervised identification of populations by genetic relationships.

### Bioinformatician IV • Scripps Research

May 2018 - Oct 2018 (San Diego, CA)

- Wrote robust automated sequencing pipelines for Oxford Nanopore data using Common Workflow Language (CWL) for realtime microbial diagnostics, *de novo* genome assembly, and variant calling.

### Independent Consultant • Juno Diagnostics (startup - \$25 million Series A closed in May 2021)

Sept 2017 - Feb 2018 (San Diego, CA)

- Developed novel IP utilizing Tensorflow deep neural networks for identifying genetic abnormalities from sequencing of cell-free DNA.
- Created a genetic abnormality simulator derived from statistical analysis of human high throughput sequencing data.
- Authored patent description concerning deep learning applications for diagnosis of genetic conditions.

### Data Science Fellow • Insight

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

- Wrote [DeepPixelMonster](#) and created an interactive Python Flask web application hosted on Amazon AWS integrated with a Tensorflow back-end for GAN based art generation.

### PhD Student Biology • UC San Diego • Scott A. Rifkin Lab

Aug 2010 - May 2017 (La Jolla, CA)

- Performed research on RNA expression noise during animal development by imaging single molecule RNA expression data >5,000 embryos and analyzing data using self-written MATLAB tools for image segmentation, fluorescence quantification, and image deconvolution.
- Wrote [DeepNuc](#) - a CNN model for classifying over 500,000 transcriptional start site (TSS) flanking sequences from humans, mice, fruit flies, and nematodes and over 60,000 microRNA target sequences (from publically available CLEAR-CLIP data).
- Transgenically modified over 70 nematode and Drosophila strains using techniques such as GIBSON assembly, CRISPR/Cas9, MosSCI, and *PhiC31* integrase.

## 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

I enjoy running, painting. During the pandemic, I developed a VR space sim game

23andMe Spitballers Ultimate Frisbee • Machine Learning Society of San Diego • 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 (tutor)

### Extracurricular Activities

