# Lawrence Du

**Machine Learning** • **Biotechnology** • **Cloud**

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##### 2911 McKinley Dr. Santa Clara, CA 95051

## Skills

#### Techniques

Neural networks (CNNs, 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, [Rust](https://github.com/LarsDu/StarRust), SQL, [C#](https://roguestargun.com), Java, [Dart](https://github.com/LarsDu/simple_flutter_audio_recorder), Bash, C/C++, Matlab, [HTML/CSS](https://dublog.net), Some Mandarin and Spanish

## Experience

#### *Senior Machine Learning Platform Engineer* • [Freenome](https://www.linkedin.com/company/freenome/mycompany/)

##### Aug 2022 - Present (South San Francisco, CA)

* Built end-to-end scalable distributed machine learning pipelines using PyTorch, Ray, and Kubernetes for cancer detection from multi-omics data (deep sequencing cell-free methylated DNA, protein, and more).
* Built out a greenfield research engineering platform/library to support both distributed data parallel (DDP) and model parallel training strategies for large-scale cancer detection models.
* Developed and refined methylated cell-free DNA based models for Colorectal Cancer (CRC) detection.
* Deployed and managed an organization-wide MLFlow based model tracking system for reproducibility, monitoring, and automated model performance reporting using Terraform, Pulumi, and Google Cloud.

#### *Software Engineer - Machine Learning Engineering •* [*23andMe*](https://www.linkedin.com/company/23andme/mycompany/)

##### 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 approaches.

#### *Data Scientist - Ancestry Product •* [*23andMe*](https://www.linkedin.com/company/23andme/mycompany/)

##### Nov 2018 - Apr 2020 (Sunnyvale, CA)

* Developed and deployed (using MLFlow + AWS Fargate) Recent Ancestor Locations (RAL) - a high precision, high recall country matching algorithm which serves >13 million customers worldwide
* Improved graph-based techniques for unsupervised identification of populations by genetically based identity-by-descent (IBD) family relationships.

#### *Bioinformatician IV •* [*Scripps Research*](https://www.scripps.edu/science-and-medicine/cores-and-services/bioinformatics-core/index.html)

##### 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 Common Workflow Language.

#### *Independent Consultant •* [*Juno Diagnostics*](https://www.linkedin.com/company/juno-diagnostics/)

##### Sept 2017 - Feb 2018 (San Diego, CA)

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

#### *Data Science Fellow •* [*Insight*](https://insightfellows.com/data-science)

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

* Built and deployed (as a Flask app on AWS EC2) [DeepPixelMonster](https://github.com/LarsDu/DeepPixelMonster) - a Tensorflow based GAN for creating pixel art, back when GANs were still relatively state-of-the art.

#### *PhD Student Biology • UC San Diego •* [*Scott A. Rifkin Lab*](http://labs.biology.ucsd.edu/rifkin/)

##### Aug 2010 - May 2017 (La Jolla, CA)

* Wrote [DeepNuc](https://github.com/LarsDu/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

* [Developing the VR game Rogue Stargun (https://roguestargun.com)](https://roguestargun.com)
* [3D modeling with Blender3D](https://sketchfab.com/3d-models/walken-23f4b6f0dcea4bf3afe714a59a9473e9)
* [Painting](https://dublog.net/images/stable-diffusion-img2img/larryd.png)
* [DuBlog (https://dublog.net)](https://dublog.net) - Self deployed using Google Cloud, Hugo, and Github Actions