# Lawrence Du

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

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

## Skills

#### Techniques

Neural networks (Transformers, CNNs, GraphNN, Diffusion), Large Language Models (LLMs), SVMs, PCA, KNN, decision trees

#### Tools

PyTorch, TensorFlow, Numpy, Numba, Pandas, Sklearn, Flask, AWS, Google Cloud, Terraform, Pulumi, Docker, Metaflow, Kubernetes

#### Languages

Python, C/C++, [Rust](https://github.com/LarsDu/StarRust), SQL, [C#](https://roguestargun.com), Java, [Dart](https://github.com/LarsDu/simple_flutter_audio_recorder), Bash, [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 - Jun 2024 (South San Francisco, CA)

* Led greenfield project building end-to-end scalable distributed machine learning platform using PyTorch, Ray, and Kubernetes for cancer detection from deep sequencing (methylated DNA) and protein data.
* Built scalable multitask learning, elastic net, and neural network based models with improved performance for classifying Colorectal Cancer risk from cell-free DNA data.
* Piloted a project to summarize biomedical literature using an LLM, first using GPT-4 and then via fine-tuning an open source LLM using DPO (direct policty optimization).
* 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 • Data Scientist (prior to 2020) - Ancestry Product* [*23andMe*](https://www.linkedin.com/company/23andme/mycompany/)

##### Nov 2018 - 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 auPRC performance metrics through model stacking approaches.
* Developed and deployed (using MLFlow + AWS Fargate) Recent Ancestor Locations (RAL) - a high precision, high recall country matching algorithm which serves >15 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 and 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