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, SQL, C#, Java, Dart, Bash, HTML/CSS, Some Mandarin and Spanish

Experience

Senior Machine Learning Platform Engineer • Freenome

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

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

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

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)

Built and deployed (as a Flask app on AWS EC2) 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

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

- Developing the VR game Rogue Stargun (https://roguestargun.com)
- 3D modeling with Blender3D
- Painting
- DuBlog (https://dublog.net) Self deployed using Google Cloud, Hugo, and Github Actions