Lawrence Du

Machine Learning • Data Science • Molecular Biology

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825 E. Evelyn Ave. Apt 414, Sunnyvale CA 94086

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, Sklearn, Matplotlib, Flask, Amazon EC2, Conda, LaTeX, Jenkins

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)

- Major contributor to a new AWS Athena backed service used by researchers for pulling imputed single nucleotide polymorphism metadata used by machine learning models and GWAS pipelines.
- Created automated model validation pipelines for supporting new deployments of country-matching algorithm*see below* (using Jenkins and MLflow).

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/Mindwerks (startup)

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, and during the pandemic,I worked on making a VR space shooter simulator.
Extracurricular Activities	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) • Triple Helix (writer) • Friends of Farmworkers (tutor)