

Machine Learning • AR/XR

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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

DuGames • Owner/Founder

- Solo-developed Rogue Stargun, a pandemic hobby gamedev project that developed into a full fledged shipped VR space shooter sim. Released to Meta Applab in Februrary 2024 and Steam in March 2024.
- Developed text-to-speech synthesis integrations for the Unity Game engine editor with ElevenLabs.io, Google Cloud, and Microsoft Azure for rapid single-player campaign dialogue generation. Rogue Stargun was an ElevenLabs Grant Recipient.
- Optimized draw calls using static batching, gpu instancing, custom shaders, and baked materials to achieve acceptable (>72 fps) frame rates for the Oculus Quest platform.

Freenome • Senior Machine Learning Platform Engineer

08/2022 - 06/2024 (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, enabling training of much larger models leveraging data distributed parallel (DDP)
 processing.
- Deployed and managed an organization-wide MLFlow based model tracking system using Terraform, Pulumi, and Google Cloud enabling live
 monitoring of deep learning model training progress, instantaneous sharing results, and completely automated and reproducible report generation.
- Built scalable multitask learning, elastic net, and neural network based models in PyTorch 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 policy optimization).

23andMe • Machine Learning Engineer • Data Scientist (prior to 2020)

11/2018 - 08/2022 (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 enabling creation of higher quality GWAS and Polygenic Risk Score (PRS) ML models.
- Built improved models for type 2 diabetes and Coronary Artery Disease by building model stacking into production PRS pipelines, improving the sensitivity and specificity of 23andme tests for tens of thousands of customers.
- 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.
- Piloted adoption of MLFlow for experiment tracking and model registry, additionally building completely automated realtime performance metric
 reporting, eliminating a key source of pipeline fragmentation and redundancy.
- Improved graph-based techniques for unsupervised identification of populations by genetically based identity-by-descent (IBD) family relationship, demonstrating an effective way to segment sub-populations in Mexico and the United Kingdom in an semi-unsupervised manner.

Scripps Research • Bioinformatician IV

05/2018 - 10/2018 (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.

Juno Diagnostics • Independent Consultant

09/2017 - 02/2018 (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.

Insight • Data Science Fellow

01/2017 - 04/2017 (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.

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

08/2010 - 05/2017 (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