Mirudhula Mukundan

Goal: To bring my interdisciplinary background in ML, Biology and Software Engineering to advance scientific research.

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Education

Carnegie Mellon University, *School of Computer Science* — ***Pittsburgh, USA***
Master of Science in Computational Biology, GPA: 3.80/4.00 — (2021 - 2023)

PES University — ***Bangalore, India***
Bachelor of Technology in Biotechnology, Minor in Computer Science, GPA: 9.31/10 — (2016 - 2020)

Skills

Programming Languages: C, Python, Java, Go, R, MATLAB, HTML, Javascript, SQL, Bash Shell Scripting
Concepts/Courses: Machine Learning, Deep Learning, Optimization, Computational Medicine, Computational Genomics
Frameworks & Tools: Pytorch, Tensorflow, Keras, Scikit-learn, Bioconductor, AWS, HPC, Scanpy, Numpy, Pandas
Bioinformatics: BLAST, Bedtools, Samtools, IGV, MEME Suite, BWA

Experience

Research Assistant
Lee Lab, Carnegie Mellon University, Pittsburgh, USA — *Jan 2022 - Present*
- Performed PCA for batch sorting of ECG data and conducted hypothesis testing for neuron selection.
- Employed convolutional recurrent neural networks (PredNet) to model spatiotemporal patterns in the brain.

Project Assistant
Cognition Lab, Indian Institute of Science (IISc), Bangalore, India — *Dec 2019 - July 2021*
- Designed attention-behavior tasks using MATLAB, Psychtoolbox and HTML.
- Performed signal processing and decoding using Logistic Regression of EEG data.

Software Developer, Intern
CGI, Bangalore, India — *June 2018 - Aug 2018*
- Developed a spelling corrector for a ChatBot platform using LSTM recurrent neural networks.
- Employed Seq2Seq encoder-decoder model to successfully make character/word corrections.

Projects

Deep Reinforcement Approach for Active Learning to Predict Small Molecule Potency — *Mar 2023 - April 2023*
- Designed a novel Deep Reinforcement model using PyTorch to actively select samples.
- Evaluated model to be significantly better than baseline Random Learning, with accuracy reaching 85%.

Machine Learning Pipeline for Accurate TSS Prediction in CAGE Data — *Mar 2023 - April 2023*
- Built an end-to-end pipeline with Convolutional NN (DeepTSS) and Large Language Model (DNABERT).
- Evaluated performance by intersecting results with RefTSS predictions of TSS.

Single-cell Batch Correction using VAE and GAN — *Mar 2023 - April 2023*
- Integrated scRNA-seq batches using generative models like VAE and Generative Adversarial Network (GAN).

A Single Cell RNA-seq Based Aging Clock for Human Neurons — *Sept 2022 - Nov 2022*
- Developed Poisson Variational Autoencoder (VAE) for efficient age prediction with MAE of 7.55.
- Improved model performance by 36% from Multilayer Perceptron model and Standard VAE.

Classification of Glioma — *Feb 2022 - Mar 2022*
- Employed Gaussian Naive Bayes and Support Vector Machine to classify TCGA glioma subtypes.
- Validated the results with a 5-fold cross-validation and achieved over 85% accuracy.