**Team ImageNomeR: Developing an Interactive Graphical Analysis Tool for Examining fMRI and Omics Data**

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During the 2022 UAB Multiomics Hackathon, our team developed ImageNomeR, a tool for viewing which features are important for a particular prediction. The tool visualized data through 4 separate interactive graphs: a feature importance bar graph, a feature distribution box plot, a cumulative brain region of interest (ROI) feature importance graph, and a brain functional network feature importance graph. ImageNomeR allows loading many sets of training/test splits (we tested up to 100 runs of a model with 34,716 features per run), and averages feature importance over all of the runs. The tool is made up of 3 components: a python library which is imported into user code, a python Flask server that receives data from the library, and a browser front end that visualizes the data. We tested ImageNomeR with two public datasets: an fMRI dataset examining fibromyalgia in middle-aged women, and a gene count dataset looking at difference between muscle biopsies from normal glucose tolerance (NGT) and type 2 diabetes (T2D) subjects during basal, post-exercise, and recovery timepoints. The best model we used had a 64% accuracy in predicting fibromyalgia (40 repetitions, 50/16 subject train/test split) and a 60% accuracy in predicting T2D vs. NGT (80 repetitions, 30/9 subject train/test split). Using ImageNomeR, we identified that default mode network (DMN) and uncertain network (UNK) regions were overrepresented in the top 20 connections by model weights, and visual network (VIS) and uncertain network (UNK) regions were overrepresented in model weights multiplied by features. ImageNomeR analysis on the omics dataset found the NEB, TTN, and MT-CO1 gene products (nebulin, titin, and mitochondrial cytochrome oxidase) consistently had high importance for diabetes prediction. Logistic regression performed better than a multi-layer perceptron for predicting fibromyalgia (p<6e-4). The post-exercise timepoint biopsies were the best for predicting diabetes, recovery biopsies were moderately good (p<0.1), and basal level predictions performed no better than chance (p<5e-4).