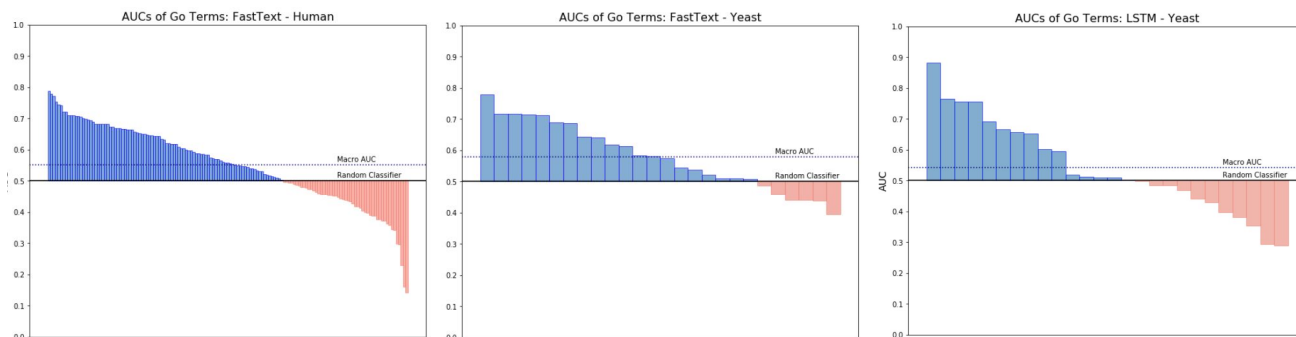
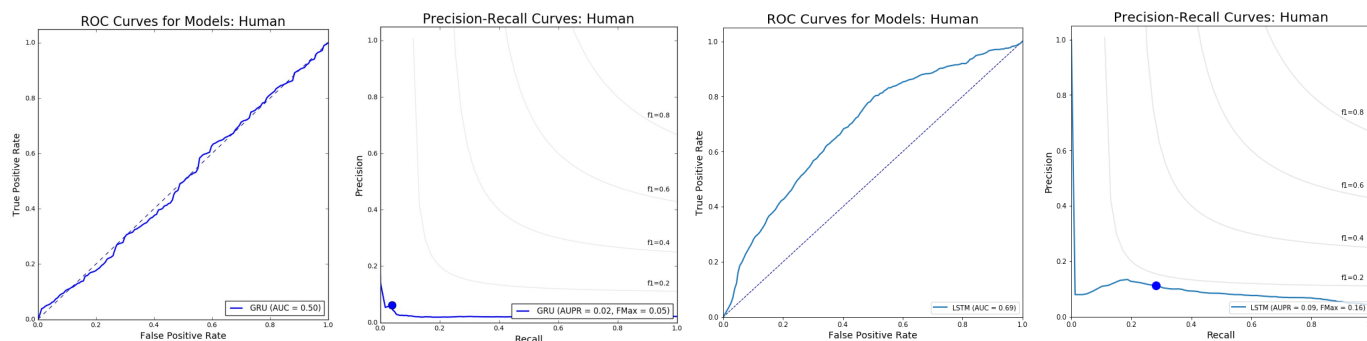


Evaluation/Results

We have now identified some encouraging results. Viewing predictions of individual GO terms reveals that over half achieve decent AUC scores. The real promise of these results is that the prediction of certain terms was feasible with minimal data and by a model that is very efficient; however, some of the terms were not well-predicted by the model. In order for this work to meaningfully contribute to the field of protein prediction research, one would need to explain what types of functions could be reliably predicted and what types tend to be poorly predicted. The plots below depict the sorted AUC scores of individual GO term predictions.



As shown below, the GRU model is not a good predictor, but the LSTM is promising.



As we planned in our last progress report, we have created k-mer features and we will incorporate them in our existing models. The final steps in our project will be to tune these 3 models (probably add another model if time permits) and to complete our written analysis. The difficulty of training so many labels from so little data has persisted throughout our project, but we will at least be able to report promising results on individual label performance. Another potential obstacle we are facing is the run time of the model : as we run the model with $k > 2$ (for K-mers), the model takes upto 24 hours for running a few epochs, which prevented us from reporting performance based on different hyperparameter values. But we are certain that we will report them in our final poster.

In anticipation of our project's conclusion and write-up, we would greatly appreciate any feedback that seems warranted from our progress thus far.