



Table 1. Sample Data Set By Protein Class

Cytosolic	Nucleic	Secreted	Mitochondrial
row4	row4	row4	row4

2.2 Classifier Training

A Random Forest Classifier was used in the training of the model, which was done with 70% of the training data. The classifier itself was implemented using the open source ‘scikit-learn’ package, and was instantiated with the a **hyperparameters of X, Y, Z**. These hyperparameters were all chosen in advance using k-fold cross validation, and a grid search on hyper parameters.

2.3 Cross Validation & Hyperparameter Tuning

In order to assess both the strength of model under certain hyperparameters, and the strength of the predictive power of certain features, a 5-fold cross validation score (*what score?*) of the model was used, each time with a 70%, 30% train-validation split. In order to search the space of hyperparameters, a grid search was established, visible in plot *plt the cross valid hyper param search*.

2.4 Ablation Study

An ablation study was performed, by removing one feature at a time and testing the 5-fold cross validation score of the model in predicting these data. The results are presented *fig xyz*

2.5 Gradient Boosting Comparison

The training set of features was then

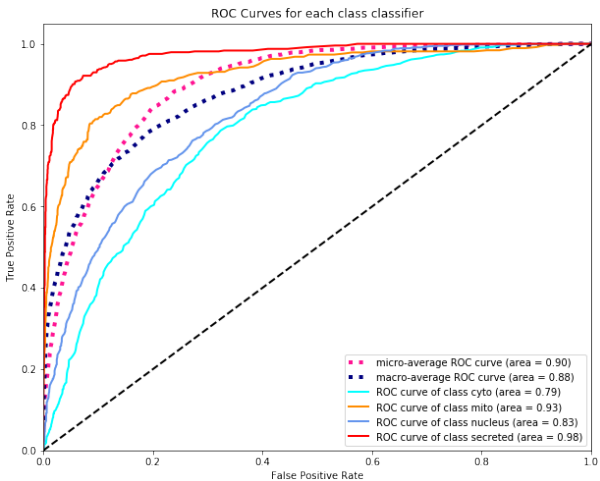
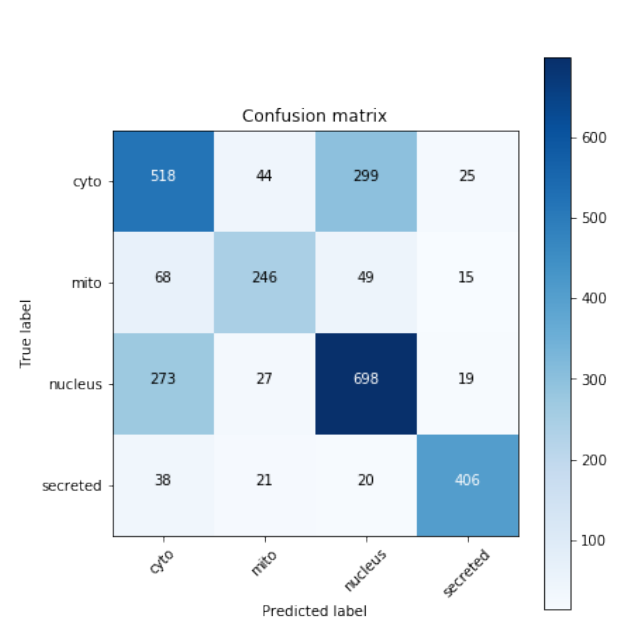


Table 2. Predictions of Test Proteins

Protein ID	Subcellular Location	Probability
row1	row1	row1
row2	row2	row2
row3	row3	row3
row4	row4	row4

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3 Results



- Results of accuracy - Confusion matrix - ablation study - results compared to xgboost

Obtained data from X files, and mixed, shuffle and split into a train and validation split. Since the proteins are all non homologous, no need to arrange by family and could split anyway.

Then took these files and processed them into feature vectors, using the biopython module. These extracted, x features from the sequence.

Then trained a random forest classifier with X trees, and also tested a XGBoost classifier.

Cross validated grid search done to find best parameters for trees. Ablation study used to investigate salient features.

Trained a random forest with X trees.

What did you do? - extract features - train -test split - homologues - cross validate - compared with a model (gradient boosting?) - ablation study

- Results of accuracy - Confusion matrix - ablation study - results compared to xgboost

end of paper

## 4 Discussion

- Examine the features - Examine the ablation study - Examine comparison to XGBoost - Compare with existing literature and approaches

## 5 Further Work

- suggestions: more data? better features/

## 6 Conclusion

## 7 Theoretical Background

What about ???





head1	head2	head3	head4
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row2	row2	row2	row2
row3	row3	row3	row3
row4	row4	row4	row4

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Funding

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