



Deep learning-based Neuron Detection in Brain CLARITY Imaging

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Background: CLARITY imaging

Clear

Lipid-exchanged

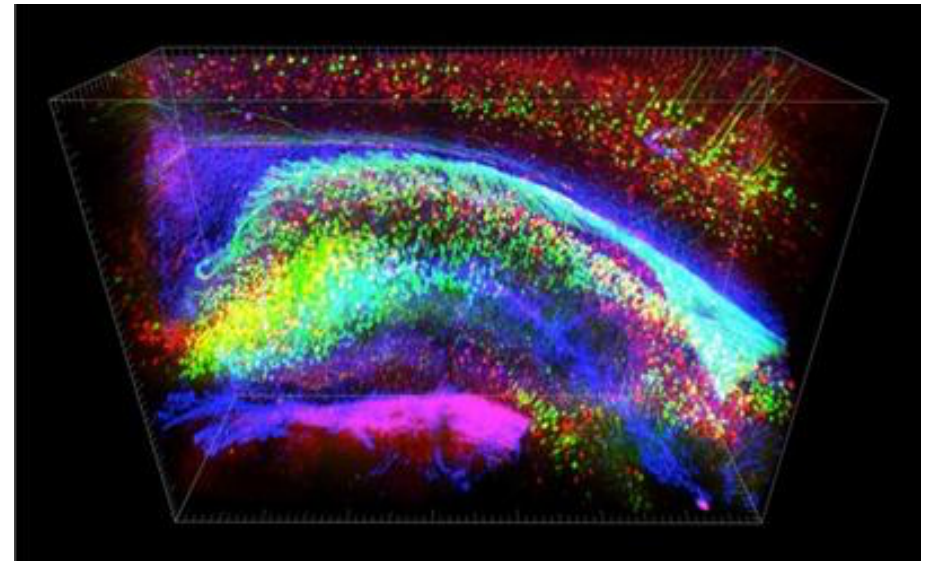
Acrylamide-hybridized

Rigid

In-situ hybridization-compatible

Tissue

Hydrogel



<https://en.wikipedia.org/wiki/CLARITY>

Significance of CLARITY for Brain Imaging

- Connectome project
 - Local circuit wiring
 - Relationships between neural cells★
- Neurological diseases
 - 3D view of brain structures





<http://www.humanconnectomeproject.org/>

Goal


- Develop a **robust 3D CNN** that can predict, with improved accuracy when compared to other models, how many fluorescent neurons are present within a section of a brain imaged with CLARITY
 - Previous models: template matching, blob detection
 - Maximum accuracy achieved was $\sim 59\%$ with these techniques

Deliverables


Minimum:

- Trained 3D CNN model (pytorch) for neuron detection 
- Report in Jupiter notebook – explains training of CNN and predictions 

Expected:

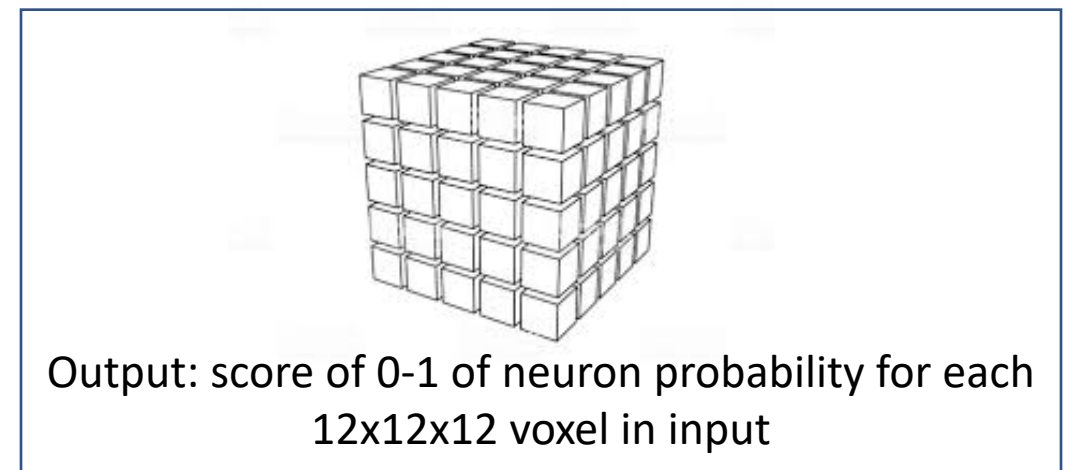
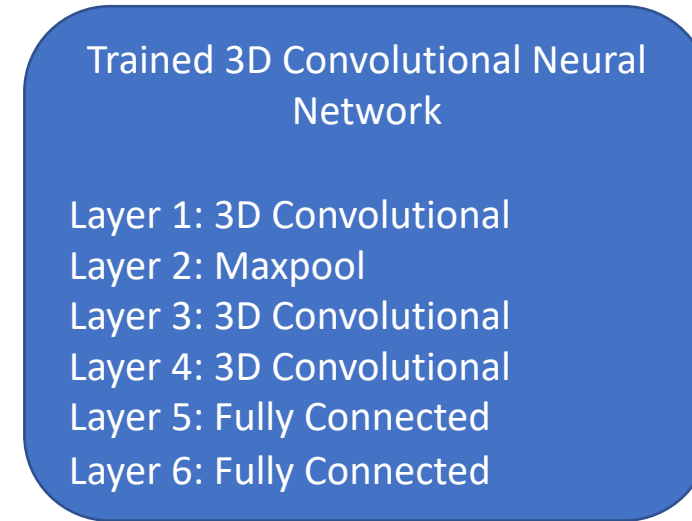
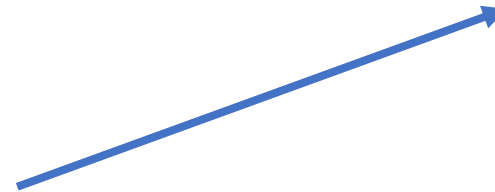
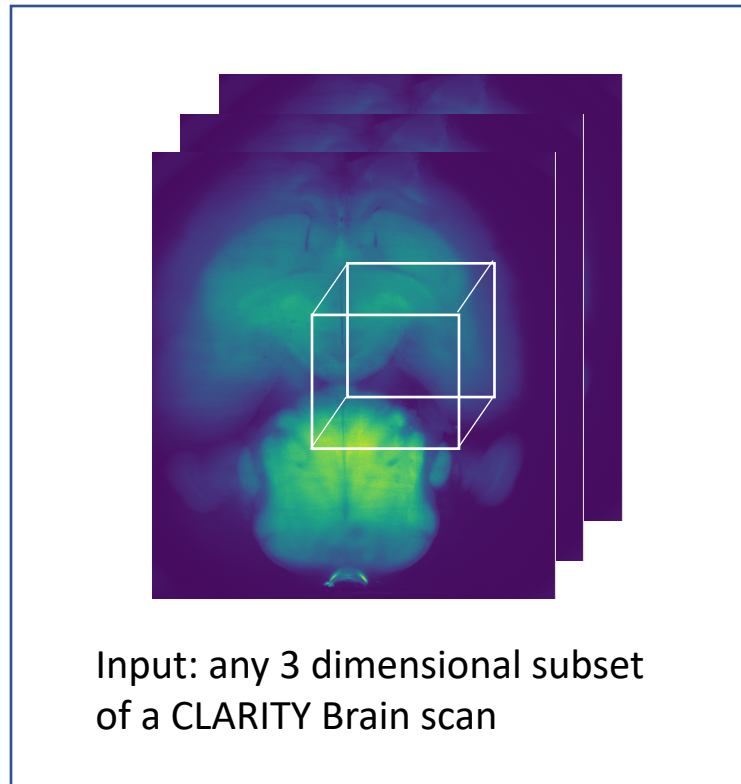
- Robust and validated trained model (pytorch) for neuron detection  Still working on it

Maximum:

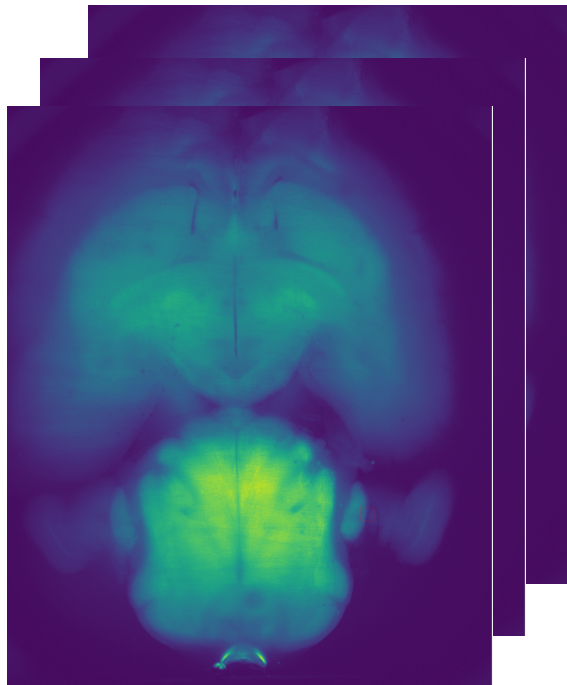
- Academic paper describing packaged model, training, validation
- Surpass baseline accuracy of previous models by a significant margin 



Technical Approach- CNN Architecture



Technical Approach – First training and validation of 3-dimensional CNN training on reduced dataset



One 3-D CLARITY Brain Imaging Data annotated for Neurons

Neuron 12X12X12 voxels
and non-neuron 12x12x12
voxels from these images
are used for training

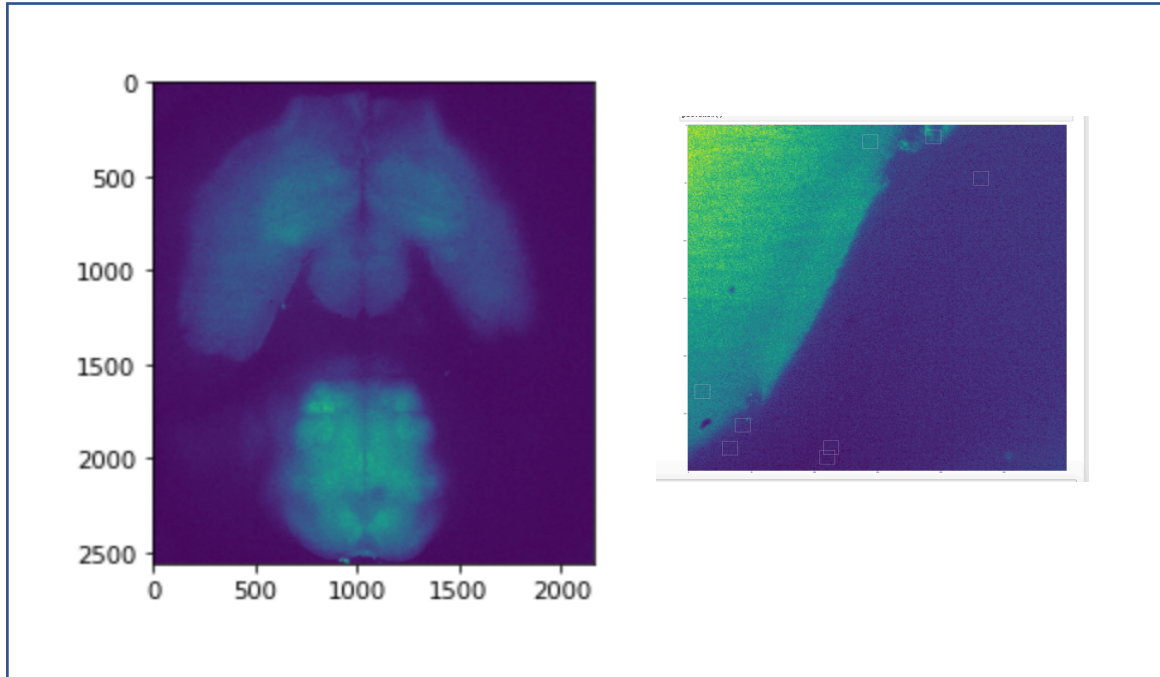


3D Convolutional Neural
Network

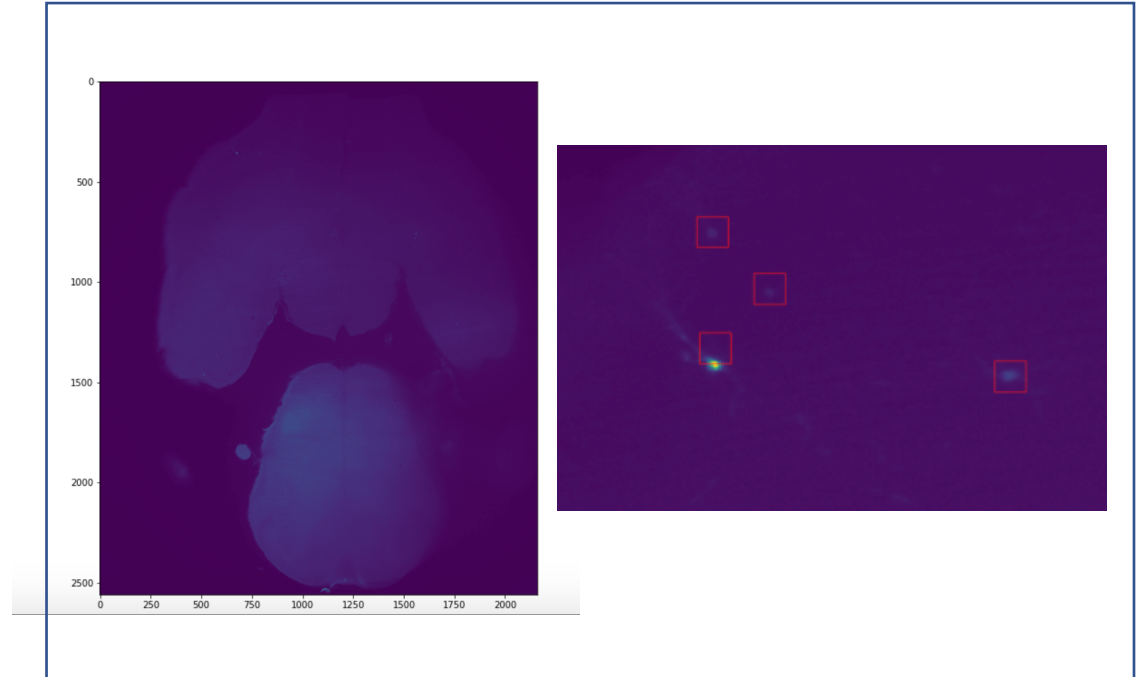
Model resulted in 99% accuracy

Problem 1: Variation in Brain Intensity

Before



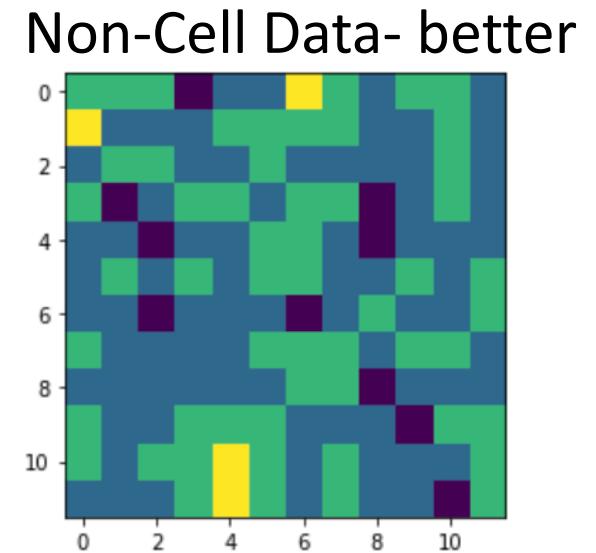
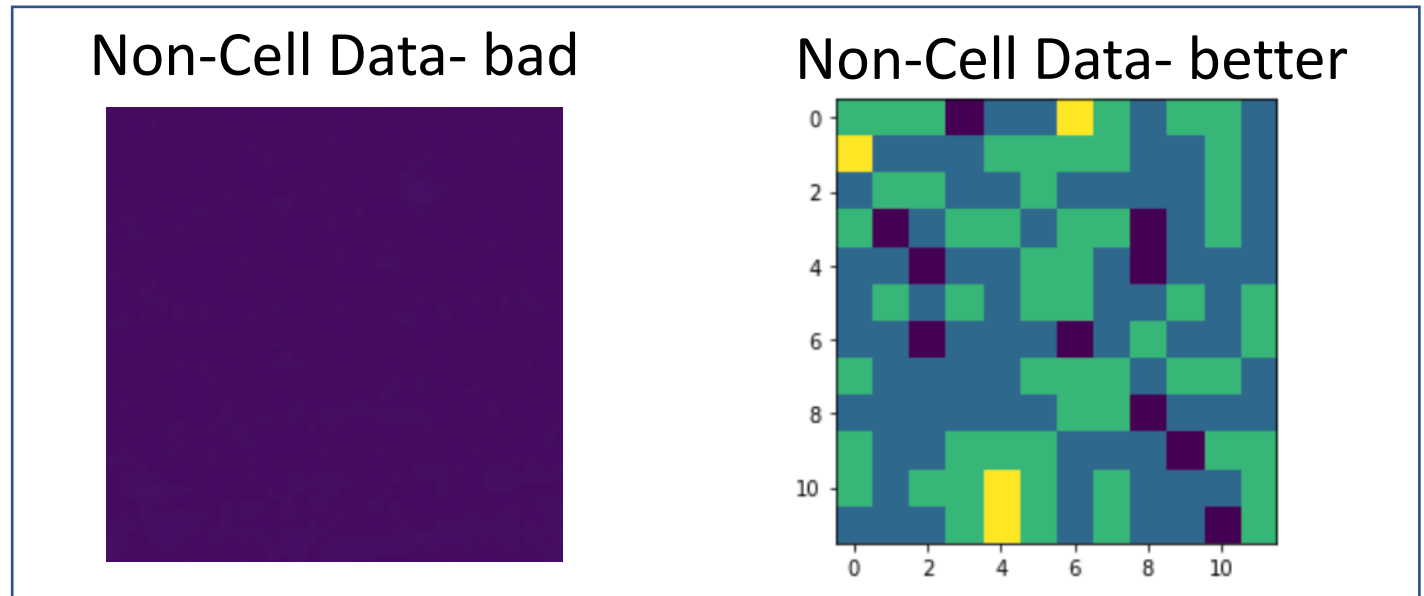
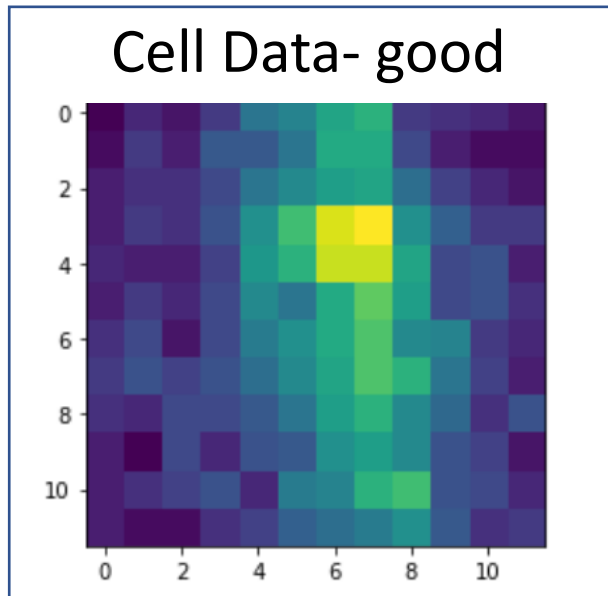
After



Solution: Brain illumination correction filter applied to the data


Problem 2: How to Extract Training Data From CLARITY Scans

- Non-cell data should be representative of brain tissue , not background



- Solution: Pick non-cell regions within 6-20 pixels of an annotated cells

Technical Approach- Large Scale Training on Complete Dataset & CNN Validation

- Data includes 8 brains
- 2376 Cell Annotations
- 23760 Non-Cell Regions Extracted
- **Coarse validation**: report metrics over a few random splits of data (5 train, 3 test) 
- **Full Leave-one-out (LOO) Cross validation**: report cross-validated metrics averaged over 6 folds. In each fold, all but 2 brains will be used for training, and the remaining 2 for testing ★

Metrics Reported

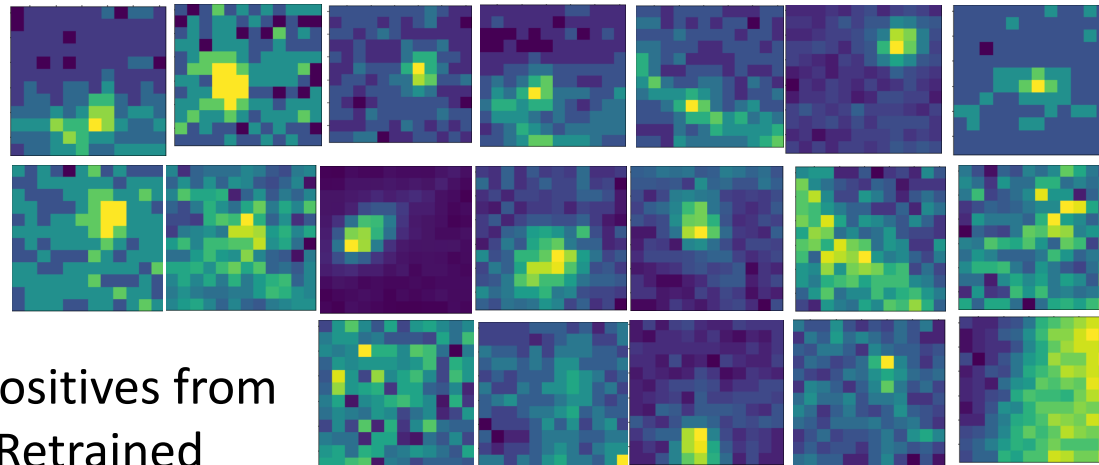
- F1 score: harmonic mean of precision and recall
- Accuracy = $(TP+TN)/(TP+TN+FP+FN)$
- Precision = $TP/(TP+FP)$
- Recall = $TP/(TP+FN)$
- False Positives: non-cell regions classified as cell regions
- False Negatives: cell regions classified as non-cell regions

*Metrics reported at threshold score of 0.5

Coarse Validation Results

Split	F1 score	Accuracy	Precision	Recall	FP	FN	AUC ROC	AUC PR	Adjusted FP
1	0.7612	0.9647	0.9867	0.6203	8	77	0.924	0.817	4
1 retrained	0.7784	0.9664	0.9733	0.6485	17	49	0.935	0.840	9
2	0.7730	0.9657	0.9701	0.6425	12	61	0.920	0.805	8
2 retrained	0.7251	0.9596	0.9493	0.5865	19	76	0.909	0.775	5

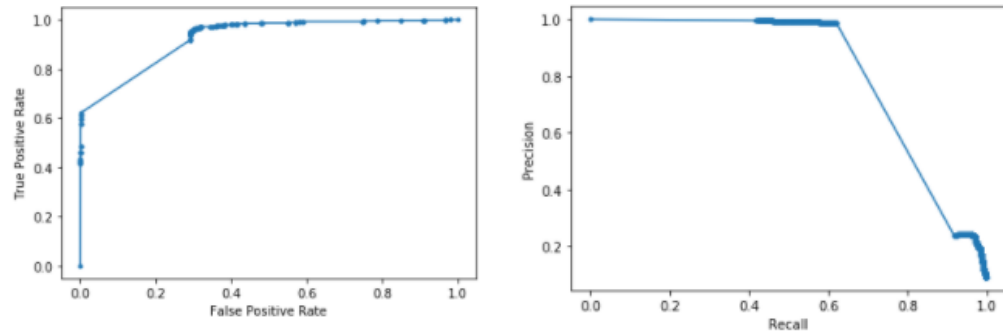
*Retrained include True False Positives and all False Negatives



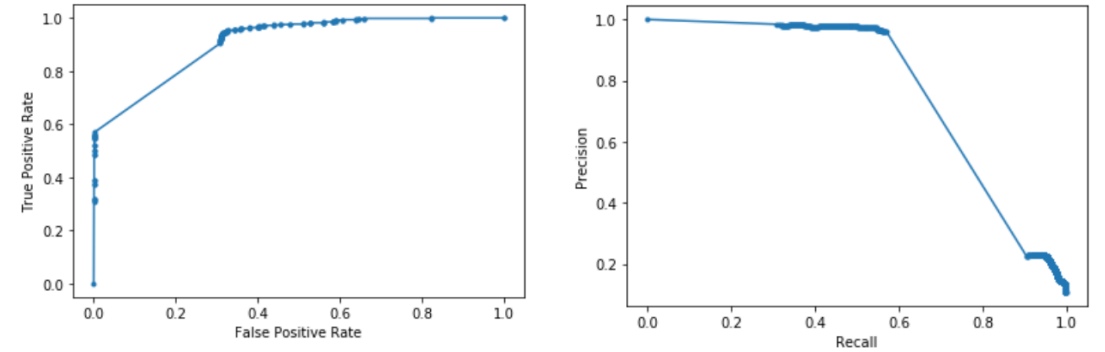
Ex) False Positives from
Split 2 Retrained

Coarse Validation Results

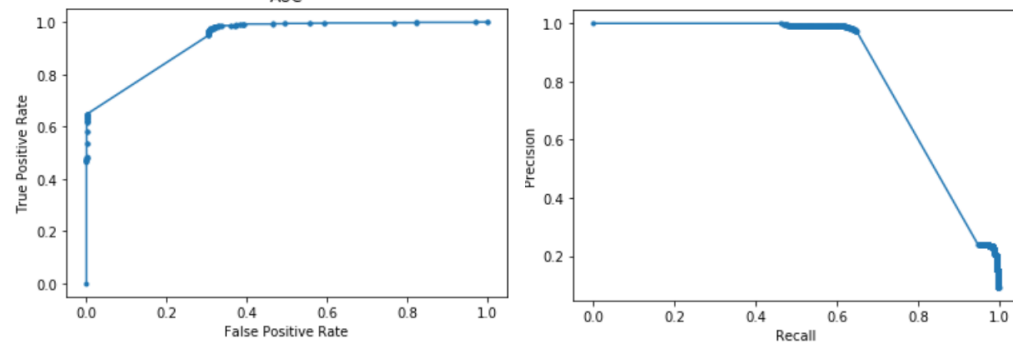
Split 1



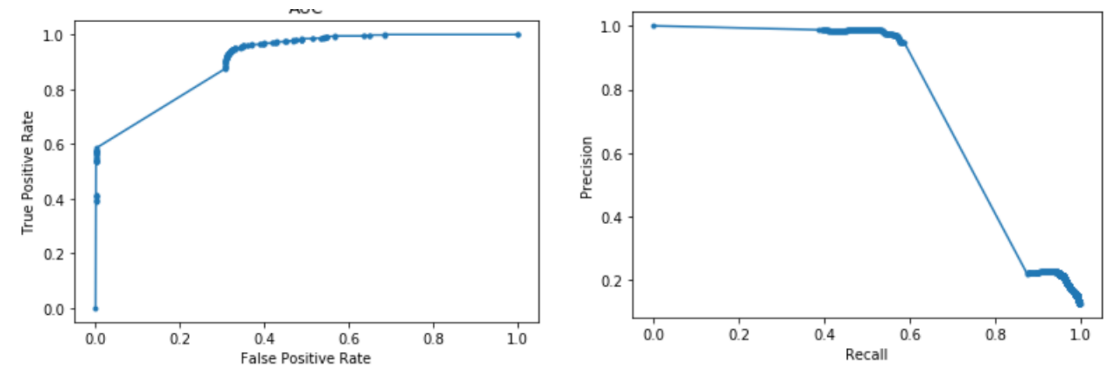
Split 2



Split 1 Retrained



Split 2 Retrained



Work Remaining

- Cross-Validation
- Academic Paper

Management

- Meetings with Dr. Sulam as necessary
- Code stored on github and MARCC
- Code backed up to github every week and more often with substantial improvements
- Communication through Slack/email

Lessons Learned

- Budget more time deemed necessary for computational difficulties (MARCC)
- Quality of training data is very important