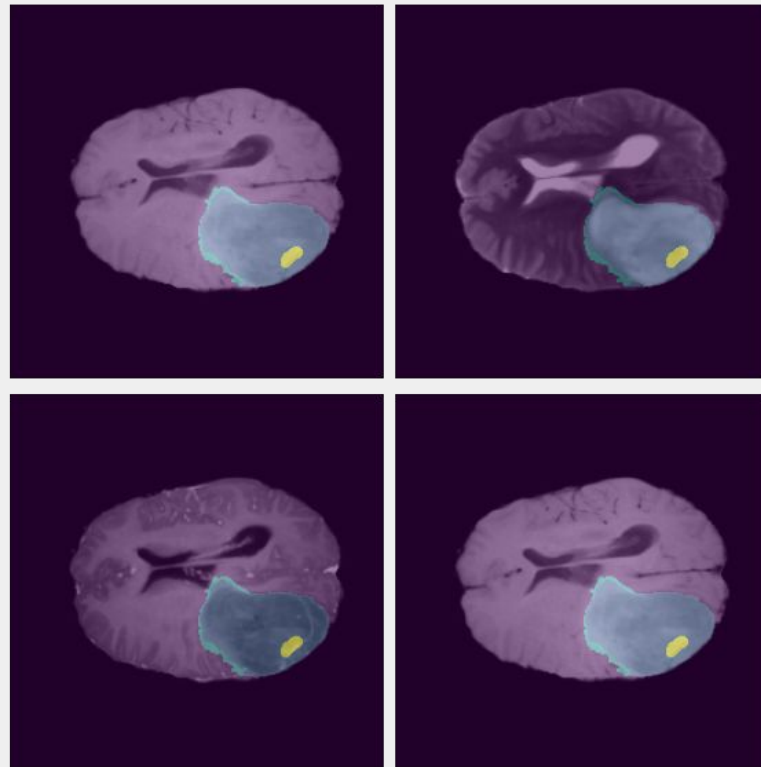




Brain Tumor Segmentation

Alejandro Cortina
Stela Lila
Vladyslav Zalevskyi





Outline



The Problem

- ❑ Dataset description

Threshold based approaches

- ❑ Isodata/Otsu

Clustering (K-Means)

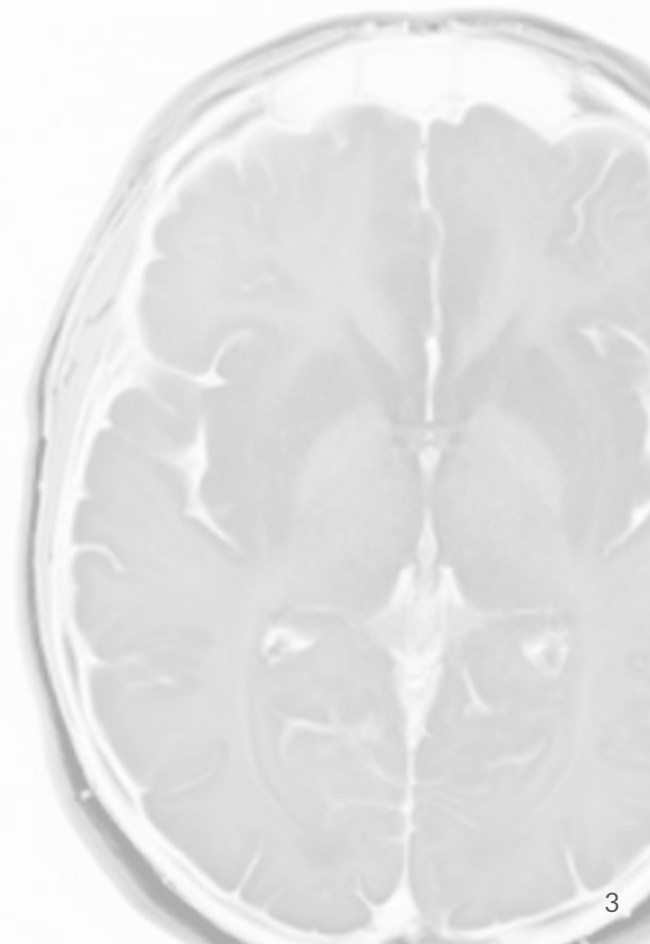
Voxel-wise classification models

- ❑ Support Vector Machines
- ❑ Random Forest Classifier

Dataset Description

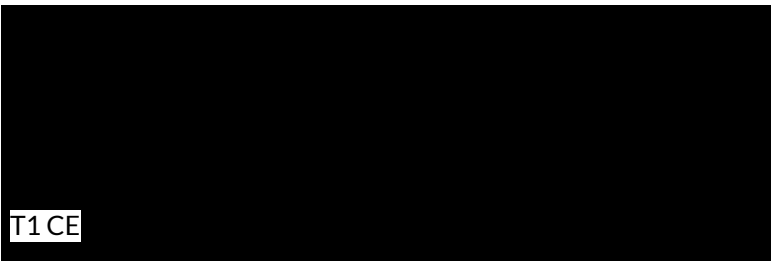
The Problem: Segmentation of gliomas in pre-operative MRI scans.

- BraTS2020 Dataset (Training + Validation)
- 369 patients
- 4 modalities
- 240x240x155 ~ 8.5 million voxels
- 19 participating institutions



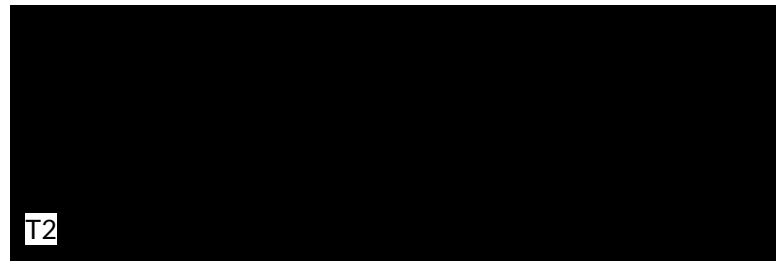


Continued...

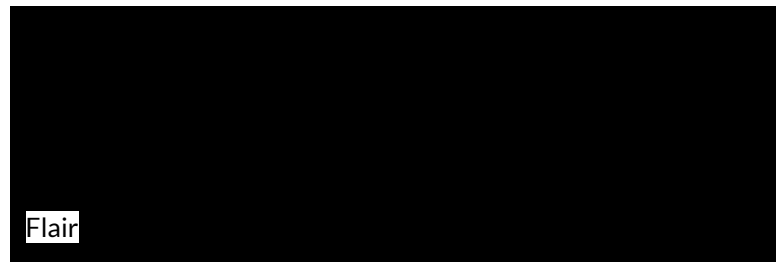
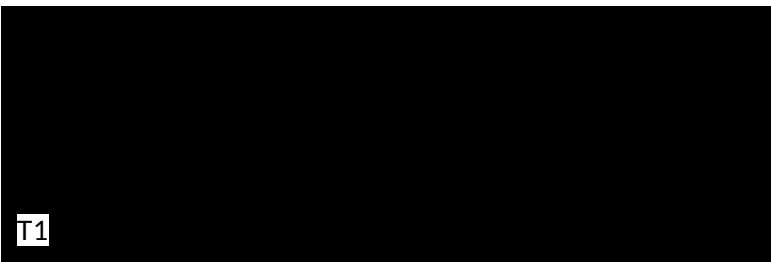


4 different
modalities

~



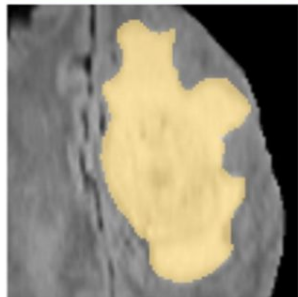
>35 million
voxels per
patient



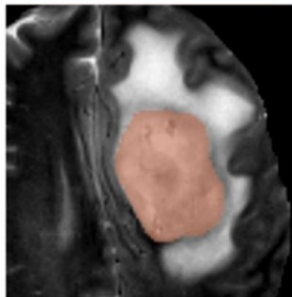


BraTS Annotations & Structures

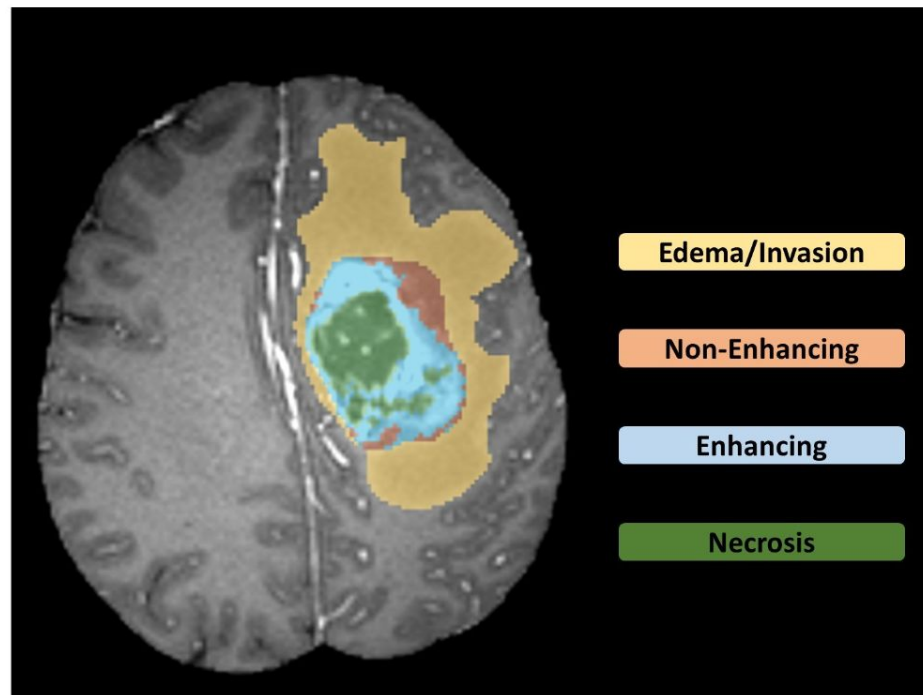
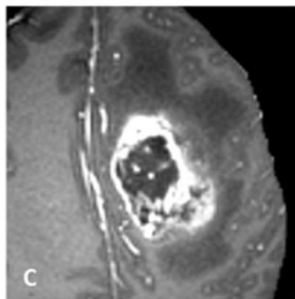
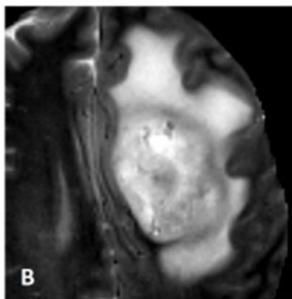
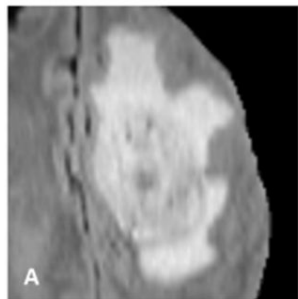
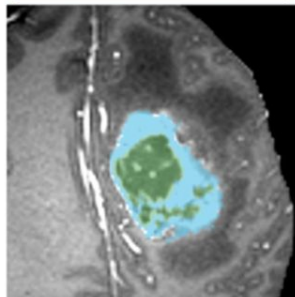
WHOLE TUMOR



TUMOR CORE

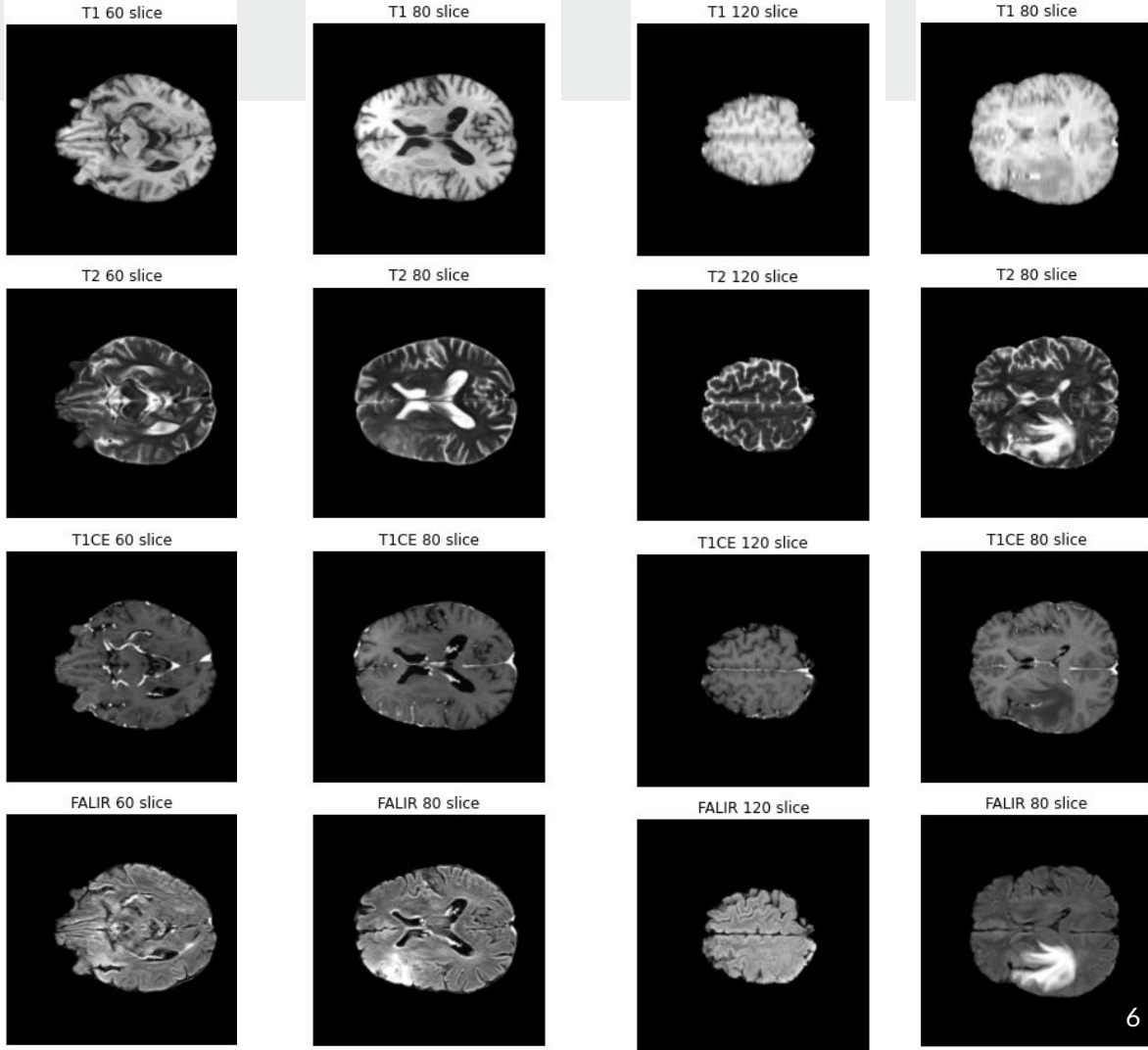


ENHANCING TUMOR



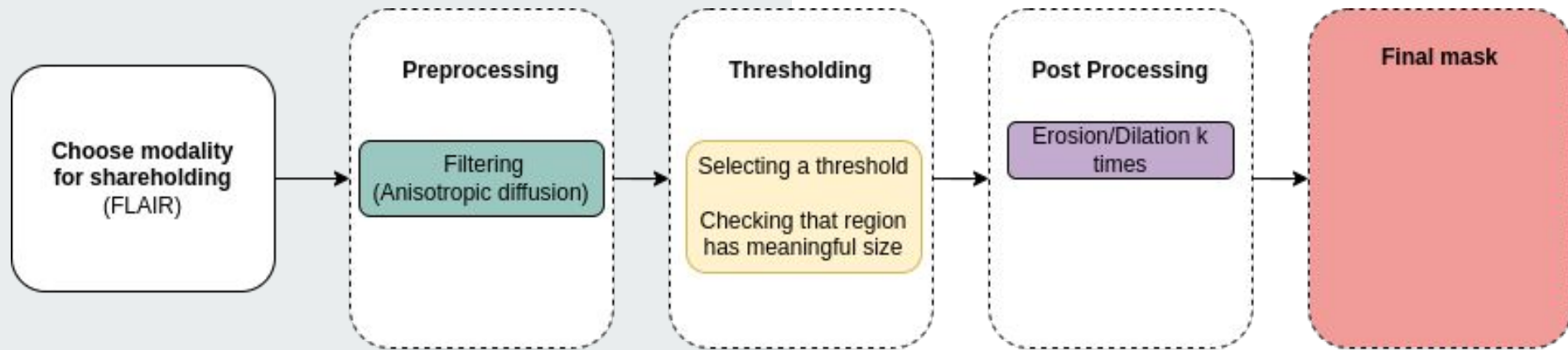
Challenges

- Image quality
- Scarcity of data
- Heterogeneity
- Complexity of brain cancer



Thresholding

Otsu
Isodata



Thresholding

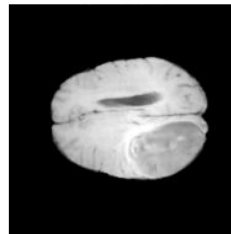
Otsu

Isodata

Advantages

- Quick (4s per patient)
- Straightforward
- Performs well on obvious cases
- Unsupervised

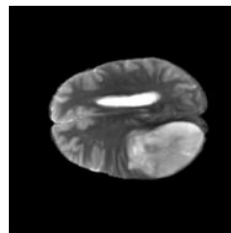
T1 95 slice



Original Mask



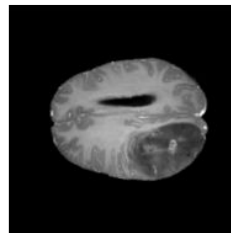
T2 95 slice



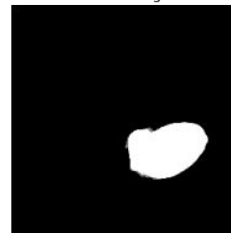
Predicted Mask



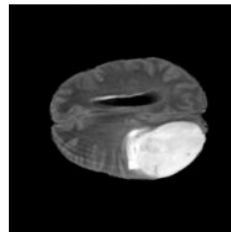
T1CE 95 slice



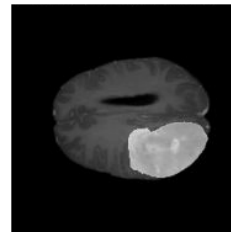
Predicted over Original Mask



FALIR 95 slice



Predicted mask over Flair



Thresholding

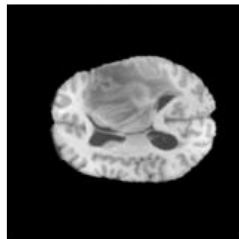
Otsu

Isodata

Disadvantages:

- Low overall accuracy
- Doesn't work for not distinct tumors
- Doesn't use modalities information
- Requires manual post processing and pre processing

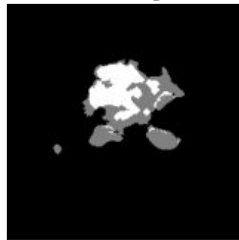
Slice T2



Otsu results dsc=0.51



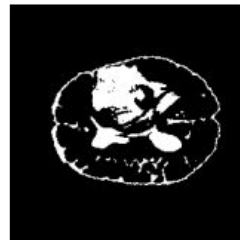
Otsu after 3 closings dsc=0.58



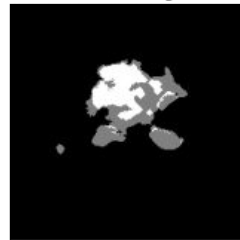
True mask



Isodata results dsc=0.51



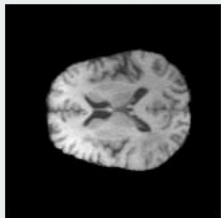
Isodata after 3 closings: dsc=0.57



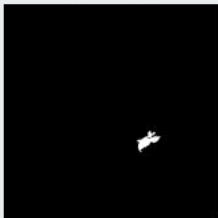
A priori information

Max tumor/brain proportion
on the train set:
34%

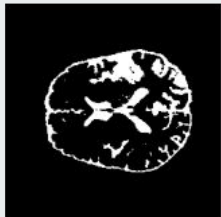
Slice T2



True mask



Otsu results dsc=0.00



Isodata results dsc=0.00



Otsu after 3 closings dsc=0.00

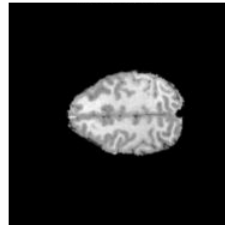


Isodata after 3 closings: dsc=0.00

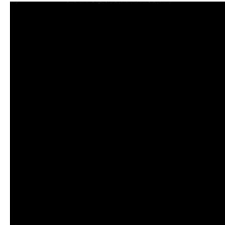


Without

T1 120 slice



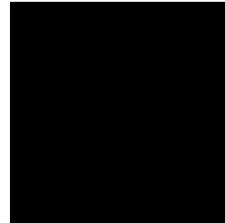
Original Mask



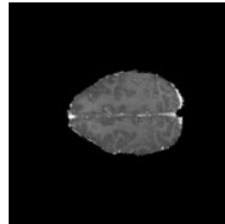
T2 120 slice



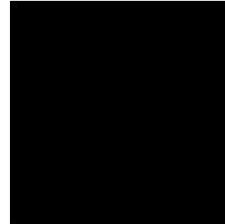
Predicted Mask



T1CE 120 slice

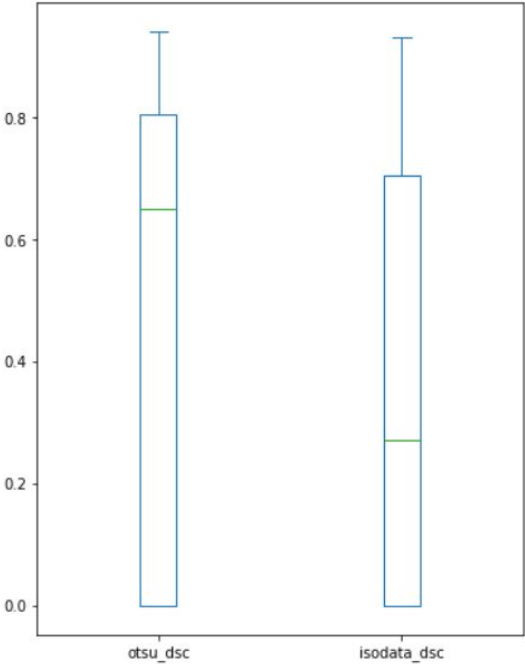


Predicted over Original Mask

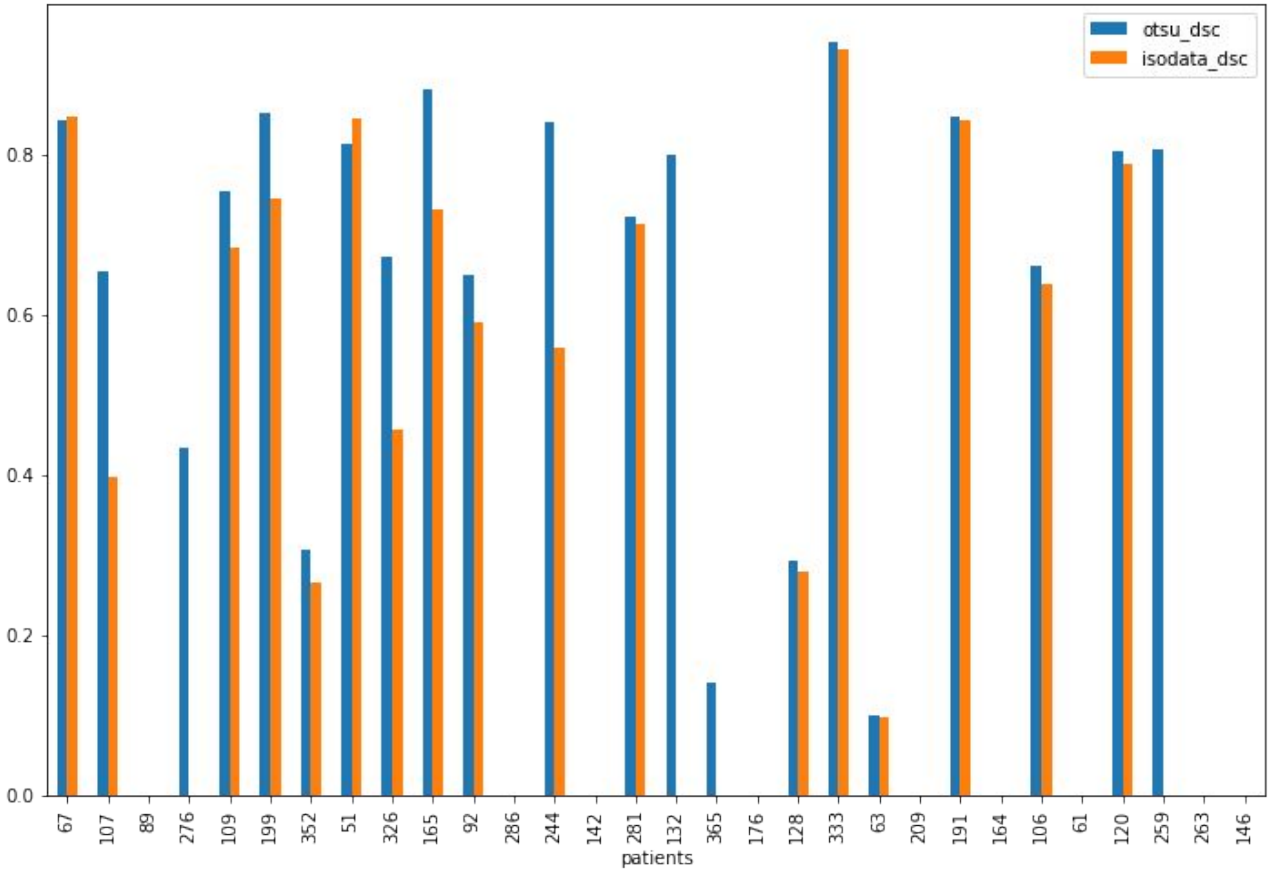


With

Results



Dice score Otsu: 0.46 ± 0.37
 Dice score ISODATA: 0.34 ± 0.356



K-Means

Improvements

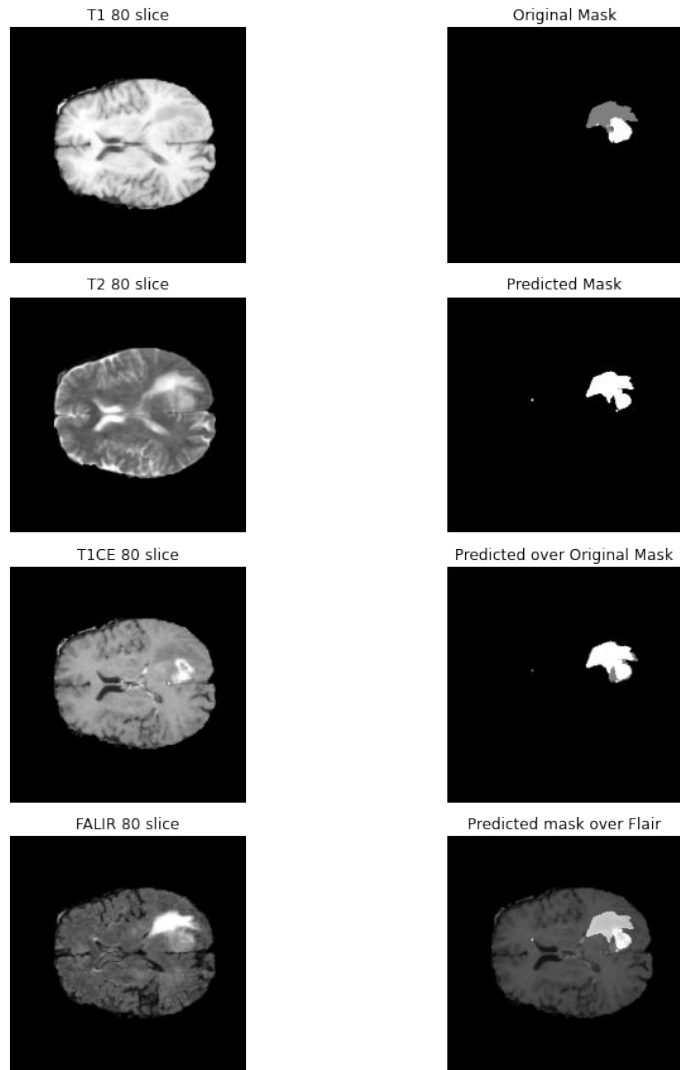
- utilizes information from all 4 modalities
- more flexible than thresholding

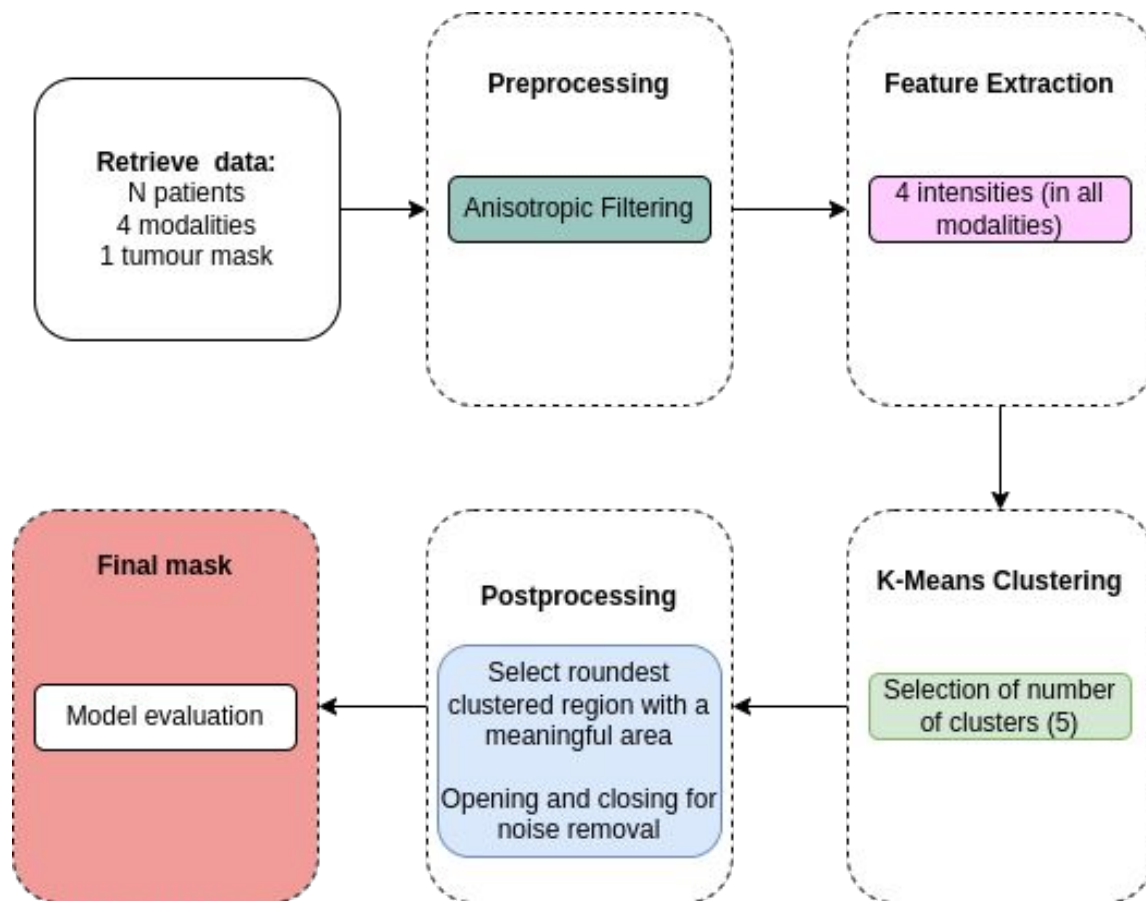
Still

- quick (12s per patient)
- unsupervised

However:

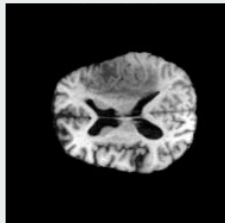
- requires manual post processing
- manual selection of # of clusters





$$Circularity = \frac{Perimeter^2}{4 \pi Area}$$

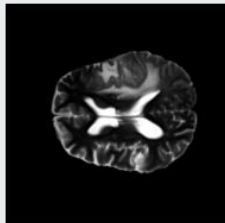
T1 80 slice



Original Mask



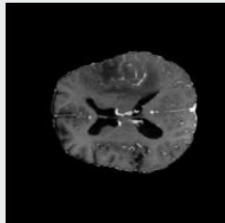
T2 80 slice



Predicted Mask



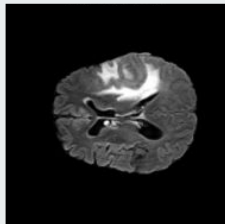
T1CE 80 slice



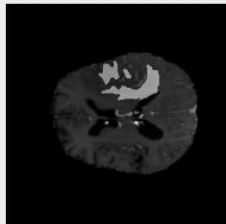
Predicted over Original Mask



FLAIR 80 slice

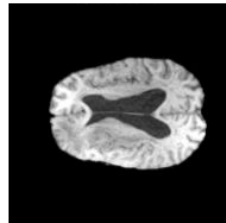


Predicted mask over Flair

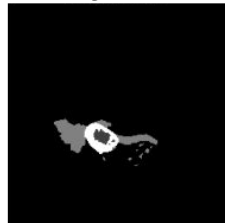


K-Means Examples

T1 80 slice



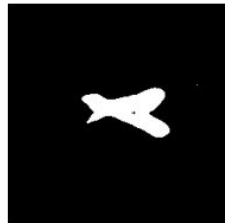
Original Mask



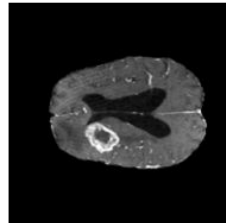
T2 80 slice



Predicted Mask



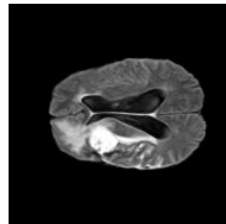
T1CE 80 slice



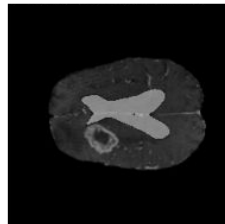
Predicted over Original Mask



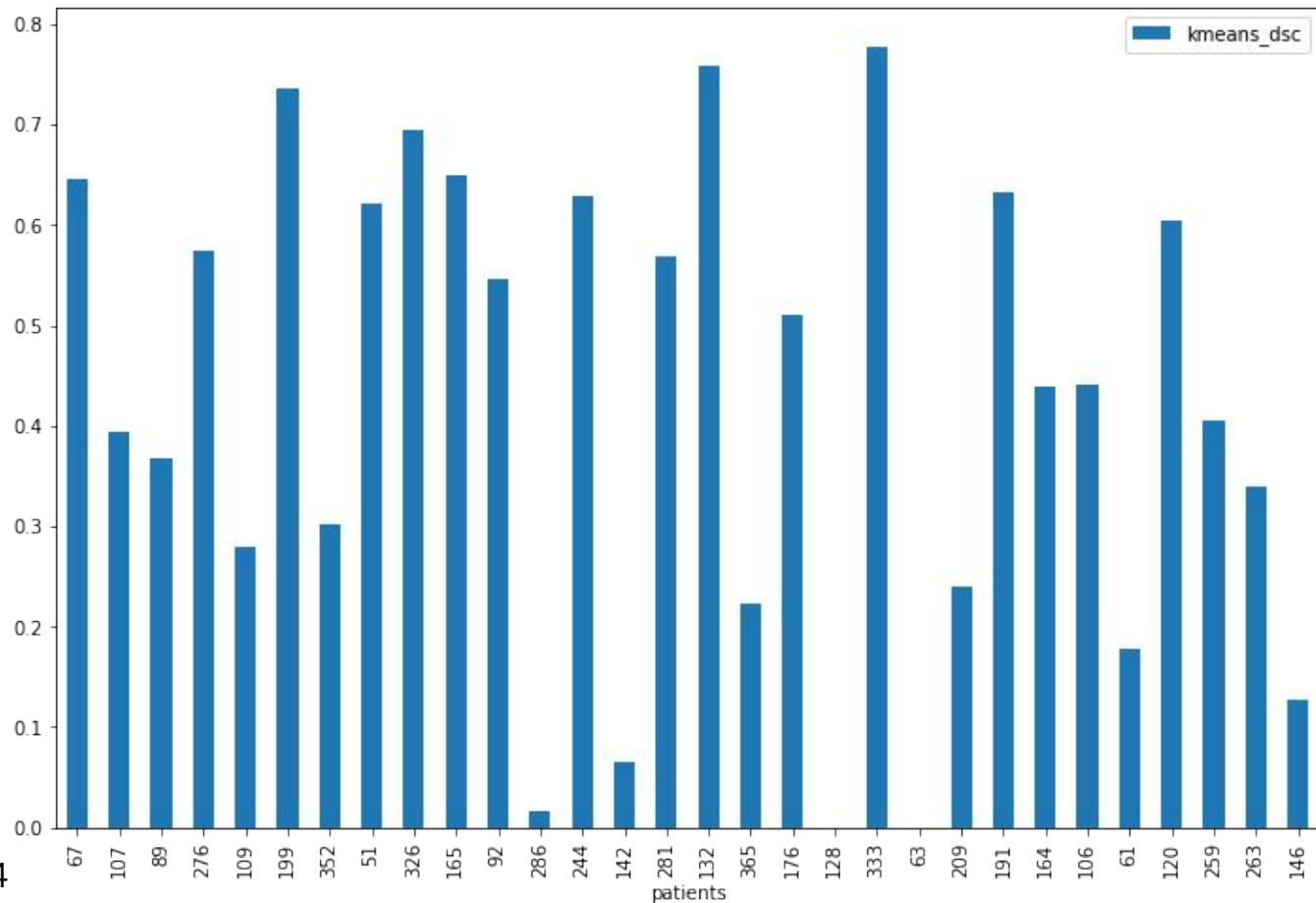
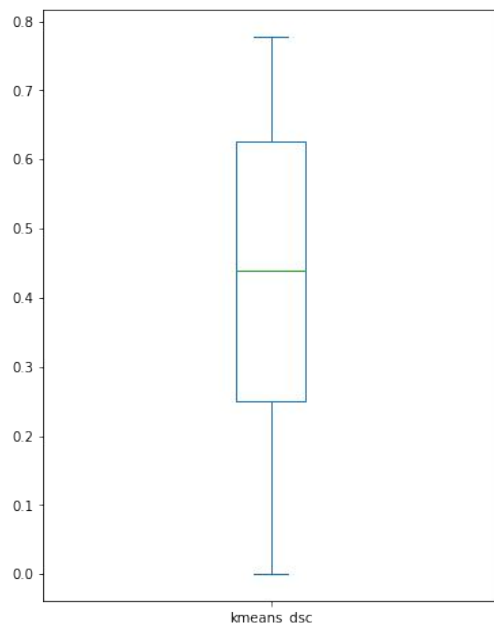
FLAIR 80 slice



Predicted mask over Flair



Results

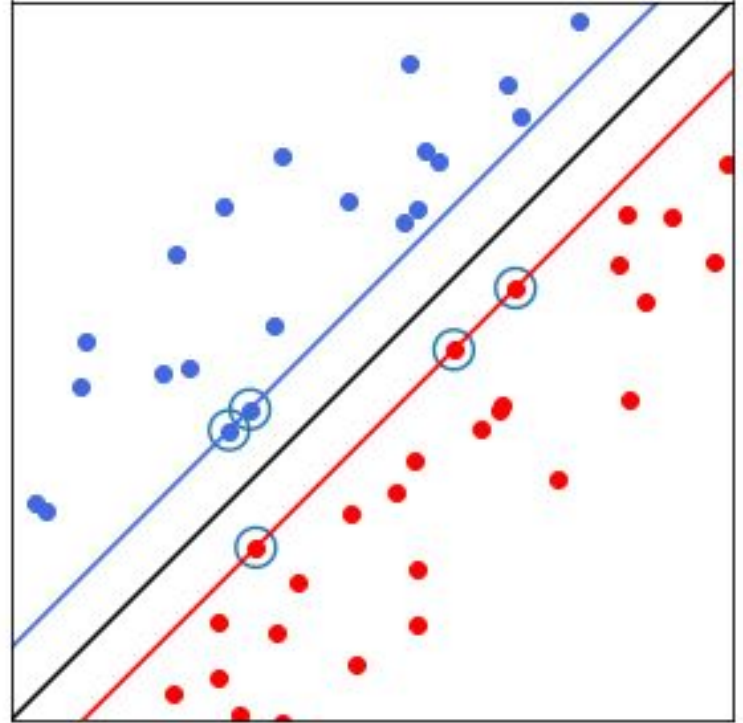


Dice score K Means: 0.43 ± 0.24

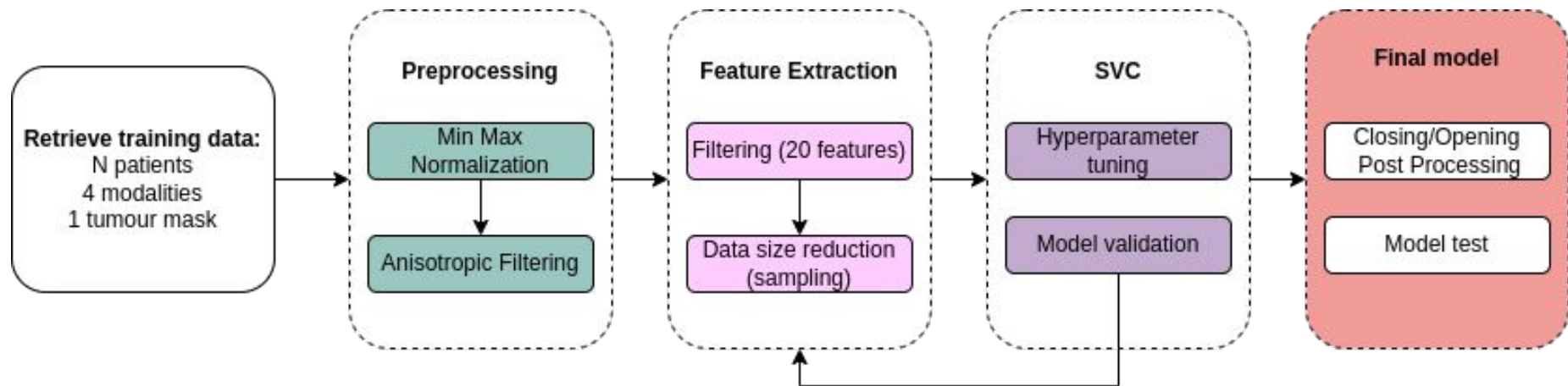
Voxel-wise classification

Support Vector Machines

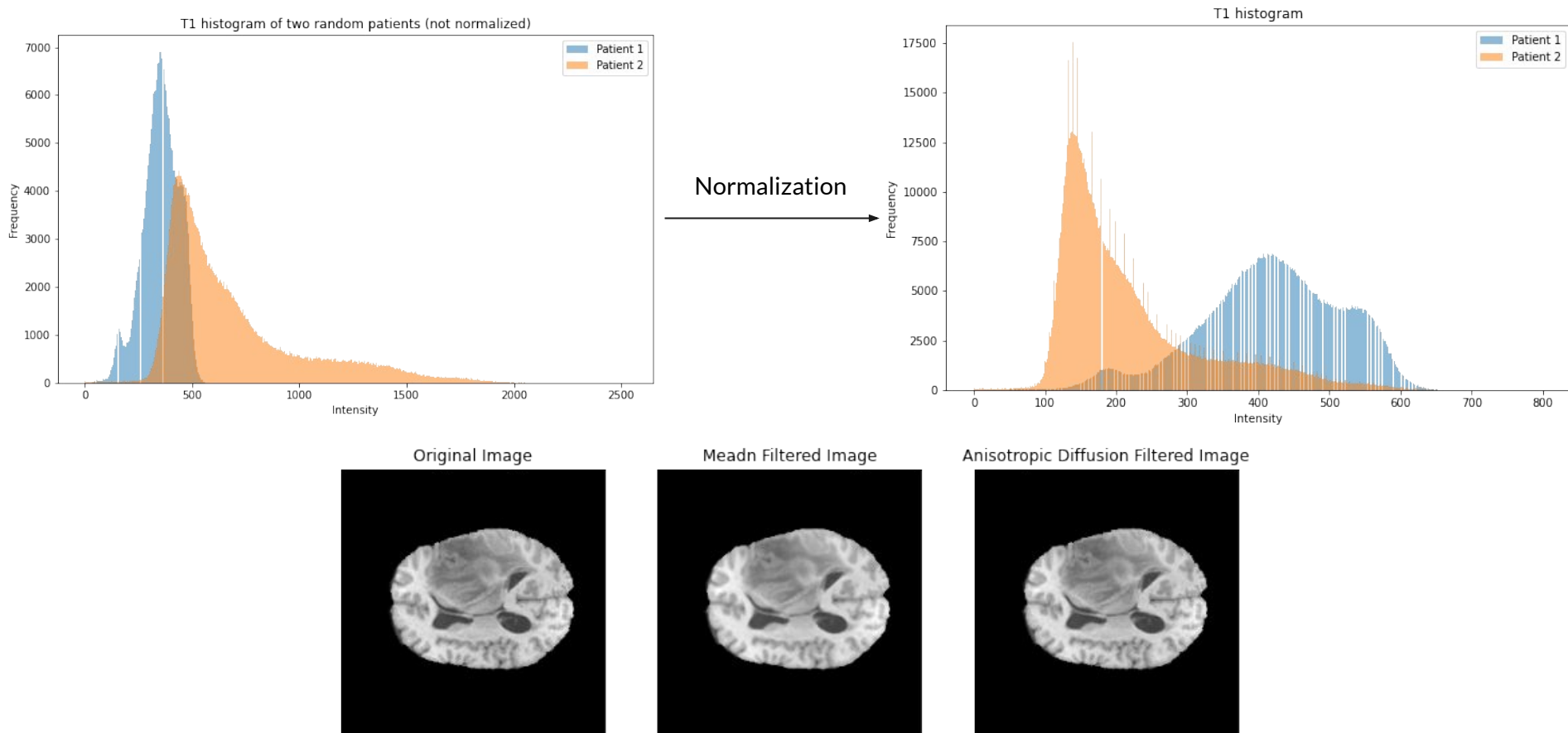
- 12 minutes per patient
- completely automated
- supervised



Pipeline



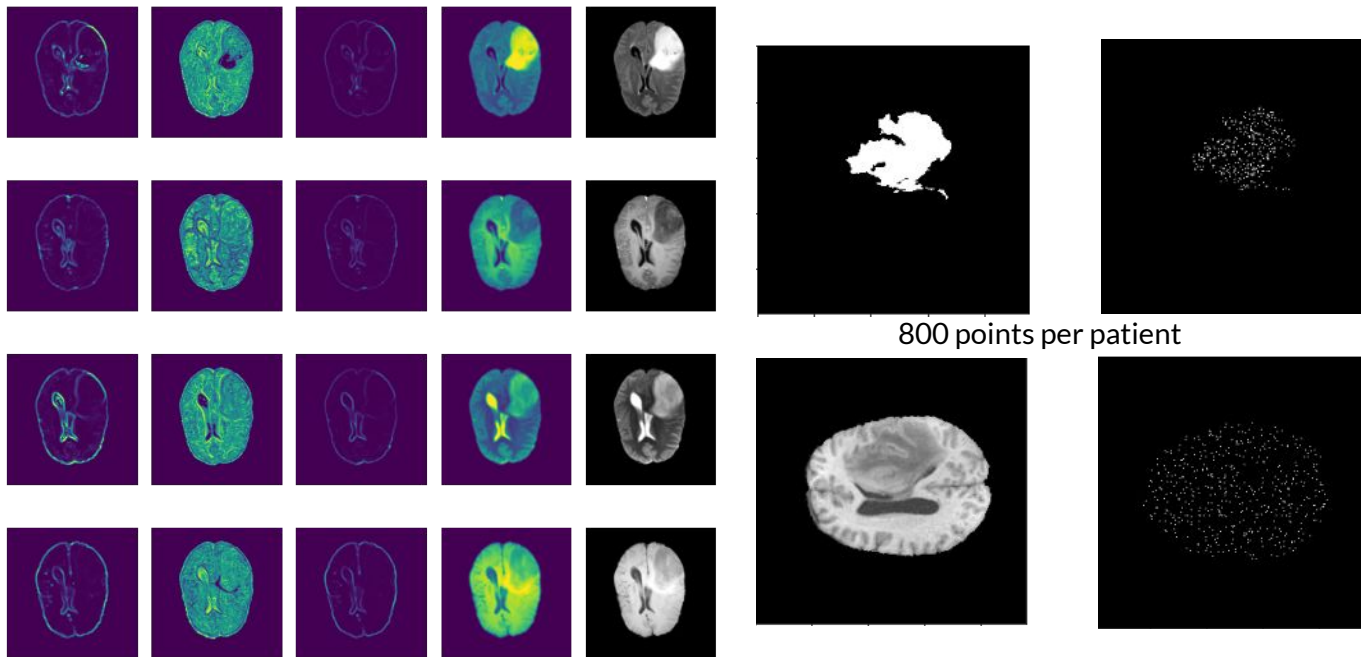
Pre-processing



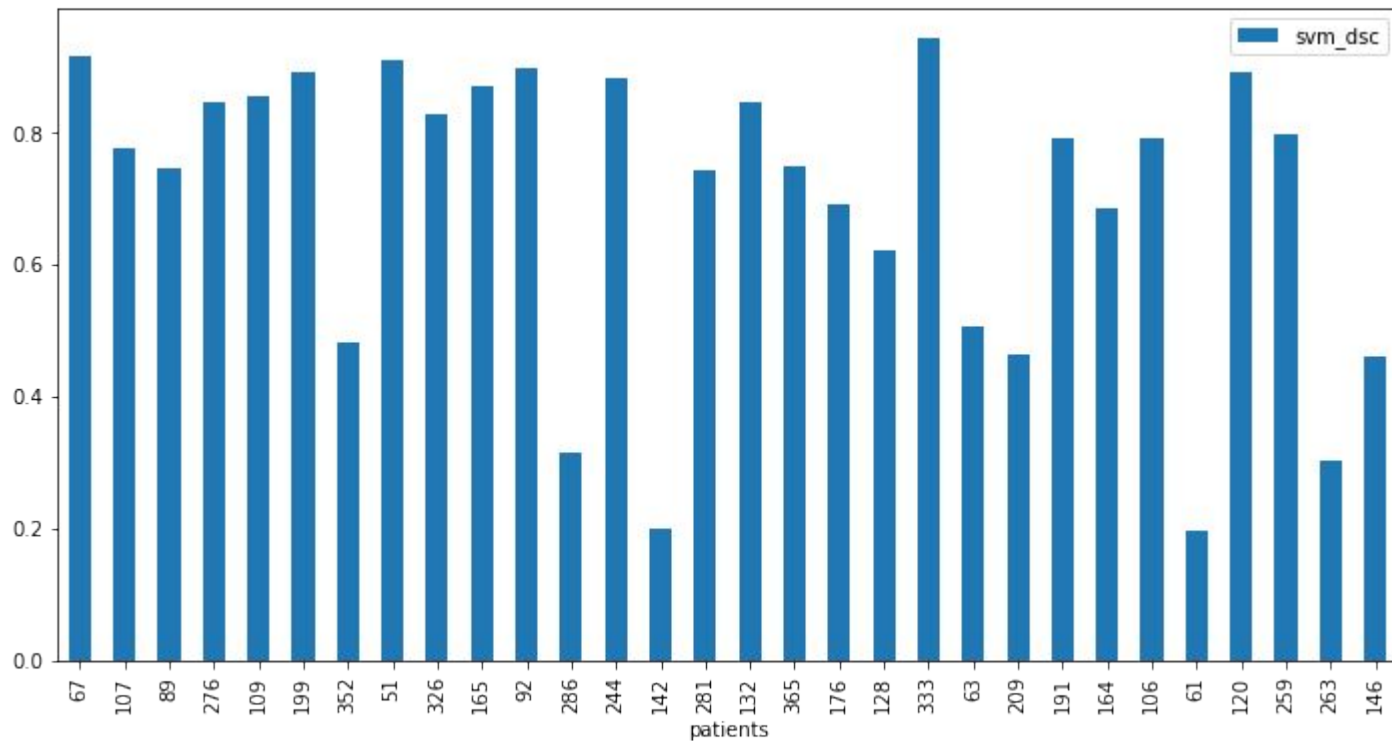
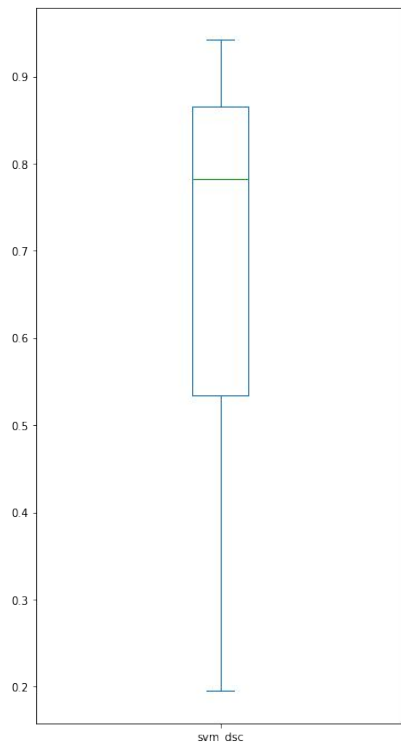
Feature Extraction and Data Sampling

20 features total:

- 4 intensities
- 4 first order texture features
 - mean
 - variance
 - skewness
 - kurtosis



Results

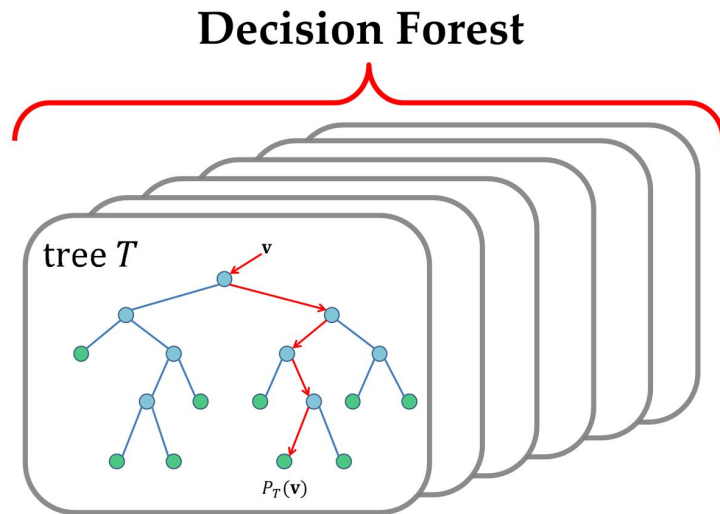


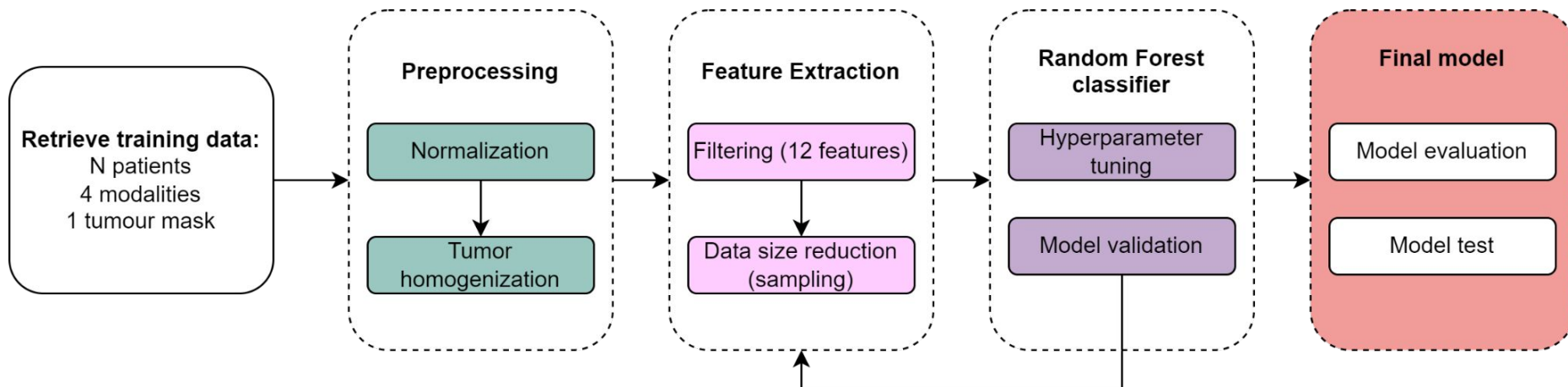
Dice score SVM: 0.695 ± 0.22

Voxel-wise classification

Random Forest

- 2 minutes per patient
- completely automated
- supervised





Made through spatial filtering in 3D volumes and 2D slices

Based on Low and high grade glioma segmentation in multispectral brain MRI data (Szilágyi et al, 2018)

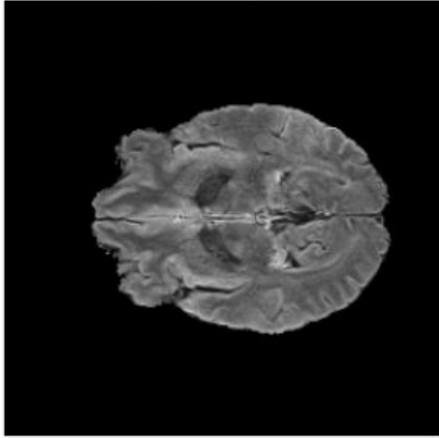
Feature (12)	Window size	Modalities
Minimum value	3x3x3	T1,T1ce,T2,Flair
Maximum value	3x3x3	T1,T1ce,T2,Flair
Median value	11x11x11	T1
Median value	11x11	T1
Mean value	11x11	Flair
Mean value	9x9	Flair

Sampling voxels: Reducing training data size (~8.9 mill voxels/px) by selecting only brain voxels and then randomly sampling 800-2000 samples per patient.

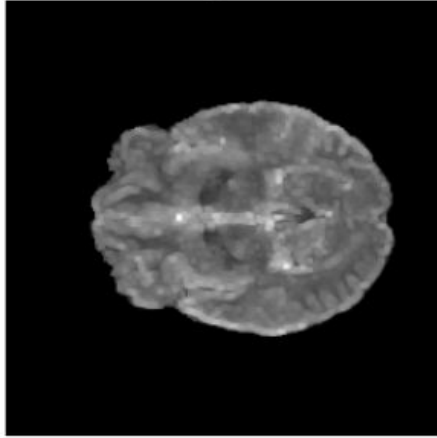
Feature Extraction:

Random Forest

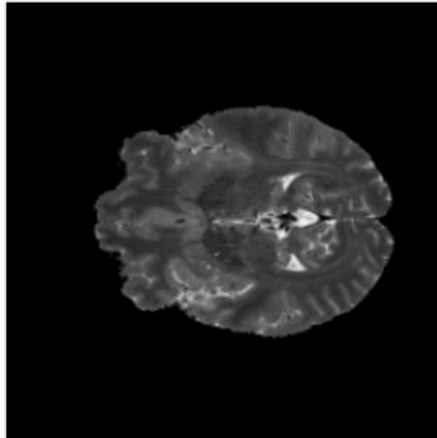
Original image Flair



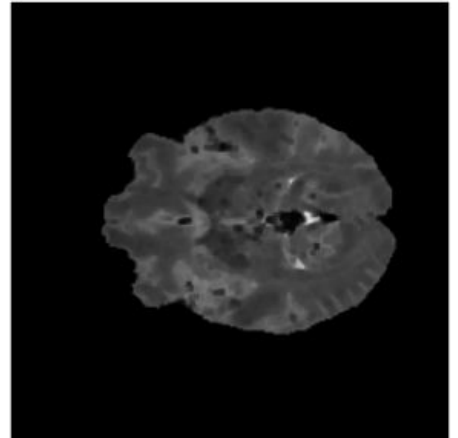
Filtered image: Max 3x3x3



Original image T2

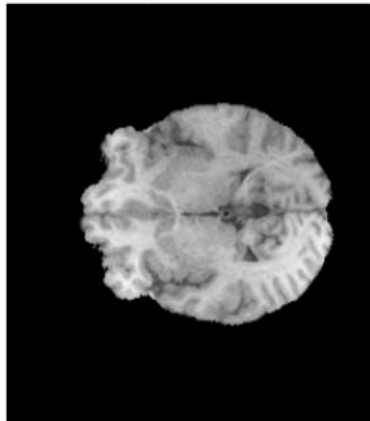


Filtered image: Min 3x3x3

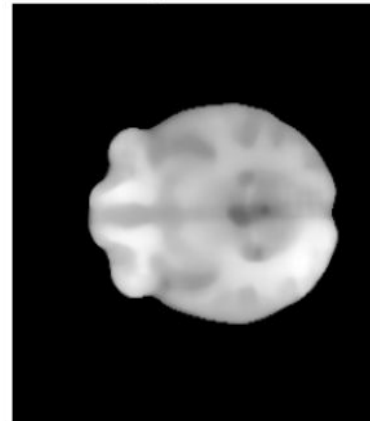




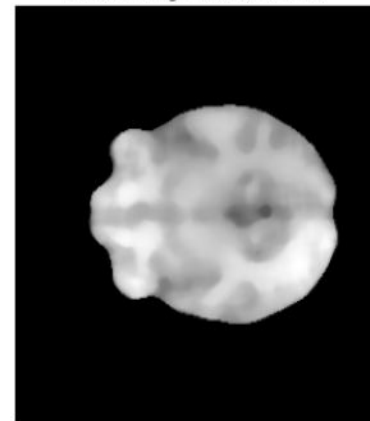
Original image T1



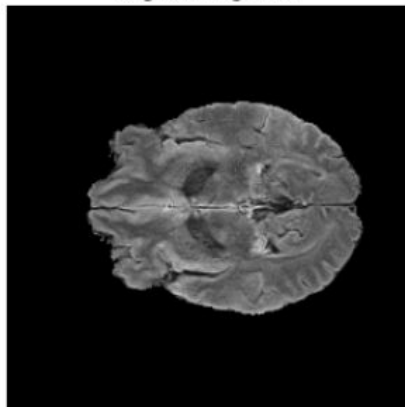
Filtered image: Median 11x11x11



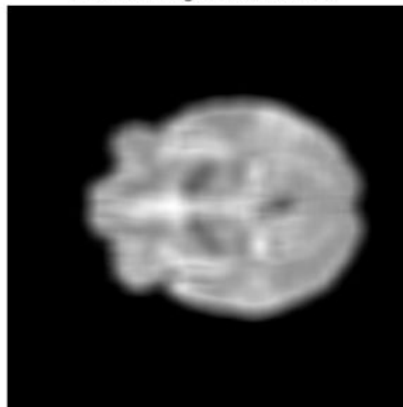
Filtered image: Median 11x11



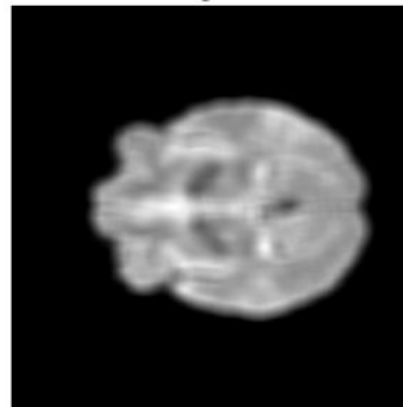
Original image Flair



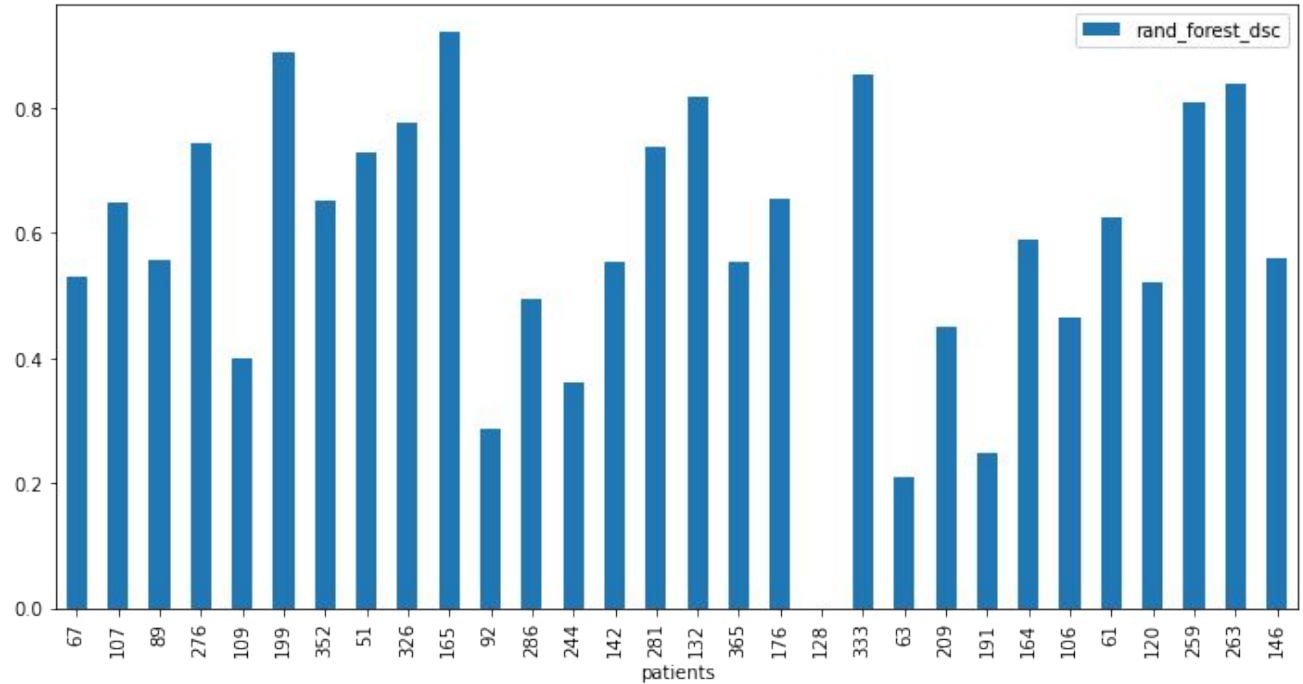
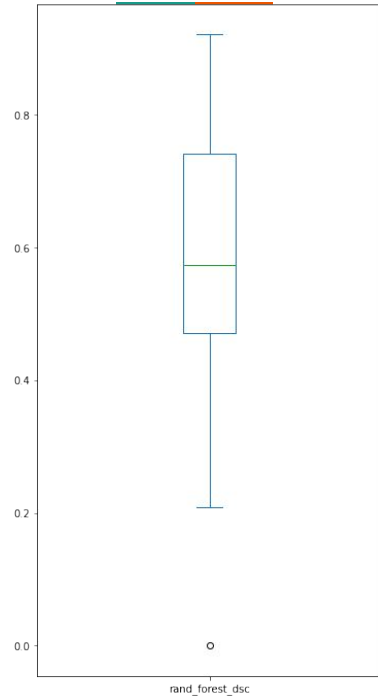
Filtered image: Mean 11x11



Filtered image: Mean 9x9

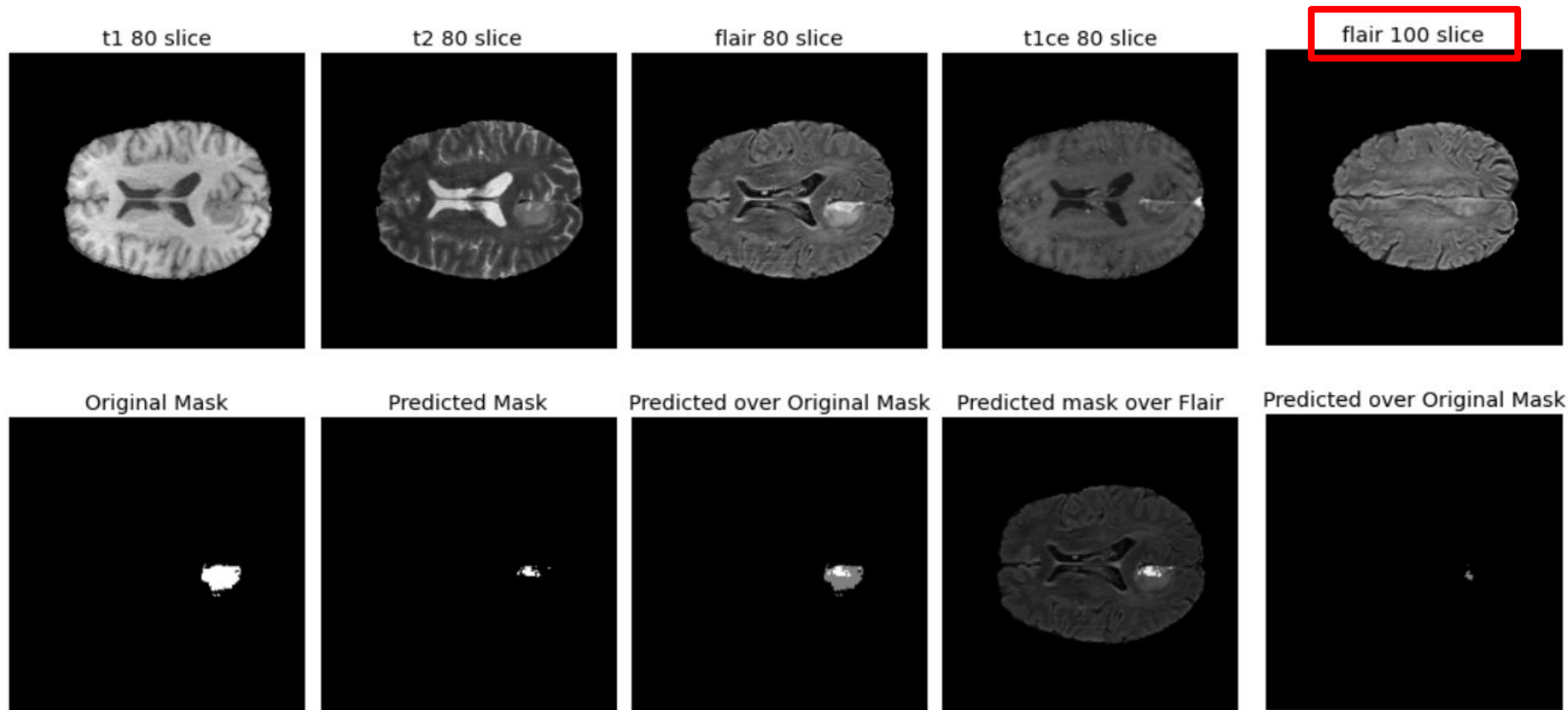


- Trained with 100 different patients (800 samples/px). [Approx time: 2 hours for FE and training]
- Test with 30 new different patients

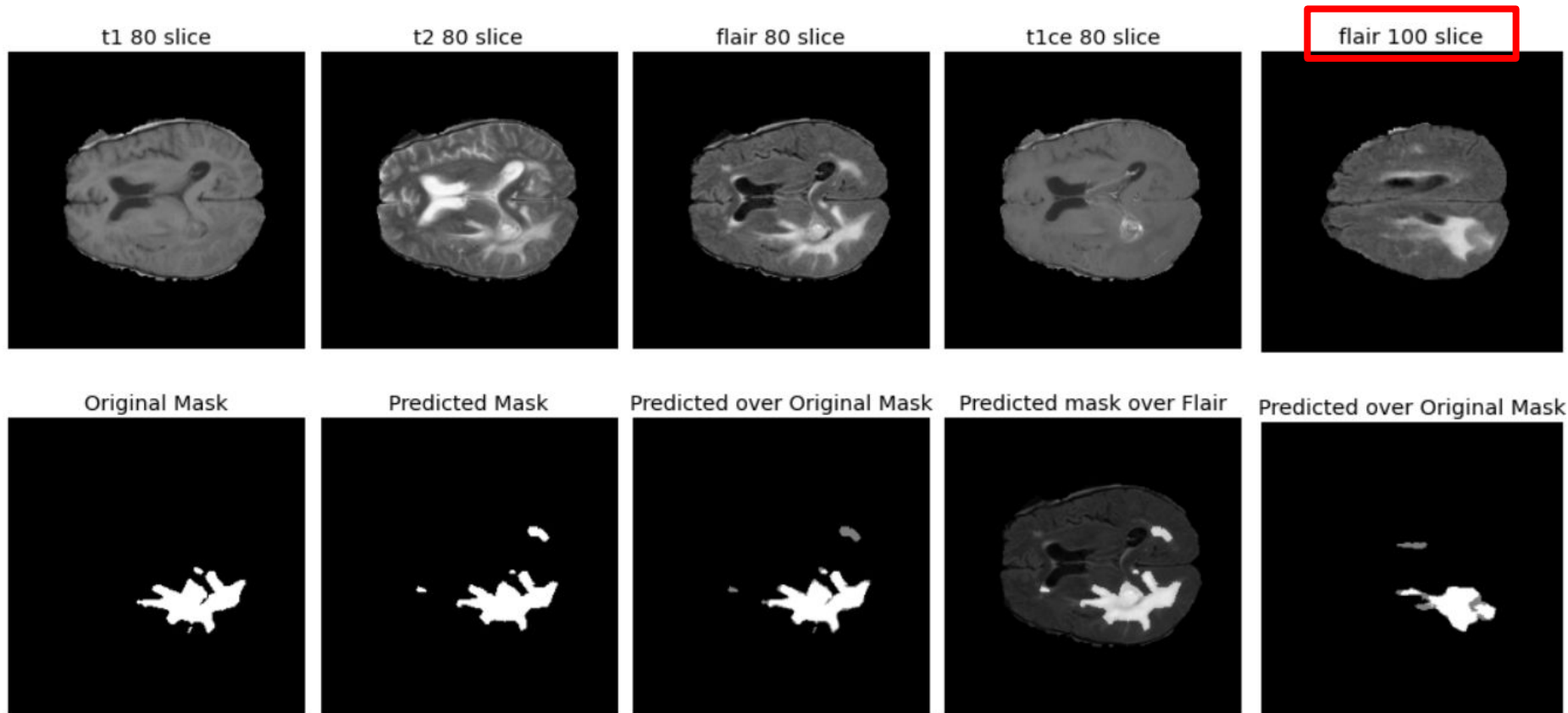


Dice score RF: 0.58 ± 0.21

- Patient 63: $DSC=0.2089$, $HD = 63.65$

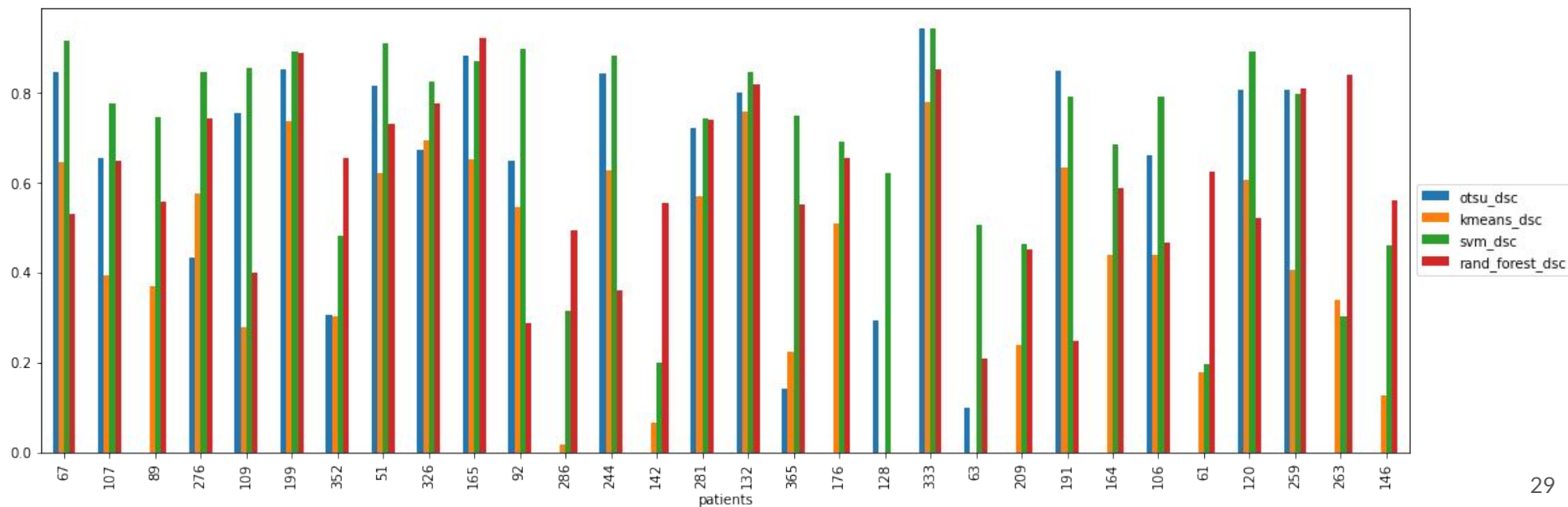


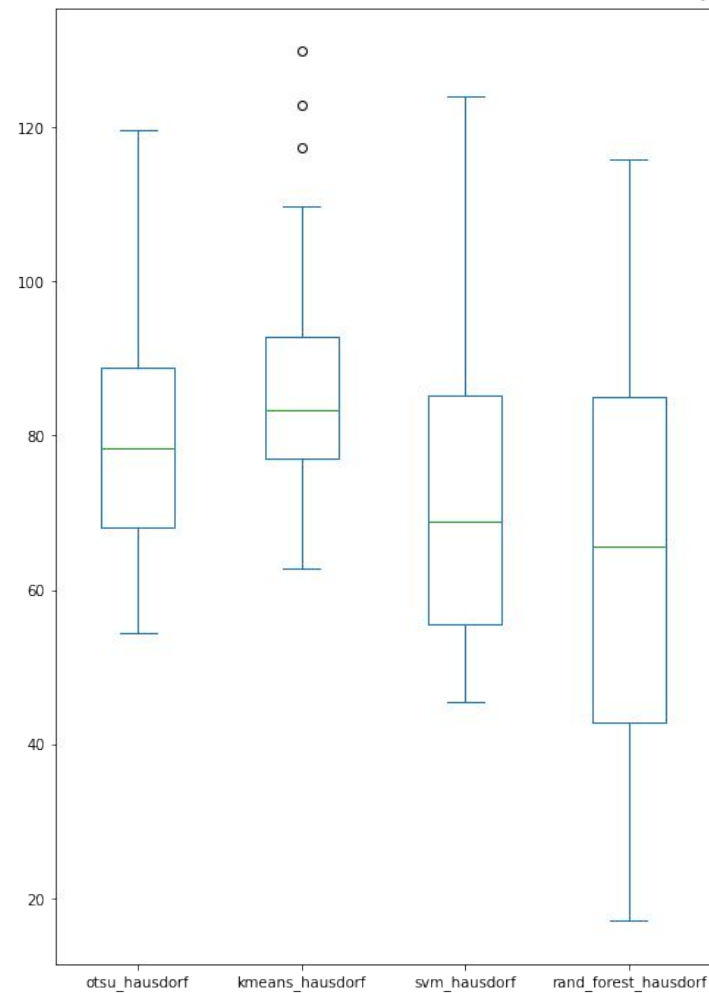
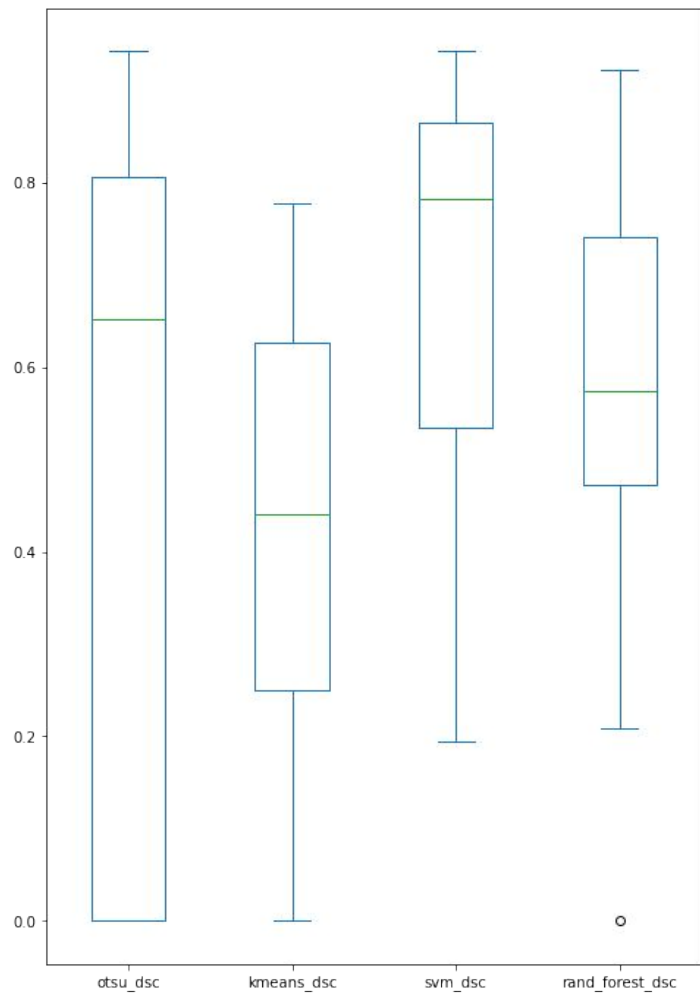
- Patient 165: **DSC=0.92.14**, HD = 53.56





Dice Score comparison

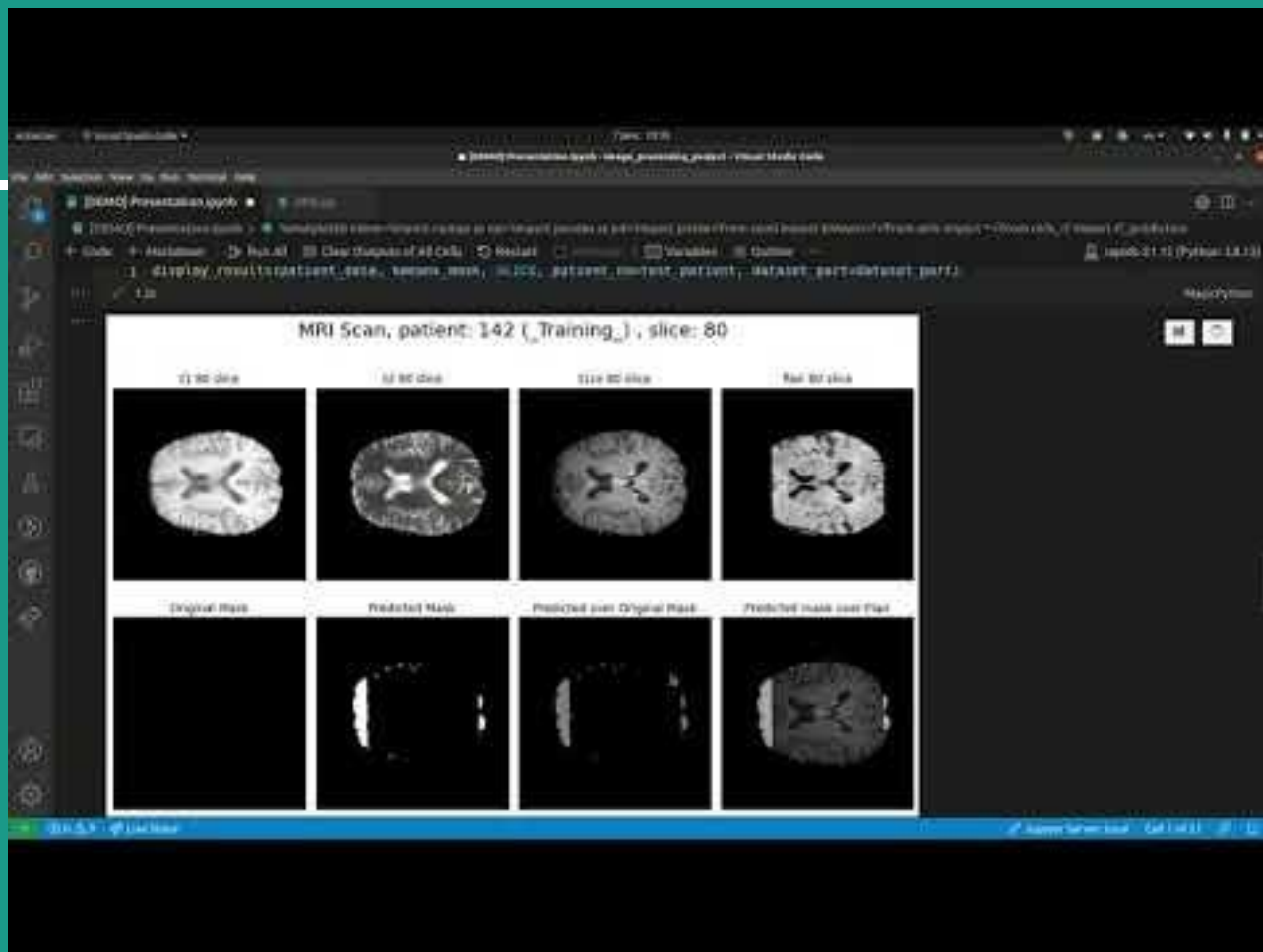




General conclusions

- High inter-patient tumor variability led to diverse results
- Each model has its own strengths and we can combine them in future work
- Traditional segmentation (thresholding, k-means):
 - Quicker but limited usability
- Voxel-wise classification (random forest, support vector machine):
 - Slower but better results

Video demo





Questions?

Thank you!