

# Comparative Study of Machine Learning and Deep Learning Multi-Class Segmentation Methods

*Elizabeth Nemeti and Shaniah Reece*

# Introduction and State of the Literature

## *MRI: non-invasive imaging for brain tumor diagnosis*

### Detection via “segmentation”:

- *manual* - radiologists annotate images
- *automated* - ML/DL classifies pixels

### Limitations of Manual Segmentation

1. Image quality
2. Experience/opinion of the analyst
3. Sheer volume of images in large dataset
4. Morphology: small size of early tumors
5. Human error + inconsistency

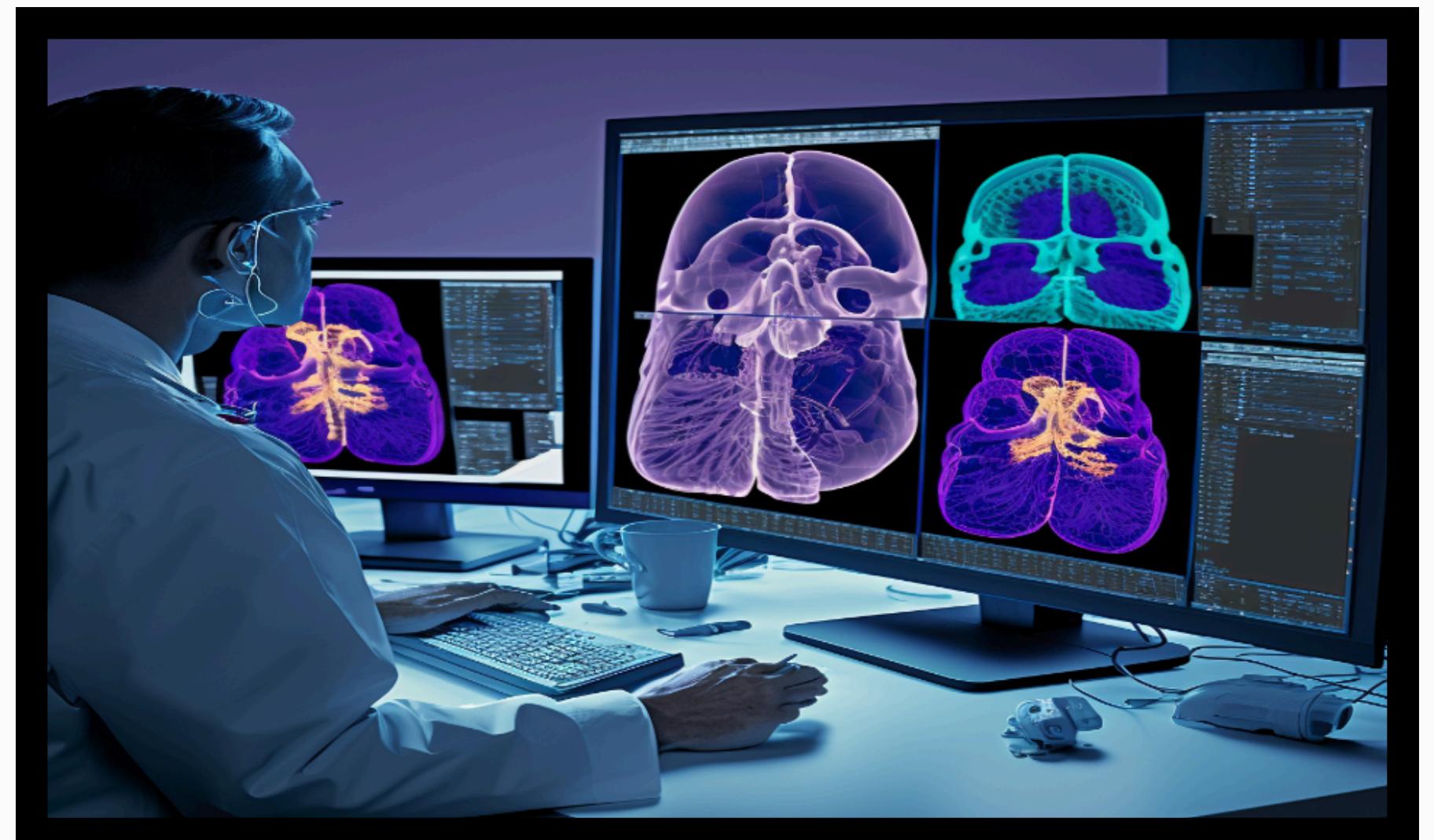


Figure. Radiologist manually segmenting MRI images with software.

# Advantages of Automated Segmentation

1. Efficiency and speed in large datasets
2. Quantitative + qualitative evaluation metrics
3. Early tumor detection
4. Speedy analysis of complex underlying patterns

## Limitations

1. Image quality (noise, blur, size)
2. Class imbalances
3. Computational resource constraints
4. Smaller unlabeled datasets

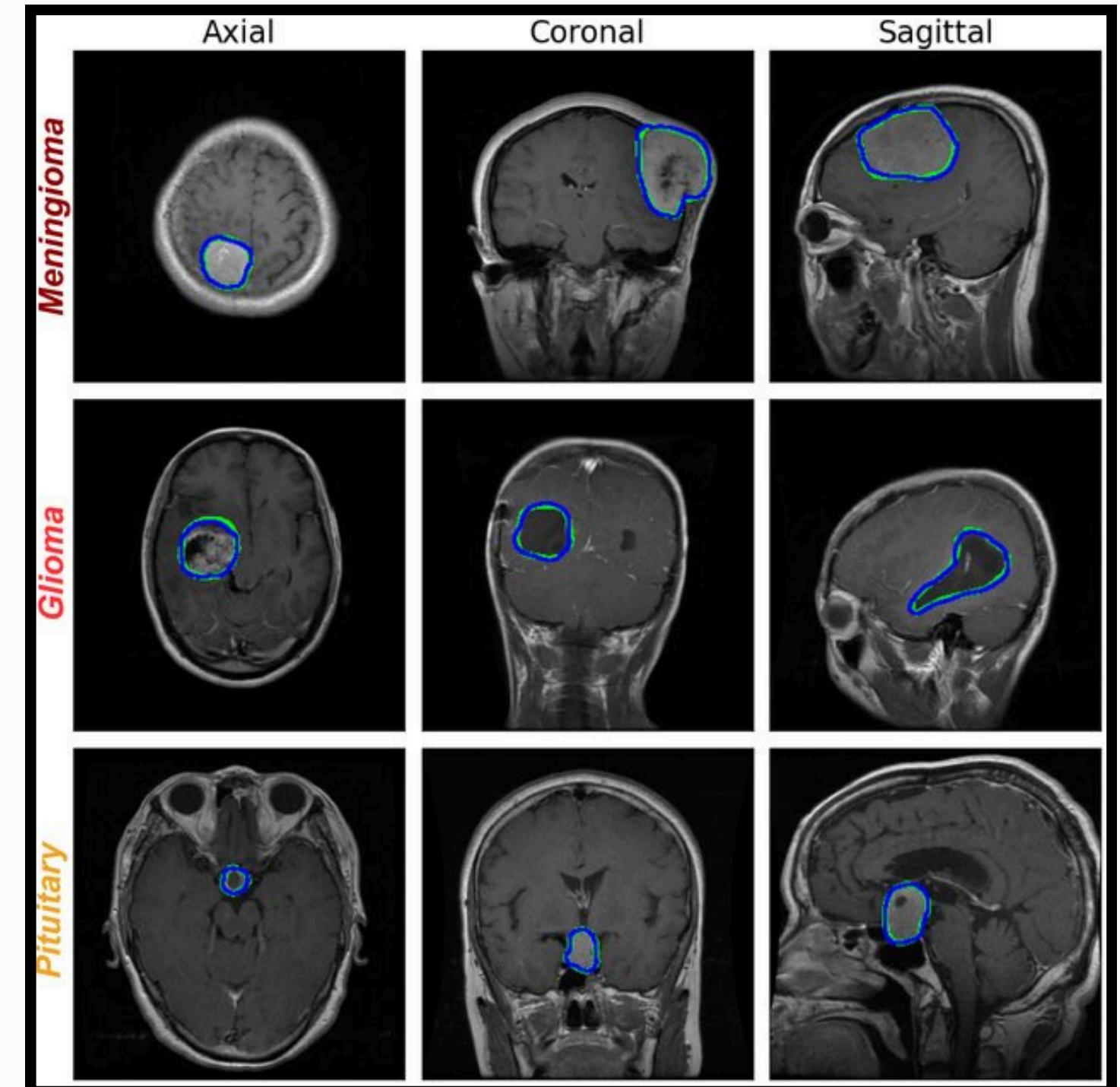


Figure. (Maas et al., 2021) Network Segmentation – High DICE Scores: Three brain tumor classes in the three different planes from our local test set. Green delineations are the radiologist annotations (ground truth) and blue borders are the network's predicted multi-class segmentations correctly classified.

# The Shift from ML to DL in the Literature

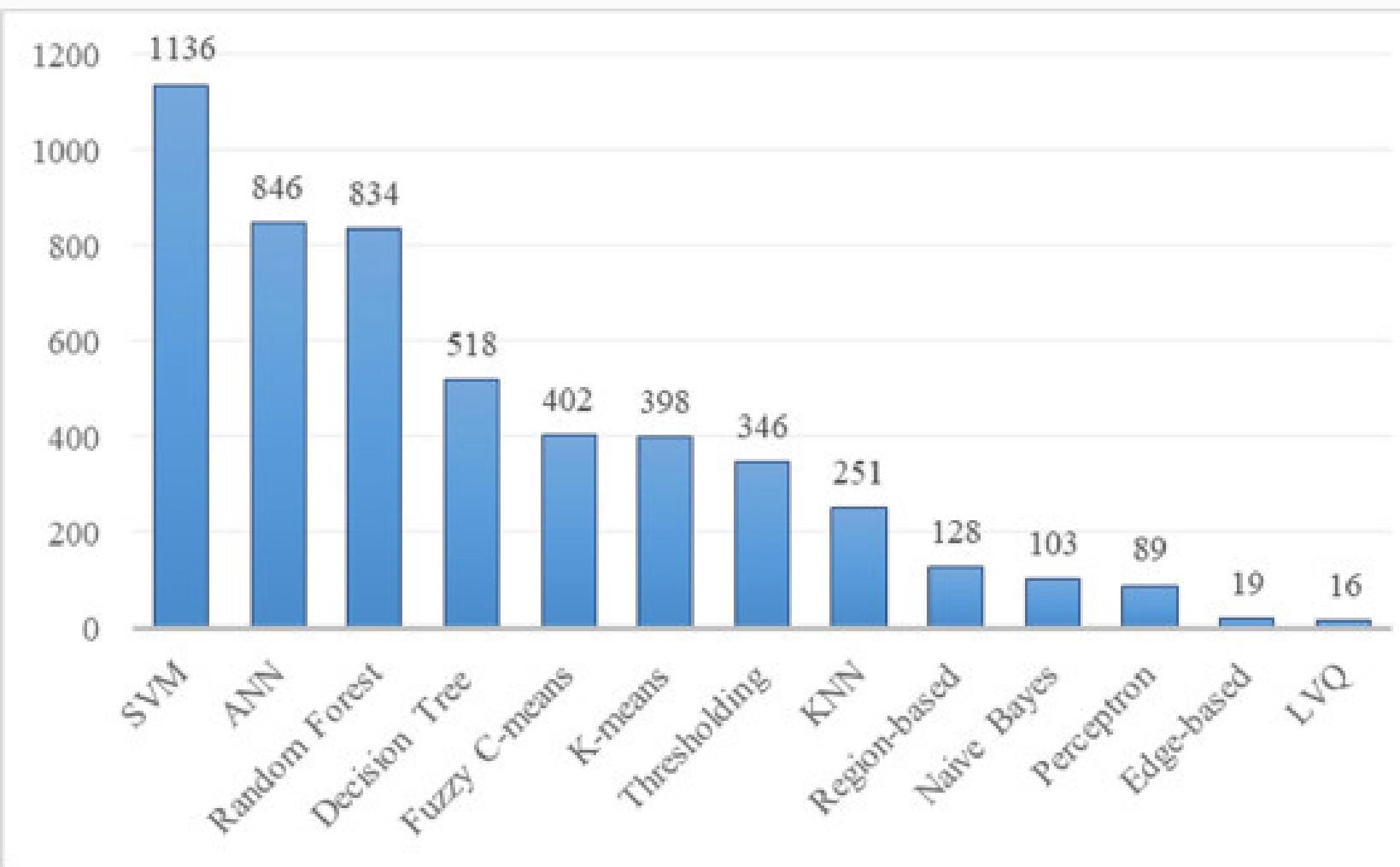


Figure. Ranjbarzadeh et al. 2023  
Number of publications between 2015 and 2022 for  
brain tumor segmentation using supervised and unsupervised  
learning techniques

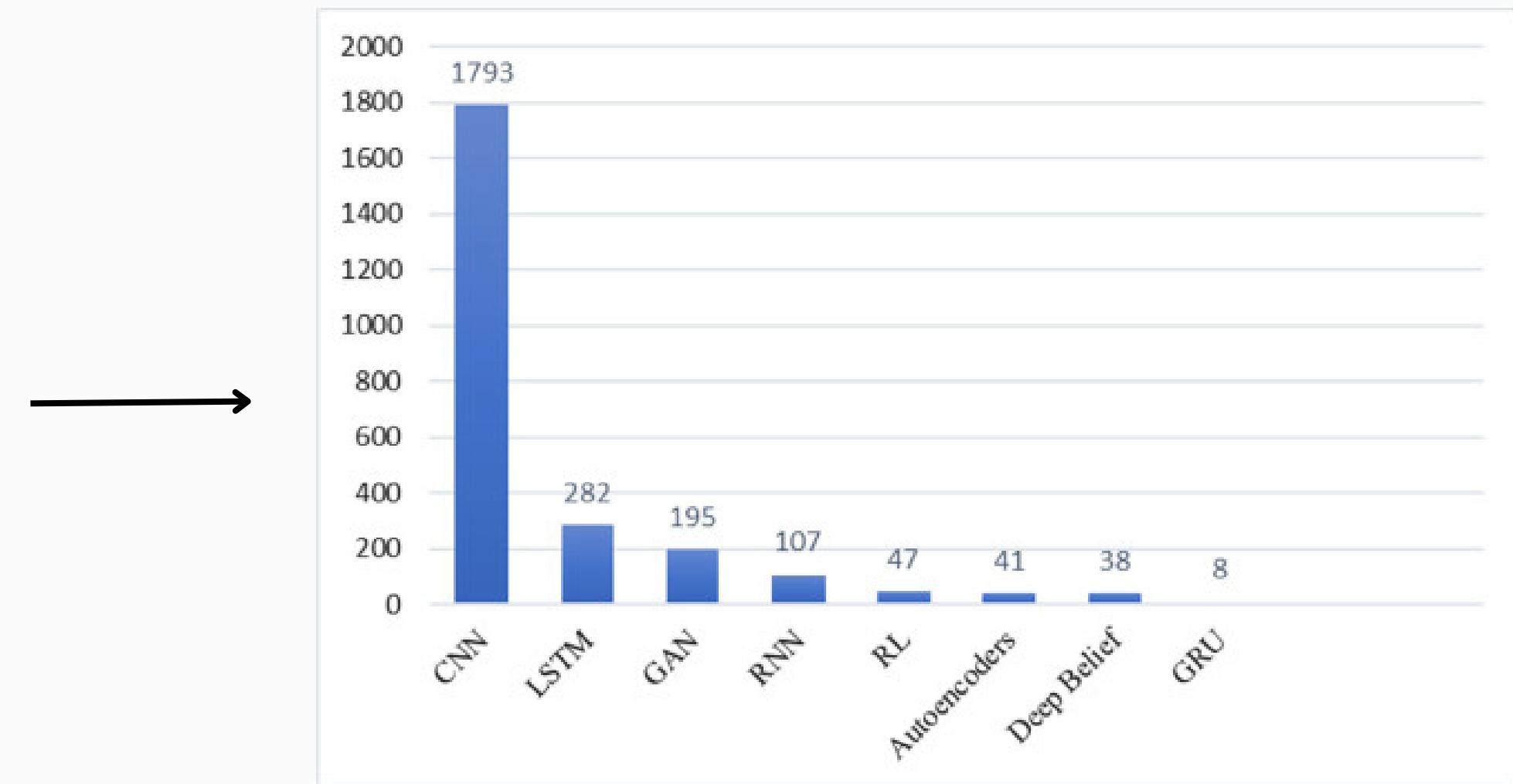
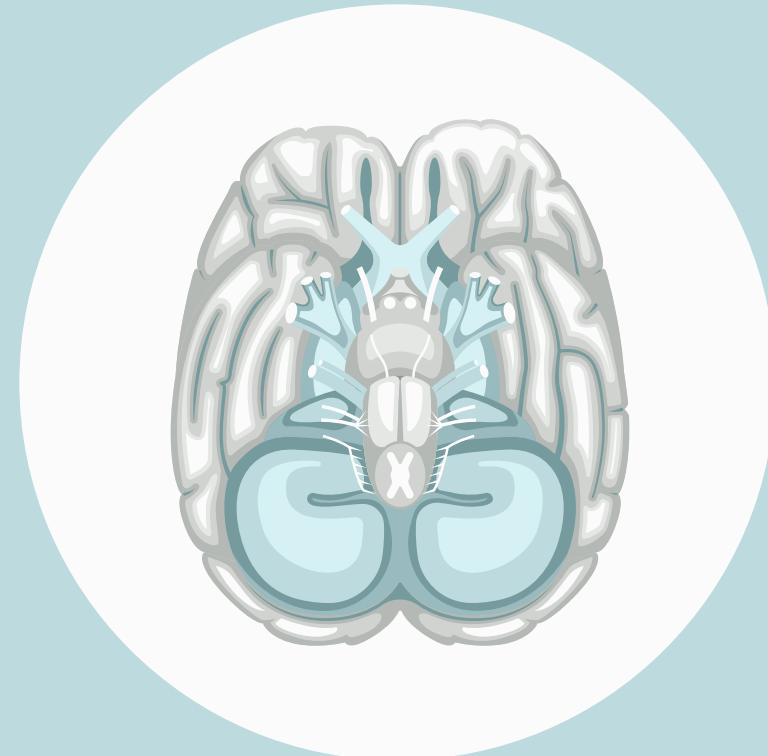


Figure. Ranjbarzadeh et al. 2023  
Number of publications between 2015 and 2022 for  
brain tumor segmentation using DL models



# A Comparative Study of Machine Learning and Deep Learning Multi-Class Segmentation Methods

# Aims/Novelty

Mass et al. 2021:

- Automated U-based deep CNN
- Used our same dataset
- Same multiclass segmentation task

We specifically address and expand upon the areas of future work outlined by Maas et al. 2021.

2021 10th International IEEE/EMBS Conference on Neural Engineering (NER)  
Virtual Conference, May 4-6, 2021

## QuickTumorNet: Fast Automatic Multi-Class Segmentation of Brain Tumors

Benjamin Maas<sup>1</sup>, Erfan Zabeh<sup>1</sup>, and Soroush Arabshahi<sup>1</sup>

**Abstract**— Non-invasive techniques such as magnetic resonance imaging (MRI) are widely employed in brain tumor diagnostics. However, manual segmentation of brain tumors from 3D MRI volumes is a time-consuming task that requires trained expert radiologists. Due to the subjectivity of manual segmentation, there is low inter-rater reliability which can result in diagnostic discrepancies. As the success of many brain tumor treatments depends on early intervention, early detection is paramount. In this context, a fully automated segmentation method for brain tumor segmentation is necessary as an efficient and reliable method for brain tumor detection and quantification. In this study, we propose an end-to-end approach for brain tumor segmentation, capitalizing on a modified version of QuickNAT, a brain tissue type segmentation deep convolutional neural network (CNN). Our method was evaluated on a data set of 233 patient's T1 weighted images containing three tumor type classes annotated (meningioma, glioma, and pituitary). Our model, QuickTumorNet, demonstrated fast, reliable, and accurate brain tumor segmentation that can be utilized to assist clinicians in diagnosis and treatment.

### I. INTRODUCTION

Fast brain tumor detection and size quantification is important in patient outcomes. Speed and accuracy are of utmost importance regarding brain tumor detection and quantification. Accurate localization of brain tumors and quantification are primary measures that dictate treatment and patient care, ultimately determining the success of treatment and patients' life expectancies. In other words, expeditious intervention and appropriate treatment in brain tumors are dependent on early tumor detection and accurate quantification which directly relate to patients' overall prognoses [1]–[3].

In our study, we look at three main brain tumor types.

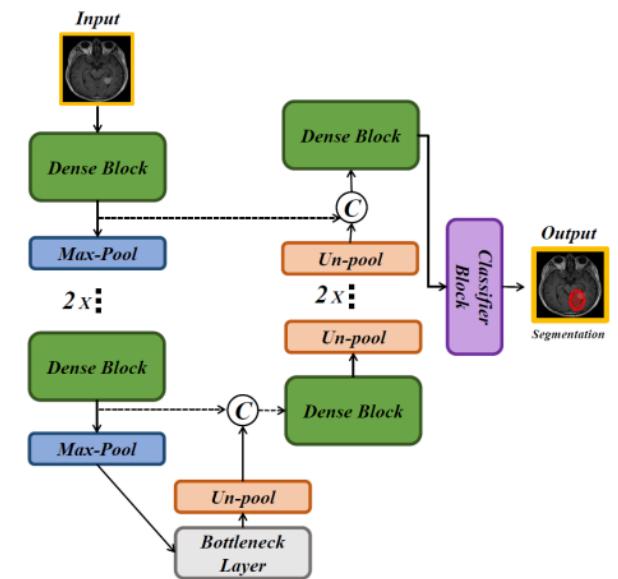


Fig. 1. Illustration of QuickTumorNet's network architecture consisting of dense, bottleneck, and classifier blocks arranged as illustrated. The C in circle symbol represents concatenation in the third dimension. Code available at: [Github Link](#)

task that requires an expert radiologist and is subjective by nature and therefore results in high inter-rater reliability variance [4]. Additionally, even expert radiologists can only perform a small amount of diagnostic reads and tumor quantifications or segmentations when compared to the amount a CNN can perform in the same duration.

In the medical discipline of radiology, the use of computer-based image processing techniques for anatomical segmentation and quantification have gained popularity as deep learning and machine learning neural networks increase in

# Aims

To address the need for comparing CNNs with simpler models to enhance interpretability, we will:

- ***Compare a U-NET (CNN) with both an SVM and FCM across multiple performance metrics and qualitative visual results.***

To address the need for utilizing more varied/diversified datasets in training, we will:

- ***Implement data augmentation for U-NET and benchmark all three models with the well-established BRaTs 2018 dataset.***

To address the labeling challenge in medical imaging (frequent noisy/inconsistent labels) we will:

- ***Assess the effectiveness of supervised (i.e. UNET and SVM) versus unsupervised segmentation methods (i.e. FCM).***

# Selected Dataset

- 3064 MRI images
- T1-weighted contrast-enhanced
- Great quality: 512 x 512 pixels
- 233 patients
- Labeled: radiologist annotated tumors

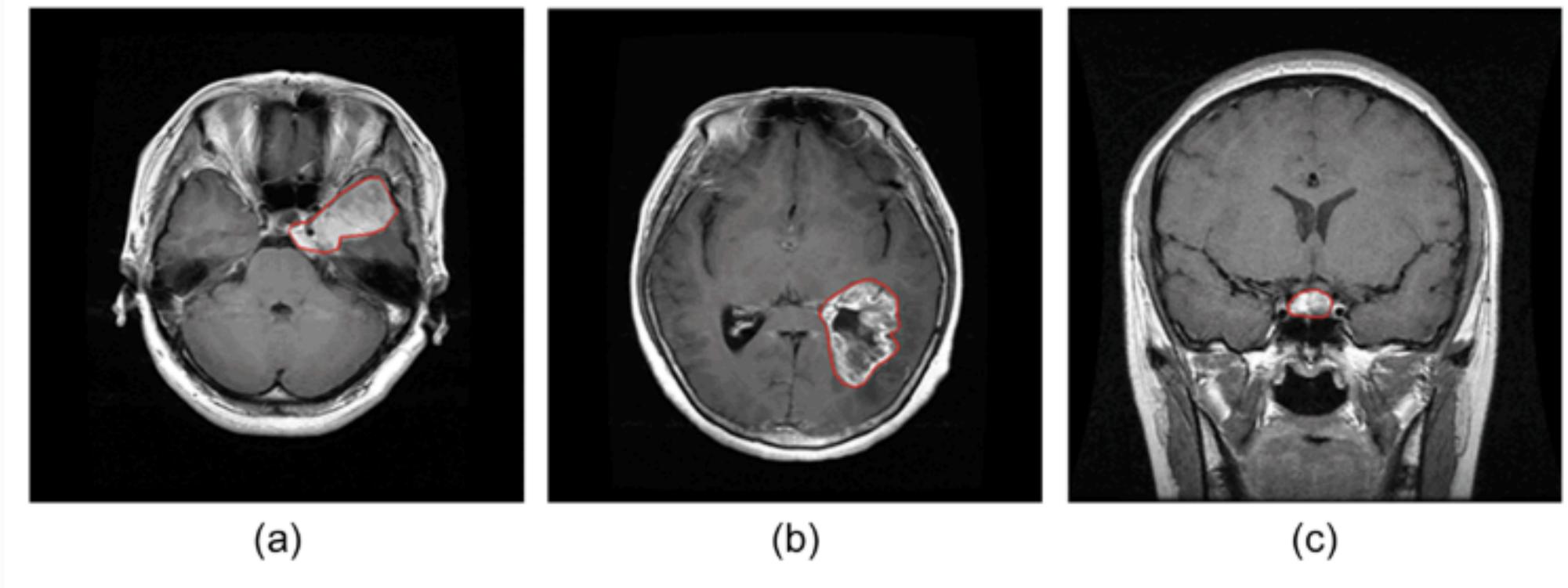


Fig. 3. Illustrations of three typical brain tumors: (a) meningioma; (b) glioma; and (c) pituitary tumor. Red lines indicate the tumor border. [3]

*Cheng, Jun (2017). brain tumor dataset. figshare.  
Dataset. <https://doi.org/10.6084/m9.figshare.1512427.v5>*

# Handling Class Imbalance

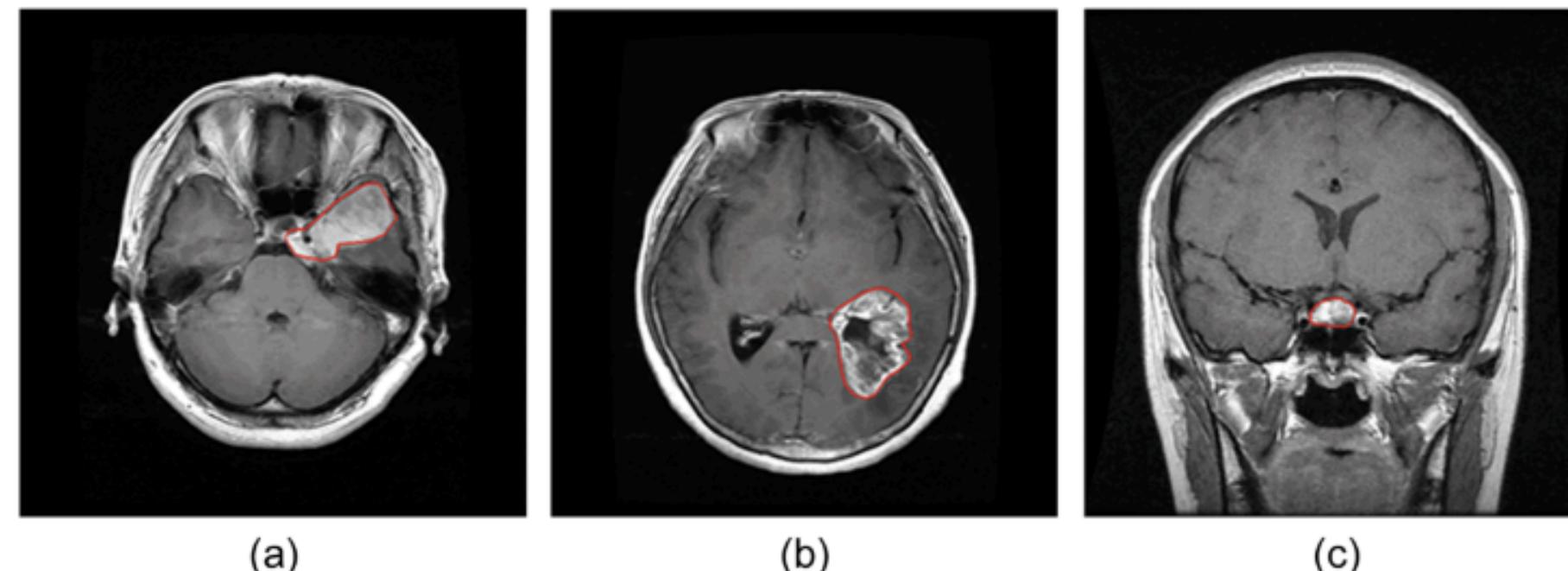


Fig. 3. Illustrations of three typical brain tumors: (a) meningioma; (b) glioma; and (c) pituitary tumor. Red lines indicate the tumor border. [3]

Original Data Distribution:  
(a) meningioma 708 images  
(b) glioma 1426 images  
(c) pituitary tumor 930 images

Balancing  
algorithm

New Data Distribution:  
(a) 708 images  
(b) 708 images  
(c) 708 images

# Benchmark Dataset

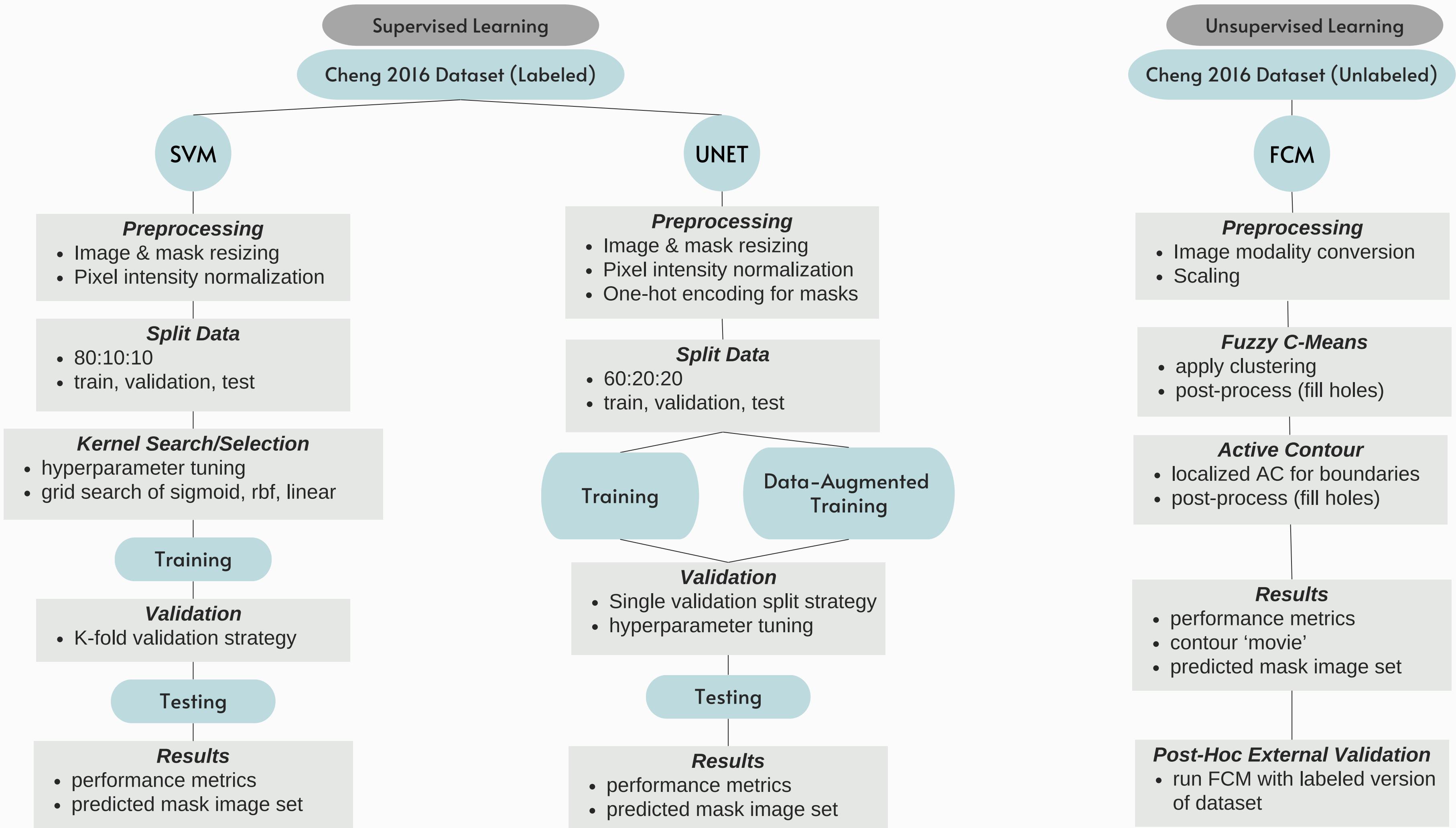
(enforces better model generalizability on unseen data)

- sourced from 19 institutions/diverse scanners
- 3gb worth of multimodal MRI images
- 4 modalities
- Labeled: radiologist annotated tumors

Multimodal Brain Tumor Segmentation Challenge 2018



<https://www.med.upenn.edu/sbia/brats2018/data.html>



## *Evaluation Metrics*

**UNET**

**Sensitivity**  
**Specificity**  
**Accuracy**  
**Precision**  
**Confusion Matrix**  
**Jaccard Index (IoU)**  
**Dice Similarity**

**SVM**

**Sensitivity**  
**Specificity**  
**Accuracy**  
**Precision**  
**Confusion Matrix**  
**Jaccard Index**  
**Dice Similarity**

**FCM + AC**

**Silhouette Score**  
**Davies - Bouldin**  
**Calinski-Harabasz**

# Preliminary Results

SVM

Accuracy: 0.83  
Precision: 0.84  
Recall: 0.83  
Jaccard Index: 0.71  
F1 Score: 0.83  
Dice Similarity: 0.79  
Specificity: 0.86

UNET

Accuracy: 0.99  
Precision: 0.01  
Recall: 0.99  
Specificity: 0.99  
IoU: 0.016  
Dice: 0.031

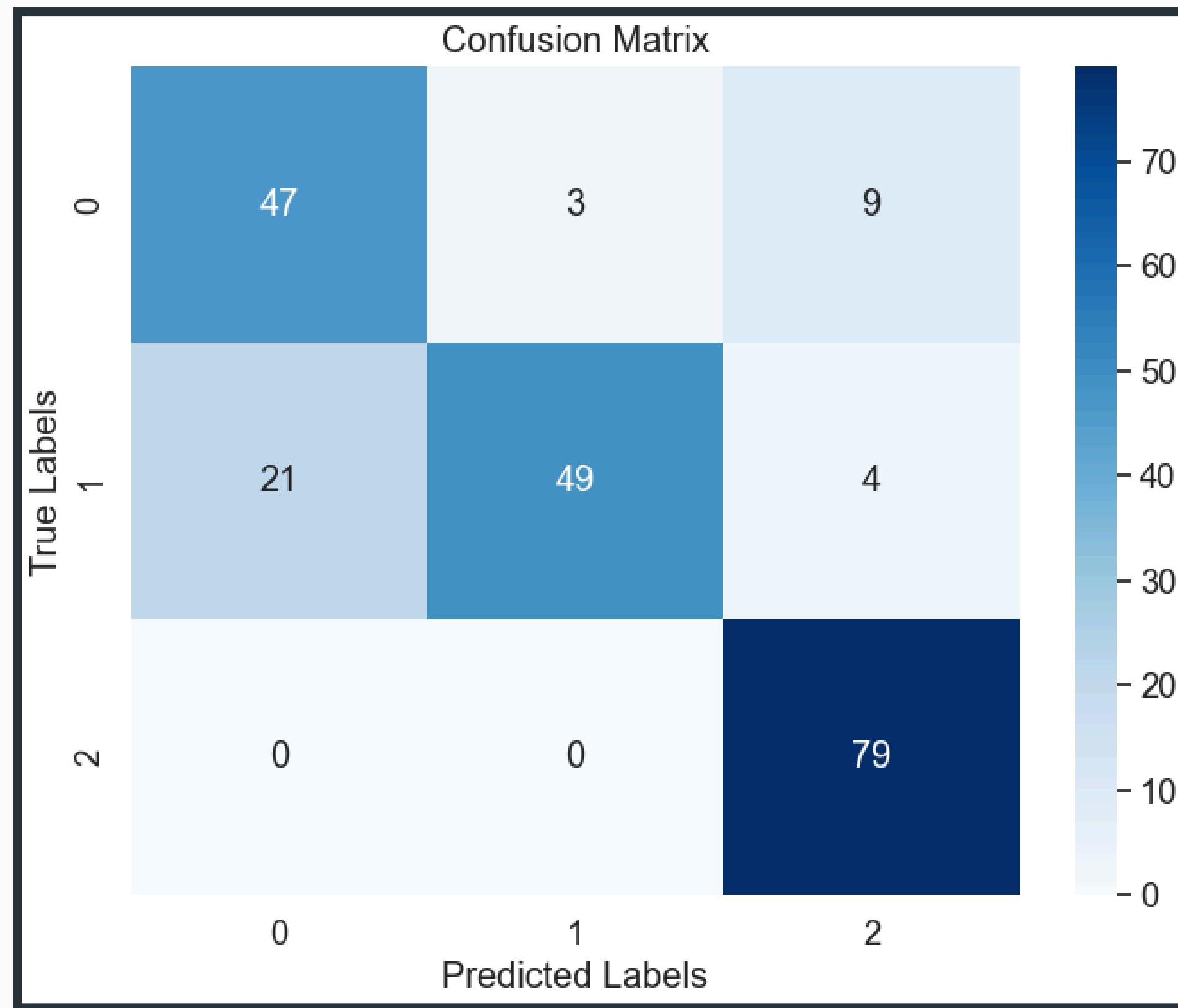
FCM

Silhouette Score  
Davies - Bouldin  
Calinski-Harabasz

# Preliminary Results

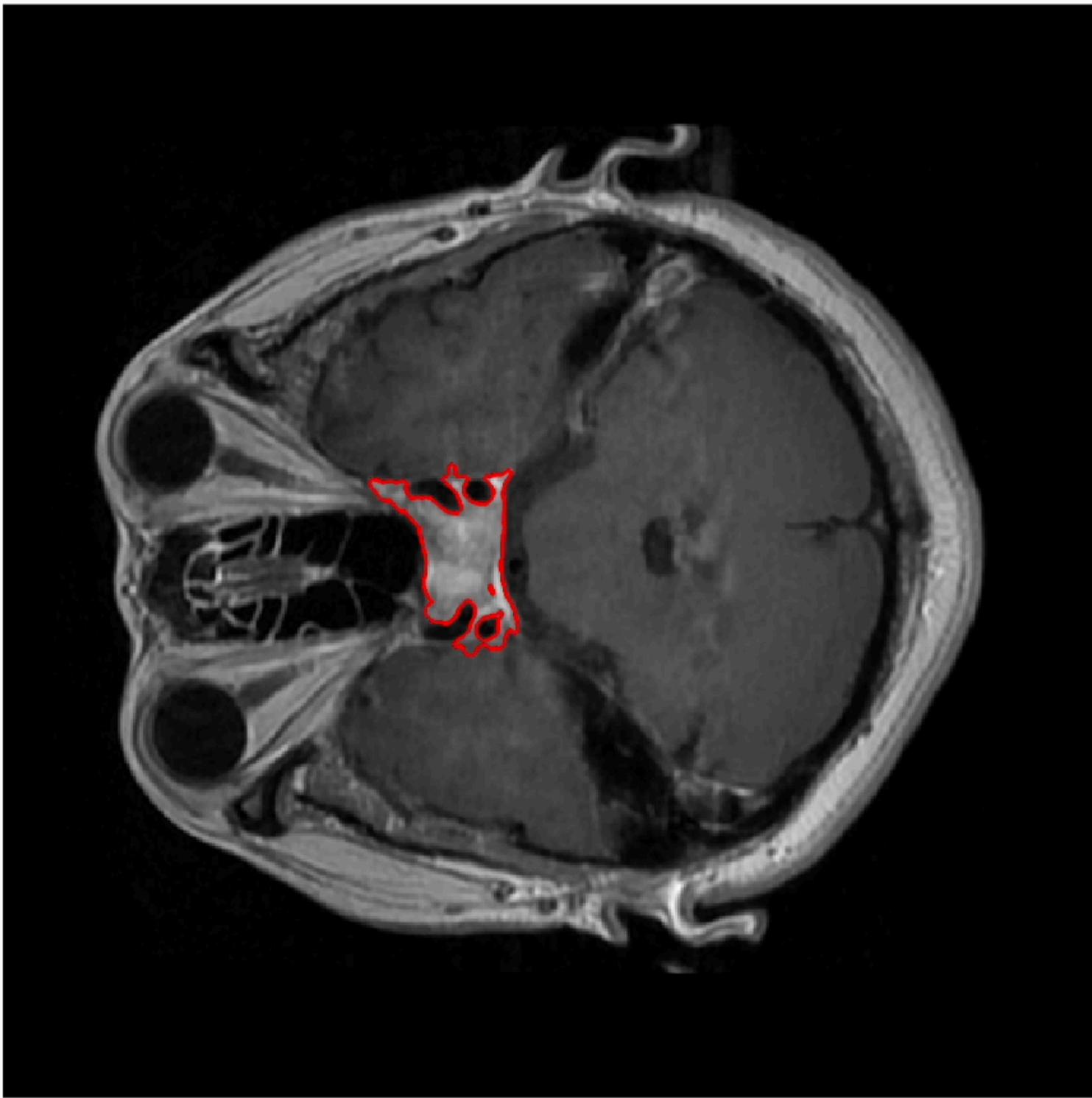
RBF	Linear	Sigmoid	Average
Accuracy: 0.83 Precision: 0.84 Recall: 0.83 Jaccard Index: 0.71 F1 Score: 0.83 Dice Similarity: 0.79 Specificity: 0.86	Accuracy : 0.81 Precision : 0.81 Recall: 0.81 Jaccard Index : 0.69 F1 Score : 0.81 Dice Similarity: 0.74 Specificity: 0.79	Accuracy: 0.53 Precision: 0.52 Recall: 0.53 Jaccard Index: 0.36 F1 Score: 0.52 Dice Similarity: 0.45 Specificity: 0.41	Accuracy: 0.53 Precision: 0.52 Recall: 0.53 Jaccard Index: 0.36 F1 Score: 0.52 Dice Similarity: 0.45 Specificity: 0.41

# Quantitative Results: SVM

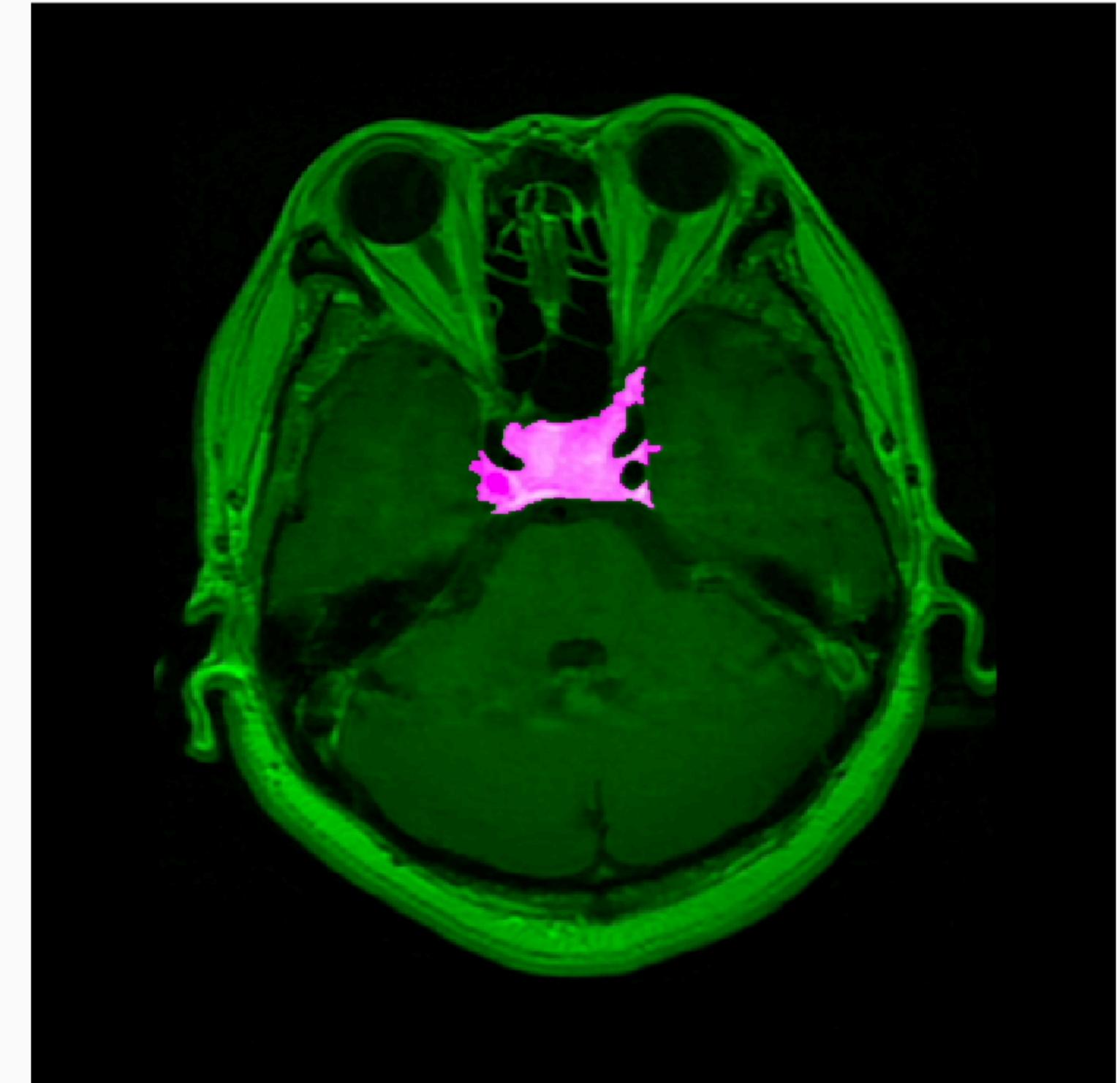


# Qualitative Results: FCM (img)

**400 Iterations**

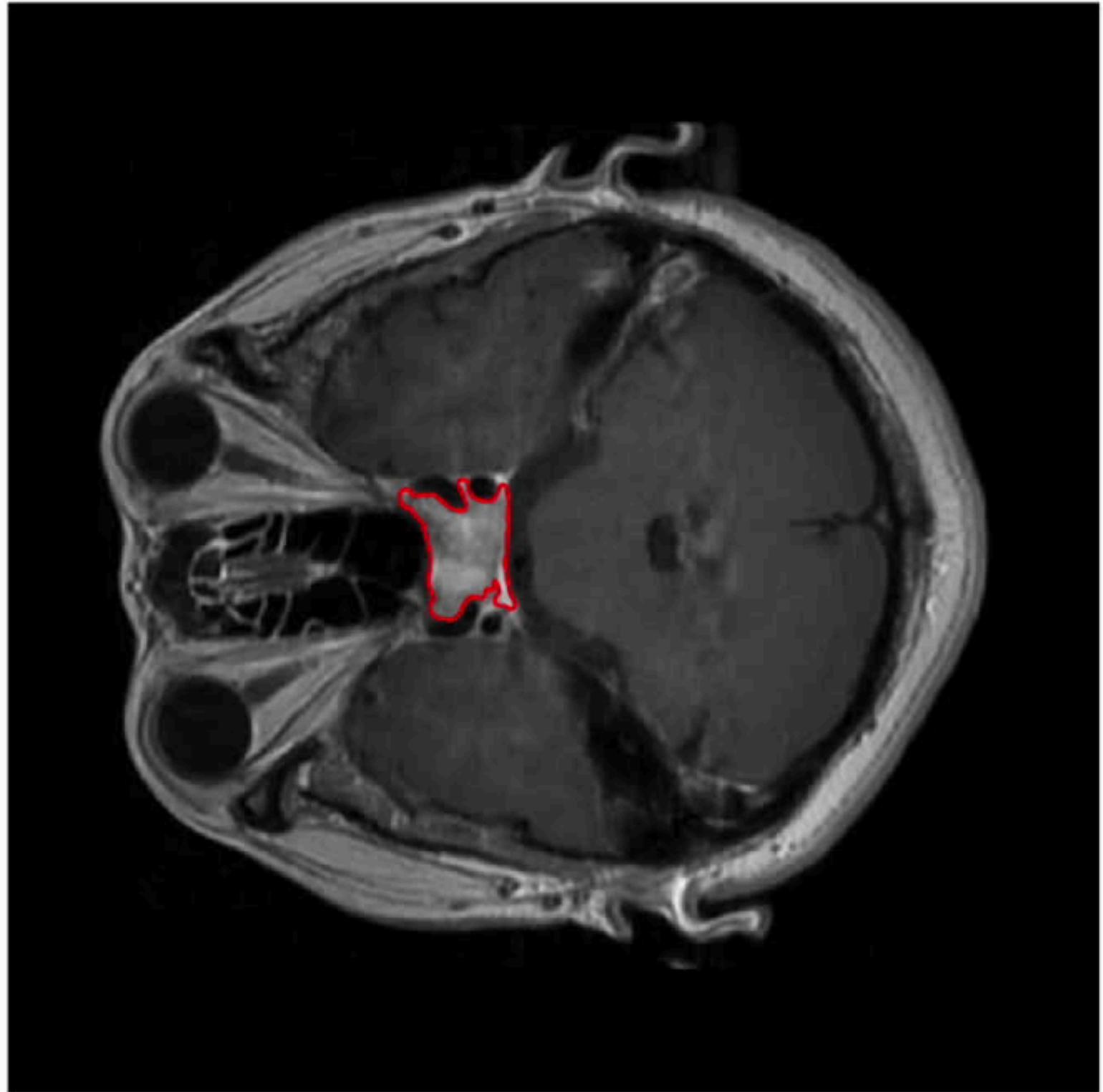


**Processed Image: 6**

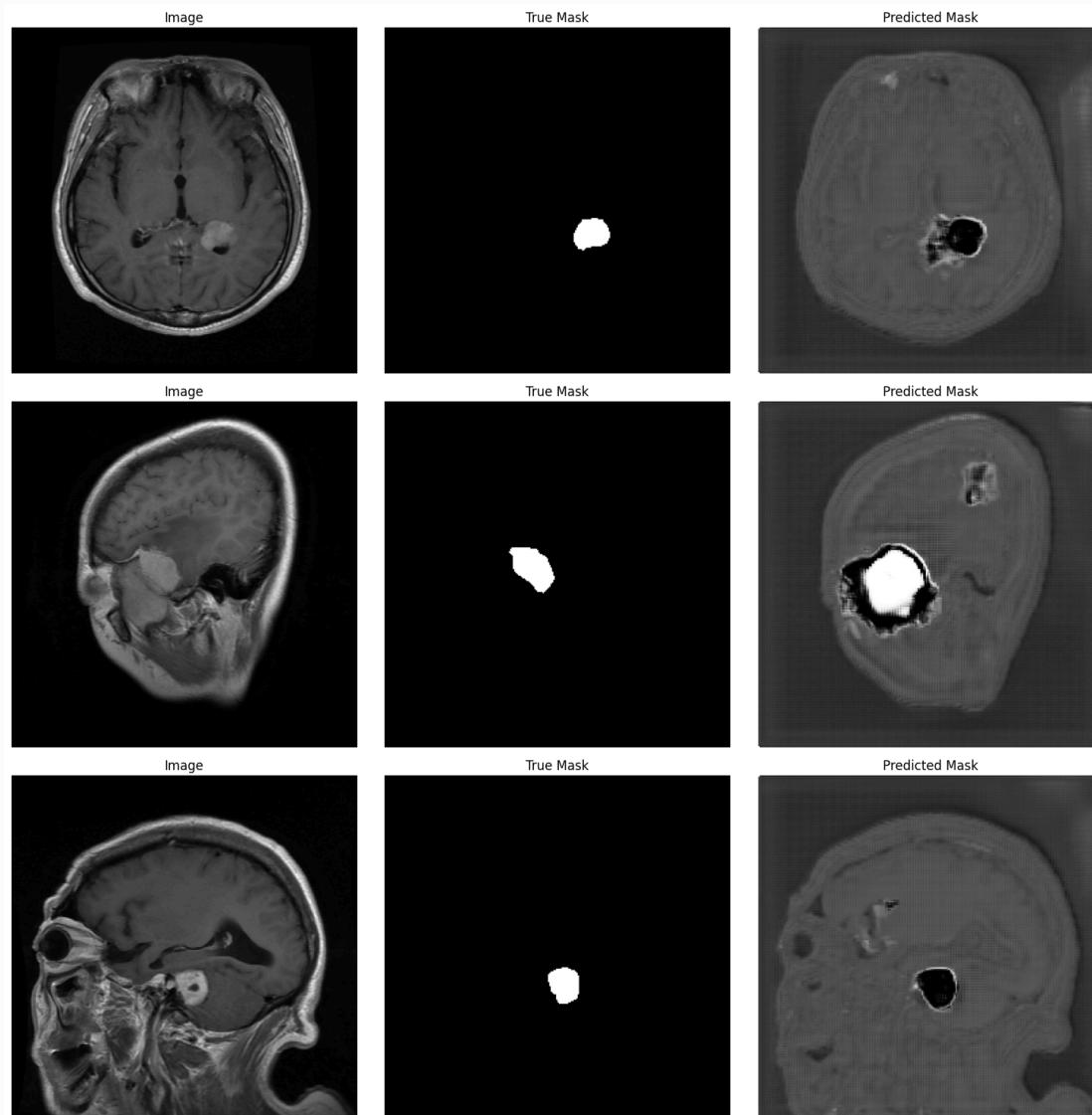


# Qualitative Results: FCM (mov)

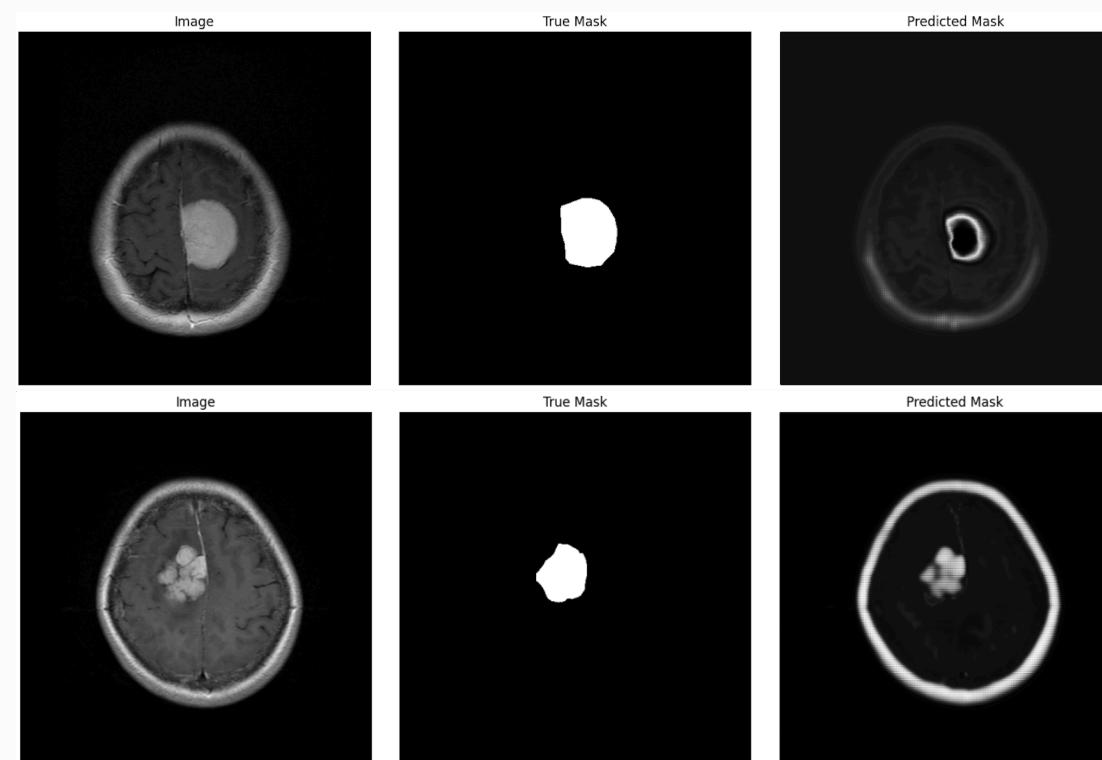
**100 Iterations**



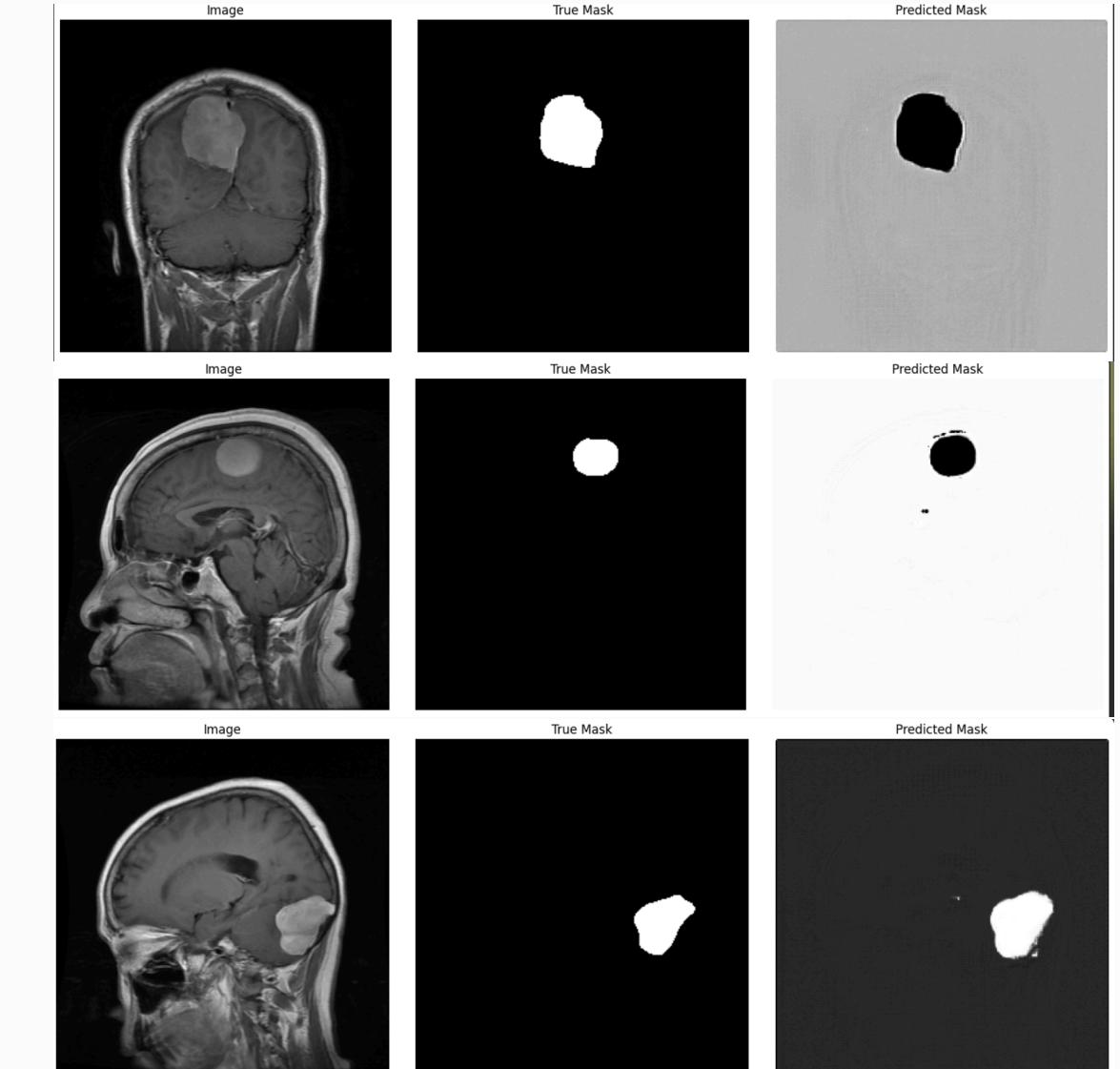
# Qualitative Results: UNET



epochs max = 100  
early stop = 46  
patience = 20  
balanced dataset  
256x256 resolution  
batch = 2



epochs max = 10  
early stop = N/A  
patience = 10  
Imbalanced dataset  
**512x512 resolution**  
batch = 1



epochs max = 50  
early stop = 17  
patience = 10  
balanced dataset  
256x256 resolution  
batch = 1

# Comparing UNET Results to Prior Studies

Table 2: Comparison of Our U-Net Model Performance with Literature on BRaTS 2018

Method	Dice Comp	Dice Core	Dice Enh	Precision Comp	Precision Core	Precision Enh
Our U-Net (512x512, 100 epochs, subset)	3.18%	-	-	1.66%	-	-
Our U-Net (256x256, subset, 50 epochs)	1.66%	-	-	1.42%	-	-
Our U-Net (256x256, balanced, 50 epochs)	3.09%	-	-	1.61%	-	-
Our U-Net (256x256, balanced, 100 epochs)	2.97%	-	-	1.56%	-	-
3D UNet [225]	86%	82%	76%	7.01	5.63	5.60
Deep CNN [226]	88%	79%	78%	5.50	6.90	2.93
3D UNet [227]	87%	77%	71%	6.50	8.31	4.14
Contour-aware 3D CNN [228]	89%	79%	72%	8.05	7.50	5.20
S3D-UNet [229]	84%	78%	69%	9.20	7.70	4.50
HITU-Net [230]	88%	89%	82%	7.53	8.81	4.43
Auto-encoder Regularization [231]	88%	81%	77%	5.90	4.80	3.80
Cascaded UNet [232]	88%	78%	72%	-	-	-
CNN [233]	87%	77%	78%	6.55	27.05	15.90
CNN+Test-time Augmentation [234]	88%	80%	75%	5.97	6.71	4.16

# Discussion



## Oversegmentation

High recall suggests the model is sensitive to tumor presence but may over-segment, capturing more than the tumor region.



## Performance Gap

E.g. U-Net Dice Coefficient significantly lags behind the literature benchmarks, indicating a need for model and training process evaluation



## Balanced data

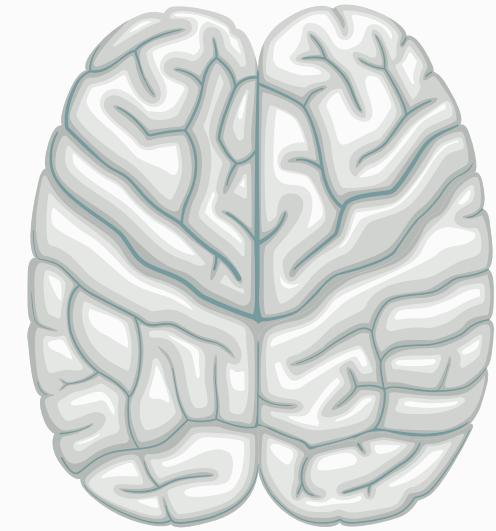
The relatively better performance of our balanced dataset runs suggests that addressing class imbalance is crucial for improving our model's segmentation ability.



## Further training/complexity

Model showed early stopping in some cases, which might have prevented it from fully converging to the best possible performance.

# Future Work



## Metrics Per Tumor Type

- measuring performance per tumor type, per model

## Using only High Quality Image

- capacity to use only 512x512 or above

## Overcoming Computational Resources

- connecting to Cluster's NVIDIA GPU

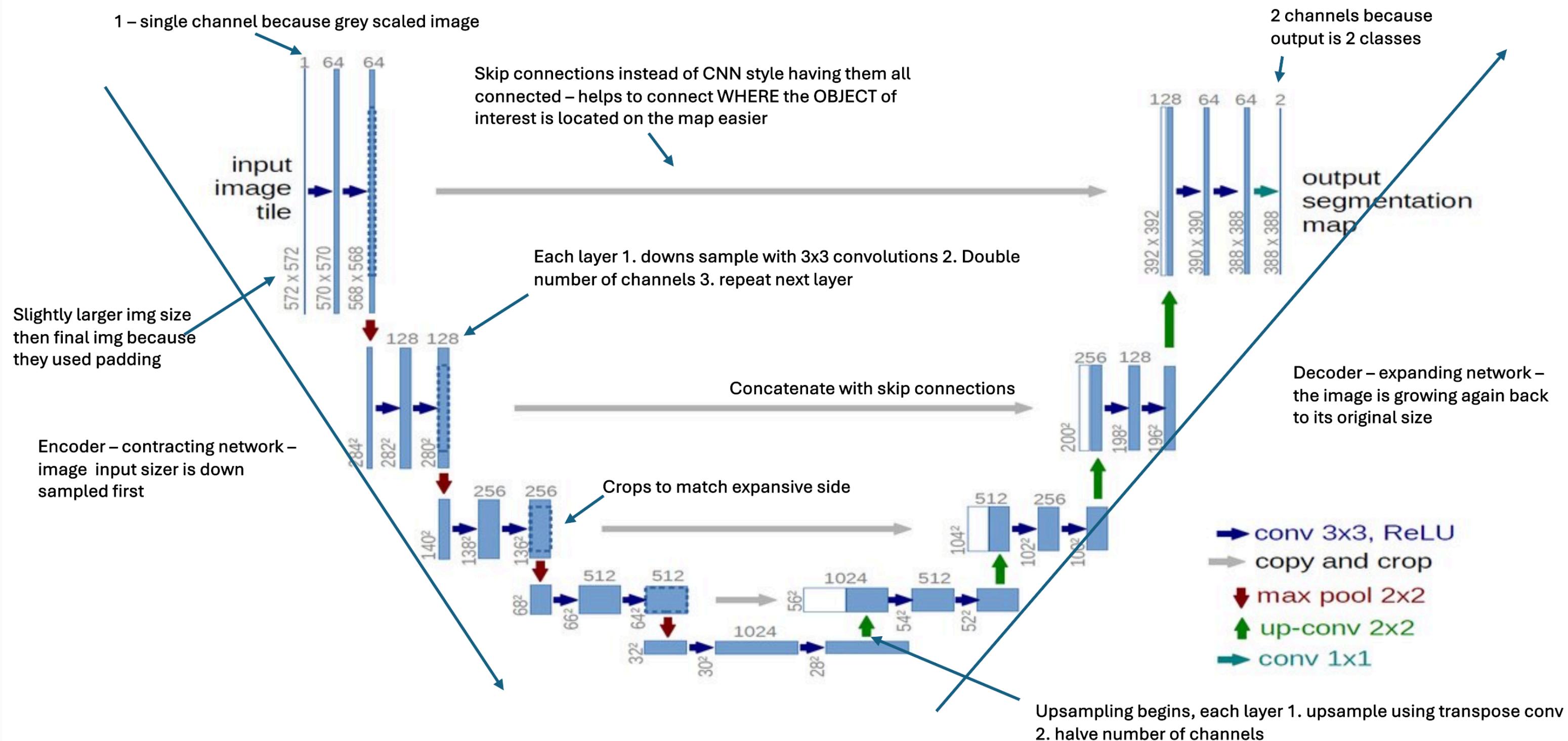
## Flag unlabeled or unrecognized tumors

- continue addressing label issue with varied datasets

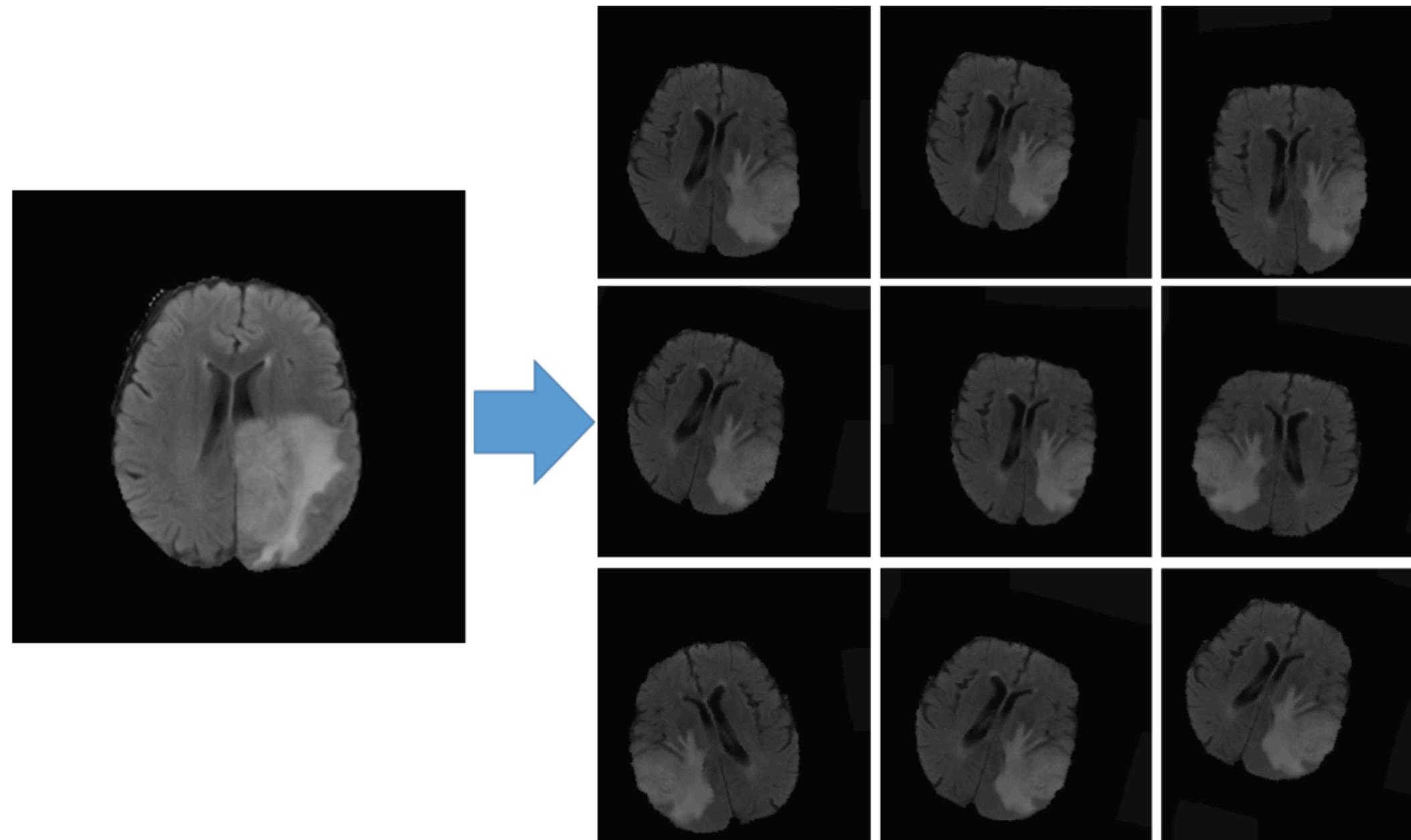
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# **Supplementary Slides**

# UNET Architecture



# Data Augmentation



- Rotation, scaling, or elastic deformations might introduce unrealistic changes in medical images
- Recognizing augmented features rather than true pathological features
- Over-application -> loss of important clinical details
- Misalign labels with the images

# FCM Methods

## Fuzziness parameter > 1

- allows for "softer clustering" -> data points can belong to **multiple clusters** with varying degrees of membership
- Name comes from here – fuzzier boundary? -> data belongs to multiple clusters

## As fuzziness approaches 1

- tends for "hard clustering" e.g. k-means -> each data point is assigned to **only one cluster**

- **The FCM objective function quantifies how good a particular clustering solution is**
- **Goal is to minimize the objective function via adjusting cluster centers and membership degrees for each point**

$$O_f = \sum_{i=1}^n \sum_{j=1}^{c=3} U_{ij}^m \|x_i - y_j\|^2$$

$n$	number of data points
$c$	number of clusters
$O_f$	objective function to be minimized
$x_i$	$i$ -th data point
$y_j$	centroid of the $j$ -th cluster
$U_{ij}$	degree of membership of $x_i$ in the $j$ -th cluster
$m$	weighting exponent on each fuzzy membership
$\ x_i - y_j\ $	Euclidean distance between the data point $x_i$ and the cluster center $y_j$

# Active Contour Methods

applies active contour model on each slice of the 2D image

- method for detecting and delineating object boundaries
- refines the contour output further by filling holes
- a low length penalty = risk of overfitting to noise/irrelevant details from the scan