Brain Tumor Segmentation using a **custom thresholding algorithm**

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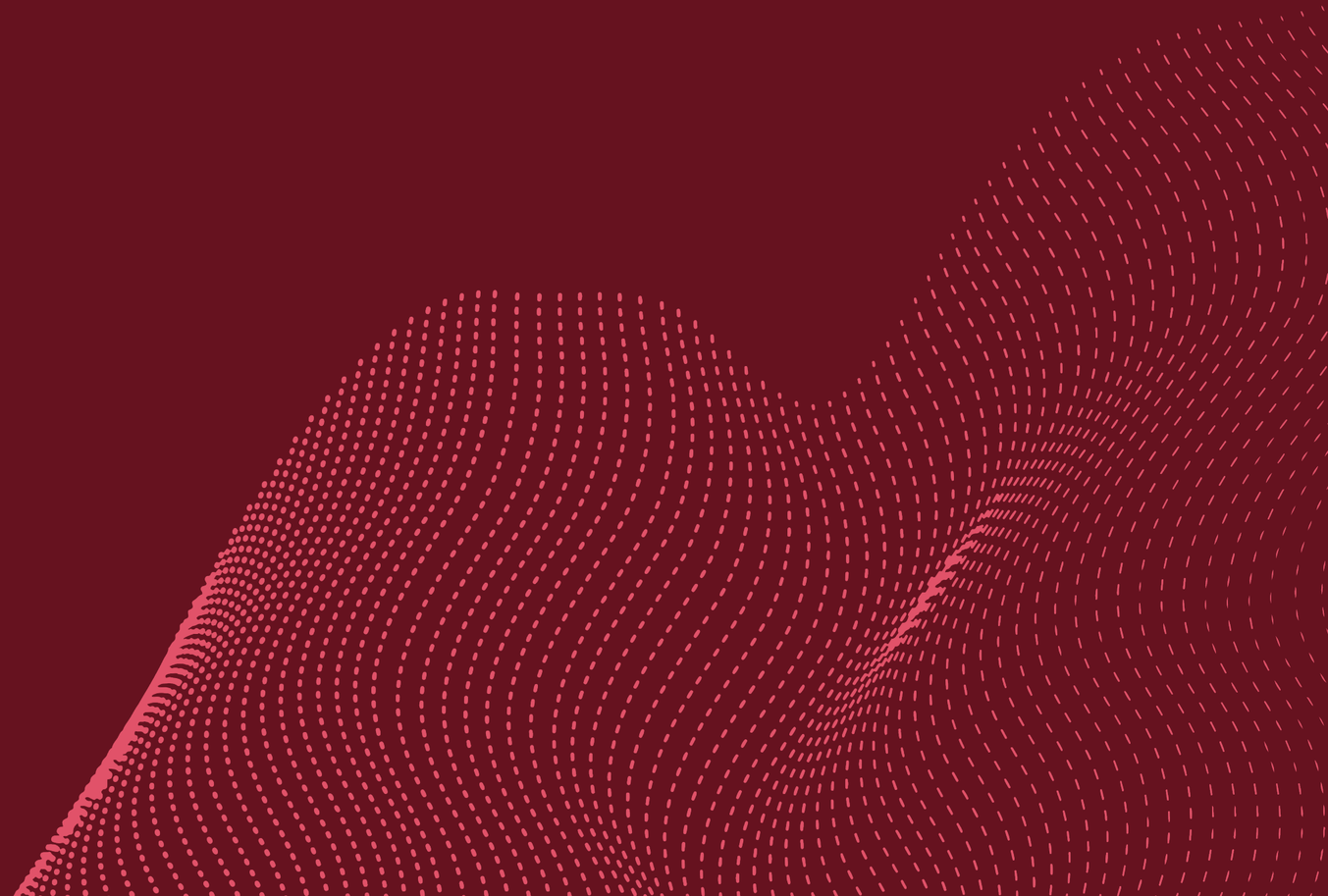
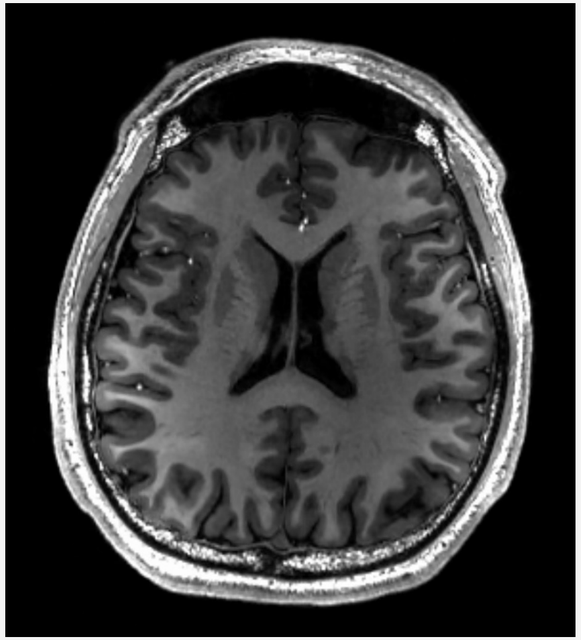
MASTER DEGREE IN COMPUTER ENGINEERING



Project's overall context



- With the rise of medical imaging in cancer diagnosis, **MRI has emerged as a pivotal tool for detecting brain tumors.**

- This project tests an approach proposed by Uhan U. Uhan A. aimed at distinctly **segment cancer affected tissues**.

- In this project it was used this **custom thresholding algorithm** that the authors proposed, for the pre-processing stage and the post-processing stage I experimented various techniques to exploit the better ones among the others.

Dataset available

- For this project, I used the **BraTS dataset**, originally composed of 750 multiparametric magnetic resonance images.

- **Only the first 100 of these were used** to test and validate the thresholding algorithm. These 100 MRIs are also provided with **ground-truth labels** that allowed me to measure the goodness of the algorithm.

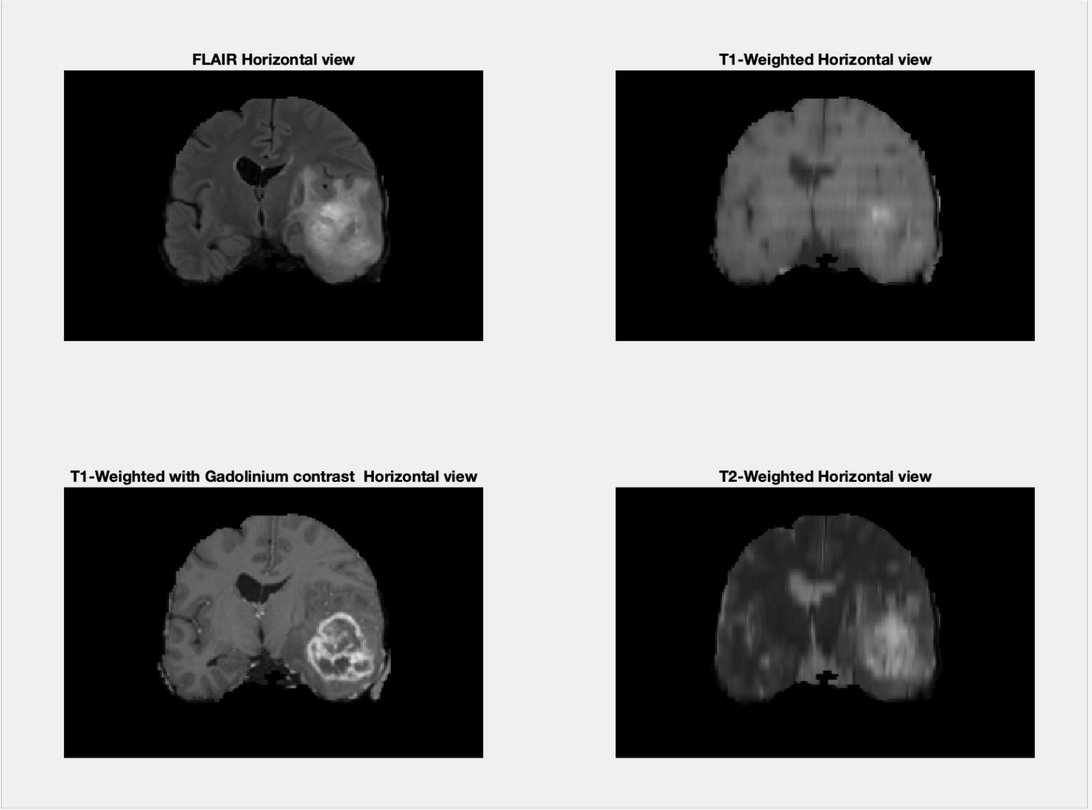
The 4 types of MRIs provided

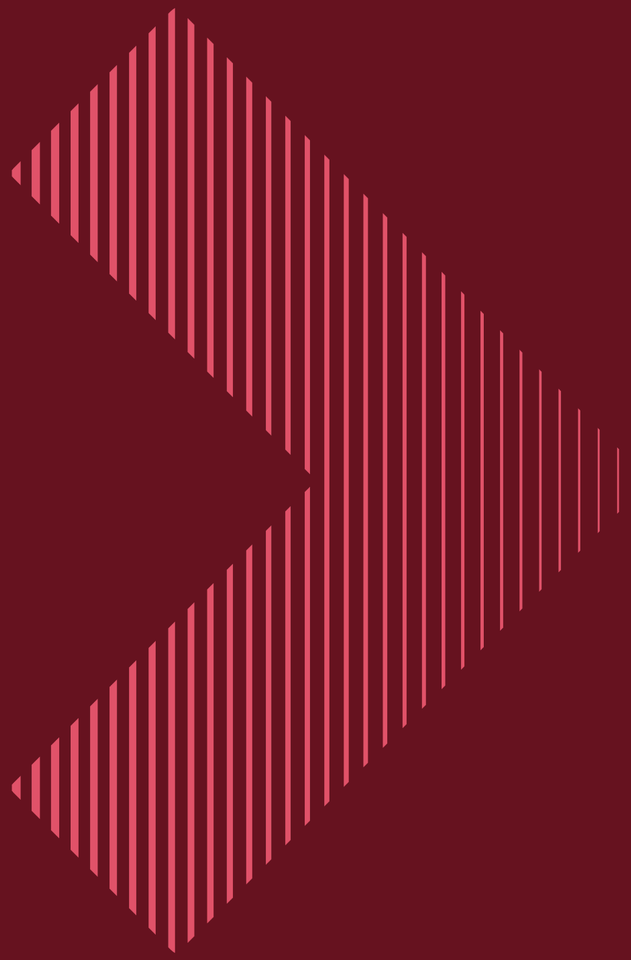
- **FLAIR** suppress the signal coming from water molecules, so it is **useful to distinct the edema from the CSF**.

- **T1w** are the most «anatomical images» resulting in images that most closely **approximate the appearance of tissues.**

- **T1gd** can make the **brain tumor borders become more brighter** because the contrast agent accumulates there due to the disruption of the blood–brain barrier in the proliferative brain tumor region.

- In **T2w** the **edema region can appear brighter** than other sequence images of MRI.



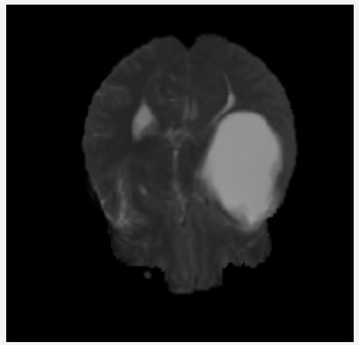


Outline of the project

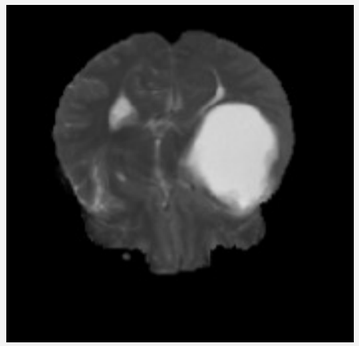
- The upcoming slides explain the methodology employed in constructing the model.

Workflow followed

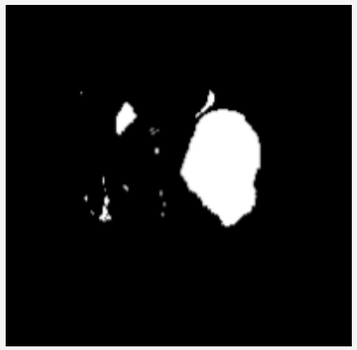
Input MRI



Pre-processing with contrast stretching

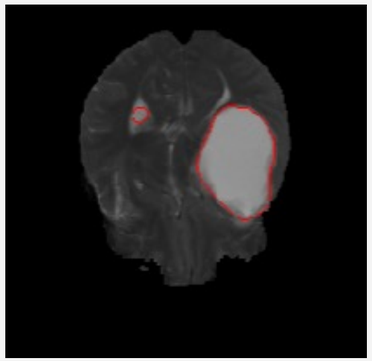


Thresholding algorithm



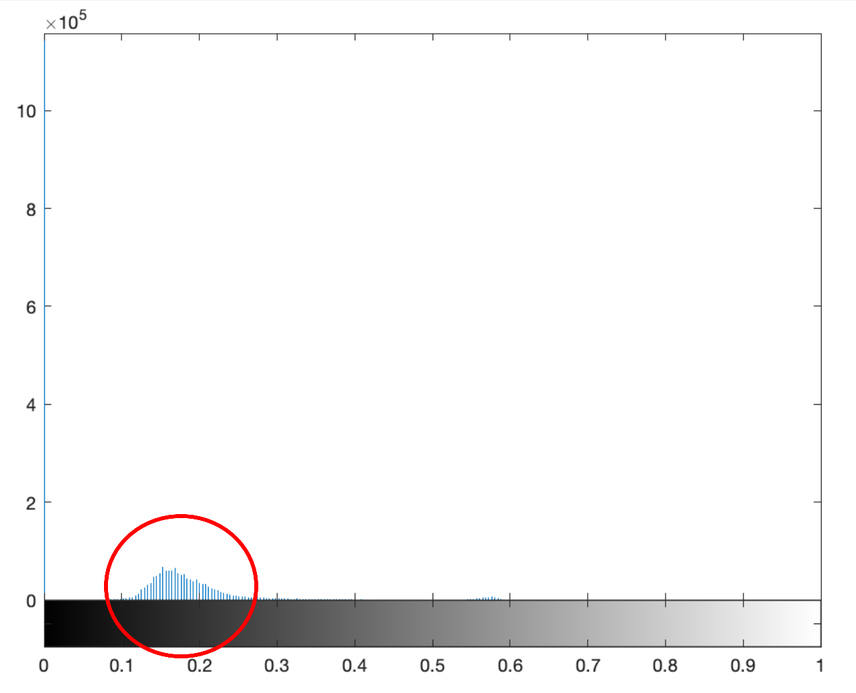
Post-processing with a median filter

Tumor segmented



Pre-processing stage: contrast enhancement

To **better distinguish** the tissues affected by brain cancer, the initial step was to **enhance the image contrast**. This was necessary because upon plotting the **histogram** of the 3D MRI image, it became evident that all gray levels were concentrated within a narrow range. Therefore, by adjusting the contrast, we could highlight the brighter regions of interest.



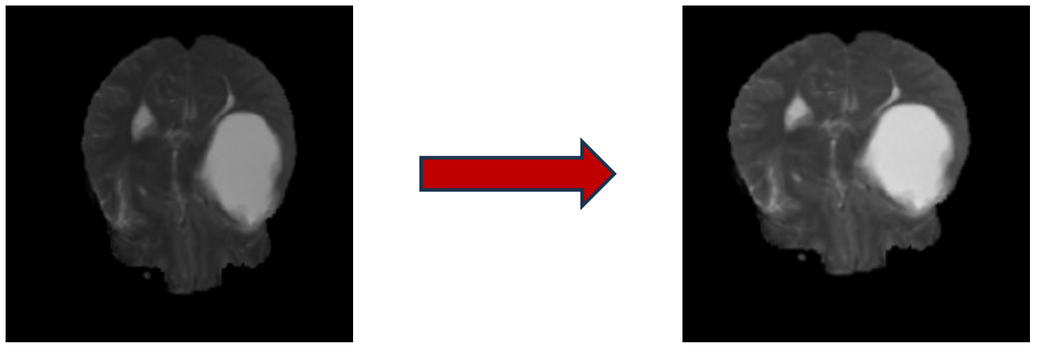
Pre-processing stage: contrast enhancement

How can we perform this contrast enhancement? By using the **imadjustn** function already implemented in MATLAB.

```
J = imadjustn(V,[low_in high_in], [low_out high_out])
```

$$f_{ac}(a) = a_{min} + (a\ - a_{low}) \cdot \frac{a_{max} - a_{min}}{a_{high} - a_{low}}$$

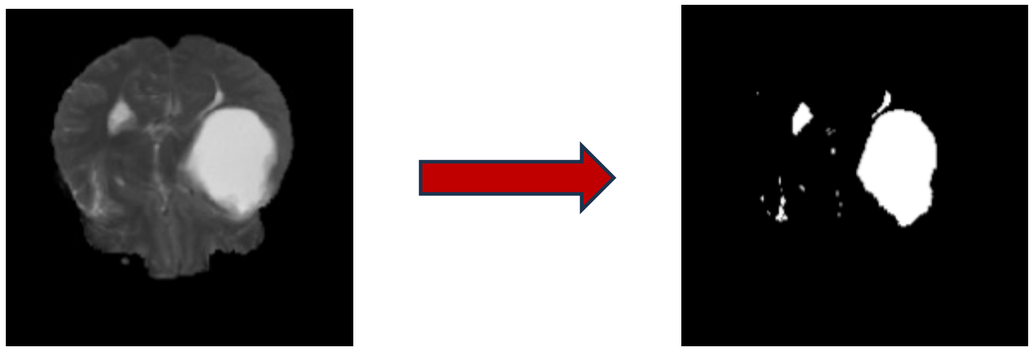
maps the values in V to new values in J such that values between low_in and high_in map to values between low_out and high_out. Values below low_in are clipped to low_out and values above high_in are clipped to high_out.



Segmentation stage: the custom thresholding algorithm

The segmentation algorithm is the following: the sum of unique pixel values excluding zeros are divided by the count of unique pixel values. By this operation, the average gray value (threshold value) is calculated to convert the grayscale image to binary image. This method can be described as:

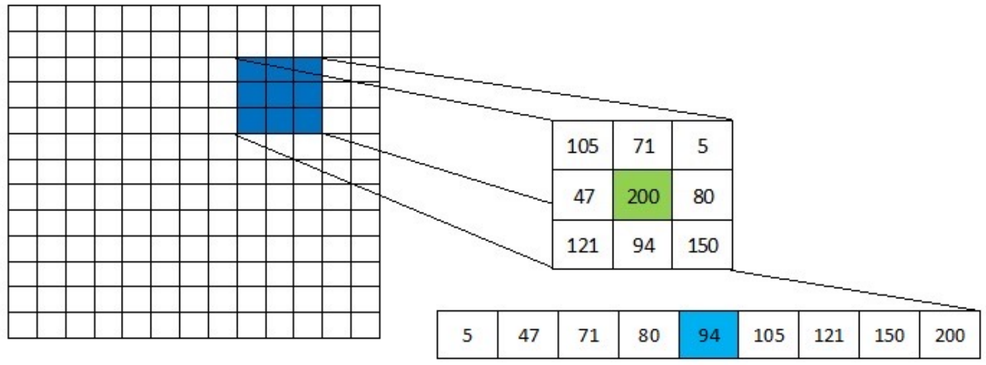
$$T = \sum_{S=1}^{n} \frac{(\forall(a,b) \in S)(a \neq b \neq 0) \rightarrow \varnothing(a,b)}{n}$$



Post-processing stage: median filtering

The **median filter** helps in reducing **”salt and pepper” noise** of the segmented regions, resulting in a more refined segmentation output. The median filter is the most commonly used non-linear filter. In this filter, the median pixel value in the neighborhood is calculated and the middle pixel value in the neighborhood is replaced by the calculated median pixel value.

In this case, the median filter is useful for **eliminating small regions** that are artifacts of the segmentation algorithm and need to be removed from the segmentation mask.

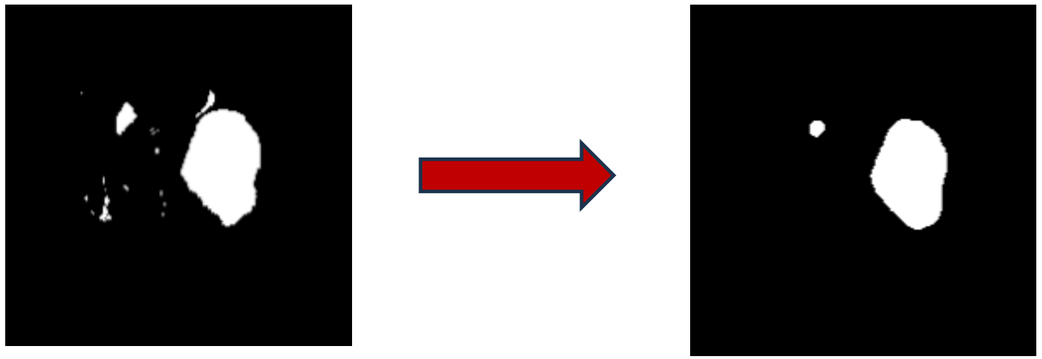


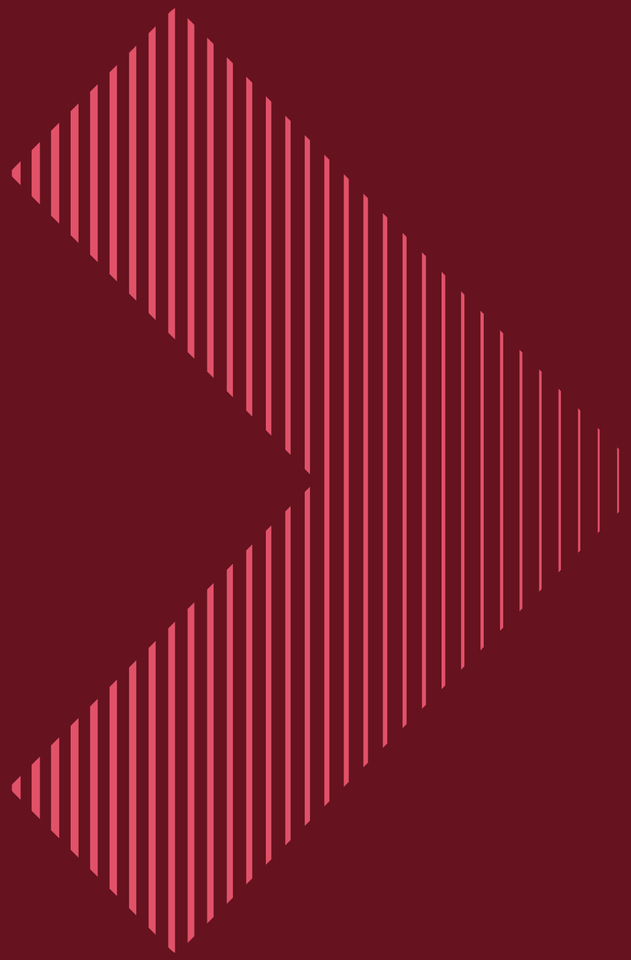
Why a median filter instead of an average one?

In this case, I chose to utilize a median filter rather than an average filter because I aimed to **preserve the structure of the tumor**.

Additionally, the decision was motivated by the fact that the mask is binary. If I had employed an average filter instead of a median filter, the output would have generated intermediate gray levels, which are not acceptable for a binary segmentation mask.

```
kernel = [13, 13, 13];
filteredBrain = medfilt3(binaryBrain(:, :, :), kernel);
```





Evaluation stage

- The upcoming slides explain all the metrics used to assess the goodness of the segmentation algorithm. This is made possible by ground-truth MRI provided by real doctors!

Accuracy

Given the ground-truth label and the segmented tumor, before calculating accuracy, we need to determine True Positives and True Negatives for all pixels in the MRI.

A pixel in the segmented MRI is classified as a **True Positive** if its intensity value is 1 and the corresponding ground-truth label indicates it as 1.

A pixel in the segmented MRI is classified as a **True Negative** if its intensity value is 0 and the corresponding ground-truth label indicates it as 0.

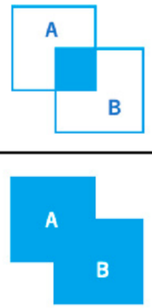
Then, **accuracy** is calculated as follows:

$$Accuracy = \frac{TP + TN}{all\ the\ pixels}$$

Intersection over Union

Intersection over Unit (IoU), also known as the **Jaccard Index**, measures the similarity between the segmented and ground truth regions, calculated as the ratio of the intersection area to the union area of the two regions. IoU ranges from 0 to 1, where 1 indicates perfect overlap and 0 indicates no overlap.

$$\text{Intersection over Unit (IoU)} = \frac{\text{Area of overlap}}{\text{Area of union}}$$

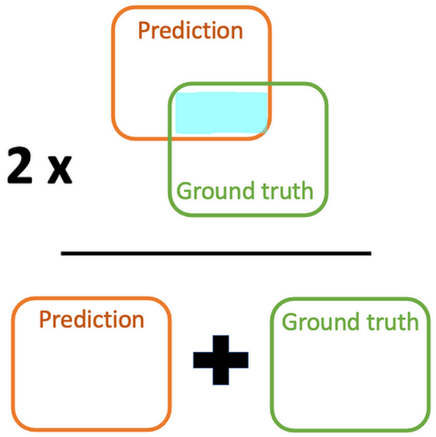


$$= \frac{|A \cap B|}{|A \cup B|}$$

DICE score

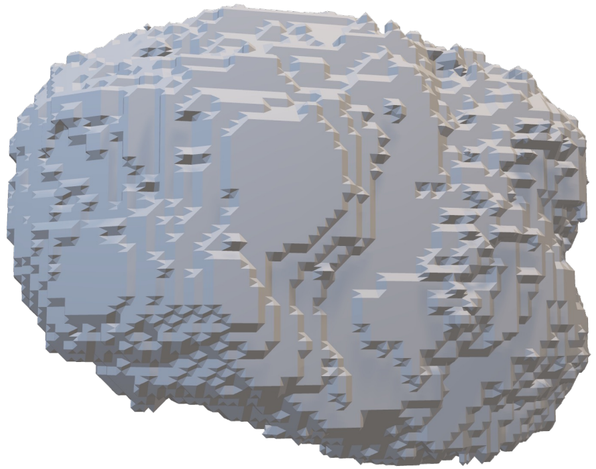
DICE coefficient quantifies the overlap between the segmented region and the ground truth region, calculated as twice the intersection of the segmented and ground truth regions divided by the sum of their areas. A Dice coefficient of 1 indicates perfect overlap, while 0 indicates no overlap.

$$\text{Dice} = \frac{2\ X\ Area\ of\ overlap}{Total\ area} =$$

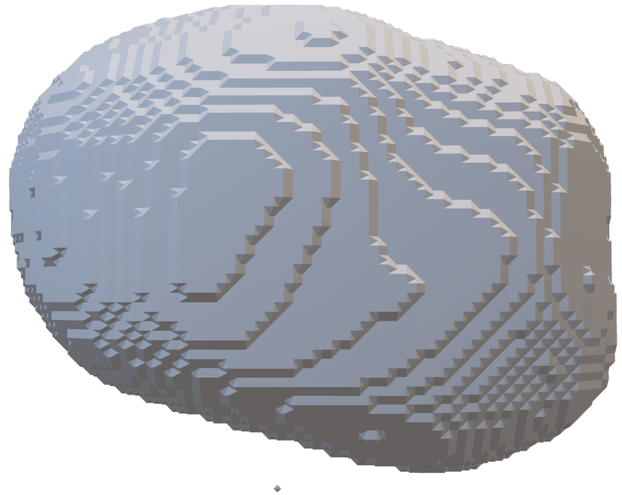


Difference between predicted and ground-truth volumes

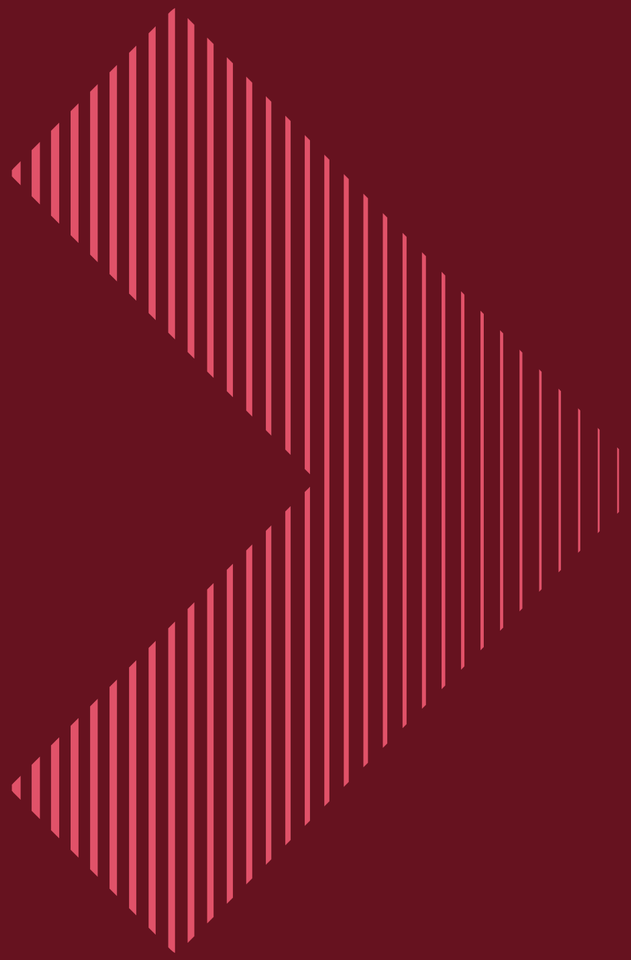
Why did I employ this metric? Because I wanted to measure not only the volume predicted compared to the ground truth but also wanted to **assess whether the algorithm tends to over-segmentation or under-segmentation** (it is not an absolute difference, the sign is useful in this case).



Segmented Tumor



Ground-truth tumor



Fine tuning stage

- After defining the metrics, it's time to determine which variables can be considered as parameters and attempt to optimize this algorithm by searching for the best combination among these parameters.

Which of the 4 MRI given is the best for this task?

That was my initial question when I began this project, and to be honest, I had some clues, but I wasn't sure if it was the optimal image to choose.

To identify the **most suitable MRI to use**, I conducted segmentations on all **100 selected MRIs**, each resulting in a distinct segmentation. Then I assessed their performance using the metrics listed before and visualized the results using **bar plots**. Here are the results:

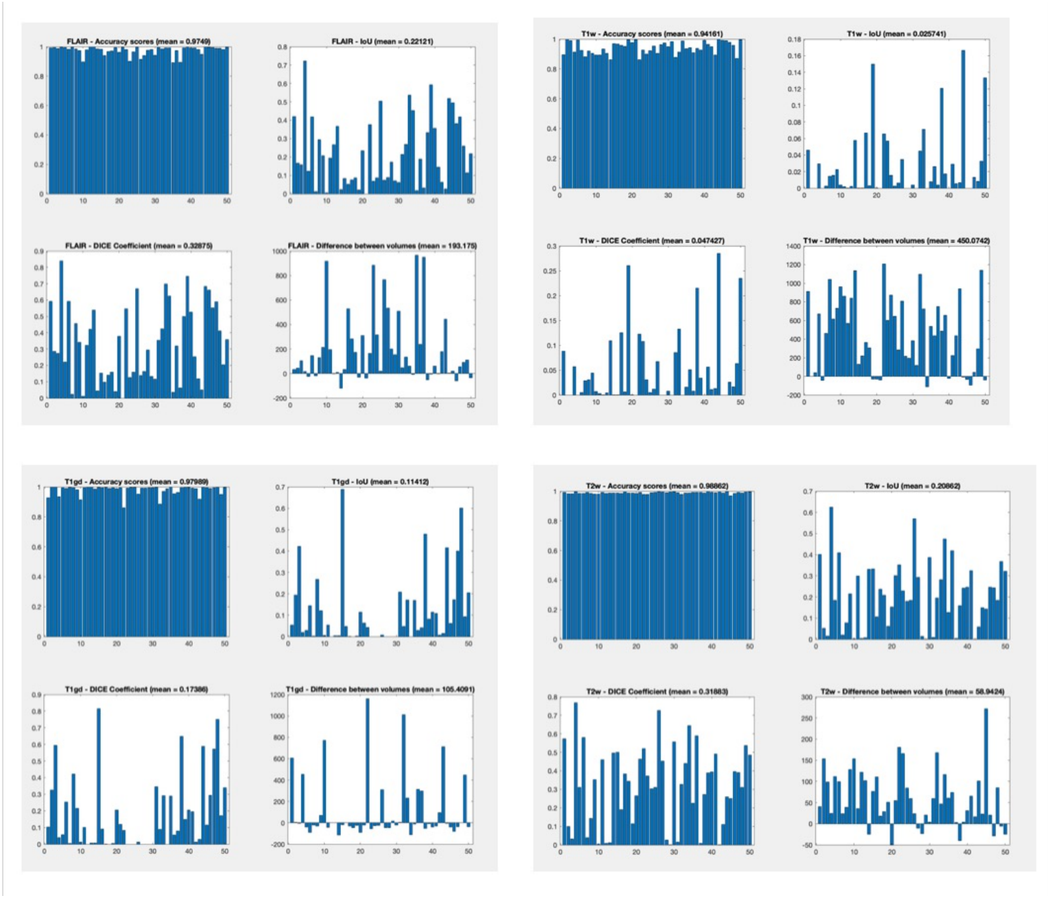
The best one is T2-w. Here's why

Here's the chain of thoughts I followed for choosing the right image.

First off, T1-w consistently scored the lowest in all four metrics, so it was quickly ruled out.

Given that this is a threshold algorithm and not a contour-based one, T1-gd isn't the ideal choice in this scenario. This is because it primarily highlights the edges rather than the entire tumor area.

Ultimately, I decided to go with T2w over FLAIR images because it exhibits significantly less over-segmentation, as evidenced by the difference in volumes.



How to properly set the median filter and the contrast enhancement

The second goal was to find the best parameters for the median filter and for the image contrast stretching functions, so I treated the **upper bound for the imadjustn** and the **dimensions of the median kernel filter** as variables to fine-tune.

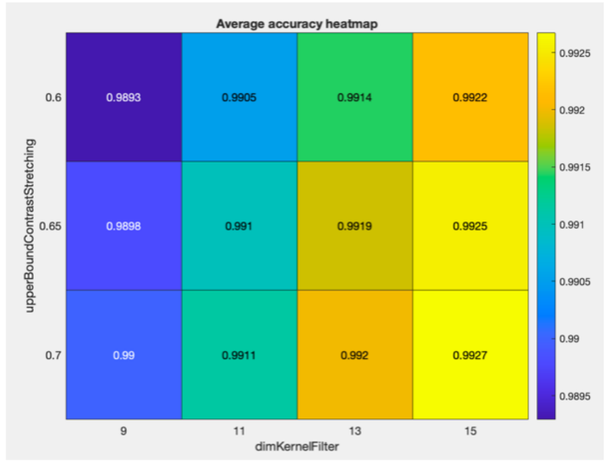
```
J = imadjustn(V,[low_in high_in], [low_out high_out])
```

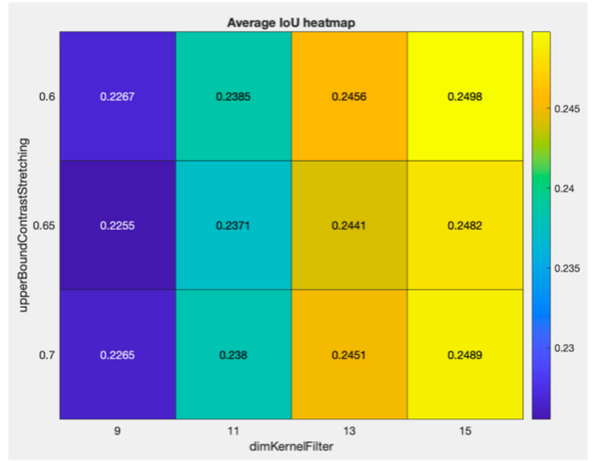
```
kernel = [13, 13, 13];
filteredBrain = medfilt3(binaryBrain(:, :, :), kernel);
```

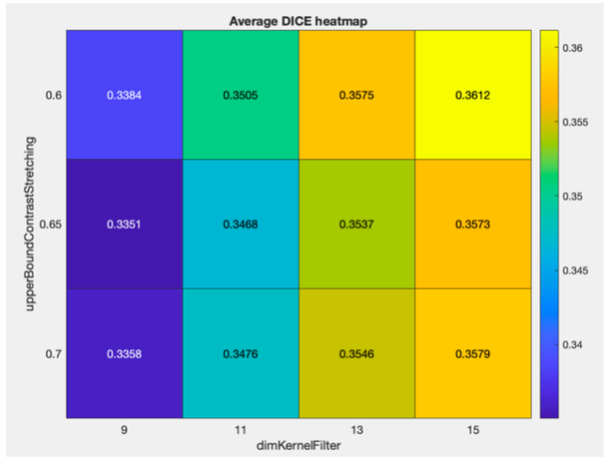
How to properly set the median filter and the contrast enhancement

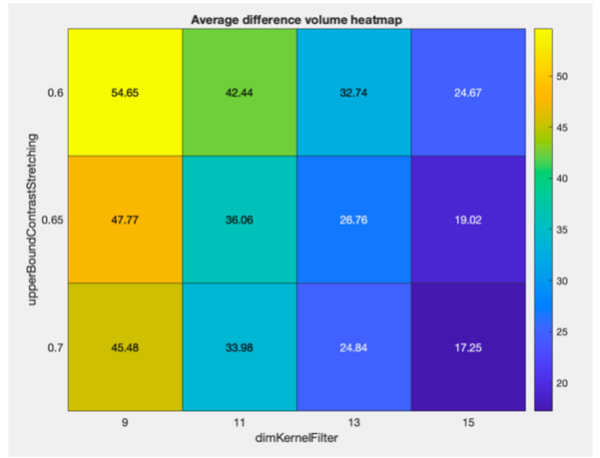
As observed, the **kernel dimension** appears to be the **primary driver** influencing all four metrics. Based on the heatmap analysis, I opted for a **kernel dimension of 15**.

Conversely, the specific value of the **upper limit for contrast enhancement** seems to have minimal impact. Therefore, I selected **0.7** as the optimal choice, as it resulted in the least discrepancy between the volume of the segmented tumor and the label given.





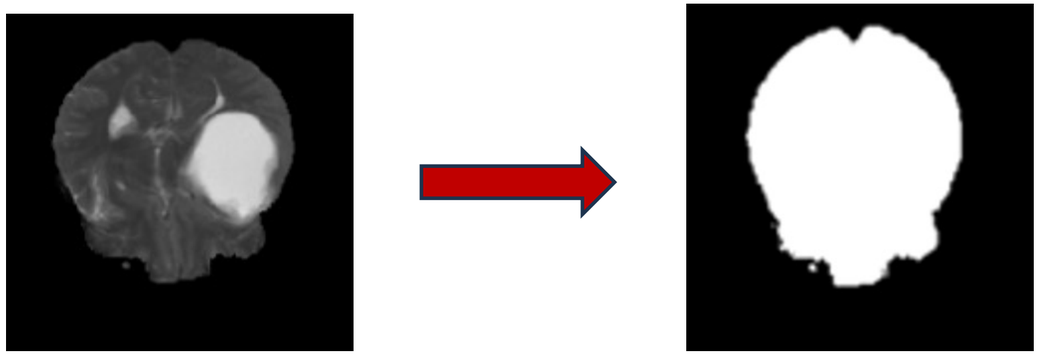




Comparing the custom thresholding algorithm with Otsu

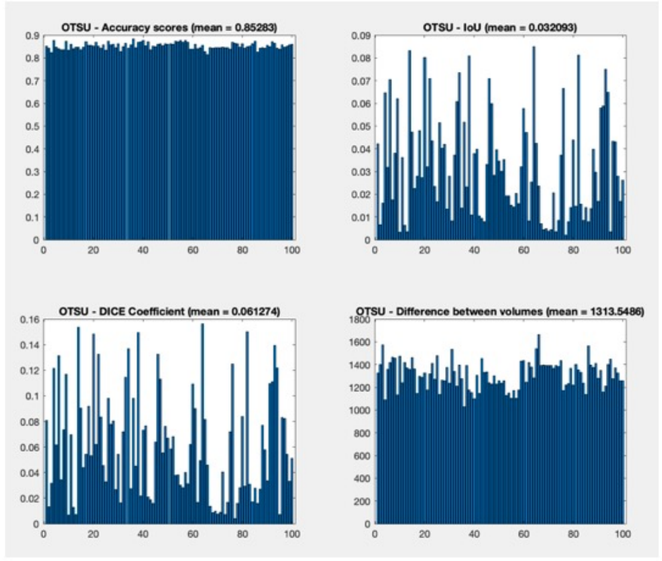
In the end, after fine-tuning the parameters of our custom thresholding segmentation algorithm, I compared this custom thresholding approach with the standard Otsu algorithm.

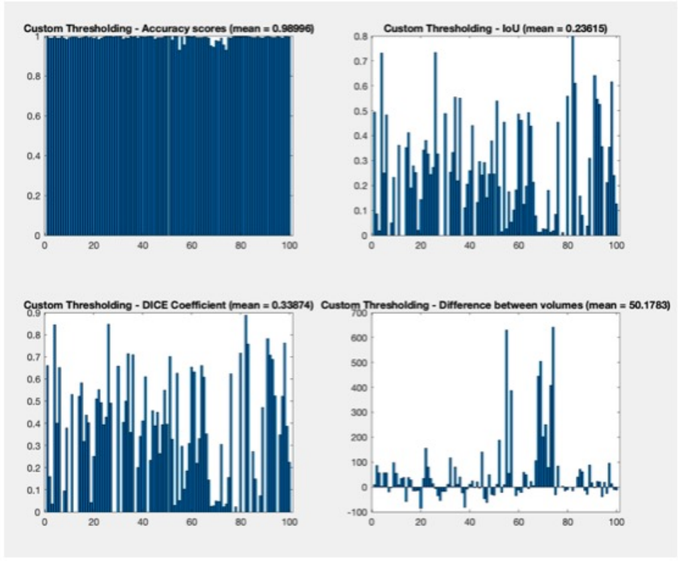
The Otsu algorithm is commonly used in various applications for finding a threshold value for binarizing images, and in the simplest form, the algorithm returns a single intensity threshold that separate pixels into two classes, foreground and background. This threshold is determined by **minimizing intra-class variance**, or equivalently, by **maximizing inter-class variance**.



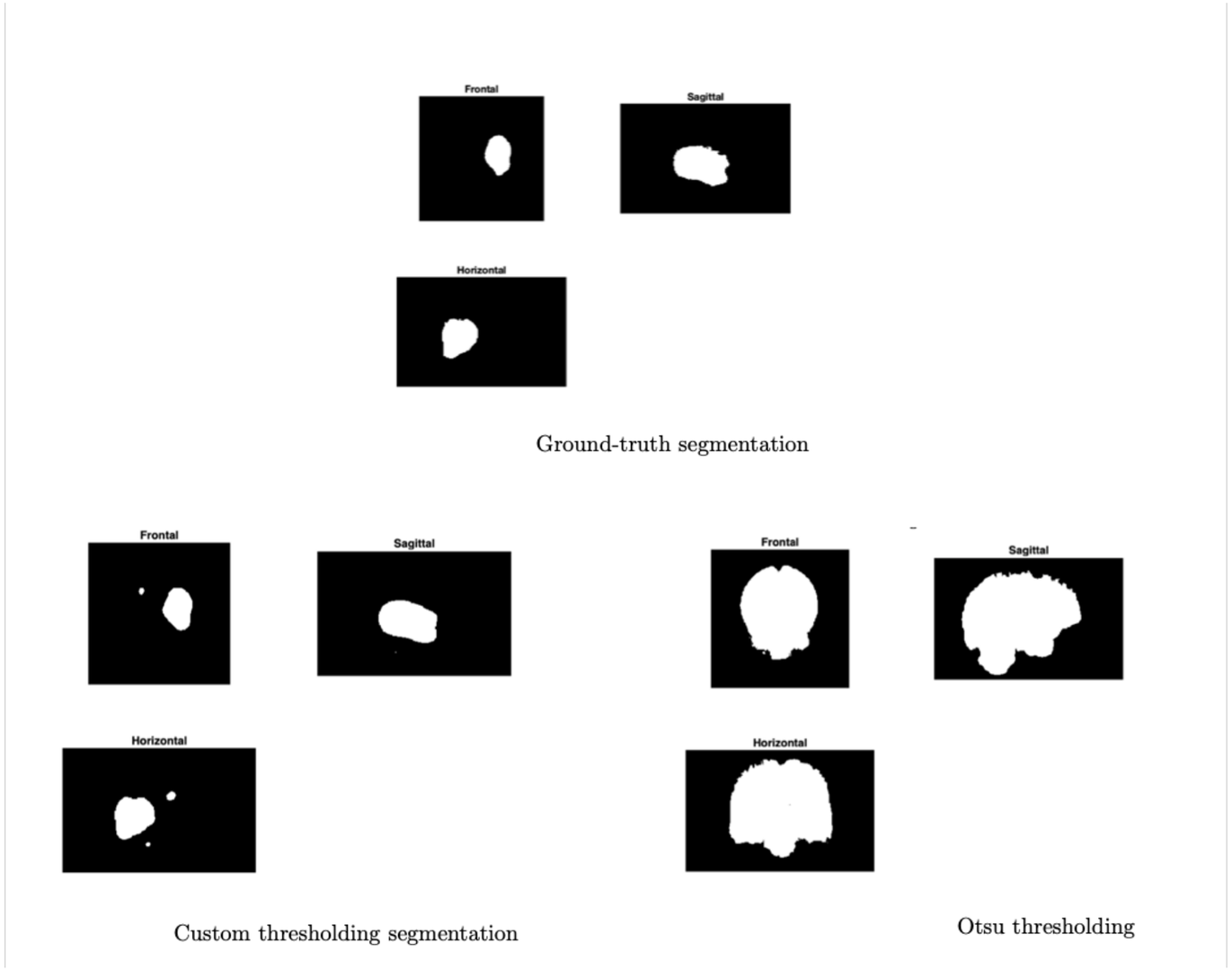
Comparing the custom thresholding algorithm with Otsu

Upon reviewing these bar plots, it's evident that **custom thresholding outperforms Otsu across all metrics**. However, to be honest, this comparison may not be entirely fair. In the paper examined, only accuracy was mentioned, which can be misleading as it tends to yield higher values anyway. When considering more appropriate metrics such as IoU or DICE coefficient, it becomes clear that the Otsu method yields nearly zero values. This indicates that **Otsu fails completely to segment tumors**, which is noticeable also by inspecting the resulting segmentation visually.





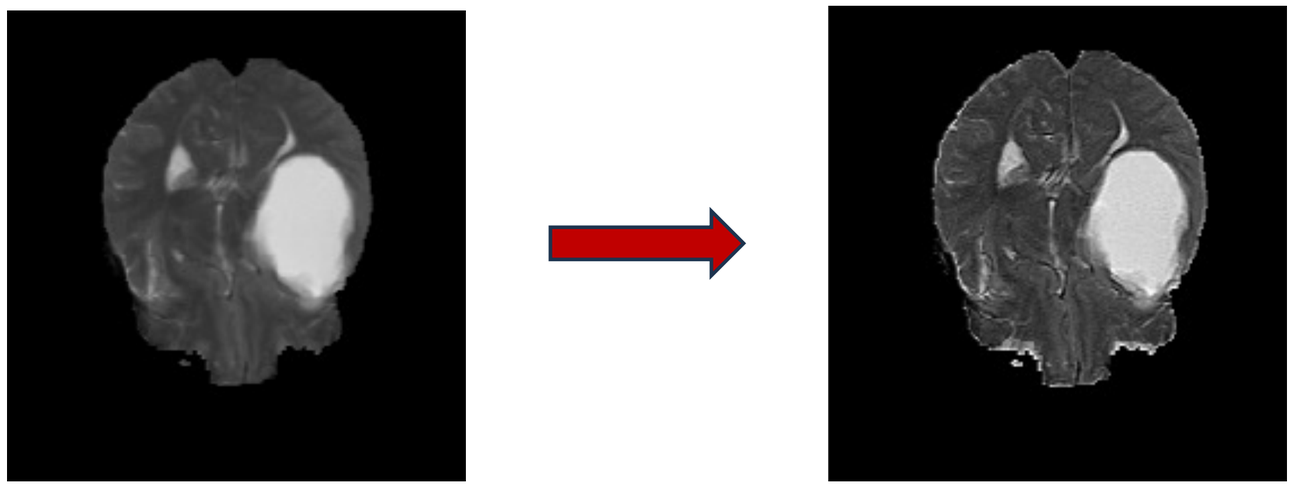
Comparing the custom thresholding algorithm with Otsu



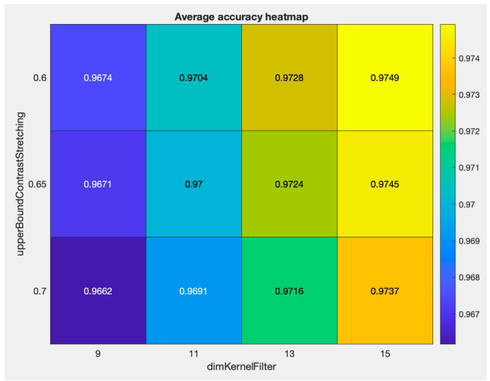
Why not sharp the image in the pre-processing stage?

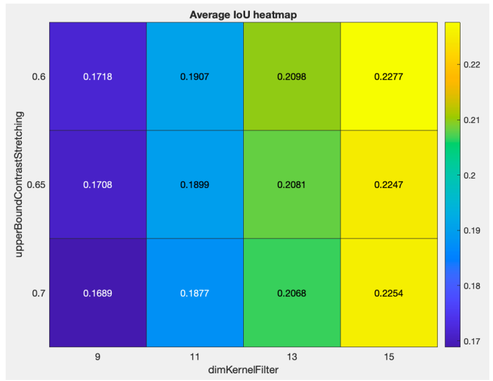
As a novice in the field of Image Processing, this was another unknown in my project. I initially assumed that sharper images would yield better results. However, this initial hypothesis proved to be completely wrong.

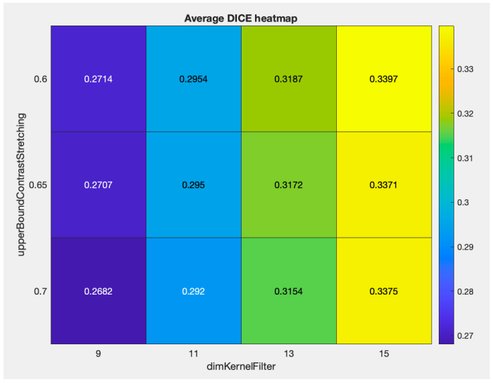
I explored the use of a **Laplacian 3D filter**, that is a type of filter used in image processing for edge detection and image enhancement. It is derived from the Laplacian operator, which is a second-order derivative operator. The Laplacian filter is designed to highlight regions of rapid intensity change in an image by enhancing the edges while suppressing noise and low-frequency details, so it can be considered as a **high-pass filter**.

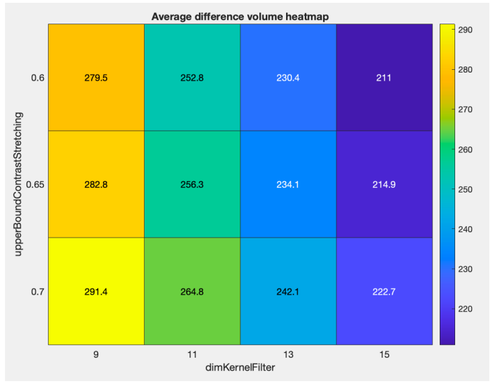


Why not sharp the image in the pre-processing stage?

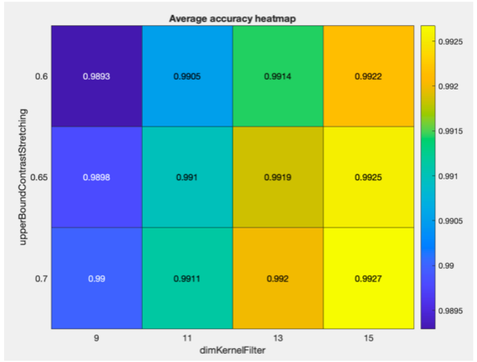


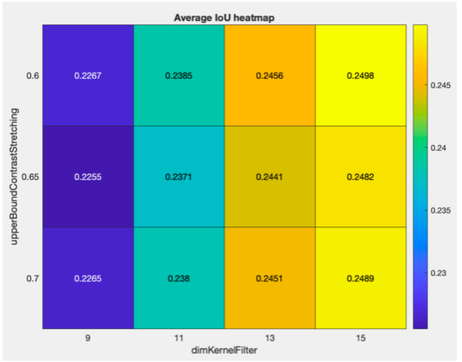


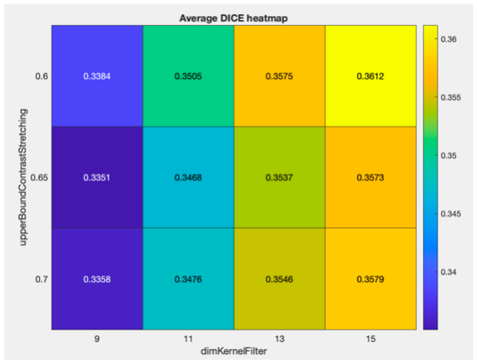


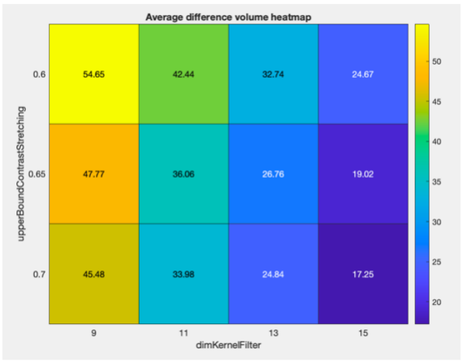


With Laplacian filter







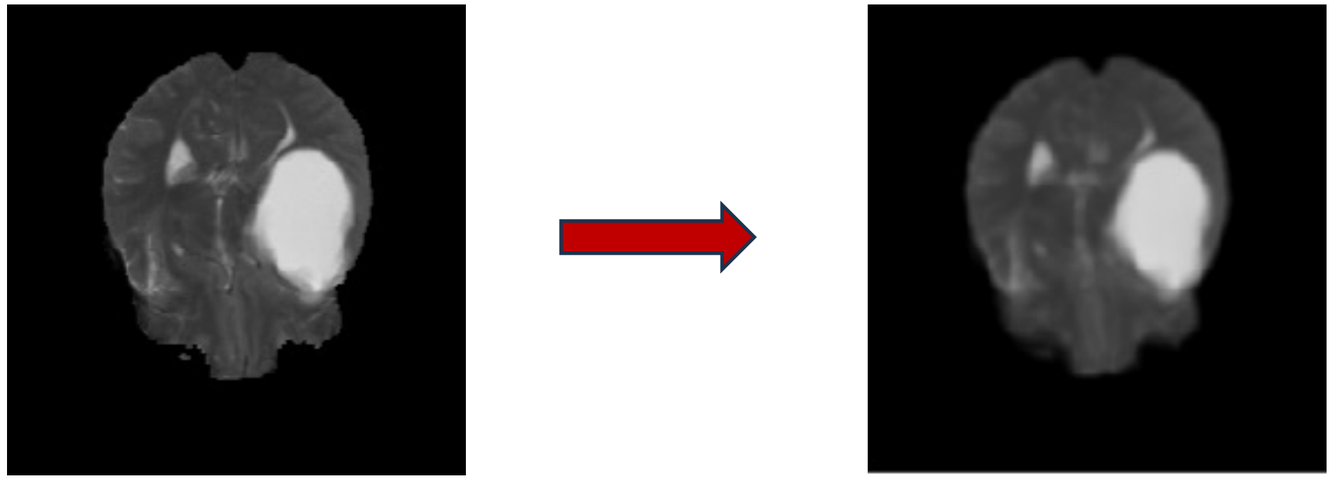


Without Laplacian filter

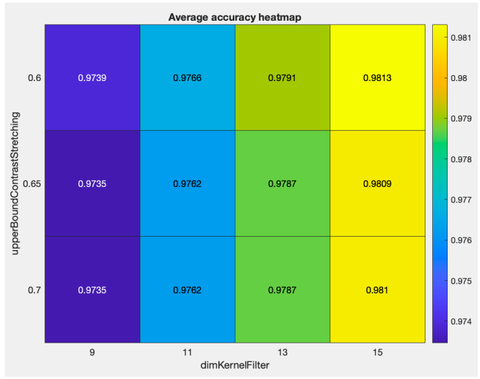
Why not average the image as a pre-processing stage?

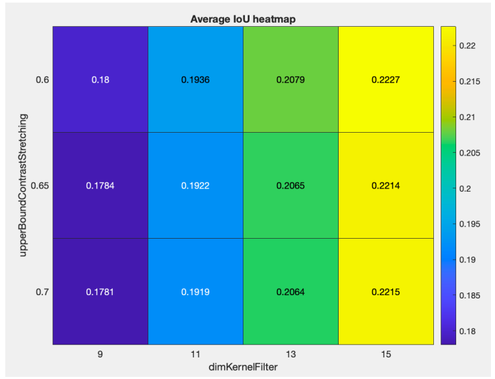
I was also intrigued by the effect of applying an average filter before the segmentation step, and once again, this turned out to be ineffective.

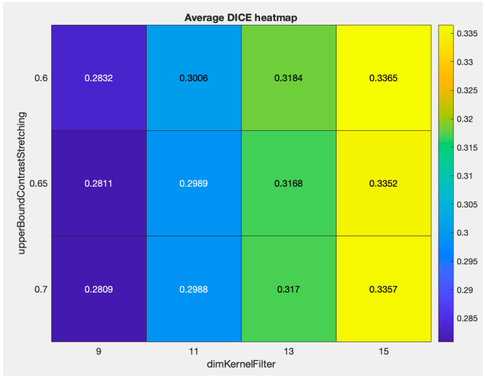
An average filter is a type of linear filter used in image processing to **smooth or blur an image** by replacing each pixel's value with the average value of its neighboring pixels. This process helps reduce noise in the image, but it may also result in loss of image detail and blurring of edges, which can negatively impact segmentation tasks.

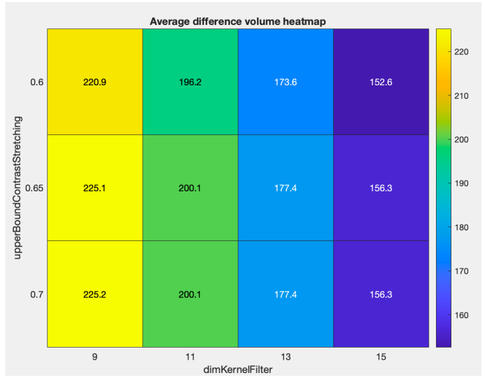


Why not average the image as a pre-processing stage?

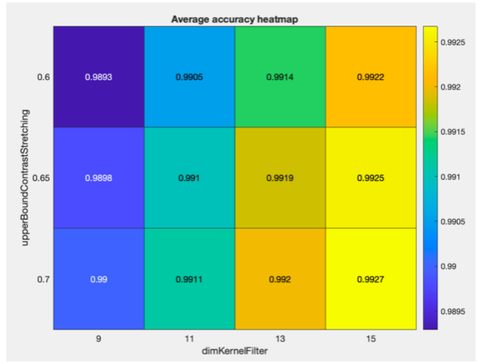


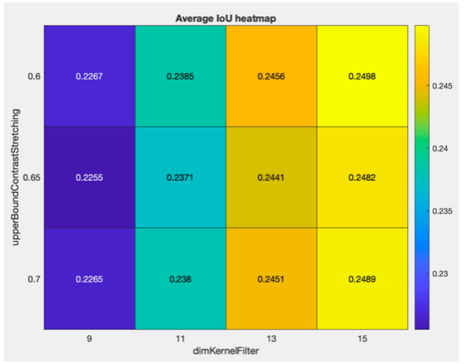


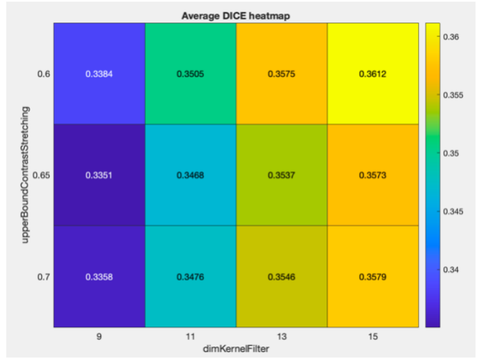


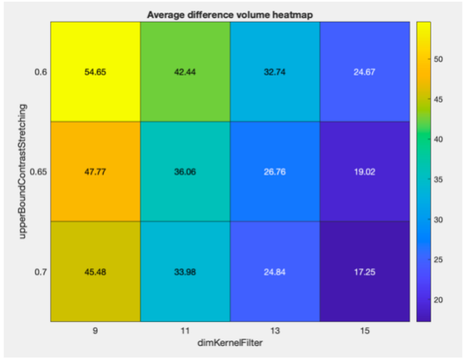


With average filter









Without average filter

3D print the result (just for fun)

Just for fun, I 3D printed the 82nd MRI segmentation (one of the best performing) and compared the result with a 1:1 scale representation of the tumor.

Ground-truth tumor

Segmented Tumor