

# BrainScope: an effective tool for brain image processing in the diagnosis and treatment of neurological diseases.

Carolain Jiménez Bedoya - 2071368<sup>1\*</sup>

## Abstract

This report presents the BrainScope application, an effective tool for brain image processing in the diagnosis and treatment of neurological diseases. The application utilizes segmentation and preprocessing techniques to obtain accurate measurements of different brain tissues. Furthermore, intensity standardization and noise removal methods are described to enhance the image quality. These techniques improve the accuracy of diagnosis and evaluation of neurological diseases, as well as the identification of brain abnormalities that require immediate treatment.

## Keywords

BrainScope — Image processing — segmentation — Intensity standardization — Denoising

<sup>1</sup> EISC, School of Systems and Computer Engineering, Universidad del valle, Cali, Colombia

\*Corresponding author: carolain.jimenez@correounivalle.edu.co

## Introduction

The human brain is one of the most complex and mysterious organs in the human body. Its proper functioning is essential for life and health, which is why neurological conditions can have serious consequences on patients' quality of life. Magnetic resonance imaging (MRI) is a non-invasive technique that allows for detailed images of the brain and its tissues. However, interpreting these images is a complex process that requires expertise and precision. Therefore, image processing tools are used, which allow for non-invasive analysis of the structure and function of the brain and precise measurements of the volume and density of brain tissues. [1]

In this report, we describe the BrainScope application, which focuses on brain image processing and provides neuroradiologists with accurate measurements of brain tissues for clinical decision-making. This application uses segmentation and pre-processing techniques to obtain precise measurements of different types of brain tissues. Segmentation divides the image into regions or segments that correspond to different types of brain tissues, such as gray matter, white matter, and cerebrospinal fluid, while pre-processing corrects image artifacts, reduces noise, and enhances image quality. The combination of these techniques in BrainScope improves the accuracy of diagnosis, evaluation, and follow-up of neurological diseases and the identification of brain abnormalities that require immediate treatment.

## 1. Materials

Medical images are a fundamental tool in the diagnosis and treatment of diseases, and their processing is crucial for their

proper interpretation. One of the most common types of medical image and the one used in the BrainScope application is magnetic resonance imaging (MRI), which uses powerful magnets and radio waves to generate detailed images of the internal structures of the brain. The high resolution and detail of the images make them an important tool for the diagnosis and monitoring of neurological diseases, and their digital processing allows for better visualization and analysis of brain tissues. These images were analyzed using digital image processing techniques to extract relevant information for diagnosis and treatment. [2]

However, before any processing could be done, it was important to ensure the security and confidentiality of patient data, as medical images contain sensitive patient information, such as their personal health data, and it is essential to protect their privacy. The images were de-identified by removing any personal information, such as the patient's name, date of birth, and medical record number. This process ensures that the images are used only for their intended purposes and that patient privacy is maintained.

Once de-identified, the images were processed using a series of digital image processing techniques. These techniques include improving image quality by reducing noise and improving contrast, and image segmentation, which separates the image into different regions based on their characteristics, such as tissue type. These techniques can be used to extract important information from the images, such as the location and extent of tumors, and help doctors make more informed decisions about diagnosis and treatment.

The medical images used for the application's interac-

tion use the DICOM (Digital Imaging and Communications in Medicine) format, which is the standard format for medical images. However, the NIFTI (Neuroimaging Informatics Technology Initiative) format, which is used in neuroimaging research, is also accepted.

In the field of magnetic resonance imaging (MRI), different methods are used to obtain images that play a fundamental role in diagnosis. This project evaluates three widely used modalities: T1, FLAIR, and IR.

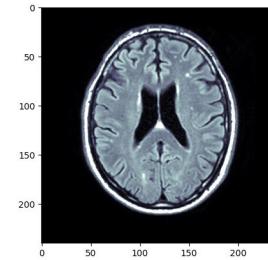
- T1: These weighted images provide a detailed structural visualization of the brain, where brain tissues with high water content appear dark, while tissues with lower water content, such as gray and white matter, appear brighter. This modality is useful for identifying anatomical regions and detecting lesions such as tumors or structural abnormalities.
- IR (Inversion Recovery): This modality is used to highlight and characterize specific types of brain tissues. It enables the identification of recent brain infarctions, tumors, and vascular anomalies, thereby facilitating a more comprehensive assessment of brain health.
- FLAIR (Fluid-Attenuated Inversion Recovery): This modality enhances the visibility of brain lesions that may be hidden or masked by cerebrospinal fluid (CSF) in conventional T1 images. It is useful for detecting and evaluating inflammatory lesions, infections, and white matter lesions.

For this project, twenty-one cerebral magnetic resonance imaging (MRI) images were utilized, obtained using a 3T scanner with multiple sequences. These images were fully annotated, employing the modalities of T1 enhancement, T1-weighted inversion recovery, and FLAIR. They were acquired at UMC Utrecht (Netherlands) from seven patients with diabetes, cognitive disorders, and matched controls at higher cardiovascular risk. These patients exhibited varying degrees of white matter lesions and atrophy, all being over 50 years old. All three imaging modalities (T1w, FLAIR, and IR) were utilized, and manual annotation of cerebral tissues was performed on the FLAIR image. Additionally, patient anonymity was ensured by cropping their faces from the T1-weighted 3D scans. It is important to note that some of the T1-weighted inversion recovery images exhibited artifacts at the lower part of the scan, which is a common occurrence in clinical scans.

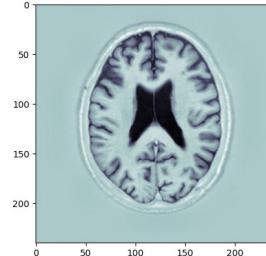
**Table 1.** Exploration details

File	Detail
T1 1mm	3D T1-weighted scan (voxel size: 1.0 mm × 1.0 mm × 1.0 mm)
T1	T1-weighted 3D scan registered with T2 FLAIR (voxel size: 0,958 mm × 0,958 mm × 3,0 mm)
T1 IR	T1-weighted inversion recovery scan with multiple slices registered with T2 FLAIR (voxel size: 0,958 mm × 0,958 mm × 3,0 mm)
T2 FLAIR	Multislice FLAIR scan (voxel size: 0,958 mm × 0,958 mm × 3,0 mm)

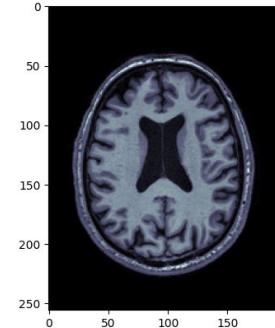
These images show the cross-sectional view of a particular patient from different modalities, demonstrating how they are visualized to achieve the mentioned objectives.



**Figure 1.** axial FLAIR.



**Figure 2.** axial IR.



**Figure 3.** axial T1.

The strategies for processing this type of images are divided into two main processes:

1. Image processing
2. Image preprocessing

## 2. Methods

The methods and techniques for medical image processing are essential for proper interpretation and analysis of images, which is crucial for the diagnosis and treatment of various diseases. Currently, there are various techniques and algorithms for medical image processing that allow for improving image quality, reducing noise, and extracting relevant information. Some of the most commonly used techniques include image segmentation and preprocessing, such as intensity standardization and noise removal using filters. It is important to understand how these techniques are applied to obtain accurate and reliable results in the diagnosis and treatment of diseases.

Image processing is based on the manipulation of digital images through various techniques to improve image quality and obtain useful information. One of the most important aspects that encompasses image processing is related to image segmentation and edge detection.

### 2.1 Segmentation

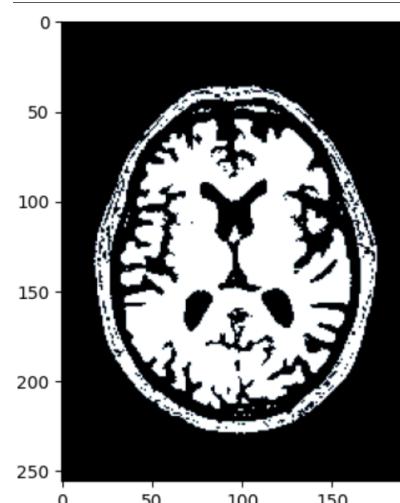
Segmentation is the process of dividing an image into different parts or regions that have similar characteristics. This technique was used in the BrainScope application for image processing in order to extract relevant information, such as the location and extent of lesions.

#### 2.1.1 Thresholding

This was the first method implemented to perform image segmentation in the BrainScope application, using an algorithm called thresholding. The algorithm was used to divide an image into two or more distinct regions based on the intensity of the pixels. [3]

The implemented method takes an image and two input parameters: tau and tol. Tau is a value that lies between the minimum and maximum values of the image and represents the initial threshold. The parameter tol is the tolerance set to determine when the segmentation is finished.

This method recursively performs a simple thresholding of the image using only the initial value of tau and then calculates a new, more optimal threshold based on the mean pixel values in the foreground and background regions. This process is repeated until the change in tau value is less than the established tolerance. Once it is found that the change is below the tolerance, the segmentation of the image is returned, with two regions: the background and the foreground, where the foreground corresponds to the pixels that are above the optimal threshold, and the background corresponds to those below it.



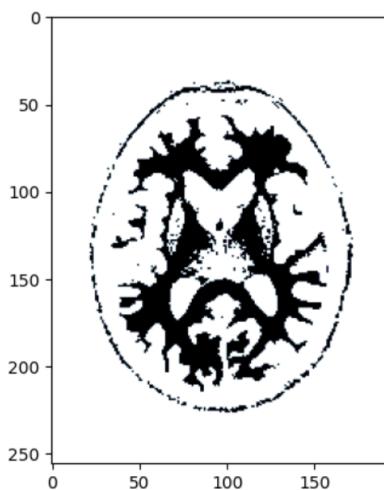
**Figure 4.** Segmented image with thresholding (T1 image).

#### 2.1.2 Region growing

The region growing method is an image segmentation technique based on the growth of homogeneous regions of pixels that share similar characteristics, such as pixel intensity. This method was used as a segmentation technique in the application, and its operation is based on a seed or set of seeds chosen within the image, which is then expanded to include neighboring pixels that meet certain predefined conditions, such as having similar pixel values or being in a homogeneous region.

This method takes as input a three-dimensional image, an initial seed position, and a tolerance value, which determines the required similarity between pixel values to add them to the segment.

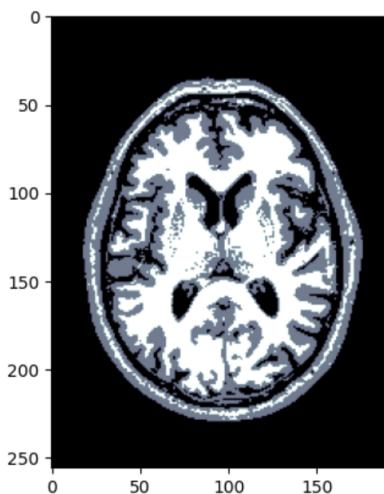
The method starts with the initial seed position and sets its value as the cluster's mean value. Then, the pixel is marked as belonging to the segment and added to the list of neighbors. As long as there are neighbors in the list, the neighbors are traversed for each pixel, and it is checked whether they meet the defined similarity criteria. If so, it is marked as part of the segment and added to the list of neighbors for further processing. The segmentation ends when all neighboring pixels meet the similarity criteria. [4]



**Figure 5.** Segmented image with region growing (T1 image).

### 2.1.3 K-means

One of the clustering algorithms implemented in the application is k-means, which is used to segment images into different regions based on the similarity of their pixel values. This method takes an image and a desired number of segments as input, and uses the pixel values as reference points to determine the center of each segment. The algorithm begins by randomly assigning pixel values as initial centers for each segment, then calculates the distance of each pixel to each center and assigns each pixel to the corresponding segment of the closest center. The center of each segment is then recalculated using the mean of the pixel values assigned to that segment. This process is repeated until the assignment of pixels to segments does not change between consecutive iterations or a maximum number of iterations is reached. Finally, the segmentation of the image into different segments is returned. [5]

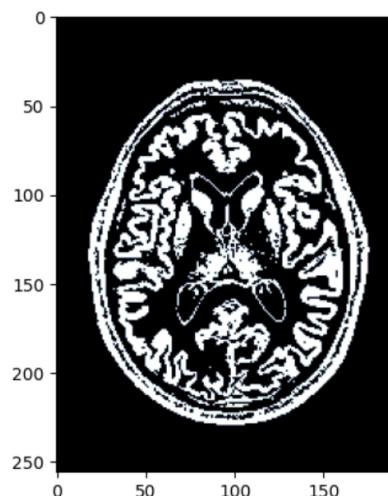


**Figure 6.** Segmented image with k-means (T1 image).

### 2.1.4 GMM

The GMM (Gaussian Mixture Model) segmentation algorithm is a technique that separates an image into multiple regions or segments by implementing the probability distribution of image data in each segment using a combination of Gaussian distributions.

In the implemented algorithm in the application, it starts with an initial estimation of the number of segments, and the mean values of each segment are set as equally spaced in the range of image values. It is assumed that the standard deviation of each segment is 1.0. Then, the probability of each pixel belonging to each segment is calculated using the probability distribution of the Gaussian mixture, and each pixel is assigned to the segment with the highest probability of membership. The mean value of each segment is updated using the average of pixel values that belong to that segment, and the processing stops until the segment assignment no longer changes. [6]



**Figure 7.** Segmented image with GMM (T1 image).

## 2.2 Edge detection

Edge detection is a technique used to identify the boundaries or contours of an image. This method is based on detecting abrupt changes in intensities between adjacent pixels. In the application, the processing of an input image is performed, which may have undergone a preprocessing stage for noise removal or not. The process involves traversing the image pixel by pixel and calculating the partial derivatives in the x, y, z directions. These partial derivatives provide information about the intensity variation at different points in the image. When there is a sharp transition in the image intensity, it is interpreted as the presence of an edge. Then, the magnitude of the gradient is calculated for each pixel, resulting in an image where pixels with higher intensity represent the edges present in the original image.

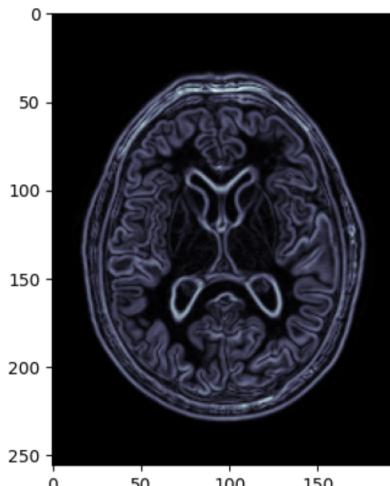
The algorithm utilizes three matrices ( $\text{dfdx}$ ,  $\text{dfdy}$ ,  $\text{dfdz}$ ) initialized with zeros and of the same size as the input image.

These matrices are used to store the results of the partial derivatives in the x, y, and z directions, respectively.

Next, an iterative loop is performed to traverse the pixels of the image, with constraints on the ranges to avoid edges that are located at the image boundaries.

Within the loop, the partial derivatives are calculated in each direction for each pixel. For example,  $\text{dfdx}[z, y, x]$  is calculated as the difference between the pixel value at position  $(z+1, y, x)$  and the pixel value at position  $(z-1, y, x)$ . Similarly, the partial derivatives  $\text{dfdy}$  and  $\text{dfdz}$  are calculated.

Finally, a matrix representing the magnitude of the gradient at each pixel is returned. This is achieved by calculating the square root of the sum of the squares of the partial derivatives in the three directions ( $\text{dfdx}$ ,  $\text{dfdy}$ ,  $\text{dfdz}$ ). [7]



**Figure 8.** Edge detection (T1 image).

Image preprocessing is a fundamental stage for proper image processing as it prepares the original image for better analysis. This preprocessing consists of intensity standardization, which reflects normalization between the grayscale scale of the image, and noise removal, which removes imperfections in the image without eliminating relevant information.

### 2.3 Intensity standardization

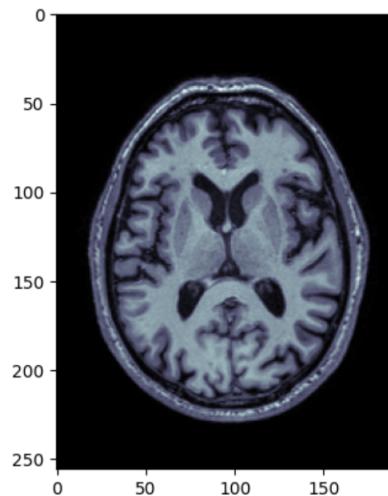
Intensity standardization was a technique used for image preprocessing in order to improve the quality and accuracy of analyses. The goal of this strategy or technique is to normalize the intensities of pixels, such that all images have a similar range of intensity, which helps to reduce variability between images and improve comparability between them.

#### 2.3.1 Global statistics: Rescaling

The rescaling method is a strategy for intensity standardization. Its main objective is to normalize the intensity range of images, so that they have a similar distribution of values. The rescaling method implemented in the BrainScope application consists of calculating the maximum and minimum intensity values of the image and then scaling each intensity value into a range between 0 and 1, by subtracting the minimum value

and dividing by the difference between the maximum and minimum values. The resulting image will have a more homogeneous distribution of intensities, which can improve the accuracy of analyses and comparisons between images. [8]

$$I^* = \frac{I - \min(I)}{\max(I) - \min(I)} \quad (1)$$

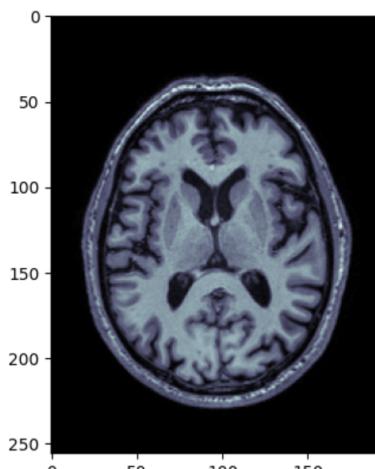


**Figure 9.** Intensity standardization with rescaling (T1 image).

#### 2.3.2 Global statistics: Z-score

The z-score method was established as another intensity standardization strategy, like the rescaling method. It is used to normalize the intensity range of images and reduce variability between them. The z-score method implemented in the BrainScope application involves calculating the mean and standard deviation of pixel intensity values in the image, excluding those values less than 10. Each intensity value is then scaled to a z-score range, by subtracting the mean and dividing by the standard deviation. The result is an image with a more homogeneous intensity distribution and z-score values that indicate how many standard deviations an intensity value is above or below the mean. This method is useful for detecting pixels with atypical intensity values and can improve the accuracy in detecting structures or patterns in the image. [9]

$$I^* = \frac{I - \text{mean}(I)}{\text{std}(I)} \quad (2)$$



**Figure 10.** Intensity standardization with z-score.

### 2.3.3 Histogram matching

For this implementation, the algorithm relies on histogram matching, aiming to adjust the histogram of an input image to resemble the histogram of a target image.

The process begins by loading the data of the original image and the target image. Then, the data is flattened into one-dimensional arrays for easier manipulation. Next, the cumulative histograms (the accumulated sum of histogram values) of the original image and the target image are computed. This is achieved by dividing the pixel values into 256 intervals and calculating the probability density for each interval.

Subsequently, a lookup table (LUT) is created using interpolation of the cumulative histograms. This table maps the values of the original image to the corresponding values in the target image.

Finally, the lookup table is applied to the data of the original image, resulting in the obtained matched image data. In this process, the pixel values are adjusted according to the histogram transformation. The algorithm returns the matched image. [10]

The following equation represents the interpolation process used:

$$I^* = \text{interpolate}(I, H_{\text{original}}, H_{\text{target}}) \quad (3)$$

Where "interpolate(x, x1, x2)" is an interpolation function that calculates the interpolated value of x within the interval [x1, x2].

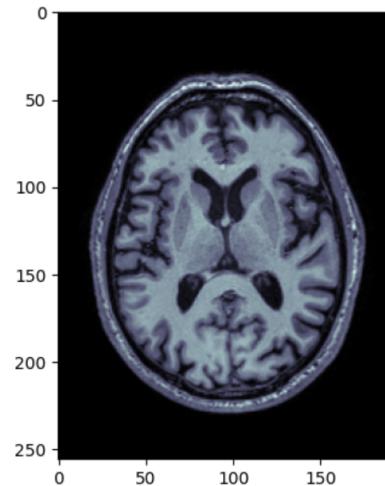
### 2.3.4 ROI based standarization: White stripe

This method focuses on improving the distribution of intensities in images, mainly in images with a large amount of background or noise. The white-stripe method is implemented in the BrainScope application through an algorithm that calculates a divisor that is used to normalize the intensity of pixels in the image.

This method first creates a histogram of the image to determine the distribution of intensity values present in it, and then finds peaks in the histogram. If at least three peaks are found, the mode value between the second and third peak is used as the divisor. Otherwise, the mode value of the entire histogram is taken as the divisor.

Once the divisor has been obtained, each intensity value in the image is divided by this value, generating a standardized image that has a more homogeneous distribution of intensities.

$$I^* = \frac{I}{ws(I)} \quad (4)$$



**Figure 11.** Intensity standardization with white stripe (T1 image).

## 2.4 Denoising

Denoising or noise removal is a fundamental process in image processing, and this preprocessing strategy is responsible for reducing the amount of noise present in an image. Noise can be caused by various factors, such as lighting or camera sensor quality, and it hinders image interpretation and decreases visual quality, which is why it needs to be removed.

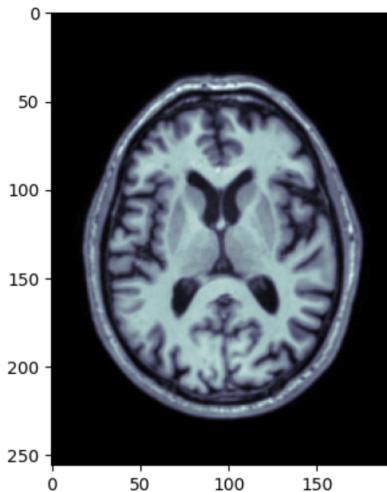
The BrainScope application has implemented Denoising algorithms to improve the visual quality of images and enhance the accuracy of the analyses performed. These algorithms use different techniques to eliminate noise, such as mean filter and median filter.

### 2.4.1 Mean filter

The mean filter method was a strategy implemented in the BrainScope application for denoising images. This method calculates the average intensity value of neighboring pixels within a neighborhood. To achieve this, each voxel of the input image is traversed, except for the voxels on the image borders. For each voxel, the intensities of its six neighbors (its upper and lower neighbors in the z-axis, its left and right neighbors in the x-axis, and its front and back neighbors in the y-axis) are obtained, as well as its own intensity value, in order to calculate the average intensity value of this set

of pixels. This calculated average intensity value is used to replace the original intensity value of the central pixel in the resulting image. By repeating this process for each pixel in the input image, the strategy generates a new output image with reduced noise and improved image quality. [11]

$$I_{(x,y,z)}^* = \{ \text{mean}(I_{(x,y,z)} + I_{(x+1,y,z)} + \dots + I_{(x,y,z+1)}) \} \quad (5)$$

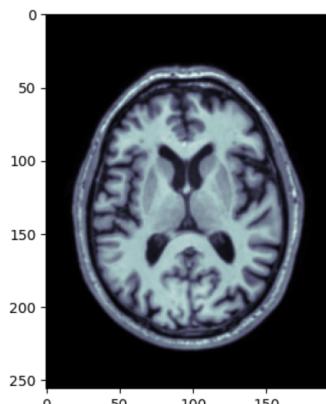


**Figure 12.** Denoising with mean-filter (T1 image).

#### 2.4.2 Median filter

The Median filter works similarly to the Mean filter, as it is also a strategy for image denoising. To execute the method correctly, firstly each voxel in the input image is traversed, except for the image borders. For each voxel, this method obtains the intensities of its six neighbors and its own intensity value, then selects the median intensity value of this set of pixels. This median intensity value is used to replace the original intensity value of the central voxel in the output image. By repeating this process for every voxel in the input image, the median filter algorithm generates a new output image with reduced noise and improved image quality. [12]

$$I_{(x,y,z)}^* = \{ \text{median}(I_{(x,y,z)} + I_{(x+1,y,z)} + \dots + I_{(x,y,z+1)}) \} \quad (6)$$



**Figure 13.** Denoising with median-filter (T1 image).

## 2.5 Registration

Medical image registration is an essential tool in medical analysis and diagnosis. It involves aligning medical images of the same patient using techniques and algorithms to ensure spatial correspondence. This allows for comparative analysis, tracking changes in the patient, and obtaining information about potential pathologies, among other applications. There are two types of registration: rigid or linear registration, and non-rigid or nonlinear registration.

Rigid registration maintains the rigid anatomical structure while applying translations, rotations, or uniform scaling to the image. This transformation aims to align the input images through geometric changes. It is used when the images have minimal movements or deformations, such as images acquired in the same session.

On the other hand, non-rigid registration enables a more precise alignment of a reference image to a target image. It is used in cases where the images exhibit significant deformations or changes, such as images acquired at different time points or positions, or those with pathological changes. It is commonly employed in tumor tracking, longitudinal image analysis, and image fusion across different modalities.

For this project, a rigid transformation of the images was performed, as they were taken at the same moment, and the goal was to obtain more information after their alignment. In the rigid registration process, four important components are considered: the transformation applied to align the moving image to the reference frame, the metric used to measure similarity between the moving and fixed images, the interpolator that transforms intensities when applying the transformation, and the optimizer responsible for adjusting transformation parameters to maximize similarity at each iteration.

## 3. Results and Discussion

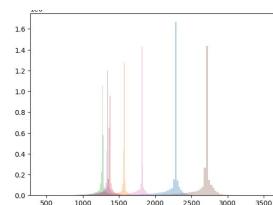
### 3.1 Qualitative results

### 3.2 Intensity standardization

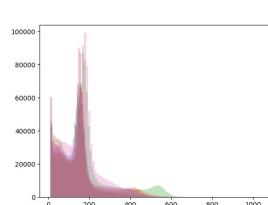
Before applying the mentioned standardization algorithms, a comparison is made of the generated histogram of the different images of the patients in the application in the 3 modalities (T1, IR, FLAIR), along with their respective frequencies and intensities. It can be observed that the peaks are not aligned in any of the modalities, and the value ranges vary considerably among them.

The “rescaling” intensity standardization method is a simple and easy-to-implement method that allows for quick normalization of the intensity of an image to a specific range. However, if the image has extreme values, i.e., values that are far outside the range of the rest of the image, normalization can negatively affect the quality of the image. Additionally, if the image has non-uniform lighting or noise, normalization may not be accurate and may affect the quality of the resulting image.

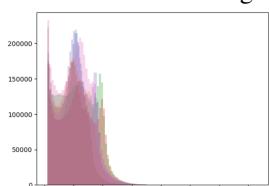
By implementing the rescaling method on the histogram of each corresponding modality for each patient, it can be observed that a better uniformity has been achieved. As a result,



**Figure 14.** Intensity histogram of IR.

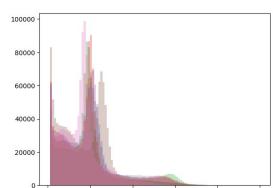


**Figure 15.** Intensity histogram of FLAIR.

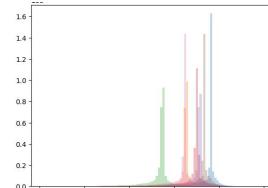


**Figure 16.** Intensity histogram of T1.

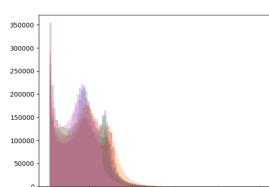
the peaks of each image, along with their respective histogram, are now more aligned compared to the initial implementation, implying a change in the range they are located. This demonstrates a successful adaptation of the method. However, in the IR modality, these peaks are highly misaligned, highlighting the disadvantages of using this standardization method for the IR modality. Based on these visual results, it can be observed that the method has a better adaptation in the T1 modality, as the peaks are more aligned.



**Figure 17.** Intensity histogram of FLAIR with rescaling.



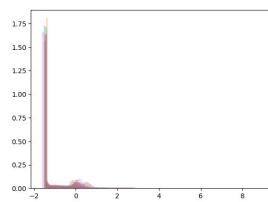
**Figure 18.** Intensity histogram of IR with rescaling.



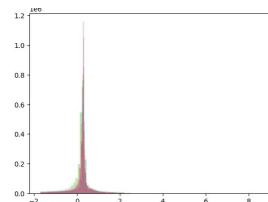
**Figure 19.** Intensity histogram of T1 with rescaling.

Similar to the rescaling method, the z-score method of intensity standardization is capable of normalizing the intensity values of an image, but it does so with respect to the mean and standard deviation of the image. This approach offers the advantage of adjusting the normalization to the distribution of intensity values in the image, allowing for a more accurate and detailed normalization. However, similar to the rescaling method, extreme values in the image can negatively impact

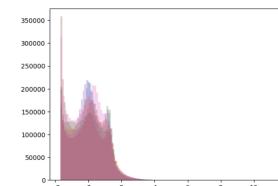
the quality of the normalization. Furthermore, the selection of the threshold value for the mean can affect the quality of the normalization and may require manual adjustments to achieve the desired results.



**Figure 20.** Intensity histogram of FLAIR with z-score.



**Figure 21.** Intensity histogram of IR with z-score.



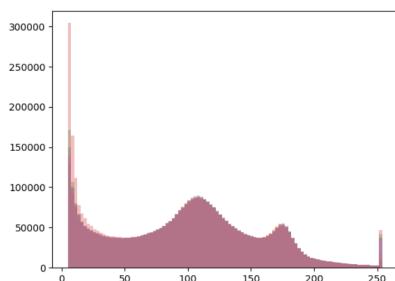
**Figure 22.** Intensity histogram of T1 with z-score.

Similarly to the rescaling method, the histograms of the images in the different modalities are visualized after applying the z-score algorithm. It can be observed that the histogram peaks are now better aligned compared to the initial state, and the range of values defining the histogram has also changed. Unlike the rescaling method, this approach adapts well to all modalities, demonstrating that is a better strategy.

The intensity matching method is capable of adjusting the normalization to the intensity distribution of the image, allowing for more accurate and detailed normalization. It is more robust than the rescaling method and others. However, the algorithm requires loading a target image to normalize the original image, which can be problematic if an appropriate target image is not available.

Now, the histograms of the T1 explorations are displayed after applying the histogram matching algorithm. A significant alignment can be observed in the peaks of each image, demonstrating its effectiveness as a technique applied to the T1 modality images. However, it was not possible to implement it in the other modalities. Currently, the strategy that has demonstrated the best performance according to the set of images and modalities available is z-score. Nevertheless, histogram matching showed better performance for the T1 modality.

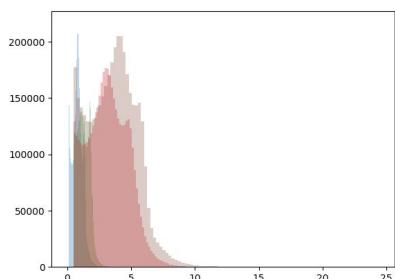
The white stripe standardization strategy, like the rescaling method, can be useful for normalizing images with non-uniform illumination. Additionally, this strategy automatically finds the divisor value for image normalization. However, this method may not be suitable for images with extreme values, as the divisor calculation is based on the peaks of the histogram and may not consider extreme values. Moreover, if



**Figure 23.** Intensity histogram of T1 with histogram matching.

the input image contains noise, the white stripe method may be inefficient.

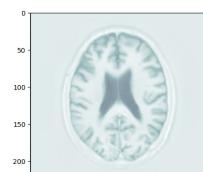
Now, the histograms of the T1 explorations are displayed after applying the white stripe algorithm. It can be observed that the peaks of the histogram are better aligned than initially. However, they are not as well aligned as the methods shown earlier, indicating the inefficiency of the method and that it is not the optimal approach to apply. Therefore, if a better preprocessing is desired, this should not be the initial method implemented for the given set of images, as its performance depends on the specific input images.



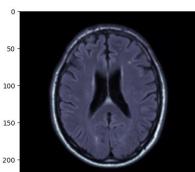
**Figure 24.** Intensity histogram of T1 with white stripe.

### 3.3 Denoising

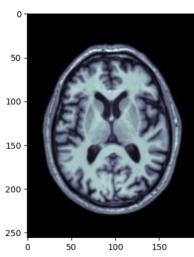
The mean-filter strategy for denoising in images is simple to understand and implement. It has fast processing and can be effective in smoothing random or uniform noise in the image. However, because it calculates the average of neighboring pixels, it can smooth fine details and edges in the image. Additionally, if the image contains outliers, the method can be negatively affected and produce undesirable results.



**Figure 25.** Mean Filter with IR.

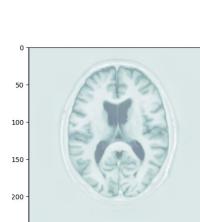


**Figure 26.** Mean Filter with FLAIR.

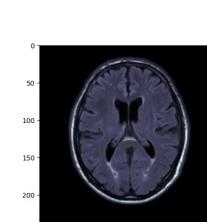


**Figure 27.** Mean Filter with T1.

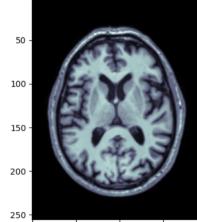
On the other hand, the median-filter method preserves edges and fine details better compared to the mean-filter. It is especially suitable for removing impulsive noise as it uses the median value of the neighbors and is more robust than the mean-filter against outliers or extreme noise values. The median value is not influenced by extreme values. However, it may remove small-sized details in the image due to its smoothing nature. In homogeneous areas, it can oversmooth and cause a blurring effect. Lastly, this strategy has a higher processing time.



**Figure 28.**  
Median Filter en  
IR.



**Figure 29.**  
Median Filter en  
FLAIR.

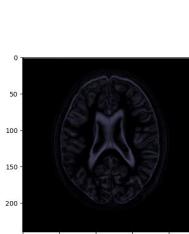


**Figure 30.**  
Median Filter en  
T1.

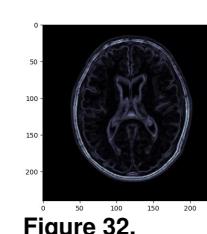
### 3.4 Edge detection

After applying filters to our images to remove noise, we sometimes find that the edges of the image blur a bit and can blend with other tissues. For this reason, the edge detection algorithm using average or median filters provides us with a much more precise and better-segmented image. The algorithm has a notable advantage as it is capable of detecting edges in different orientations and performs well on low-contrast images. Additionally, it can be applied to both noisy and noise-free images.

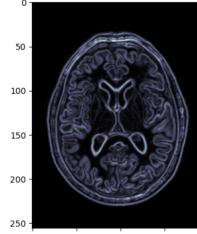
However, the algorithm may have some drawbacks. There is a possibility of detecting false edges in areas where the intensity changes gradually instead of abruptly. Moreover, the algorithm can be sensitive to noise in the image, leading to false edge detection or an image with an excessive number of edges. It is also important to consider that the algorithm requires high computational cost due to the need to iterate over each pixel of the image in three dimensions.



**Figure 31.**  
Median Filter with  
edge detection IR.



**Figure 32.**  
Median Filter with  
edge detection FLAIR.

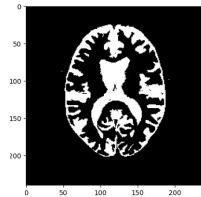


**Figure 33.**  
Median Filter with  
edge detection T1.

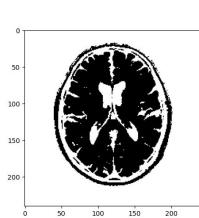
### 3.5 Segmentation

The thresholding (ISODATA) method is a simple and fast way to segment black and white images, and it does not require prior knowledge about the image, making it a good method for segmenting regions. However, it should be noted that it does not work well on images with uneven illumination or noise, as threshold values can vary too much. This method has a limitation in that an appropriate initial threshold needs to be chosen, which can be difficult for some images, and due to threshold updating, it can lead to incomplete segmentation of objects with poorly defined edges. [13]

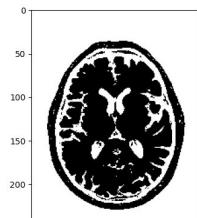
Here is a comparison between the segmentation of the image of a patient in the three modalities without any intensity standardization or noise removal, and the segmentation of the image after applying these preprocessing algorithms.



**Figure 34.**  
Segmentation  
isoDATA with  
IR.

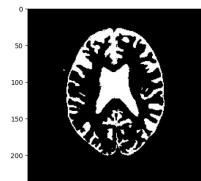


**Figure 35.**  
Segmentation  
isoDATA with  
FLAIR.

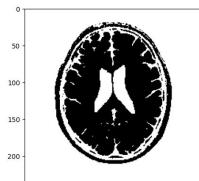


**Figure 36.**  
Segmentation  
isoDATA with  
T1.

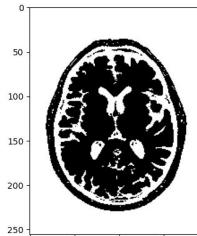
It can be observed that the difference between preprocessing the image with a rescaling standardization strategy and not doing so does not generate a highly significant change. However, it allows for capturing details that were previously overlooked, as processing the image results in a brighter appearance, thus enabling a better visualization of the segmentation. This emphasizes the importance of adjusting intensity levels before performing image processing.



**Figure 37.**  
Segmentation  
isoDATA with  
Rescaling  
IR.



**Figure 38.**  
Segmentation  
isoDATA with  
Rescaling  
FLAIR.

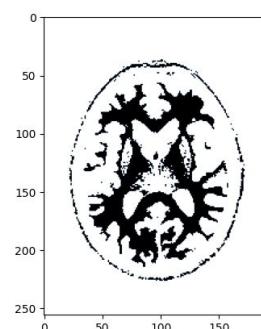


**Figure 39.**  
Segmentation  
isoDATA with  
Rescaling  
T1.

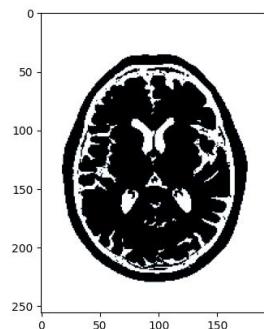
Upon analyzing the proposed region growing method, it was found that this strategy allows for segmentation of images with irregular or complex shapes, and unlike the thresholding method, it does not require manual selection of the threshold. Furthermore, multiple seeds can be used to segment objects more accurately, and due to its implementation, it can also

be adapted for edge detection. However, its execution time is very high as it requires a lot of computation time for large images, and since the seeds are sensitive to user selection, they can result in inaccurate segmentations. The tolerance inputted should not be too restrictive or too permissive to obtain a correct segmentation.

Here we present a comparison between the region growing segmentation of a patient's T1 image without any intensity standardization or noise removal, and the segmentation of the image after applying these preprocessing algorithms. It can be observed that the difference is clear, and better results are obtained by standardizing the image intensities. In this case, the intensities were standardized using the z-score method.



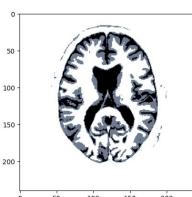
**Figure 40.** Region  
growing en T1.



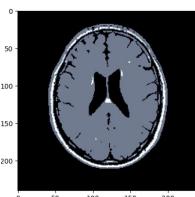
**Figure 41.** Segmentation  
using region growing  
with z-score T1.

The k-means segmentation strategy represents a fast and efficient method for segmenting images due to its simplicity and ability to work with large datasets. It is very useful as it allows for segmentation based on the similarity of pixel values, which can be beneficial in many cases, and it does not require much processing time. However, it is sensitive to the initial centroid values, which can lead to suboptimal solutions, and specifying the number of clusters in advance can result in not knowing the optimal number of clusters.

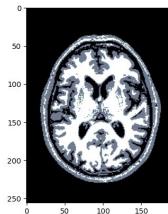
Here we present a comparison between the k-means segmentation of a patient's image in different modalities without any intensity standardization or noise removal, and the segmentation of the image after applying these preprocessing algorithms. The difference can be observed, and better results are obtained by standardizing the image intensities, as more details are visible, enabling early diagnosis. In this case, the intensities were standardized using the rescaling method.

**Figure 42.**

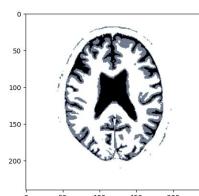
k-means with 3 clusters IR.

**Figure 43.**

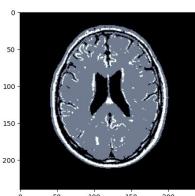
k-means with 3 clusters FLAIR.

**Figure 44.**

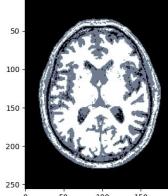
k-means with 3 clusters T1.

**Figure 45.**

k-means using Rescaling IR.

**Figure 46.**

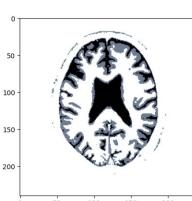
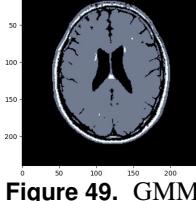
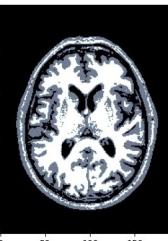
k-means using Rescaling FLAIR.

**Figure 47.**

k-means using Rescaling T1.

One advantage of the GMM segmentation algorithm is its ability to model non-symmetric distributions, allowing for the segmentation of images with regions of different shapes and sizes. Moreover, this algorithm is very flexible and can be adapted to different types of images and segmentation tasks. However, one disadvantage of this algorithm is that it can be sensitive to outliers and image noise, which can affect segmentation accuracy. Additionally, selecting the number of clusters can be challenging, as an incorrect selection can produce inaccurate or incomplete segmentations.

For this example, we will display a segmentation on a standardized image using GMM with three clusters in the T1 modality of one of the patients. For this purpose, the standardization algorithm and the rescaling algorithm were utilized.

**Figure 48.** GMM using rescaling IR.**Figure 49.** GMM using rescaling FLAIR.**Figure 50.** GMM using rescaling T1.

### 3.5.1 Registration

Registration in medical image processing is the process of aligning and combining images acquired from different modalities with the aim of creating a coherent and complete representation of a region of interest in the human body, in this case, the brain.

In the context of our project, registration is a fundamental component. Techniques and algorithms were employed to align and fuse these images to obtain a more comprehensive and accurate understanding of the brain's structures.

This registration process allows us to compare and analyze images acquired at different time points or from different modalities, facilitating diagnosis, disease progression monitoring, and treatment planning.

The registration technique initially used in this project is rigid registration, which enables precise alignment of the images while preserving their original shape. This technique was implemented using the SimpleITK (sitk) library.

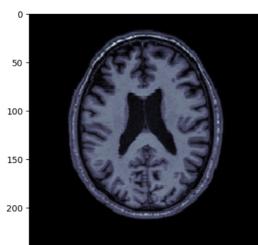
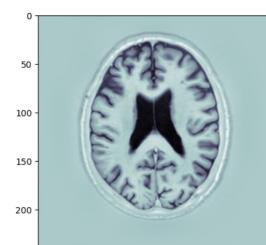
The chosen registration metric at the beginning is called "MattesMutualInformation," which evaluates the similarity between the images using Mattes' mutual information. This metric helps determine the degree of overlap and resemblance between the images.

During the registration process, the sitkLinear interpolator was applied, using linear interpolation to adjust the images. This ensures a smooth and continuous transition while aligning the pixels of the images.

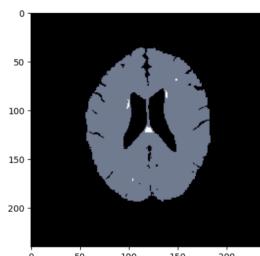
The optimizer configuration was based on the gradient descent method. This method aims to find the best solution by gradually minimizing the difference between the images over multiple iterations.

Once the linear transformation between the images was established, adjustments were made to the contraction settings and smoothing sigmas. These parameters control the rigidity and smoothness of the transformation, respectively.

Finally, the registration process was executed, and the registered image was resampled. This involved adjusting the position and scale of the image to properly fit the reference space. As a result, a final registered image was obtained that is coherent and precisely aligned.

**Figure 51.** T1 to FLAIR with rigid registration**Figure 52.** IR to FLAIR with rigid registration

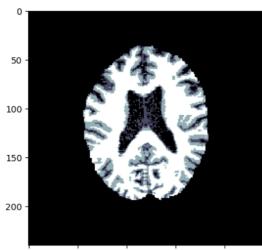
Tests were conducted during the image registration process, in which a segmented FLAIR image was used as a fixed reference using the k-means algorithm, followed by the registration of the segmented T1 image using the same k-means algorithm. After considering various options, it was decided to continue utilizing this approach. It is important to note that the majority of the algorithms implemented in this study are approximations and/or simplifications of the algorithms used in practical applications.



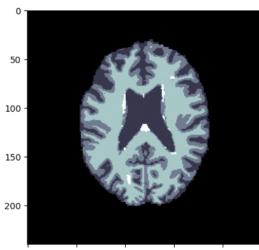
**Figure 53.** Rigid registration. Segmented T1 registered to segmented FLAIR with skull removal.

To conclude the project objectives, after testing various algorithms at each stage, we successfully obtained segmentations of the MRI images from the described patients in the materials section. Initially, we applied standardization to the T1 and FLAIR images using the z-score algorithm. Subsequently, we performed segmentations using the k-means algorithm on both images. Next, we proceeded with the registration of the segmentations, and finally, we applied the skull removal method using the "robex" function from the pyrobex library in Python. This method provided us with a segmentation mask using the IR image, which was then applied to the registered image. As a result, we obtained the following results:

#### Patient 1:

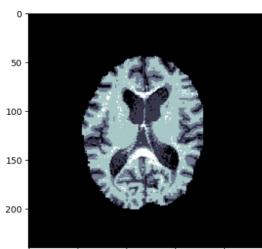


**Figure 54.** Segmented T1 Image with K-means Registration.

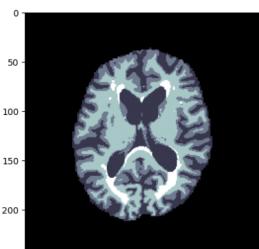


**Figure 55.** Reference Segmented Image for Patient 1.

#### Patient 4:

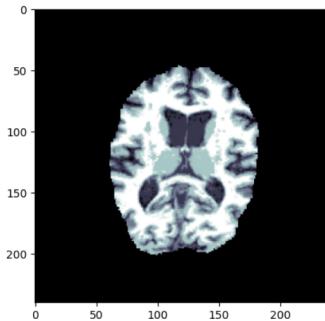


**Figure 56.** Segmented T1 Image with K-means Registration.

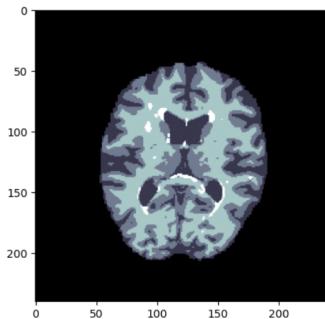


**Figure 57.** Reference Segmented Image for Patient 4.

#### Patient 5:

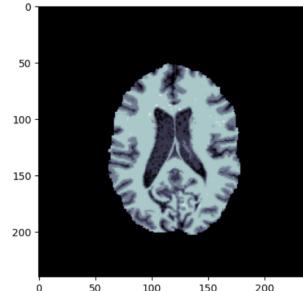


**Figure 58.** Patient 5: Segmented T1 Image with K-means Registration, FLAIR Alignment, and Skull Removal

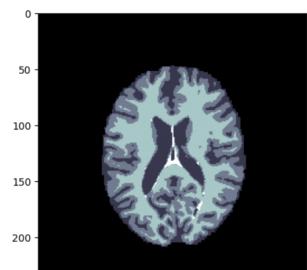


**Figure 59.** Reference Segmented Image for Patient 5.

#### Patient 7:

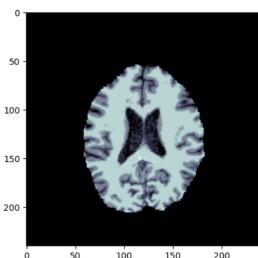


**Figure 60.** Patient 7: Segmented T1 Image with K-means Registration, FLAIR Alignment, and Skull Removal.

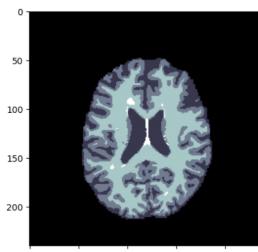


**Figure 61.** Reference Segmented Image for Patient 7.

#### Patient 14:

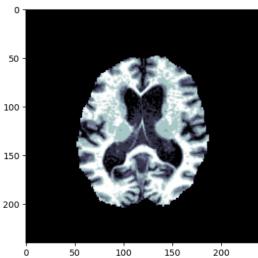


**Figure 62.** Patient 14:  
Segmented T1 Image  
with K-means  
Registration, FLAIR  
Alignment, and Skull  
Removal.

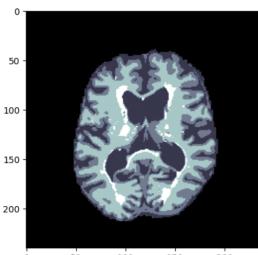


**Figure 63.** Reference  
Segmented Image for  
Patient 14.

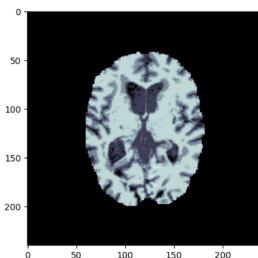
#### Patient 070 and Patient 148:



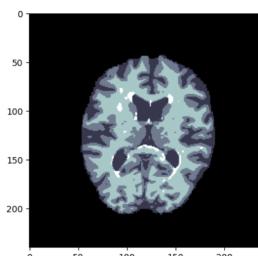
**Figure 64.** Patient 070:  
Segmented T1 Image  
with K-means  
Registration, FLAIR  
Alignment, and Skull  
Removal



**Figure 65.** Reference  
Segmented Image for  
Patient 070.



**Figure 66.** Patient 148:  
Segmented T1 +  
K-means Registration  
and Skull Removal



**Figure 67.** Reference  
Segmented Image for  
Patient 148.

#### 3.6 Quantitative Results

The following section presents the numerical results obtained during the image segmentation process. Segmentation plays a vital role in the analysis of medical images as it enables the identification and delineation of regions of interest within an image.

Analyzing the accuracy and coherence of the achieved segmentations is crucial, as it allows for evaluating the proposed method's ability to accurately capture relevant anatomical

structures and distinguish them from the background. These numerical results provide a detailed and comprehensive understanding of the quality and applicability of the obtained segmentations, which holds significant importance for their interpretation and clinical application.

Multiple evaluation algorithms were employed to assess these results.

- **Similarity of volumes:** To assess the similarity of volumes, a volumetric similarity measure is utilized to compare two segmentations. Firstly, the volumes of each cluster in both segmentations are obtained. Then, the volumes are summed to obtain the total volume for each segmentation. Finally, the volumetric similarity is calculated based on these measurements.
- **The Jaccard Index,** implemented in the Python library medpy, is a valuable measure for evaluating the quality of segmentations. In contrast to the Dice Score, the Jaccard Index focuses on the overlap between segmentations rather than considering the number of voxels in each segmentation individually.

The Jaccard Index value ranges from 0 to 1, where 1 indicates a perfect overlap or identical segmentations, and 0 indicates a lack of overlap or completely different segmentations.

The Jaccard Index is calculated by dividing the intersection of the segmented regions by their union. It provides a quantitative measure of the similarity between the segmentations, with higher values indicating a greater degree of overlap.

- **The Dice Score,** derived from the Python library MedPy, is a widely used measure to evaluate the quality of segmentations. This metric takes into account both sensitivity to detection and specificity in segmentation. It ranges from 0 to 1, where a value of 1 indicates perfect overlap or identical segmentation, while a value of 0 indicates no overlap or completely different segmentations. The Dice Score provides an objective measure to assess the quality of segmentations based on their similarity to the reference object.

The following table presents the consolidated results obtained after comparing the segmentations generated by the application with the reference segmentations:

File	DiceScore	JaccardIndex	Vol.Similarity
1	0.8485	0.7368	0.4999
4	0.8227	0.6988	0.4999
5	0.8378	0.7209	0.5
7	0.8221	0.6979	0.5
14	0.8257	0.7031	0.5
070	0.7570	0.6090	0.5
148	0.8182	0.6923	0.4999

For each patient, the obtained volume results for our segmentation and the reference segmentation were:

Patient 1:

Cluster	Segmentation	reference
1	157121mm <sup>3</sup>	375190mm <sup>3</sup>
2	341816mm <sup>3</sup>	539174mm <sup>3</sup>
3	464381mm <sup>3</sup>	386808mm <sup>3</sup>
4	1038mm <sup>3</sup>	6871mm <sup>3</sup>

Patient 4:

Cluster	Segmentation	Reference
1	170332mm <sup>3</sup>	426500mm <sup>3</sup>
2	304433mm <sup>3</sup>	526897mm <sup>3</sup>
3	474363mm <sup>3</sup>	478629mm <sup>3</sup>
4	73429mm <sup>3</sup>	30359mm <sup>3</sup>

Patient 5:

Cluster	Segmentation	Reference
1	119468mm <sup>3</sup>	369671mm <sup>3</sup>
2	191988mm <sup>3</sup>	524412mm <sup>3</sup>
3	326591mm <sup>3</sup>	397405mm <sup>3</sup>
4	307109mm <sup>3</sup>	18151mm <sup>3</sup>

Patient 7:

Cluster	Segmentation	Reference
1	124326mm <sup>3</sup>	322678mm <sup>3</sup>
2	286828mm <sup>3</sup>	508936mm <sup>3</sup>
3	412545mm <sup>3</sup>	356752mm <sup>3</sup>
4	8466mm <sup>3</sup>	1391mm <sup>3</sup>

Patient 14:

Cluster	Segmentation	Reference
1	127833mm <sup>3</sup>	340585mm <sup>3</sup>
2	343547mm <sup>3</sup>	598599mm <sup>3</sup>
3	481409mm <sup>3</sup>	415598mm <sup>3</sup>
4	3030mm <sup>3</sup>	4380mm <sup>3</sup>

Patient 070:

Cluster	Segmentation	Reference
1	192671mm <sup>3</sup>	542508mm <sup>3</sup>
2	236013mm <sup>3</sup>	540304mm <sup>3</sup>
3	365503mm <sup>3</sup>	572105mm <sup>3</sup>
4	237923mm <sup>3</sup>	39570mm <sup>3</sup>

Patient 148:

Cluster	Segmentation	Reference
1	170225mm <sup>3</sup>	441141mm <sup>3</sup>
2	332413mm <sup>3</sup>	497111mm <sup>3</sup>
3	506266mm <sup>3</sup>	462315mm <sup>3</sup>
4	3628mm <sup>3</sup>	61352mm <sup>3</sup>

#### 4. Conclusions

BrainScope offers a comprehensive and effective tool for processing brain images in the context of diagnosing and treating neurological diseases. The algorithms used, such as segmentation, edge detection, intensity standardization, and noise removal, contribute to improving the interpretation and comparability of the images. This facilitates clinical decision-making and the development of more precise and personalized treatments.

During the preprocessing of the images, various algorithms were employed for intensity standardization. These algorithms were predefined, and each one was applied to the T1 images of each patient. The resulting histograms were compared, and it was observed that the Z-score algorithm provided the highest significance. This algorithm is adaptable to all modalities, preserves information without loss, and offers a better representation of intensities, especially when atypical values are present. By adjusting the normalization based on the intensity distribution in the image, a more accurate and detailed normalization is achieved. Although the rescaling method was also effective and executed within an optimal time frame, Z-score demonstrated greater precision in the histograms.

After intensity standardization, the feasibility of applying noise removal techniques was analyzed. It was observed that using the Z-score intensity standardization method, applying techniques such as mean, median filter, and median filter with edges resulted in volumes that significantly differed from the reference volume. This outcome was attributed to the high likelihood of noise removal eliminating or modifying parts of the original image information. Consequently, important details or structures in the image were lost, affecting the accuracy of segmentation and resulting in incorrect or distant cluster volumes.

Therefore, it was decided to perform intensity standardization using the Z-score method without employing noise removal. This approach prevents significant information loss, ensuring that the obtained cluster volumes closely match the reference values with minimal differences.

For selecting the algorithm that would represent the image segmentation in the processing stage, a simpler analysis was conducted. Given that the image segmentation needed to be performed with multiple clusters due to the presence of more than two regions to be segmented, most methods had limitations in this regard. For instance, the isodata algorithm only allowed segmentation of two different regions or two clusters,

which did not offer an advantage in the final application and was therefore discarded. Region growing, on the other hand, presented complex implementation within the coding, resulting in slow performance. Consequently, two algorithms were considered for processing the final images: Clustering or k-means and Gaussian Mixture Model (GMM). Both algorithms allow segmentation into multiple regions, with clusters being user-selectable. They offer a more inclusive user experience and enable the differentiation of various regions, including cerebrospinal fluid, normal gray matter, normal white matter, and hyperintensities of white matter.

Ultimately, the k-means algorithm was chosen over GMM due to its relative simplicity and computational efficiency. In comparison, GMM is a more complex probabilistic model based on Gaussian distributions, requiring the estimation of various parameters. K-means produces clear and easily interpretable partitions of the data, where the obtained centroids represent the central points of each region. This simplicity makes the algorithm easier to understand and apply, unlike GMM, which employs a mixture of Gaussian distributions to model the data.

The registration was implemented using the SimpleITK library, which provides the necessary tools to implement it properly. It was decided to implement rigid registration because it is used in the image registration process when aligning images of the same patient acquired at different times or with different modalities. By implementing this type of registration, subtle movements and deformations are corrected, ensuring registration stability. Non-rigid registration is primarily used for registering images of different patients, capturing more complex local deformations. Similarly, the "MatteMutual-Information" metric was selected for registration due to the differences in intensity ranges between the images. These differences in intensity range can pose challenges in the registration process, as traditional similarity metrics may not be suitable for capturing correspondence between intensities of different modalities. However, this metric effectively addresses this challenge.

The NearestNeighbor interpolator was chosen primarily because it represents the simplest and most direct interpolation method. It does not compute or modify existing pixel values in the input images. Each new pixel in the registered image simply takes the value of the nearest pixel in the original image. This ensures that no additional information or alteration is introduced into the original data during registration, and it has low computational complexity, allowing for efficient registration. Using gradient descent as an optimizer enhances computational efficiency.

The choice of these methods is critical for achieving appropriate segmentation. However, even with this analysis, there were cases where metrics deviated from the reference values, as observed in patients 070 and 148. Visually, it can be seen that certain clusters in the segmentation exhibited a higher pixel presence, resulting in larger cluster volumes, such as in cluster 4. Consequently, the metrics showed more

variation. Another reason for deviating metrics is the presence of artifacts in medical images, such as noise, distortions, or lack of contrast. These artifacts can affect image quality and, consequently, influence the segmentation accuracy.

In general, it can be concluded that:

1. Intensity standardization improves the uniformity of histograms, indicating better adaptation of pixel intensities and reduced variability among the images. However, it is important to consider the limitations of the intensity standardization methods used. In some cases, the presence of outliers or uneven lighting can affect the quality of normalization. Therefore, manual adjustments or alternative standardization methods may be necessary.
2. The preprocessing stage of image analysis is crucial as it prepares the original images for better processing. BrainScope utilizes intensity standardization techniques such as rescaling, z-score normalization, and histogram matching to normalize pixel intensities and reduce variability among the images. This improves comparability and accuracy in the conducted analyses, although using Z-score is recommended in this implementation.
3. Image segmentation employs algorithms like region growing, k-means, and GMM to divide the image into different regions or segments based on the similarity of pixel values. These algorithms can identify and delineate relevant brain structures for the diagnosis and treatment of neurological diseases.
4. Edge detection is a technique used to identify the boundaries or contours of an image. BrainScope implements an edge detection algorithm that uses partial derivatives to identify abrupt changes in pixel intensities, indicating the presence of edges. This technique is useful for highlighting brain structures and facilitating their analysis.
5. An automated solution for measuring the volume of brain tissues using magnetic resonance imaging (MRI) is presented. Through preprocessing and image processing techniques, precise and reliable results are achieved.
6. Rigid registration is a valuable technique in medical image processing and computer vision that allows aligning images to facilitate their analysis and comparison. The SimpleITK library provides efficient implementations for rigid registration and other registration techniques, making it easy to use.

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