# Influence of filtering on automated brain segmentation in MRI

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*Abstract*—The focus of this project is the influence of prepro-cessing MRI datasets on automated segmentation of a human brain, using a Random Forest Classifier network. Different filters were tested and compared and the two best performing filters (normalization and histogram matching) were then used in a combination. An improvement in the dice score of 3.79% was achieved when using the SimpleITK normalization filter followed by the SimpleITK histogram matching filter.

*Index Terms*—Magnetic resonance imaging, Brain segmenta-tion, Random Forest Classifier, preprocessing, filters, SimpleITK

## I. INTRODUCTION

Every year, an estimated 13.8 million patients worldwide require neurological surgery. The majority of neurosurgical care includes traumatic brain injuries, tumors, stroke-related conditions and epilepsy [1].

Due to the opportunity of having high resolution images of soft tissue, MRI is the state-of-the-art imaging method in Neurol-ogy, but to differentiate the brain strucures, segmentation is necessary. This is mostly done by clinicians and is very time consuming. To facilitate this process, automated segmentation using machine learning (ML) is being researched.

The use of Random Forest Classifier (RFC) and conditional random fields for the segmentation in MRI has been investi-gated by Pereira et al. [2].

When segmenting automatically, there often is an influence from noise or other artifacts, affecting the quality of the outcome. To reduce this, preprocessing is often applied. The influence of preprocessing on the segmentation of MR images using a convolutional neural network was already investigated by deRaad et al. [3].

In this project we focus on using a selection of preprocessing filters from the SimpleITK library. These filters are applied on a dataset of human brain MR scans from the Human Connectome Project (HCP).

We hypothesize that the segmentation accuracy improves when applying a combination of the two best-performing filters, as opposed to using no preprocessing filters.

## II. MATERIAL AND METHODS

### A. Material

The dataset employed in this project comprises 3-tesla head MR images obtained from 30 unrelated healthy subjects sourced from the Human Connectome Project (HCP) dataset of healthy volunteers [4]. Each subject's data includes a T1-weighted MR image volume, which is not skull-stripped but defaced for anonymization, and subjected to bias field correction. Additionally, a T2-weighted MR image volume is processed in a similar manner as the T1w image. Both modal-ities are presented in native T1w subject-space. The dataset also provides ground truth label maps and brain masks in the native subject-space, generated through automated labeling.

### B. Methods

*1) Libraries and Frameworks:* The implementation uti-lized the codebase available from the Git repository "ubern-mia/MIALab." The experiments were conducted in a Python (version 3.10.6) environment, utilizing conda (version 4.10.3) on personal laptops. The primary library employed for image processing was SimpleITK (version 2.4.0)

*2) Pipeline structure:* The implementation followed the pipeline structure provided by the "ubern-mia/MIALab" code-base. The foundational structure of this codebase guides our approach, providing a well-established framework for the various stages of our Medical Image Analysis (MIA) pipeline. This groundwork, briefly elucidated below, serves as the backbone for our methodology:

**Registration:** Aligning the two MR images is initiated to establish spatial correspondence.

**Preprocessing:** Diverse preprocessing techniques are applied to enhance the image quality, ensuring optimal input for the subsequent ML algorithm.

**Feature extraction:** The extraction of meaningful features from the MR images to facilitate subsequent classification.

**Classification:** Voxel-wise tissue classification is performed based on the extracted features. The classification process is akin to the method proposed by Pereira et al. [2], wherein a Random Forest encoding the likelihood function is employed for brain tissue segmentation. This entails leveraging intensi-ties, gradients, probability maps, and locations as features to achieve accurate results.

**Postprocessing:** Following classification, a postprocessing step refines and improves the overall classification results.

*3) Filters:* Various SimpleITK filters were applied individ-ually to the brain segmentation preprocessing task.

**Normalization** is a filter which standardizes pixel intensities to a common scale.

**Mean** is a simple spatial smoothing filter by averaging pixel values.

**Gaussian** smoothing with the standard deviation $\sigma = 1$ and once with $\sigma = 0.5$ for blurring and smoothing.

**Laplacian** enhances edges by emphasizing intensity changes.

**Curvature Flow** is an anisotropic diffusion filter for noise reduction which was used once with one iteration and once with ten iterations.

**Bilateral** filtering smoothens images while preserving edges, considering both spatial and intensity differences.

**Grayscale Opening Morphology** and **Grayscale Closing Morphology** are operations for image enhancement. With these filters we can try to eliminate small outliers.

**Histogram Matching** adjusts image intensities to match a reference histogram which was chosen to be the atlas image.

**Adaptive Histogram Equalization** enhances contrast by adjusting intensity distribution locally.

*4) Evaluation:* The evaluation of the brain segmentation results was performed using the Dice score and Hausdorff distances. A baseline was established for comparison. The Dice score measures the spatial overlap between predicted and ground truth segmentation, while Hausdorff distances quantify the dissimilarity between two point sets.

To test the hypothesis that segmentation accuracy improves with filter combinations, we employed the two best-performing filters in serial combination, conducting the experiment twice to assess the potential impact of filter sequence on segmentation results.

For better visualization the experiments were split up into three groups we will look at in the results section:

- **Filters 1:** separate application of the following filters - Normalization, Mean, Gaussian, Laplacian, Curvature Flow.
- **Filters 2:** separate application of the following filters - Bilateral, Grayscale Opening/Closing Morph, Histogram matching Adaptive Histogram Equalization
- **Filter Combinations:** explores the combinations of the two best filters in a sequence.

## III. RESULTS

*1) baseline:* The performance of the baseline segmentation was evaluated by using dice score metric as well as the Hausdorff distance. Fig. 1

For the remainder of the report we focus solely on the dice score due to similar performance of the filters in both metrics across all tested filters.

*2) filters 1:* To compare the filters to the baseline the relative dice score in comparison to the baseline dice has been measured. It was evident from the graph in Fig. 2, that the largest improvement in comparison to the baseline was achieved with the normalization filter with 3.31%.

*3) filters 2:* To compare the advanced filters the achieved dice score was reviewed in comparison to the baseline dice score. When comparing the different advanced filters with
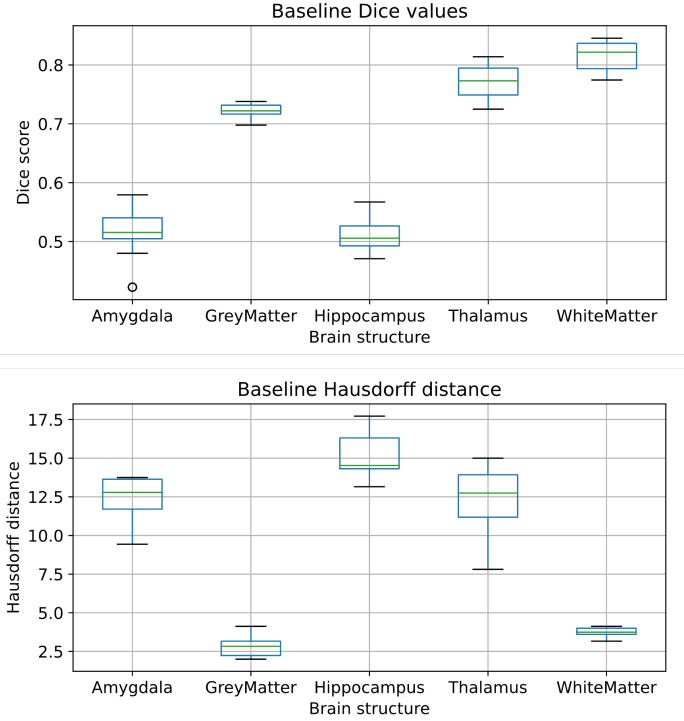


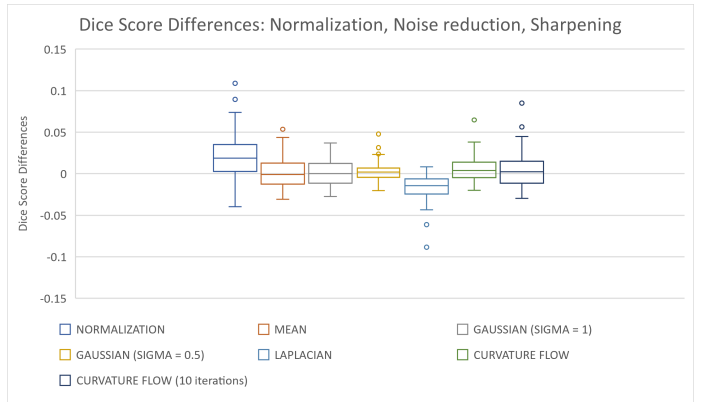Fig. 1. Dice and Hausdorff of baseline.
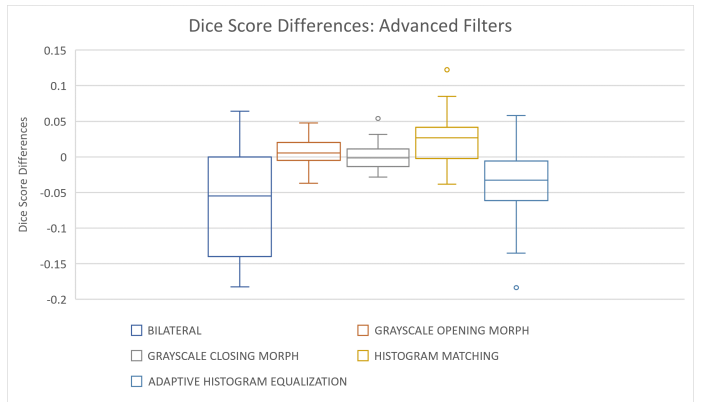


Fig. 2. Dice difference of filters 1.



Fig. 3. Dice difference of filters 2.

each other, the graph in Fig. 3 highlighted the improvement of 3.56% when using the histogram matching filter in comparison to the baseline.

*4) filter combinations:* The two combinations of the normalization and the histogram matching filter were compared to the baseline as relative dice score. An improvement of the mean dice score by 0.94% and 3.79% respectively was achieved. Fig. 4
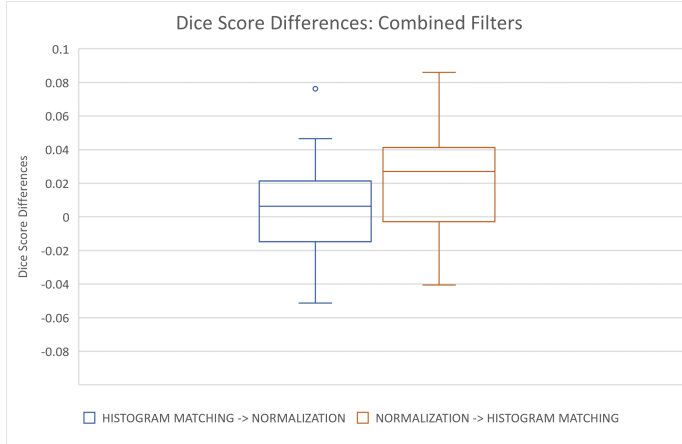


Fig. 4. Dice difference of filter combinations.

## IV. DISCUSSION

Our hypothesis was the improvement of segmentation accuracy when applying a combination of the two best-performing filters, as opposed to using no preprocessing filters. Thus, our hypothesis is accepted due to the mean dice score improving by 3.79% (Fig. 2) with the use of the **Normalization** filter followed by the **Histogram Matching** filter, where the T1- or T2-atlas image is used as reference image.

The **Normalization** filter has been chosen due to improving the mean dice score by 3.31% (Fig. 2). Normalization is common practice in combination with Machine Learning (ML) algorithms to achieve improved results. Hence, the improvement of the mean dice score with the **Normalization** filter could be due to our usage of the Random Forest Classifier (RFC) in the pipeline. Similarly, the RFC receives as input less varying pixel intensities for the same region when histogram matching is done with the same corresponding T1- or T2-atlas image as reference. Hence, the RFC should be able to distinguish easier between the different brain regions: Applying the **Histogram Matching** filter resulted in an improvement of the mean dice score by 3.56% (Fig. 3).

In comparison to these two selected filters, the other filters did either have no or a negative influence on the mean dice score. **Mean** and **Gaussian** filters were intended to reduce random noise by blurring the image but did not improve the mean dice score (Fig. 2). As opposite, sharpening the images using the **Laplacian** filter did also reduce the mean dice score by -2.85% (Fig. 2).

**Bilateral** and **Curvature Flow** filters use algorithms to preserve edges and blur homogeneous segments to counteract the loss of information or the amplification of random noise through blurring and sharpening: The mean dice scores did in fact increase by 1.00% (1.01% with 10 iterations) for the **Curvature Flow** filter (Fig. 2); however, the **Bilateral** filter reduced the mean dice score by -10.88% (Fig. 3), while also increasing the computational costs of the whole pipeline from an average 30 minutes to 8 hours.

The use of morphological filters such as the **Grayscale Opening Morphology** filter is another approach to reduce potential noise in images to improve segmentation of structures. However, this filter did also not improve the mean dice score significantly with 0.97% (Fig. 3).

Finally, all previous observations indicate that the noise reduction in the data was not the key factor for the improvement of segmentation but the preprocessing of the data for the ML approach of this pipeline. Accordingly, the best performance was achieved with the **Normalization** and **Histogram Matching** filters, where only the latter might have a negligible effect on the noise of data.

## V. CONCLUSION

In conclusion, the different preprocessing tests might show different results with another ML algorithm than the RFC. Additionally, more extensive research could be done on the effect of the filters, for example the difference between the order of applying the **Normalization** and **Histogram Matching** filters. Nonetheless, at least the **Normalization** filter should be kept if a ML algorithm is implemented in the pipeline.

Further, new combinations of filters in serial or parallel application could be tested in another project with corresponding hypotheses.

Finally, regarding the data set, the preprocessing steps with noise reduction could show better improvements if a data set with more noise would have used. This effect could be simulated by adding random noise to the same data set prior to feeding it into the pipeline.

### REFERENCES

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## REPOSITORY

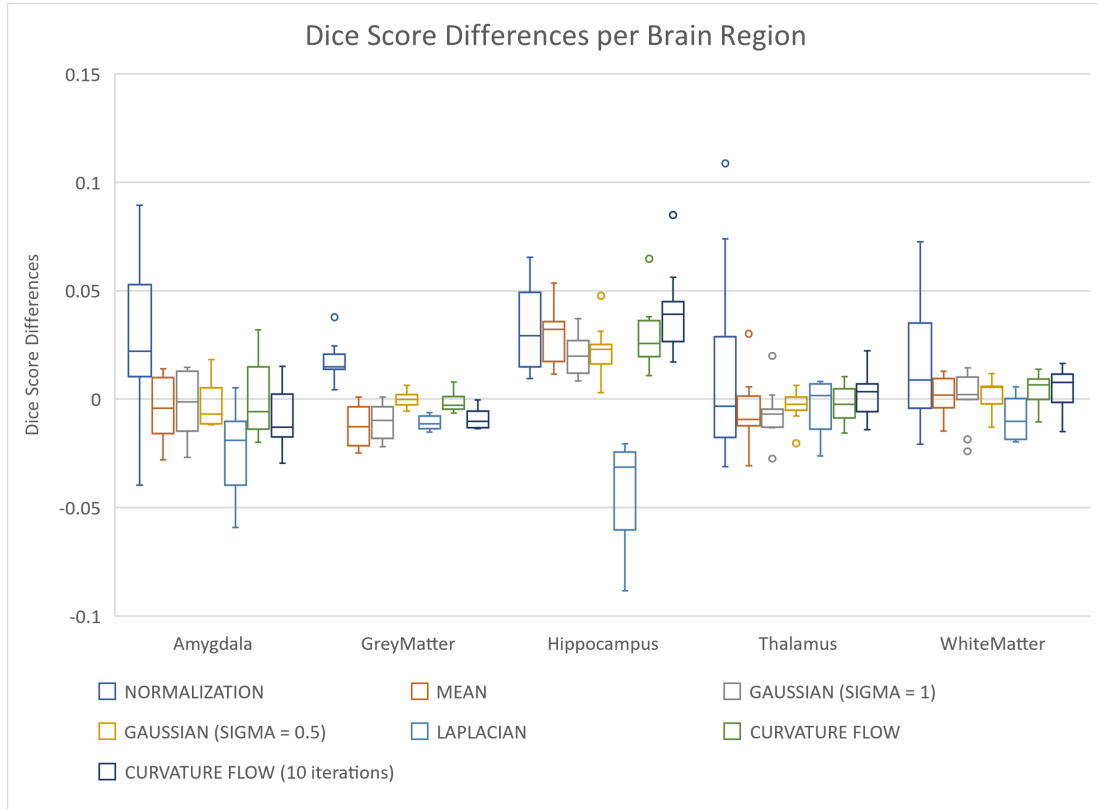https://github.com/randakan/MIALab_Preprocessing_2023

Fig. 5. The Dice Score Differences of the first filter group for each brain region separately.
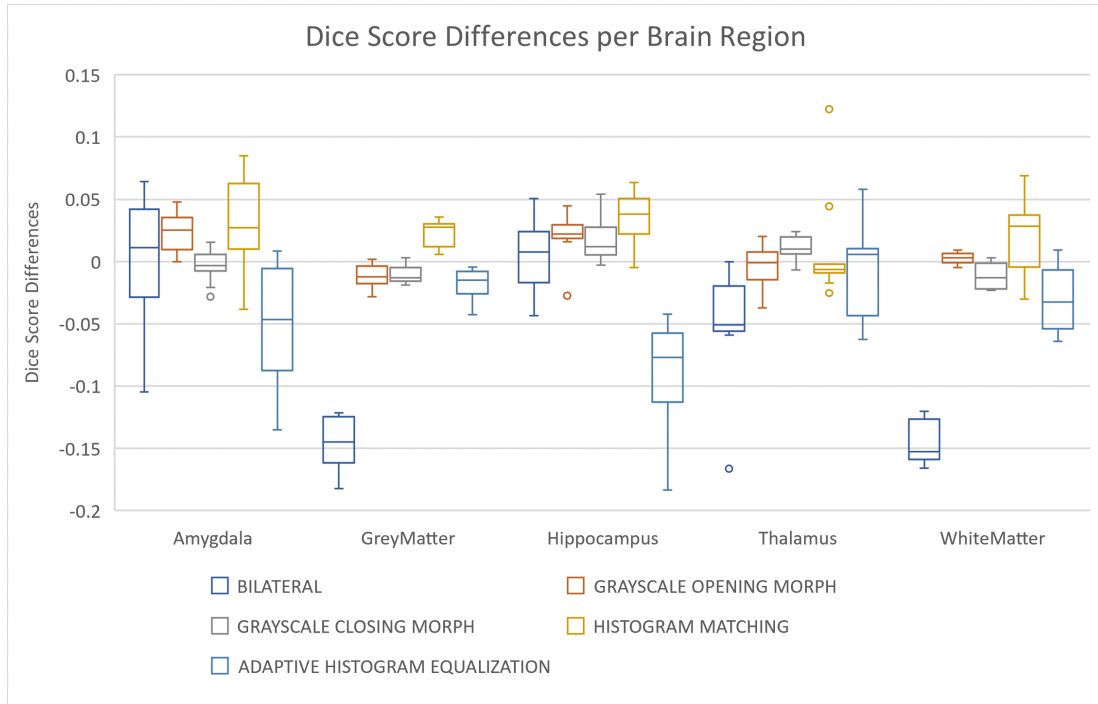


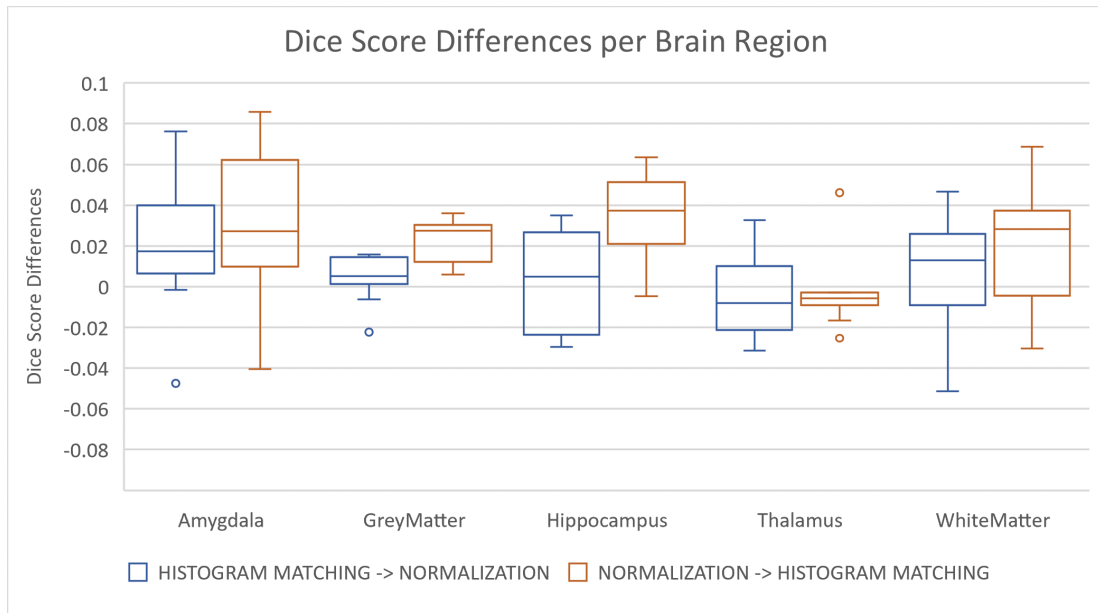Fig. 6. The Dice Score Differences of the second filter group for each brain region separately.

Fig. 7.  The Dice Score Differences of the filter combinations for each brain region separately.



Fig. 8.  Visualization of the brain segmentation realized in the software ITK-Snap, with the sequential use of Normalization and Histogram Matching during preprocessing.