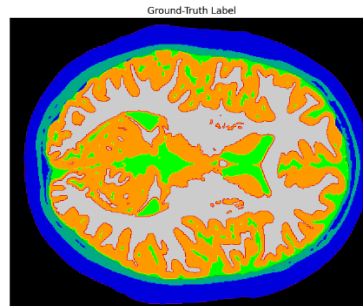


6 dic 2024

1. Aim

The objective of the following model development is to analyze and segment 10 consecutive 'axial' cross sections from MRI images of a single human brain. The following labels, which were previously defined as follows are what the algorithm is trying to segment:

- Label 0 = air
- Label 1 = skin/scalp
- Label 2 = skull
- Label 3 = CSF
- Label 4 = Gray Matter
- Label 5 = White Matter



2. Methods

The segmentation task has developed several preprocessing and clustering techniques to extract meaningful regions from the image. On the one hand, the raw MRI slice undergoes outlier removal using minmax scaler, standard scaler, and quantile transformation to eliminate outlier values, ensuring the data is normalized and is ready for the following transformations, like Gaussian smoothing, which is applied to reduce noise and enhance image quality by blurring minor intensity variations where the degree of smoothing is determined by the standard deviation with the objective of preserving meaningful anatomical structures. The following method has been applied for edge detection; the techniques that have been explored are Sobel, Prewitt, Roberts, Laplace, and Canny, with the objective of extracting using image transformations such as gradient-based methods to identify boundaries between regions and finding the best technique that can give us our best result in the segmentation task.

For the segmentation task, K-Means clustering is implemented due to computational efficiency in comparison of SVM and multi-level thresholding models. K-Means is an unsupervised learning algorithm. The reason to use this algorithm is that we do not have data to train a supervised model, which requires a large sample of labeled data. The K-Means model groups pixels into distinct clusters based on the similarity of their intensity and edge features. This model iteratively assigns pixels to clusters and updates cluster

centroids in order to minimize the variance within clusters. The result is a segment image where each cluster corresponds to a different tissue type or region. Finally, the segmented results are visualized and overlapped with the original image and its intensity histogram to assess the model's performance.

2.1 Evaluation Metrics

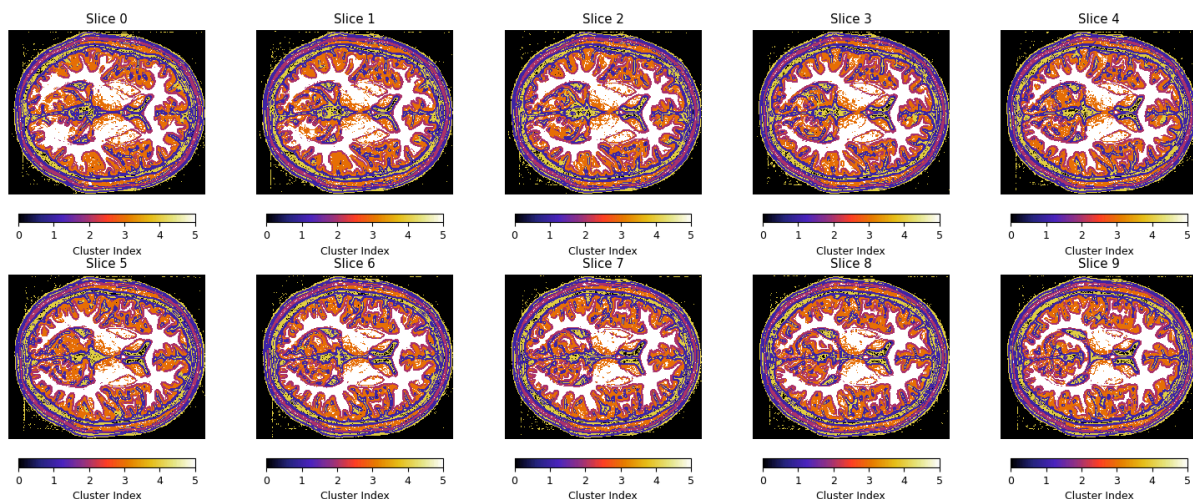
The F1-Score was chosen to evaluate the balance between precision and recall for each segmentation method. The implementation of the F1 score as our precision metric is the harmonic mean between the ground truth and the segmentation results from each cluster, and the main metric is the mean of all cluster's scores between all the slices, which ensures a balanced evaluation when both false positives and false negatives need to be minimized.

In addition, we develop a Gaussian optimization technique in order to find our best parameters and preprocessing techniques by applying just the best features, which gives us a higher score in the model training. Gaussian optimization is a probabilistic model-based approach to hyperparameter tuning to maximize the F1 score. The combination of Gaussian optimization and the F1 score ensures that the best parameters are chosen to achieve optimal segmentation performance in terms of both precision and recall.

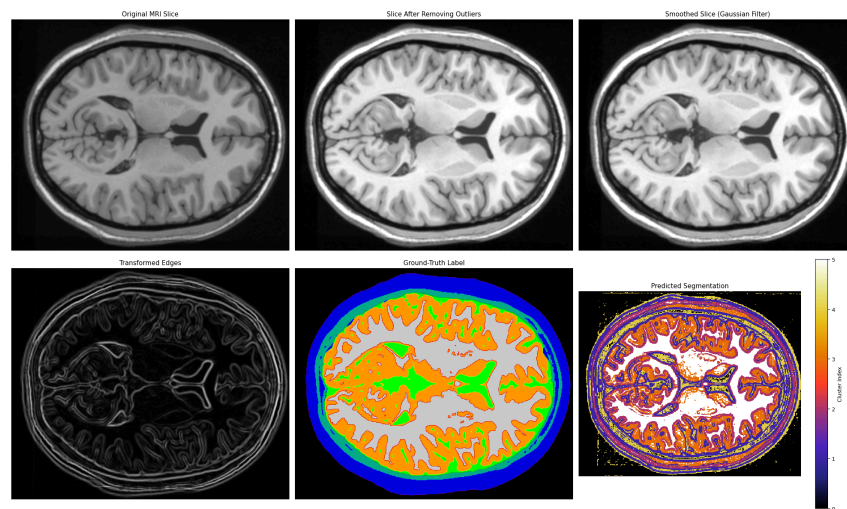
3. Results

After implementing the K-Means model and applying Gaussian optimization, the results are the following:

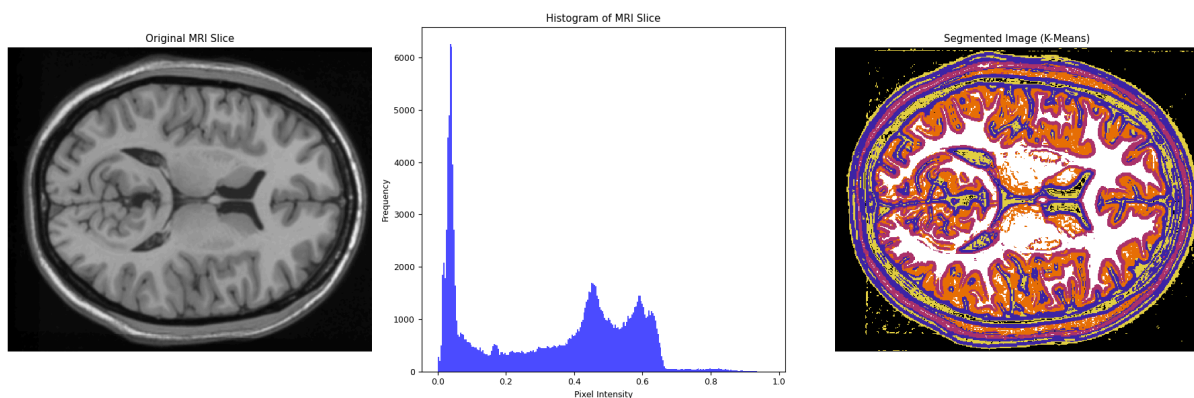
- **F1 Score:** .7902
- **Initiator:** random
- **Transformation:** Novel
- **Gaussian Smoothing Sigma:** .1477
- **Scaler:** Quantile



Model Pipeline



Pixel Density




3. Conclusions and 3D image segmentation

A 3D segmentation algorithm for processing MRI slices is going to improve the relationships between slices to capture slice continuity and leverage the segmentation consistency for the biggest anatomical structures like white and gray matter. This can be achieved by transforming the IMR images as a tensor, applying volumetric preprocessing, and segmentation algorithms like 3D KMeans clustering or 3D convolutional neural networks. In comparison with 2D slice by slice methods, 3D segmentation could minimize inconsistencies and produce more accurate results, but it requires more computational resources and careful parameter tuning. Using the F1 score to evaluate performance, 3D segmentation typically excels in segmenting large, continuous regions but may face challenges with small structures. It offers significant advantages for applications like volumetric brain analysis, though its computational demands may restrict its use in some scenarios.

References

Kragsterman, P. (2024, August 28). *The Ultimate Guide to Preprocessing Medical Images: Techniques, Tools, and Best Practices for Enhanced Diagnosis*. Collective Minds Radiology. Retrieved December 3, 2024, from <https://about.cmradiology.com/articles/the-ultimate-guide-to-preprocessing-medical-images-techniques-tools-and-best-practices-for-enhanced-diagnosis>

Schmid, S. (2023, August 15). *Image Intensity Normalization in Medical Imaging*. Image Intensity Normalization in Medical Imaging. <https://medium.com/@susanne.schmid/image-normalization-in-medical-imaging-f586c8526bd1>

Source Code:  kmeans_img_segmentation.ipynb