Corpus Callosum Segmentation Using CNNs

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1 Motivation and Dataset Selection

The segmentation of the corpus callosum in brain MRI images is crucial for neurological studies, particularly for analyzing structural differences in disorders such as autism. This project aims to develop an efficient Convolutional Neural Network (CNN) model for precise segmentation of the corpus callosum using publicly available MRI datasets.

The datasets used in this study include:

- **OASIS**: Contains brain MRI scans of healthy individuals.
- **ABIDE**: Includes MRI scans of individuals diagnosed with autism spectrum disorder (ASD).

Both datasets provide sagittal MRI slices, and the ground truth segmentation masks were used for training the model. Preprocessing steps included resizing images to 128×128 pixels, normalization, and data augmentation to enhance model generalization.

2 Segmentation as a Classification Problem

Image segmentation is a specialized case of classification, where each pixel in an image is assigned a class label. In binary segmentation, such as this project, each pixel is classified as either belonging to the corpus callosum (foreground) or not (background). This problem is closely related to semantic segmentation in computer vision, where models predict a class label for every pixel in an image [1].

3 Model Architecture

The segmentation model is based on an encoder-decoder architecture similar to U-Net [2]. The encoder extracts feature representations using convolutional and max-pooling layers, while the decoder reconstructs the segmentation mask using upsampling and convolutional layers. The final layer uses a sigmoid activation function to produce a probability map.

The layers in the model are as follows:

['conv2d_7', 'max_pooling2d_3', 'conv2d_8', 'max_pooling2d_4', 'conv2d_9', 'max_pooling2d_5', 'up_sampling2d_3', 'conv2d_10', 'up_sampling2d_4', 'conv2d_11', 'up_sampling2d_5', 'conv2d_12', 'conv2d_13']

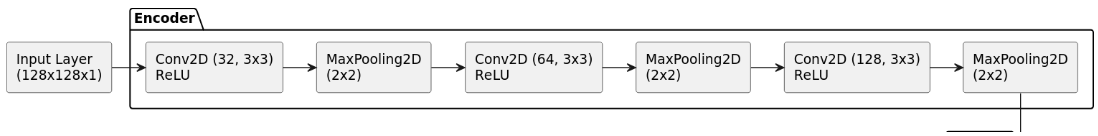

Figure 1: Encoder Structure

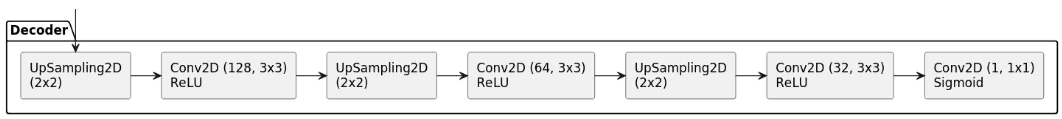

Figure 2: Decoder Structure

4 Training and Evaluation

The model was trained for 50 epochs using early stopping and model checkpointing. The dataset was split into training (70%), validation (15%), and test (15%) sets.

4.1 Accuracy

- **Training Accuracy**: 99.70%
- **Validation Accuracy**: 99.68%
- **Test Accuracy**: 99.83%

4.2 Custom Evaluation Metric: Weighted MSE and SSIM

To better evaluate the segmentation quality, a combined metric was used:

$$\text{Combined Metric} = (MSE \times \text{mse\_weight}) + ((1 - SSIM) \times \text{ssim\_weight})$$

Where:

- MSE was below 0.012 per image.
- SSIM was over 0.985 on average.
- The combined metric averaged below 0.008 per image.

4.3 Visual Results

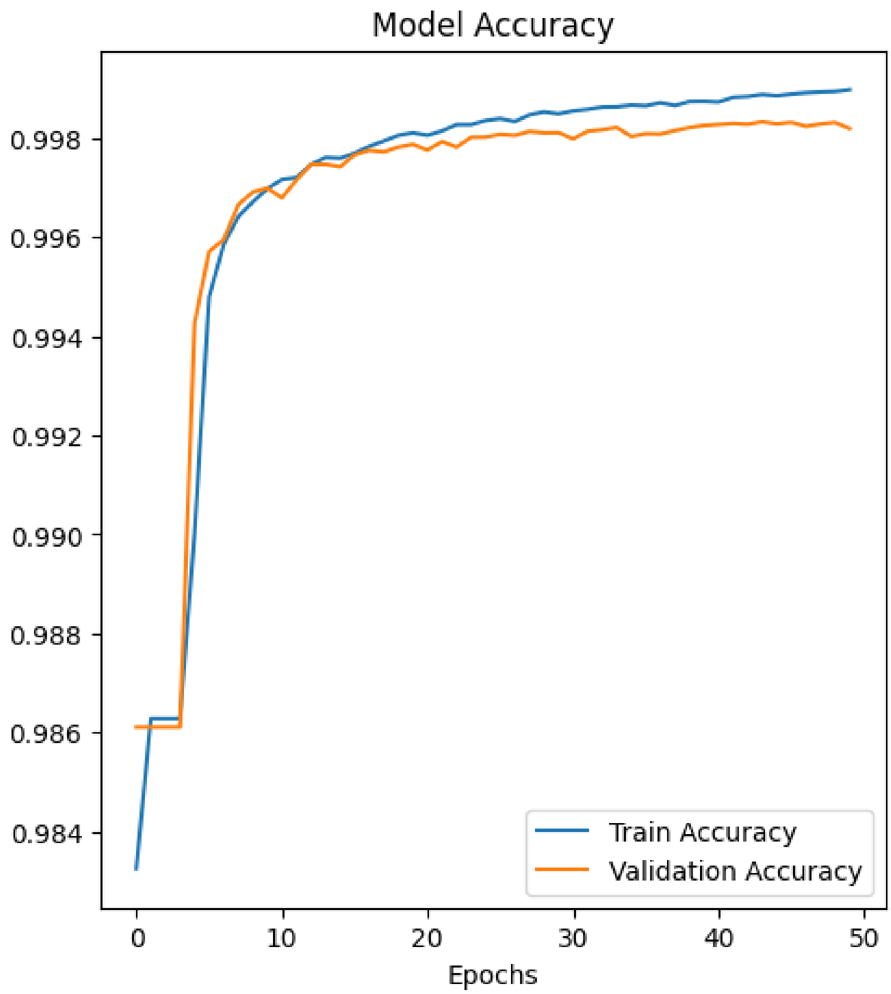

Figure 3: Training and Validation Accuracy

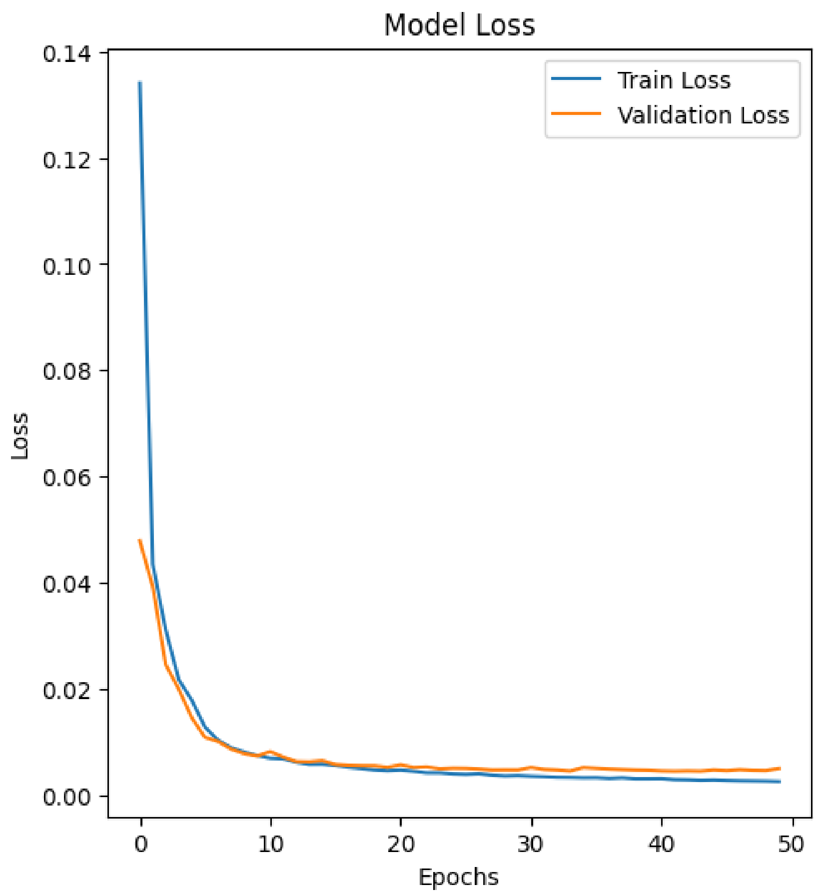

Figure 4: Training and Validation Loss

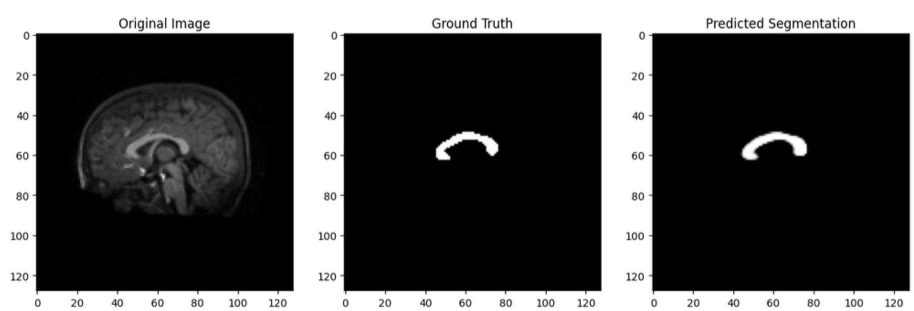

Figure 5: Predicted vs Ground Truth Segmentations

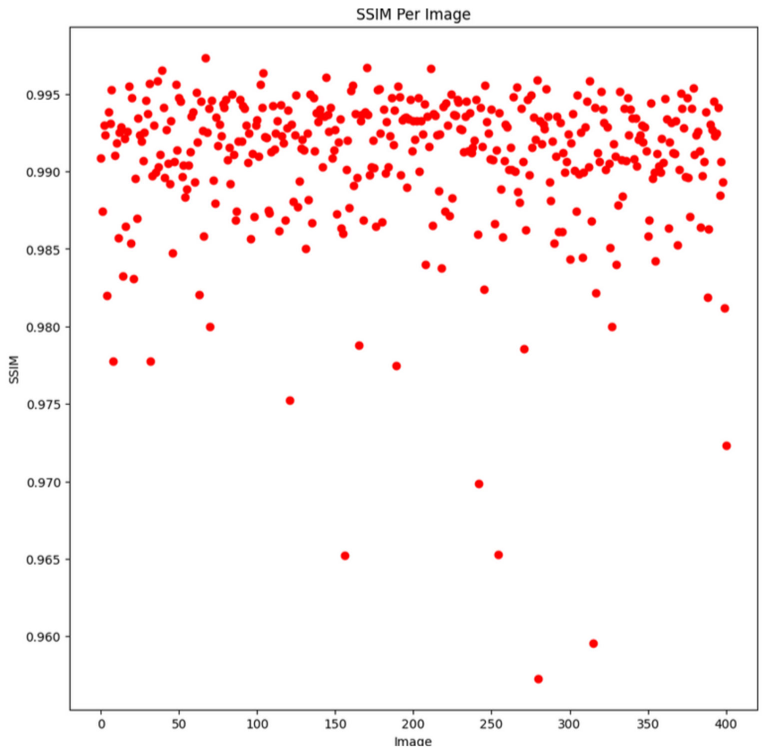

Figure 6: SSIM

5 Conclusion

The developed CNN model demonstrated excellent performance in segmenting the corpus callosum, with high accuracy and low error metrics. The combination of MSE and SSIM as an evaluation metric provided a robust assessment of segmentation quality. Future work includes fine-tuning the architecture and exploring alternative loss functions to further improve segmentation accuracy.

References

[1] J. Long, E. Shelhamer, and T. Darrell, "Fully convolutional networks for semantic segmentation," in *Proceedings of the IEEE conference on computer vision and pattern recognition*, 2015.

[2] O. Ronneberger, P. Fischer, and T. Brox, "U-Net: Convolutional networks for biomedical image segmentation," in *Medical Image Computing and Computer-Assisted Intervention*, 2015.

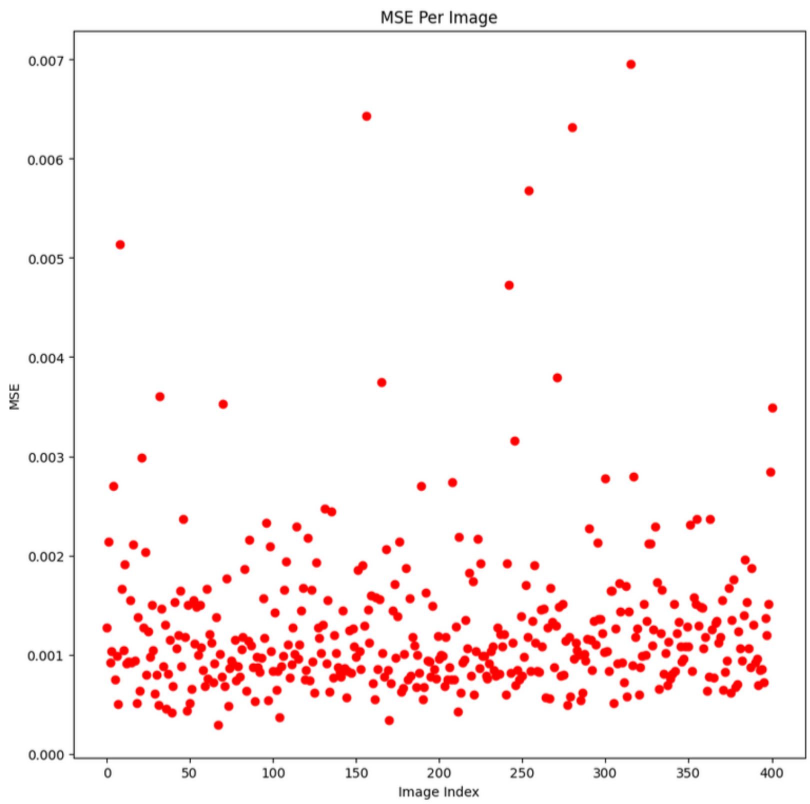
MSE Per Image
MSE
0.000
0.001
0.002
0.003
0.004
0.005
0.006
0.007
0
50
100
150
200
250
300
350
400
Image Index

Figure 7: MSE

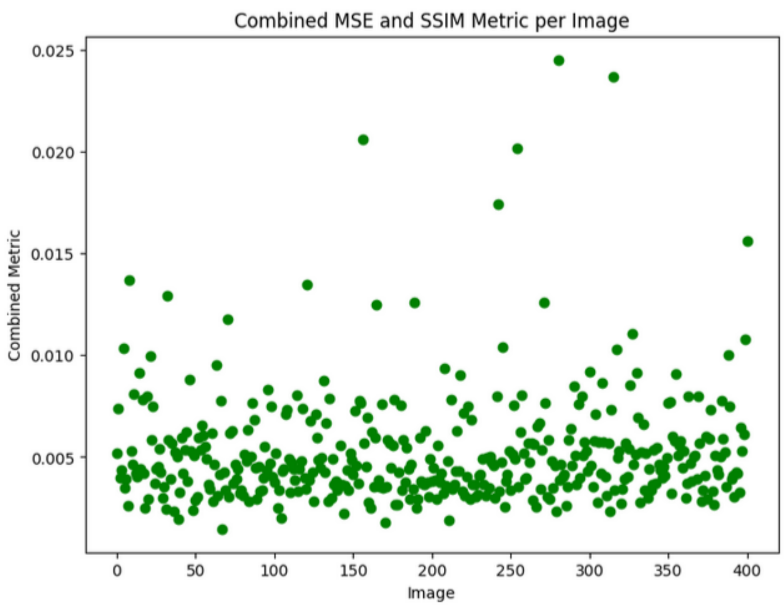

Figure 8: Combined metric

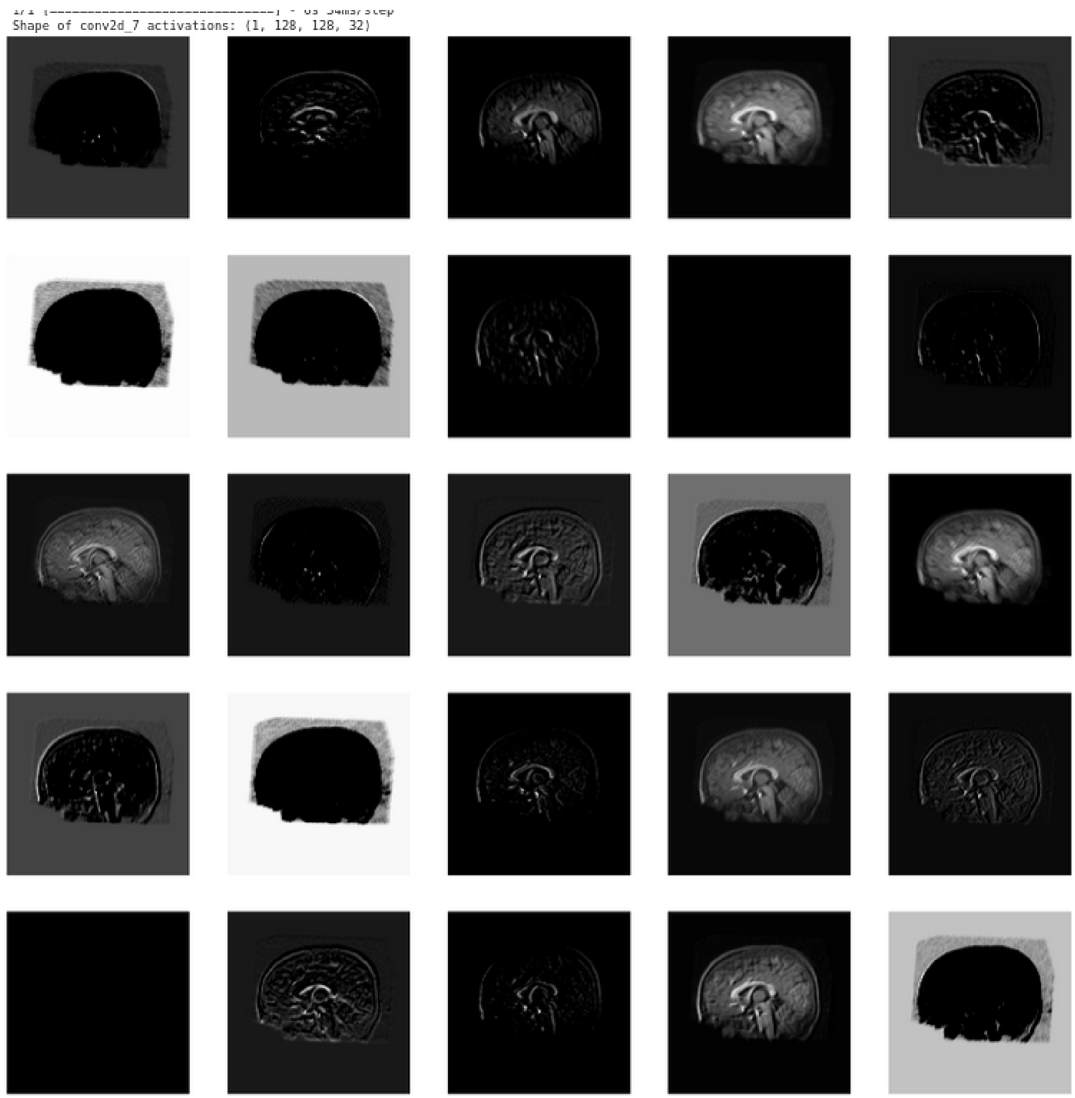

Figure 9: Activation Maps of a Convolutional Layer