Training a model to classify Alzheimer's disease using PET scans.

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February 2024

Abstract

In this project, we're collaborating to implement and train a deep learning model for classifying Alzheimer's disease using PET scans. Alzheimer's, a progressive neurodegenerative disorder, presents diagnostic challenges, but PET imaging provides crucial insights. Our focus is on leveraging deep learning techniques to enhance classification accuracy. We're tasked with refining a baseline model and evaluating its performance against our custom model. Please see figure 1 for an extract of this datasets PET scans.

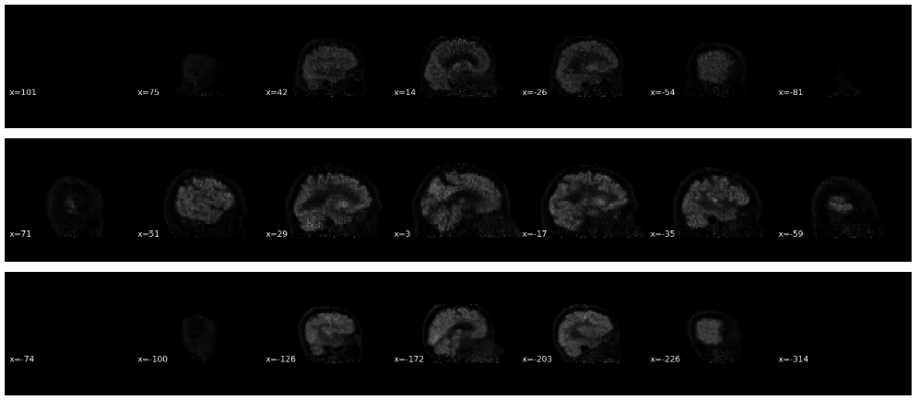

Figure 1: Example of PET scans.

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1 Pre-Processing

PET scans often exhibit variations in size, brightness, and contain irrelevant information, such as the skull, which can complicate the analysis process. Software packages like Statistical Parametric Mapping (SPM) and tools like MATLAB offer robust solutions for preprocessing PET scans. Through SPM's image processing capabilities, various preprocessing techniques can be employed. These may include image registration to align scans, intensity normalization to mitigate brightness differences, and segmentation to isolate relevant brain regions while removing extraneous structures like the skull. By incorporating these preprocessing steps, the quality and consistency of PET scan data will be improved for the model, resulting in more accurate classification of Alzheimer's disease.

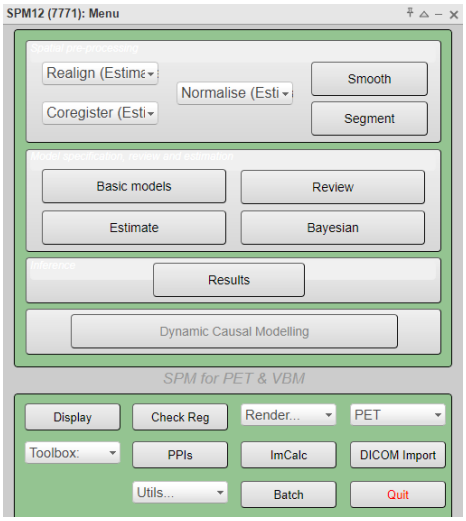

Figure 2: Overview of the SPM menu.

1.1 Importing dicom images

PET scans typically arrive as DICOM files, comprising individual slices that must be compiled into a 3D NIfTI file for analysis. This transformation was executed using SPM, which assists in assembling the slices.

1.2 Setting the Image origin

3 After converting the DICOM files to NIfTI format, it's essential to establish the image origin, crucial for subsequent plotting and preprocessing. This was achieved by centering the image around the anterior commissure of the brain, ensuring accurate analysis and interpretation. Please refer to Figure 3 For the reoriented Image.

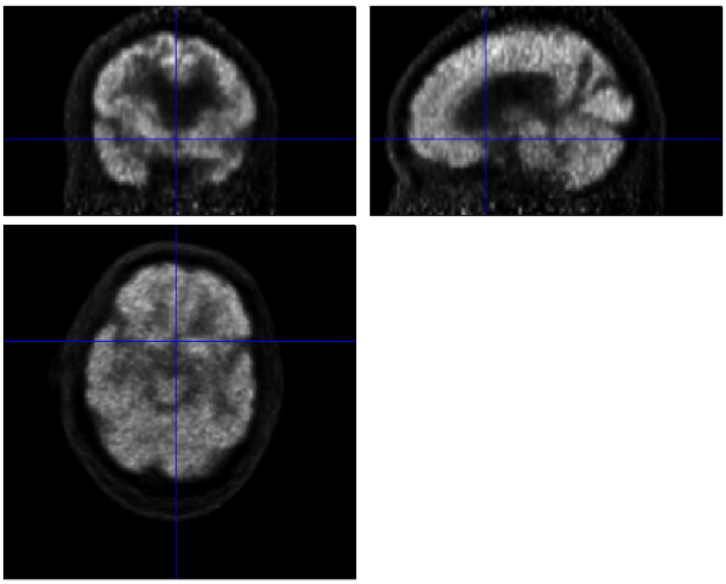

Figure 3: Overview of the reoriented Image.

1.3 Brightness Normalization

To ensure even signal strength for all images, I normalized their brightness using the "Normalise (Est & Wri)" function in SPM. I clicked on the drop-down menu "Normalise" and selected "Normalise (Est & Wri)." Then, in the new window, I clicked on "Data ¡-X" and set the image to align and the image to write to the NIfTI file where I had set the origin. Finally, I clicked the green triangle in the taskbar to start the normalization process, see Figure 4 for the process window.

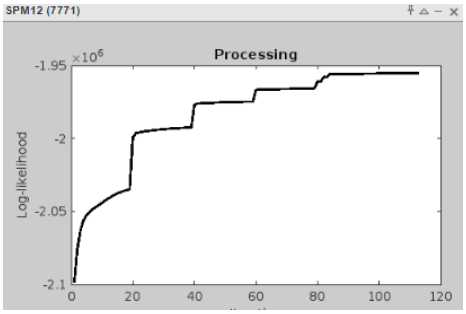

Figure 4: Normalization processing window.

1.4 Segementation: Keeping the Brain

Following image normalization, I conducted segmentation to isolate the brain, the critical component. Segmentation of the brain is vital as it allows for the removal of non-brain tissues such as the skull and scalp, thereby focusing the analysis specifically on the brain region of interest. This was done correctly, as seen by comparing the processed, Figure 6, and the original, Figure 4.

1.5 Final image calculation

The last preprocessing step using SPM is to combine them into a final single nifti file. This is done by selecting the w, c1-c3 files as input files and typing in the expression $i1. * ((i2 + i3 + i4) > 0.5)$, as seen in figure 5

After all of the preprocessing steps above, the final image was plotted, which turned out positively much better than the original image, please see figure 6 for the final result.

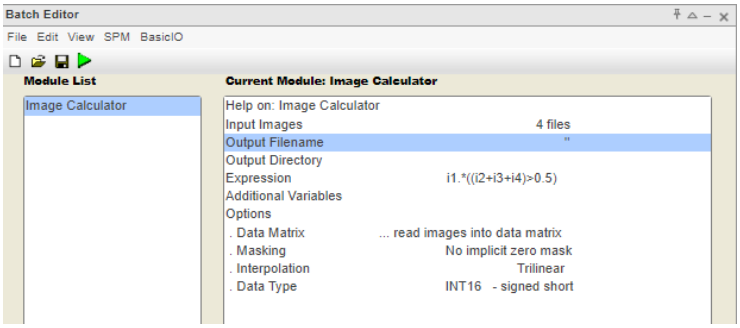

Figure 5: Overview of final step

Figure 6: My final preprocessed image.

2 Model-Building

Upon initial training attempts on the entire dataset without employing k-fold cross-validation, the model exhibited immediate signs of overfitting. Consequently, I opted to incorporate k-fold training to address this issue effectively.

Through experimentation, I determined that a learning rate of 0.005, coupled with a batch size of 64, yielded optimal results. Additionally, to enhance the model's complexity, I introduced a dropout layer between the two dense layers and expanded the network architecture to include three convolutional blocks instead of two. These blocks comprised 16, 32, and 64 filters, a notable increase compared to the previous configuration of 4 filters in each block. Notably, I observed that the Adam optimizer outperformed Stochastic Gradient Descent (SGD) in terms of training efficacy. For both models, I selected the "binary_crossentropy" loss function, given the binary nature of the classification task. Moreover, I augmented the sizes of the dense layers from 32 and 16 to 128 and 64, respectively, to accommodate the heightened complexity of the network. Finally, the best AUC epochs weights are also saved, making sure the best one is used. A comparison of these hyperparameters is summarized in Table 2.

	Epochs	LR	BatchSize	Optimizer
Baseline:	50	0.01	20	SGD
Custom:	300	0.005	64	Adam

Table 1: The Hyperparameters Baseline model and the Custom model.

3 Results

As depicted in Table 1, the baseline method exhibited a rather basic performance, characterized by an average AUC of approximately 0.69 and a standard deviation of 0.05. In contrast, the Custom model showcased superior outcomes across the board.

	Fold 1	Fold 2	Fold 3	Fold 4	Fold 5	μ	σ
Baseline AUC:	0.4816	0.7532	0.9083	0.7756	0.7246	0.7286	0.1386
Custom AUC:	0.9215	0.9211	0.9527	0.8662	0.9231	0.9169	0.0280

Table 2: A table containing the results of the diverse kfolds, the mean, and the standard deviation for both the Baseline and Custom models AUC

4 Visualization

4.1 Filters

When plotting the filters for each layer, i found somehing interesting. When plotting the filters of the first convulutional layer, it is seen that they focus on different parts of the brain, as expected, however there are some of the filters that are mostly black, implying that the patterns they are designed to detect were not present. The other filters show various levels of activation with different

patterns and intensities, which indicates that they are responding to different features in the image. The plots of the diverse layers are in the notebook, due to the reports page restriction.

4.2 SHAP

In the SHAP plot (Figure 7), a detailed look shows that the central and left parts of the brain have the biggest impact on whether someone has Alzheimer's disease, as observed from the perspective depicted in Figure 7. This is clear from the colors in the Figure – there's lots of red and blue, which means strong connections in different directions across many cases. These findings suggest that these areas of the brain play a crucial role in Alzheimer's, giving us clues for further study and potential treatments.

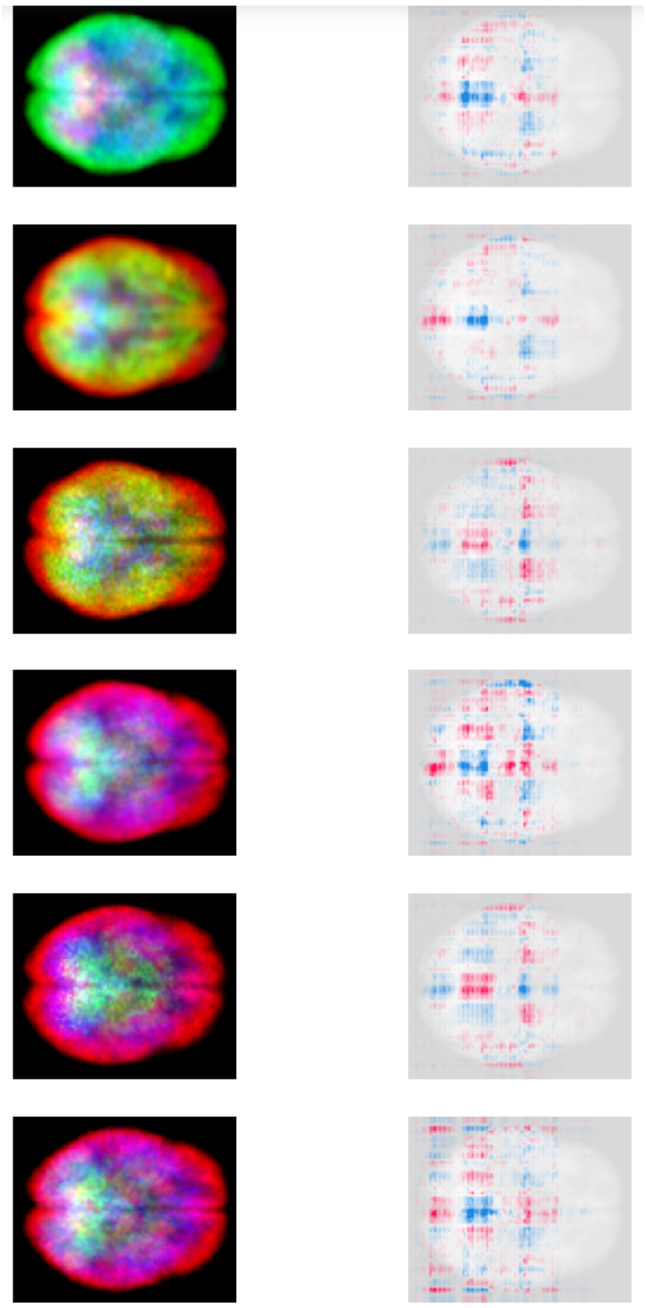

Figure 7: SHAP Plots for six samples, indicating what the model has learned.