BMENE4460 - Deep Learning in Biomedical Imaging
Project Proposal

Applying deep learning models to structural MRI for stage prediction of Alzheimer's disease

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I. Introduction

Alzheimer's disease is a progressive disease that is usually noticed when a person's memory and thinking skills worsen, eventually affecting their performance on daily activities over time [1]. It is the leading cause of dementia, and in 2020, an estimate of 5.8 millions of Americans were suffering from Alzheimer's disease [1]. In 1906, German neurologist and psychiatrist Alois Alzheimer discovered in one its late patient's brain what are today considered the main physiological features of the disease: abnormal clumps (amyloid plaques) and tangled bundles of fibers (tau or tangles) [2]. Before imaging was available, such physiological features could not be obtained in vivo, and the disease was diagnosed only through clinical symptoms, and confirmed through an autopsy. Thankfully, advances in lab and imaging tests made biomarkers available for clinicians to diagnose Alzheimer's, such as CSF levels of Ab42 and Tau proteins [3]. There have been several studies around the development of imaging biomarkers for Alzheimer's disease [4]. In this project, we would like to use deep learning and CNNs applied to brain MRI in order to assess Alzheimer's disease.

II. Previous work review and proposed approach

We intend to implement and possibly extend the work of Yiğit, A., & Işık, Z. in their paper "Applying deep learning models to structural MRI for stage prediction of Alzheimer's disease" [4]. The authors used two different datasets for training (Open Access Series of Imaging Studies, OASIS) and testing (Minimal Interval Resonance Imaging in Alzheimer's Disease, MIRIAD). Both contain three dimensional T1-weighted MRI records of patients, along with sex, age and Mini Mental State Examination (MMSE) scores. We will only use a subset of the OASIS dataset in our approach, and the balance between Alzheimer's patient, MCI patients and healthy controls will be detailed in the data augmentation paragraph.
These images first go through a preprocessing pipeline, that we will modify:

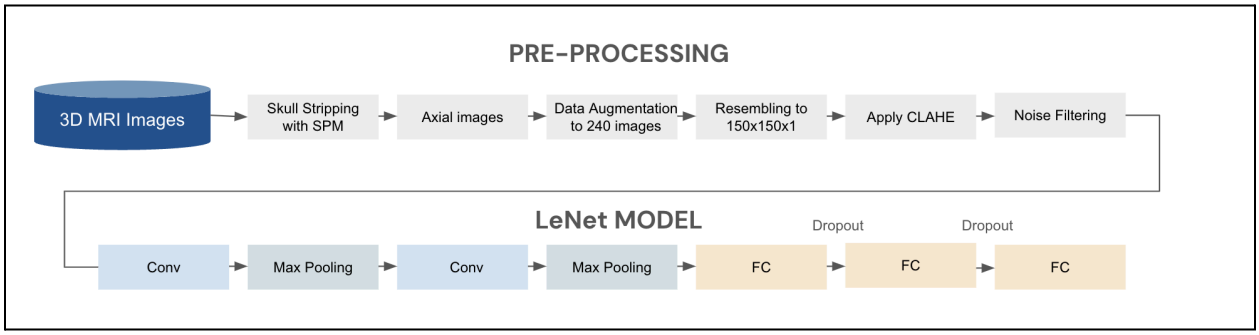
- *Skull stripping:* The MRI images are first being processed with brain extraction tools. The original paper used BET, but we decided to use the software SPM instead, as it

has been shown that the qualitative evaluation of the brain segmentation using Dice and Jaccard metrics shows SPM8 performs better [5].

- *Bypassing slice selection:* In the original paper [4], authors decided to select ten slices in axial, sagittal, and coronal projections for each patient, choosing a specific part of the brain. Since we lack the time to do so, we decided to use the only 10 axial slices of each patient's volumetric data.
- *Data augmentation:* The OASIS dataset is limited in size and presents class imbalance between Alzeigmer patients, MCI and healthy subjects. We will be using data augmentation techniques to increase each of these classes to 80 instances each. The previous paper augmented it to 380 images for each class, which resulted in computation times up to 40 hours, which is too high for this project. The dataset size must be a trade off between accuracy and computational efficiency.
- *Resampling, CLAHE, Noise filtering:* As in [4], we will resample our image using bicubic interpolation on a 4x4 interpolation to be 150×150 pixels, and apply contrast transformation using CLAHE (Contrast limited adaptive histogram equalization). Finally, we will filter out potential noise in our image. We will determine through trial and error whether to use Gaussian filtering as in [4] or another method (median filtering, morphological operations, etc.)

After being put through this pipeline, our images will be ready to be used as input for our model. We will train two models, derived from the LeNet architecture [6] :

- Model 2 from [4], as is: two convolutional layers, two pooling layers that output a 100 features into three fully connected layers. It has 1,311,697 parameters.
- Our own model, derived from the previous one with improvements of our own. Through trial and error, we will tweak the learning rate, dropout out rates, convolutional filter size, feature map size and other parameters to improve from the results of the first model. We will also add BatchNorm to the convolutional layers.



Workflow of our proposed approach

We will use the same loss as [4] for training, which is binary cross-entropy, for the training. Then we will use different metrics (AUC, accuracy, specificity and sensitivity) to compare the performance of the two models.

III. References

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