University of Utah
UNDERGRADUATE RESEARCH JOURNAL

SIMULTANEOUS MULTI SLICE AND ITS APPLICATIONS TO AGE PREDICTION IN DIFFUSION MRI

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I. Introduction

Brain age predictions are an important tool in predicting health and potential diseases such as Alzheimer's or HIV [1]. People with diseases will have abnormal (older) age predictions than their true age [2]. Brain age is characterized by size changes to cerebrospinal fluid (CSF) and gray matter, as well as microstructural changes to white matter [3]. Currently the biggest issues in age prediction are the lack of a method of determining healthy ages, and the slow scan times required for high resolution images. The best current approaches use T1 weighted MRI images and 3D convolutional neural networks (CNN) to predict age using changes in CSF and gray matter size. Diffusion MRI using 3D CNNs may provide better predictions because it can characterize microstructure in white matter in addition to the size changes in CSF and gray matter [3]. Simultaneous multi slice (SMS) methods combined with a separate previously trained network for model fitting allow for significant reductions in processing and scan times [4]. SMS gathers data from multiple slices simultaneously, thus heavily decreasing scanning time. These slices are combined together and need to be dealiased in the reconstruction process. Many techniques exist for SMS reconstruction, however the main goal is to separate the images using the coil sensitivities. Coils closer to a specific slice will have higher sensitivities and more information about that slice is gathered from that coil. Once the data is dealiased, a small set of 60 diffusion directions are selected for preprocessing. These 60 pre processed directions can then be fed into the network described in [4] to obtain finalized parameter maps. The use of 3D CNNS with diffusion parameter maps created by the network will allow significant reductions in scan and processing time, and potentially more accurate age predictions.

II. Materials and Methods

We used publicly available data from the Human Connectome Project in Aging (HCPA) which uses multi-shell q space imaging to provide diffusion-weighted images [5,6]. The data was gathered using SMS multiband 4 which a significantly speeds up scan times. We used 204 healthy female subjects aged between 36 to 78 years and uniformly split into testing and training sets (training/testing: 140/66). 60 diffusion directions were selected randomly for preprocessing and then fed into the previously trained network to produce 11 parameter maps of each subject (Figure 1) [4]. This network allowed for significant reduction in scan and model fitting times. The 11 parameters came from 3 diffusion models, DTI, DKI, and NODDI.

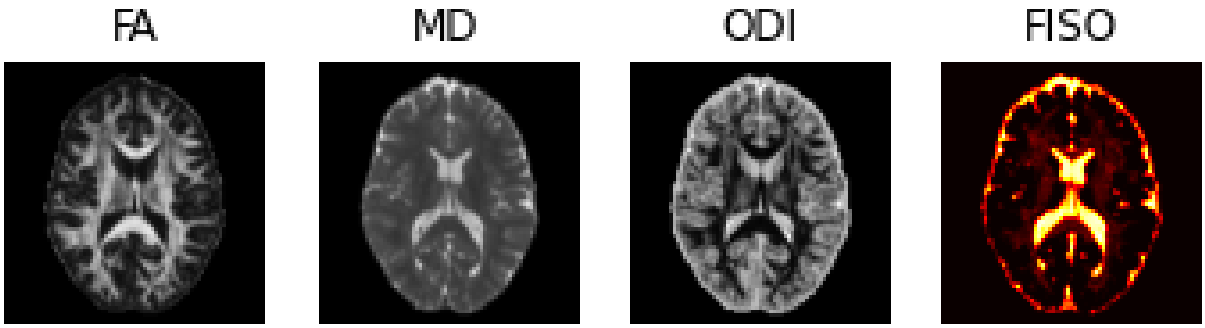

Figure 1 – Example of a slice of parameter maps created by a previously trained network on a random test subject

For age prediction, we used a 3D CNN implemented with PyTorch (Figure 2). The CNN contained 7 convolutional blocks, containing two sets of a convolutional layer and ReLU activation followed by batch normalization and a max-pooling of 2x2x2. The convolutional blocks were followed by two fully connected layers. The final layer outputs two values that were mapped to a unit semicircle to normalize age differences and reduce network bias in predicting a small range of ages. That value is then converted to a final age estimation. The network was trained separately on each diffusion parameter map.

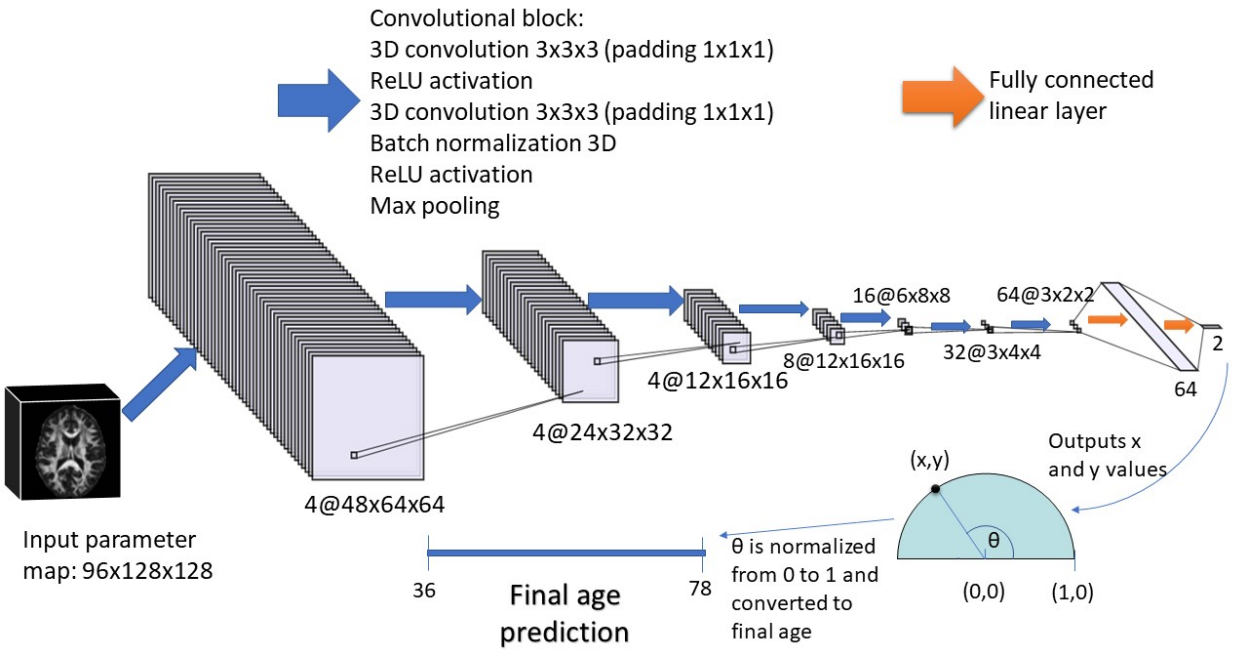

Figure 2 – Network architecture and mapping from semicircle

III. Results and Discussion

Our network could distinguish the age of the testing set with a mean absolute error (MAE) of 5-10 years based on which of the 11 parameters were trained. The best parameters were the ones like mean diffusivity or the isotropic volume fraction, which are related to CSF size. Parameters like orientation dispersion index or fractional anisotropy which are based on white matter

microstructure also worked, but less well (Figure 3). These results are comparable to many of the current best methods reported for diffusion or T1 imaging [2]. Parameters related to radial diffusion predicted age poorly.

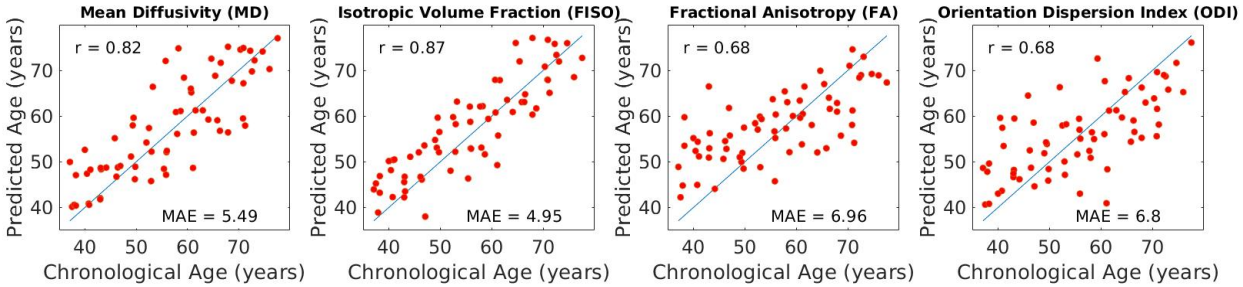

Figure 3- Predicted vs chronological age of test subjects and their MAE and Pearson correlations

IV. Conclusions

By using a 3D CNN with diffusion imaging, we were able to predict age with similar accuracy to T1 studies with much larger datasets. Diffusion imaging has the potential to accurately predict age for clinical uses. The use of SMS and a separate network for estimating parameter maps allowed for significant reductions in scan and processing time. Fast and accurate age estimations are necessary for imaging to predict age related health outcomes. Future diffusion MRI studies combining multiple parameter maps could predict age with greater accuracy by simultaneously looking at CSF, gray matter, and white matter.

V. Acknowledgements

Data used in the preparation of this abstract were obtained from the National Institute of Mental Health (NIMH) Data Archive (NDA). Dataset identifier(s): 10.15154/1522592.

VI. References

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