Predicting Age of Children and Adolescents with T1 Images in a Convolutional Neural Network

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Abstract

Brain age can be used as a biomarker to monitor brain development and aid in the diagnosis of psycho- and neuro-pathological disorders. Deep learning models have been effective in measuring brain age given a T1-weighted scan, though a lot of this research has been primarily conducted on adults. This research aims to create a convolutional neural network that can predict the brain age of a child or adolescent given a T1-weighted neuroimage. The model was trained on a dataset containing 650 children and adolescents between the ages of 5 and 21 years from the Human Connectome Project Development. The convolutional neural network was able to achieve a validation mean absolute error of 2.03 ± 0.13 and an R^2 value of 0.61 ± 0.04. This data suggests the model was moderately successful in brain age prediction, and there is potential for the model to improve by increasing the dataset size with data augmentation.

Keywords: brain age prediction, neuroimaging, convolutional neural networks, deep learning, childhood neurodevelopment

Introduction

Deep learning models, such as convolutional neural networks, are being implemented in medical imaging to help aid in a range of topics such as disease classification and lesion detection (Ker et al., 2017). In neuroimaging, these models have been used to monitor brain development using a metric called "brain age," a biomarker of brain health that assesses the age a person should be given the state of their brain's development (Franke and Gaser, 2019). This metric has been very useful in predicting diseases such as dementia and Alzheimer's (Biondo et al. 2022, Millar et al. 2023).

A lot of brain age prediction models have been focused on adults, but there is a growing body of research around neurodevelopmental abnormalities associated with mental illness starting in childhood (Shaw et al. 2010). Delays in neurodevelopment could indicate disorders such as ADHD, and tracking brain development could be beneficial in diagnosis (Kakuszi et al. 2020). Findings such as these could suggest that brain age could be used as a biomarker to monitor childhood development for signs of psychopathology. However, accurate models need to be developed and tested with typically developing children's brains before moving forward with atypical development.

Some deep learning models involving children's brains have already been created. For example, Hu et al. (2021) created a dimensional-attention-based 3D convolutional neural network to predict subjects (n = 808) aged 6 to 18 and achieved a mean absolute error of 1.01 ± 0.05 years and an R^2 value of 0.73 ± 0.04. The number of parameters the model utilized was 16.8 million, making predictions computationally heavy compared to simpler models. Another study by Mendes et al. (2021) used voxel-based morphometry to preprocess gray and white matter to train a deep-learning model to predict the ages of children between the ages of 6 and 20 years.

Not all the children from this dataset were typically developing, with about 40% of the subjects having autism spectrum disorder or attention-deficit disorder. Despite this, the model was able to achieve a mean absolute error of 1.43 ± 0.22 years. While both of these models achieved a fairly high success rate, they implemented computationally expensive models, which may not be as applicable in practice.

This project aims to create a convolutional neural network that can accurately predict age given a minimally processed T1-weighted MRI scan of a child or adolescent's brain. To decrease computational resources, the model will be implemented to be parameter-efficient. The Human Connectome Development Project will be used to train and evaluate the model's performance between the age ranges of 5 and 21 years.

Methods

T1-weighted images from the Human Connectome Project -- Development were used in this model (n = 652), with two subjects being excluded for missing MRI data. This dataset collected MRI data from typically developing children and adolescents between the ages of 5 – 21 on a Siemens 3T Prisma.

Preprocessing was mostly conducted by the Human Connectome Project, where each T1 image was aligned to an MNI152 template. Outside of the Human Connectome Project, skull stripping was conducted using FSL, and the dimensions of the image were reduced from (227, 272, 227) to (113, 136, 113).

A simple architecture was implemented for the convolutional neural network to reduce the memory requirements. The model consists of five blocks, each containing a 3D convolutional layer with a 3 x 3 x 3 kernel size, a ReLU activation, and a varying filter size (64-128-256-512-128), each followed by a batch normalization layer and a 2 x 2 x 2 3D max pooling layer. The

last block contains a global average pooling layer, a dropout layer with a 30% dropout rate, and a fully connected dense layer with linear activation. The output consists of an age estimate in years given a T1 image.

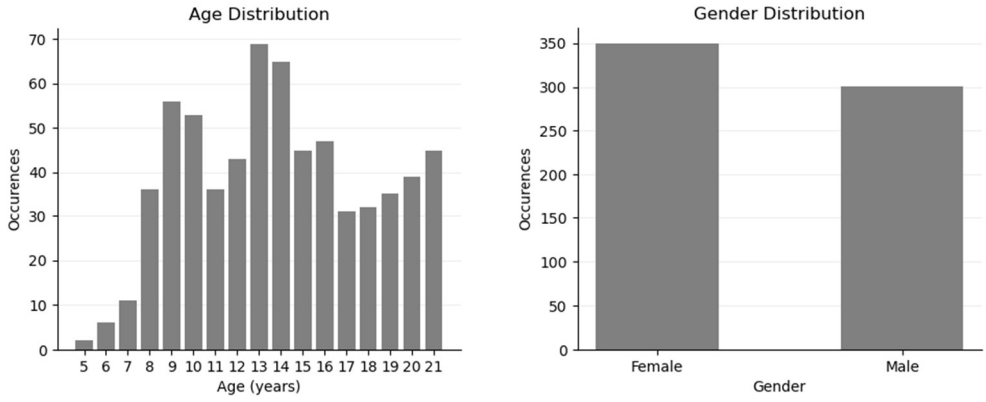
The model was compiled using mean squared error as a loss function, an Adam optimizer, and a learning rate of 0.000001. Training occurred over 25 epochs on an A100 GPU with mean absolute error and R^2 values collected. Due to the small sample size, only a training set and a validation set were used when training the model. The data was split so that 80% of the data was used toward training, while the other 20% was used for validation. In total, there are 6,421,633 parameters in this network.

Results

Information about the Human Connectome Project Development dataset is displayed in Figure 1. In total, 521 subjects were used in the training set, with the remainder being included in the validation set. Due to the small sample size, the test set was omitted, and this study used the validation set for hyperparameter tuning.

Figure 1

Age and Gender Distribution in Human Connectome Project Cohort

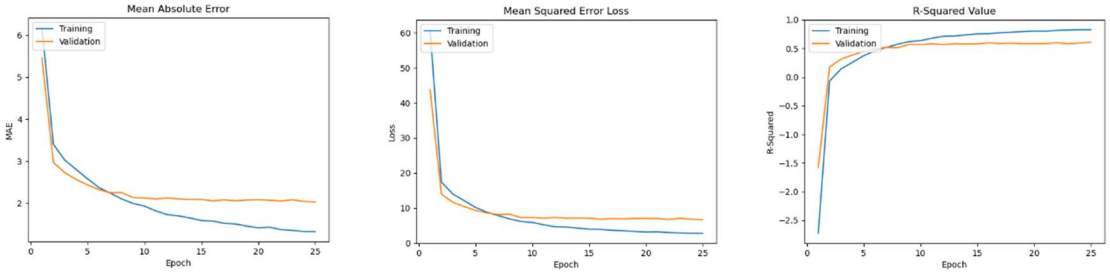


Note. These graphs show the distribution of gender and age in the subjects used in this study. The dataset is unbalanced regarding age, where ages 5-7 are grossly under-represented compared to the rest of the cohort.

Grid search and trial-and-error methods were used for hyperparameter tuning of the dataset. A random seed was not used, so ten trials of each run were conducted to ensure reliability. Epochs were gradually increased until a plateau was reached in the validation set, which would end up being between 20 to 25 epochs per run. Figure 2 shows the training and validation performance averaged over 10 trials and 25 epochs with the mean absolute error, the mean squared error, and the R^2 value. The figure also displays a table of the results of all the metrics in five epoch intervals for both the training and validation set.

Figure 2

Metrics for evaluating the efficacy of the convolutional neural network



Epoch	Train Loss	Train MAE	Train R^2	Validation Loss	Validation MAE	Validation R^2
5	10.22 ± 0.88	2.55 ± 0.12	0.38 ± 0.05	9.38 ± 0.83	2.43 ± 0.11	0.44 ± 0.05
10	5.93 ± 0.52	1.93 ± 0.10	0.64 ± 0.03	7.35 ± 0.73	2.12 ± 0.14	0.57 ± 0.04
15	4.02 ± 0.28	1.58 ± 0.06	0.75 ± 0.02	7.13 ± 0.97	2.09 ± 0.15	0.58 ± 0.06
20	3.21 ± 0.19	1.41 ± 0.05	0.80 ± 0.01	7.04 ± 0.76	2.08 ± 0.12	0.59 ± 0.04
25	2.84 ± 0.26	1.32 ± 0.05	0.83 ± 0.02	6.68 ± 0.68	2.03 ± 0.13	0.61 ± 0.04

Note. The standard deviation for each metric is included in the table to better understand the distribution across all ten trials.

Discussion

The convolutional neural network model aimed to accurately identify the ages of children and adolescents between the ages of 5 and 21. This model achieved moderate success, with the R^2 value in the final epoch reaching a value of 0.61 ± 0.04 and the mean absolute error reaching 2.03 ± 0.13. While these results are not remarkable, they could indicate that the model could make more accurate predictions given some changes to the design.

In comparison to a study by Peng et al. (2021), which used a similar lightweight deep neural architecture with a similar range of ages, the mean absolute error for the validation set was around the same value as this study. The mean absolute error for the study was 2.73 ± 0.03 compared to 2.03 ± 0.13. However, Peng et al. (2021) had a larger dataset (n = 14,503), which gave more strength to their results.

A study by Hong et al. (2020) created a convolutional neural network to predict brain age with a smaller dataset (n = 220), but used data augmentation to increase the size of their training set. Their model had an age range of 0 through 5 years, but their prediction labeled how many days old the subject was. This model was able to achieve an R^2 value of 0.971, suggesting that data augmentation may prove beneficial.

There are several limitations to this project. As stated earlier, the sample size is relatively small compared to other deep-learning models, and the dataset is unbalanced. There were limited data samples for children within the range of 5 through 7, and the model may be improved by omitting this age range. Additionally, while extensive psychological testing is conducted on the subjects, there is a certain level of uncertainty regarding whether the children in the Human

Connectome Project will go on to develop psycho- or neuro-pathology. If so, then some subjects in the dataset may not be "typically developing," and should not be included in the model.

Future directions to this research could be using data augmentation to increase the sample size to see if the metrics could be improved. This dataset could also be used in conjunction with other datasets containing younger age ranges to create a more balanced sample. Seeing as the results of the model are heading in a positive direction, implementing these changes along with more hyper-parameter tuning may improve the overall efficacy of the model. As the model currently stands, the predictions are not reliable enough to conclusively determine brain age throughout childhood development.

Conclusion

Brain age could be a useful predictor in childhood brain development as evidenced by the growing body of research suggesting delays in brain maturation could be indicative of pathology. More models with a younger age range need to be trained before research into using this as a biomarker can be implemented. This project created a convolutional neural network that achieved moderate success in identifying the brain age of a participant between the ages of 5 and 21. Based on the mean absolute error and the R^2 value, the network does not perform at the level of other machine-learning prediction models. However, training the model with an augmented dataset would increase the sample size and may improve the overall performance of the model at the expense of a higher computational load.

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