

Introduction

From childhood to adult, the functionality of the human brain undergoes progressive changes. EEG records the electrical activity of brain cells in real time, which is a planar map that records the correlation between potential and time. For people of different ages, the EEG is most likely to contain features that characterize the level of brain maturation. Studies have shown that the difference between a person's true age and brain maturation level leads to better characterization of genetic factors associated with brain aging [1], and this difference, we call the **BrainAge Index (BAI)**. It can be used to reflect the extent to which the brain deviates from normal developmental levels. In this course project, we found a resting EEG dataset in the OpenNeuro database containing **111 healthy individuals resting with eyes closed for 4 min**. Based on this dataset we built a deep learning model for BA prediction, which contains four layers and can better extract the spatiotemporal features of EEG. We used K-Fold Cross Validation for training and obtained **a mean error of 8.7 years** between BA and true age.

Dataset

This EEG dataset contains resting-state EEG extracted from the experimental paradigm used in the Stimulus-Selective Response Modulation (SRM) project at the Dept. of Psychology, University of Oslo, Norway.

The data is recorded with a BioSemi ActiveTwo system, using 64 electrodes following the positional scheme of the extended 10-20 system (10-10). Each datafile comprises four minutes of uninterrupted EEG acquired while the subjects were resting with their eyes closed. The dataset includes EEG from 111 healthy control subjects (the "t1" session), of which a number underwent an additional EEG recording at a later date (the "t2" session). In this project, we selected all EEGs from the "t1" time period and pre-processed them.

Methods

Data preprocessing

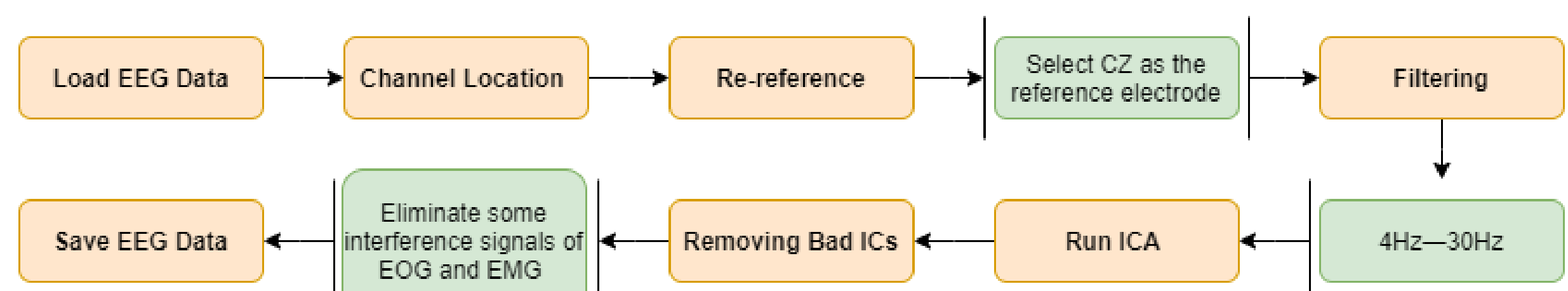


Figure 1: Data preprocessing flow chart

1. Load EEG Data: Import the raw data.
2. Channel Location: Information about the locations of the recording electrodes is required to plot EEG scalp maps and to estimate source positions for data components.
3. Re-reference: Select CZ as the reference electrode.
4. Filtering: EEG data was band-pass filtered between 4 and 30Hz.
5. Run ICA: Run Independent Component Analysis(ICA).
6. Removing Bad ICs: Eliminate some interference signals of EOG and EMG.
7. Save EEG Data: Save the preprocessing data.

Model - BAPM

Brain Age Prediction Model (BAPM) (Figure 2) is a model composed of four layers, namely:

1. **StCNN (Short-term temporal convolutional layer)**: a 1-dimensional convolutional layer which aggregates groups of timestamps along the time dimension. It aims to extract short-term patterns from the preprocessed EEG signals. Meanwhile, the layer effectively reduces the data size during the training process.
2. **Spatial Attention Layer**: This layer includes a multi-head GaAN (Gated Attention Network) module which aggregates information among the channels (electrodes) using a pre-calculated graph (using Pearson Correlation Coefficient).
3. **Temporal Layer**: This layer is simply a GRU to run through all the reduced "timestamps" and aggregate the temporal features. The output will be a fully aggregated spatial-temporal embedding feature tensor.
4. **Transfer Layer**: This layer uses two fully-connected sub-layers (and ReLU as the activation function) to first aggregate the information along the channel dimension, then aggregate the features along the feature dimension. The final output will be the prediction age value.

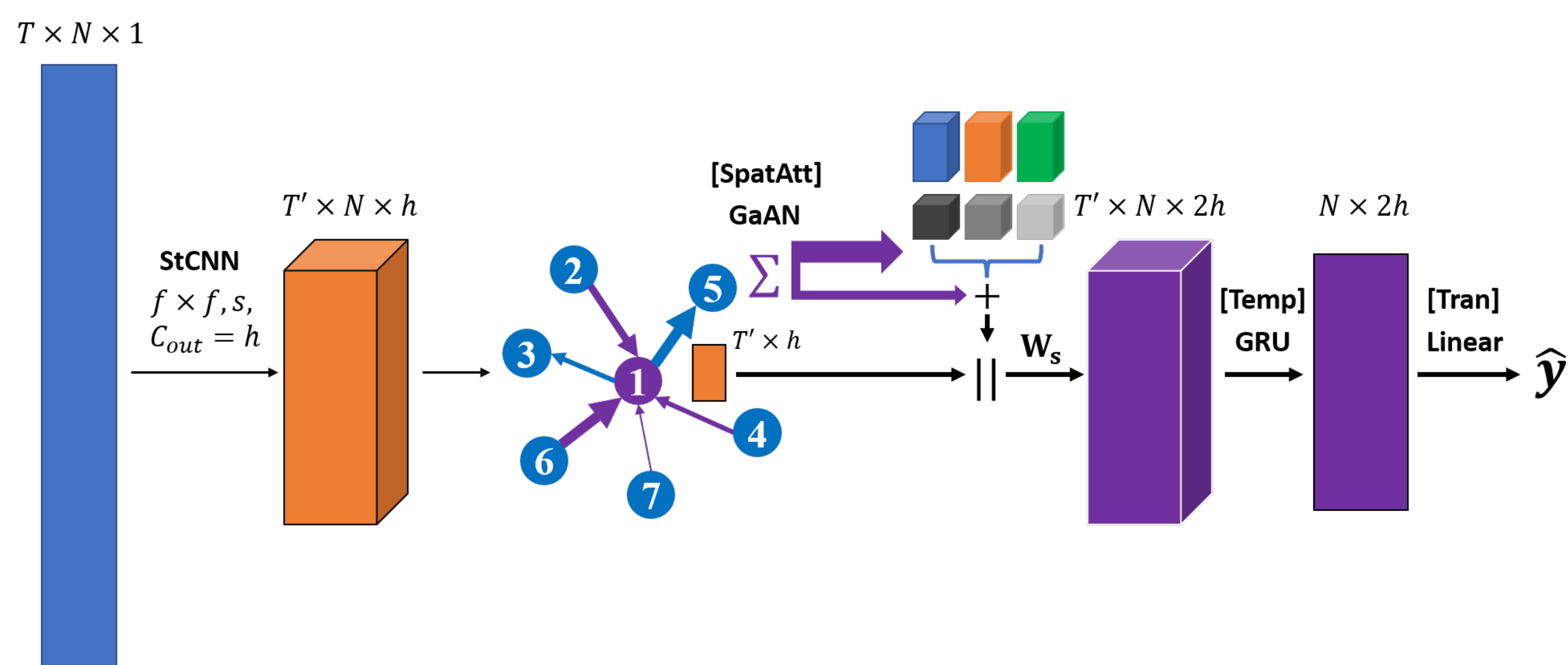


Figure 2: Model structure of BAPM (from left to right): 1. Input (blue rectangle) 2. StCNN (Short-term CNN) 3. Short-term features (orange block) 4. Spatial Attention Layer (multi-head GaAN) 5. Spatial features (purple block) 6. Temporal Layer (GRU) 7. Spatial-temporal features (purple rectangle) 8. Output \hat{y}

Experiment

Settings

For metrics, we use MAE (Mean Absolute Error), RMSE (Rooted Mean Squared Error) and MAPE (Mean Absolute Percentage Error) to evaluate the model performance. The preprocessed EEG data contains 245760 timestamps (240s). The frequency is 1024Hz and the number of electrodes is 63. The data includes 111 subjects, 11 of which are removed. The data of each subject is further split uniformly into multiple samples. For the train-validation-test split, we first shuffle the samples and select the last 20% as the test data. Then the rest of the data is split 4 : 1 for the training and validation set. We perform K-Fold Cross Validation on our model with settings as s16-stf4. The implementation uses PyTorch and DGL and the experiments are run on *Tesla P100-PCIE-16GB*. The batch size, total training epochs, learning rate, hidden dimension, number of attention heads are specified as 5, 100, 0.01, 5 and 3 respectively. The selected optimizer is Adam

and the loss function is SmoothL1Loss which is more resistant to noises than MSELoss. For StCNN, several stride values are tested.

We use two comparison models, namely FeedForward (simple fully-connections) and GRUNet (simply use GRU to extract temporal features). We also propose three variant models from BAPM, namely BAPM-CG (use a customized graph to perform graph convolution), BAPM-1 (StCNN + TranLayer) and BAPM-2 (StCNN + SpatAttLayer + TranLayer). BAPM-1 and BAPM-2 are used for ablation experiment on BAPM (StCNN + SpatAttLayer + TempLayer + TranLayer).

For more details, refer to <https://github.com/WingsUpete/EEG2Age>.

Results

The experiment results are shown in Table Set 3.

| <i>a</i> | Model | SRM Resting-state EEG | | |
|----------|-------------|-----------------------|----------------|--------|
| | | s16-stf4 | | |
| | | MAE | RMSE | MAPE |
| | FeedForward | 37.1000 | 39.5578 | 1.0000 |
| | GRUNet | 11.5837 | 14.0128 | 0.3384 |
| | <u>BAPM</u> | 8.0607 | 10.8924 | 0.2423 |
| | BAPM-1 | 11.4550 | 14.3746 | 0.3191 |
| | BAPM-CG | 8.5720 | 11.2067 | 0.2730 |

| <i>b</i> | Model | SRM Resting-state EEG | | |
|----------|-------------|-----------------------|----------------|--------|
| | | s16-stf4 | | |
| | | MAE | RMSE | MAPE |
| | <u>BAPM</u> | 8.0607 | 10.8924 | 0.2423 |
| | BAPM-1 | 11.4550 | 14.3746 | 0.3191 |
| | BAPM-2 | 11.1898 | 14.0586 | 0.3140 |

Figure 3: **a (left): results on SRM Resting-state EEG data for the models. b (right): ablation experiment results for BAPM.**

It can be discovered that **BAPM performs the best on all three metrics, achieving MAE = 8.0607**. Furthermore, a K-Fold Cross Validation process has proven that our model performs relatively stably with an average MAE = 8.7286, RMSE = 11.3910, MAPE = 0.2759. BAPM-CG performs slightly worse than BAPM, indicating that our customized graph design may be inadequate to show the true relationships among the electrodes.

The results of BAPM-1 and BAPM-2 prove the importance of performing both spatial and temporal feature extractions. When we gradually add back the modules, the results improve step by step. The performance largely increases as soon as both spatial and temporal feature extraction layers are recovered.

The crucial hyper-parameters are also tested with different settings. The results are shown in Table Set 4.

| <i>a</i> | Stride Factor | SRM Resting-state EEG | | |
|----------|---------------|-----------------------|----------------|---------------|
| | | s16 | | |
| | | MAE | RMSE | MAPE |
| | 1 (1s) | 9.8407 | 12.7894 | 0.2935 |
| | 2 (0.5s) | 8.4396 | 11.0257 | 0.2547 |
| | 4 (0.25s) | 8.0199 | 10.7034 | 0.2428 |
| | 8 (0.125s) | 7.9656 | 11.4174 | 0.2464 |

| <i>b</i> | Metrics | SRM Resting-state EEG | | | | |
|----------|---------|-----------------------|---------|----------------|---------------|---------|
| | | BAPM (stf4) | | | | |
| | | s8 | s12 | s16 | s24 | s32 |
| | MAE | 8.6207 | 8.2052 | 8.0607 | 8.3351 | 8.8679 |
| | RMSE | 10.9219 | 11.3111 | 10.8924 | 11.1475 | 11.9708 |
| | MAPE | 0.2610 | 0.2374 | 0.2423 | 0.2347 | 0.2594 |

Figure 4: **a (left): results for BAPM, with a sample split of 16 (s16) and different stride factor settings. b (right): results for BAPM, with a stride factor of 4 (stf4) and different sample split settings.**

It can be discovered that the results vary as the number of **sample split** from one subject increases. For MAE and RMSE, a sample split of 16 gives the best results while for MAPE, a sample split of 24 gives the best results. This is explainable, since as the sample split increases, the total number of samples increases, enabling the model to converge more stably without overfitting. On the other hand, the number of timestamps for each sample decreases, which might break certain pattern along the time dimension when the sample is too short. The results are best when the **stride factor** is 4 (MAE is not much worse than that of s8). Our 16GB GPU has been overloaded when the value is over 8, but theoretically, there should also be a stride factor value between 1 and 1024 which provides the best results.

Conclusion

With limited time, we designed a model - BAPM to predict the age of human beings according to the EEG signals. Our model managed to outperform two baseline models on all three metrics efficiently. Nevertheless, there is still plenty space for improvement and more data is required to test the performance of the model.

Prospect

There have been many research reports on BA in recent years, such as EEG-based BA metrics can be used as a marker for dementia patients, predicting the brain maturation level of adolescents [4], and also illuminating the link between BA and lifespan [2]. More and more reports demonstrated that BA can be used as a biomarker for neuroscientific diseases, especially for the early prevention, control and treatment of chronic neurodegenerative diseases with high significance.

In this course project, we completed BA predictions from resting-state EEG data only, which is not far from the results of current cutting-edge articles in the field [3]. After this class, the sample size can be increased and the parameters can be optimized in order to achieve better standards. Meanwhile, the accuracy of BA as a disease indicator can also be evaluated by using publicly available patient data sets for various diseases.

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