Surface Learning for Clinical Neuroimaging
An MLCN Workshop Challenge

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Abstract. Documentation of our submission for https://slcn.grand-challenge.org/.

1 Data preprocessing and augmentation

Each cortical sphere, corresponding to the left or right cerebral hemisphere of a neonatal subject, contains 40962 vertices. There is a 4-dimensional feature vector assigned to each vertex (myelin, sulcal depth, curvature, cortical thickness). We concatenated this feature vector with the feature vectors of the 6 neighbouring vertices, resulting 28 channels per vertex. We separated the left and right hemispheres using a reference left hemisphere: if the mean absolute error between the data and the reference was over a certain limit (1.0 in template space, and 1.385 in native space), then we identified the data as right hemisphere. Using this method, we could separate the hemispheres in the train and validation sets with 100% accuracy. We then rearranged the vertex order such that each right hemisphere was reflected across the sagittal plane, such that its orientation matched with the left hemispheres. We computed the mean and standard deviation of the train dataset along the feature dimension, and standardized both the train and validation datasets.

2 Method description

We used a 6-layer perceptron (MLP) with 28 hidden units and tanh activation in each layer. We performed batch normalization after each of the first 4 layers. After the fourth layer, we performed mean pooling along the vertex dimension. We used mean squared error as loss function. Our MLP had 3 output units: beyond the target variable (gestational age at birth), we incorporated two more variables into the loss function (postmenstrual age at scan and birthweight). These variables were provided as metadata. According to our measurements, the joint prediction of these 3 variables increased the generalization ability of our models. If validation MAE did not decrease in the last 100 epochs, we stopped the training, and restored the parameters of the best performing model. Even though our model has as few as 4371 parameters, it is able to outperform previous models.

3   Results

Our best validation MAE was 1.181 in template space, and 1.255 in native space. Our best test MAE (evaluated by Grand Challenge) was 1.226 in template space, and 1.386 in native space.

4   Link to public code repository

Our code is publicly available at:
https://github.com/daniel-unyi-42/MICCAI-2022-SLCN-solution

References

1. Fawaz, A., Williams, L. Z., Alansary, A., Bass, C., Gopinath, K., da Silva, M., ... & Robinson, E. C. (2021). Benchmarking geometric deep learning for cortical segmentation and neurodevelopmental phenotype prediction. bioRxiv, 2021.12.01.470730.