

Brain Cortical Functional Gradients Predict Cortical Folding Patterns via Attention Mesh Convolution

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1 Functional Gradients and Cortical Folding Patterns

In brief, for each subject, a functional connectivity matrix was calculated using the correlation coefficient for all pairs between vertices (32,492 per hemisphere) on HCP grayordinate mesh system. For each row of this “dense” functional connectome matrix, the values of the top 10% of connections were retained, whereas all others were zeroed. The negative values in the remaining connections were zeroed as well. The similarity of the connectivity matrix \mathbf{A} was ensured by calculating the cosine distance between all pairs of rows, yielding a symmetric affinity matrix \mathbf{L} . On this matrix, diffusion embedding [1] that allows local and long distance connections to be more effectively projected into a common space, was employed to yield unitless components, also known as functional “gradients”. The positions of nodes on these embedding axes encode the differences in nodes’ connectivity patterns. In this work, the number of gradients was set to 5. Results of other numbers of gradients were compared. It is noted that each functional gradient is associated with an eigen value that suggests its dominance. It has been demonstrated that gradients decomposed from different subjects are consistent, whereas their dominance could vary across subjects [2]. Hence, the algorithm in [2] used the group-mean matrix to yield the group-wise gradients, that were further used as templates to identify the cross-subject correspondence of gradients from individuals. The top-left panel of Figure 1a illustrates the aligned 5 functional gradient maps from one subject. Surface mean curvature k was used to segment surface to gyri ($k > 0$) and sulci ($k < 0$) (the right-top panel of Figure 1a).

2 Dataset & Preprocessing

Important imaging parameters are: T1-weighted MRI: TR=2400 *ms*, TE=2.14 *ms*, flip angle=8 *deg*, image matrix=260×311×260 and resolution=0.7×0.7×0.7 *mm*³. Diffusion MRI: TR=5520 *ms*, TE=89.5 *ms*, flip angle=78 *deg*, FOV=210×180 *mm*², matrix=168×144, resolution=1.25×1.25×1.25 *mm*³, echo spacing=0.78

ms; rsfMRI: TR=0.72 *s*, TE=33.1 *ms*, flip angle=52 *deg*, in-plane FOV=208×180 *mm*², matrix=90×104, 220 *mm* FOV, 72 slices, 1200 time points, 2.0 *mm* isotropic voxels, BW = 2290 *Hz/Px*. T1-weighted MRI was used to reconstruct a cortical surface, since it provides more precise anatomical information due to its higher spatial resolution. Preprocessing of T1-weighted MRI includes skull stripping, tissue-segmentation and white matter surface reconstruction. The surfaces were transferred to the grayordinate system, a common surface template, *via* cross-subject registration to standard volume and surface spaces. It is noted that the aligned surface of each subject was re-sampled such that vertices have cross-subject correspondence. Preprocessing of fMRI signals includes: ICA-denoise, spatial artifact/distortion removal. Within-subject cross-modal registration was applied such that each grayordinate vertex was associated with a preprocessed fMRI signal. More details of data acquisition and preprocessing are referred to [3].

In order to make the above data available to the proposed model, we further processed the data. Firstly, remeshing input data. SubdivNet requires meshes with Loop subdivision sequence connectivity as input, the 'obj' format mesh data of HCP was remeshed to be available that has 131072 faces and 65538 points by a method in [4]. Then, we used the nearest neighbor method to map the values on the original surface to the new surface both on gradient and curv data. Next, values on points are converted to values on faces by 'paraview'. Last, the data above was normalized and written to 'json' format file, every subject then has a surface data and a value data includes input features (gradients) and labels (binarized by curvs).

References

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