



Joint Representation of Functional and Structural Profiles for Identifying Common and Consistent 3-Hinge Gyral Folding Landmark

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Abstract. The 3-hinge is a form of cortical fold, which is the intersection of the three gyri. And it has been proved to be unique anatomically, structurally, and functionally connective patterns. Compared with the normal gyri, the 3-hinge gyri have stronger structural connectivity and participate in more functional networks. Therefore, it is of great significance to further explore the 3-hinge regions, which could give more new insights on the study of mechanism of cortical folding patterns. However, for the large differences in brain across subjects, it is difficult to identify consistent 3-hinge regions across subjects and most previous studies on 3-hinges consistency merely focused on a single mode. In order to study the multi-modal consistency of 3-hinge regions, this paper proposes a joint representation of functional and structural profiles for identifying common and consistent 3-hinges. We use the representation of 3-hinge patterns in the functional network to obtain the functional consistency of 3-hinges cross subjects, then the distance between 3-hinge regions and Dense Individualized and Common Connectivity-Based Cortical Landmarks (DICCCL) system to obtain the structural consistency. Combining these two sets of stability, 38 functionally and structurally consistent 3-hinge regions were successfully identified cross subjects. These consistent 3-hinge regions based on multi-modal data are more consistent than that merely based on structural data and experimental results elucidate those consistent 3-hinge regions are more correlated with visual function. This work deepens the understanding of the stability of 3-hinge regions and provides a basis for further inter-group analysis of 3-hinge gyral folding.

Keywords: 3-hinge Gyral Folding · Multimodal Data · Brain Landmark

1 Introduction

Cortical folds have been shown to be related to brain function, cognition, and behavior. Based on the research of the past decades, the cortex can be further decomposed into fine-grained basic morphological patterns, such as gyri and sulci. Gyri are more potential

to be functional connection centers, which are responsible for exchanging information among remote gyri and nearby sulci; on the contrary, sulci exchange information directly with their nearby gyri [1].

Recent studies have shown that gyri can be further separated by the number of hinges it comprises, both for anatomical analysis and for functional timing analysis. Thus, the 3-hinge cyclotron fold pattern was gradually introduced and determined. It has been demonstrated that the 3-hinge regions have a thicker cortex [2], a stronger pattern of fiber connections [3], and a greater diversity of structural connections [4]. These studies revealed the salient features and potential value of the 3-hinge region. In a recent study, it was claimed that 3-hinges have been found as “connector” hubs in the brain [5].

Although these works have achieved great success, there remain several obstacles to studying and comprehending the role of 3-hinge gyral folding patterns. One of the most significant challenges is identifying common and consistent 3-hinge gyrus folding patterns across subjects, which has yet to be resolved and has impeded group-level 3-hinges analysis. The morphology of cortical folds varies greatly between individuals, so identifying stable 3-hinge regions between individuals is difficult. In 2017 Li *et al.* addressed this issue by manually labeling 3-hinges across subjects and species (macaques, chimpanzees, and humans), demonstrating that six 3-hinges have functional correspondence across subjects and even across species [4]. In 2020, Zhang *et al.* proposed a semi-automatic approach that combines the fold morphology of the cerebral cortex and the characteristics of white matter nerve fibers to estimate the correspondence of the 3-hinge regions across subjects [6]. In a recent study, by transferring Dense Individualized and Common Connectivity-Based Cortical Landmarks (DICCCOL) stability across subjects to the 3-hinge regions, a DICCCOL-based K-nearest landmark detection method was proposed, which automatically identified 79 consistent 3-hinge regions [7]. These studies have shown the possibility of automatically identifying consistent 3-hinge regions via data-driven approach. However, those identified consistent 3-hinge regions were still studied by single modality.

To identify the three-hinge regions with multi-modal stability via data-driven approach, we present a joint representation of functional and structural profiles for identifying consistent 3-hinges in this paper. We use functional network representation and fiber connectivity pattern of the DICCCOL system to obtain functional and structural consistency, respectively. And combine these two consistencies to identify 38 3-hinge regions that are consistent in both function and structure. We further compare these results with those based solely on structural data, which deepens our understanding of the 3-hinge region. Our work provides a basis for further inter-group analysis of the 3-hinge gyrus.

2 Method

2.1 Dataset and Preprocessing

We used the Q1 release of Human Connectome Project (HCP) [8] consortium and randomly selected 50 human brains from it in this study. The acquisition parameters of functional magnetic resonance imaging (fMRI) data are as follows: 90×104 matrix, 220 mm FOV, 72 slices, $TR = 0.72$ s, $TE = 33.1$ ms, flip angle = 52° , $BW = 2290$ Hz/Px, in-plane FOV = 208×180 mm, 2.0 mm isotropic voxels. For fMRI images,

the preprocessing pipelines included skull removal, motion correction, slice time correction, spatial smoothing, global drift removal. All of these steps are implemented by FMRIB Software Library (FSL) FEAT [9]. We use resting state fMRI and task fMRI data. Among them, task fMRI data contains a total of seven tasks, which are EMOTION, GAMBLING, LANGUAGE, MOTOR, RELATION, SOCIAL and WM.

For diffusion weighted imaging (DWI) data, the parameters are as follows: Spin-echo EPI, TR = 5520 ms, TE = 89.5 ms, flip angle = 78° , refocusing flip angle = 160° , FOV 210×180 (RO \times PE), matrix 168×144 (RO \times PE), slice thickness 1.25 mm, 111 slices, 1.25 mm isotropic voxels, Multiband factor = 3, and Echo spacing = 0.78 ms. Fiber tracking and cortical surface can be reconstructed from DWI dataset. Please refer to [10, 11] for more pre-processing details. One subject is randomly selected as template and 10 subjects are randomly selected as referential subjects. The remaining subjects are used as predictive subjects to predict consistent 3-hinges.

2.2 Joint Representation of Functional and Structural Profiles

We introduce a joint representation of functional and structural profiles for identifying common and consistent 3-hinges. The method contains four steps, as shown in Fig. 1.

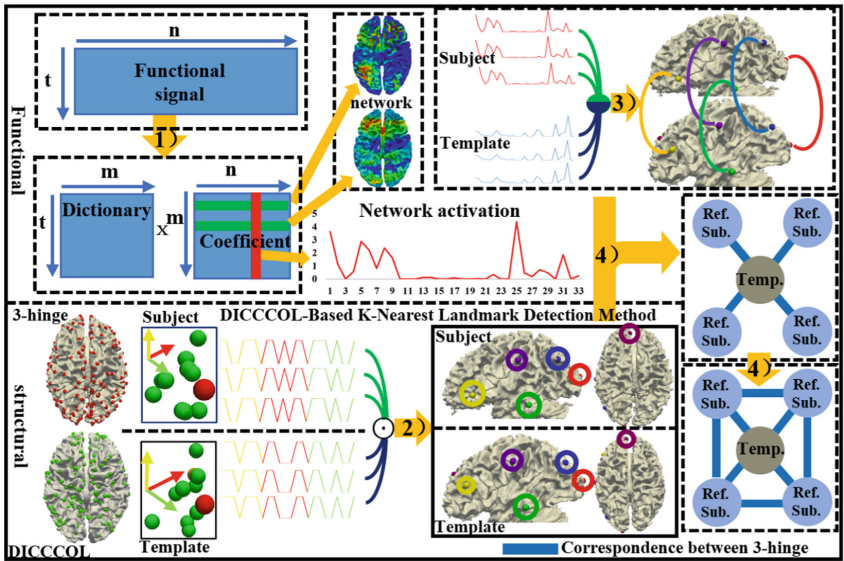


Fig. 1. Joint representation of functional and structural profiles. 1) Dictionary learning and sparse representation algorithm. 2) DICCOCOL-based K-nearest landmark detection method. 3) Obtain functional consistency by functional network. 4) Combine the functional and structural consistency.

First step is to obtain the functional network. The 4-dimensional data of the resting state and the fMRI of 7 tasks are stretched into 2-dimensional data, which are input into dictionary learning and sparse representation algorithm [12]. 400 functional networks

were obtained on the data of each modality. Based on prior knowledge, we select 10 functional networks from the resting state data and 23 functional networks from the task state data for this work. In the second step, we randomly select a subject as a template and use it as a bridge to study the consistency of 3-hinges across subjects. The second step is to obtain the corresponding of 3-hinges between the template and subjects using structural data. We improved the DICCCOL-based K-nearest landmark detection method [7] and retained the 3-hinges with the same spatial position and the same nearest DICCCOLs as the candidate matching set D_s . The third step is to obtain the corresponding of 3-hinges between the template and subjects using functional network. We register the functional network to all subjects, denote activation intensity vector of functional network with 3-hinge i on the template as A_i^t , and on other subjects as A_i^s . The candidate set D_j^f on subjects match 3-hinge j on the template based on functional network is given by formula 1:

$$D_j^f = |i|P(A_j^t, A_i^s) > \max P(A_j^t, A_i^s) - \text{th}| \quad (1)$$

where $P(A_j^t, A_i^s)$ represents the Pearson correlation coefficient of A_j^t and A_i^s , and the threshold is set to 0.1.

The fourth step combines the results of the second step and the third step to obtain stable 3-hinges across subjects. Firstly, the overlap in D_s and D_j^f is found as a matching result of 3-hinges between the template and subject. If multiple ones are found, the one with higher functional similarity is selected. Secondly, 10 subjects are selected as referential subjects. The stable sequence is obtained on the template by statistical matching information between the referential subject and the template. According to the stable sequence and matching information, the consistent 3-hinge regions cross subjects are identified. And it can be used to predict consistent 3-hinge regions on new subjects.

2.3 Consistency Analysis from Anatomical, Structural and Functional Perspective

From the previous section, a group of the consistent 3-hinges were identified. Then, it is important to come up with the evaluation operations and check the consistency of these 3-hinges. In this section, the evaluation operations are designed from structural, functional, and anatomical perspectives.

For the anatomical perspective, we calculate the voxel-wise distance of 3-hinges across subjects to measure their consistency. We register all subjects into the Montreal Neurological Institute (MNI) standard space. After obtaining the coordinates of 3-hinges, we calculated the voxel-level distance of 3-hinges between different subjects.

For the structural perspective, we use the similarity of fiber connection pattern passing through 3-hinges to evaluate the consistency of them. In detail, we count the nerve fibers passing through each 3-hinge region, and then used the trace-map method [13] to convert the nerve fiber bundles into vectors that could be quantified, and evaluated the consistency of the 3-hinges among groups by the Pearson correlation coefficient between these vectors. The trace-map is a computational model that transforms the directional

information in the trajectory of an arbitrary bundle to a standard spherical surface, for quantitative comparison of structural connectivity patterns.

For the functional perspective, we count the activation intensity of the 3-hinge regions among different functional networks as vector and used the Pearson correlation coefficient of these vectors across different subjects to quantify the functional consistency of 3-hinge regions.

2.4 Comparative Analysis of Consistent 3-hinges for Structural Data and Multimodal Data

Both joint representation of functional and structural profiles and DICCCOL-based K-nearest landmark detection method are methods that identify consistent 3-hinges by using templates as bridges. We compare the results of the two methods and study the distribution and corresponding functions of the two groups of 3-hinges on the cortical surface. We register consistent 3-hinges on all subjects to the MNI standard space and calculate the distribution of consistent 3-hinges on the Automated anatomical labelling (AAL) template [14]. Since the 90 brain regions of the AAL template are symmetric between the left and right brain, we combine the left and right brain regions. For statistics, we count the distribution of consistent 3-hinges over 45 AAL brain regions on each subject and average across all subjects. We then investigated the functions with consistent 3-hinges distributions according to the functions corresponding to AAL regions.

3 Result

3.1 Visualization of the Identified Consistent 3-hinges

The consistent 3-hinges of subjects are shown in Fig. 2.

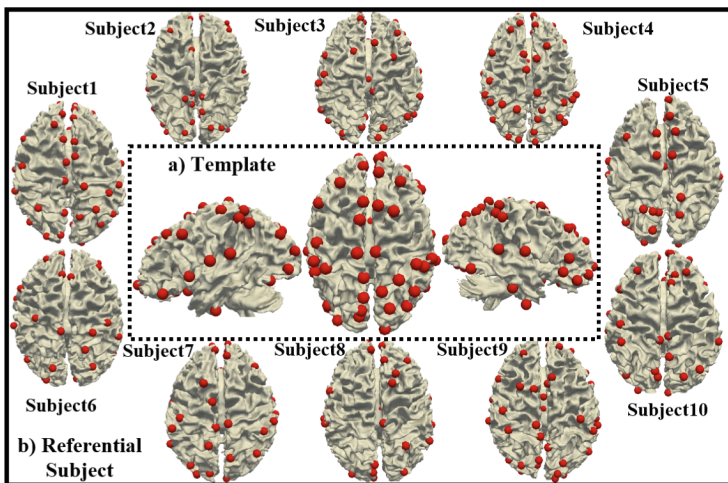


Fig. 2. Visualization of the distribution of identified 3-hinges in the cerebral cortex

Through adopting a joint representation of functional and structural profiles, stable sequences of length 65 are determined on the template and average 38 consistent 3-hinges can be successfully identified on subjects. Figure 2 shows the consistent 3-hinges of 10 referential subjects and the template subject. And we can see that those identified common and consistent 3-hinges are indeed consistent across the subjects.

In order to show the consistency of the identified 3-hinges among different subjects subjectively, in Fig. 3, we select 11 subjects (including a template, five referential subjects, and five predictive subjects) and mark the identified 3-hinges with the same color. As shown in Fig. 3, most of the 3-hinges can be found in the corresponding 3-hinges regions between different subjects, and these consistent 3-hinges regions are relatively close. We will quantitatively analyze the consistency of the 3-hinges identified in the following section.

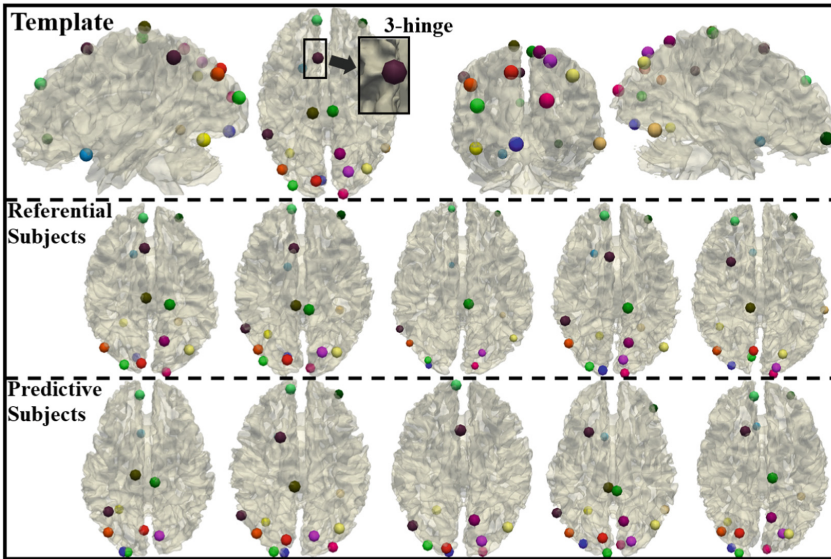


Fig. 3. Visualization of the corresponding distribution of identified 3-hinge region.

3.2 Effectiveness of the Proposed Consistent 3-hinges

After the identification of 3-hinges, it is important to evaluate whether they are common and consistent. To evaluate the consistency of these identified 3-hinges, we conduct quantitative experiments from three perspectives of anatomy, structure, and function to evaluate the performance mentioned in Sect. 2.3.

From the anatomical perspective, all the subjects are registered into the MNI standard space via a linear algorithm. Then, for each corresponding 3-hinge, the voxel-level distances are calculated to measure the distance between the template and other subjects. As shown in Table 1, consistent 3-hinge regions based on multi-modal data have better inter-population stability than three-hinge regions based on structural data.

Table 1. Voxel-level distances between the 3-hinges.

Consistent 3-hinge	Based on structural data	Based on multi-modal data
Referential subjects	6.03	5.31
Predictive subjects	6.10	5.31

From the structural perspective, the average Pearson correlation coefficient of fiber connection patterns of identified 3-hinges is as high as 0.44. As a comparison, the similarity is 0.37 for consistent 3-hinges based on structural data. This shows that the method of adding functional data to identify the consistent 3-hinges also has a great improvement in the structural stability of the identified 3-hinges.

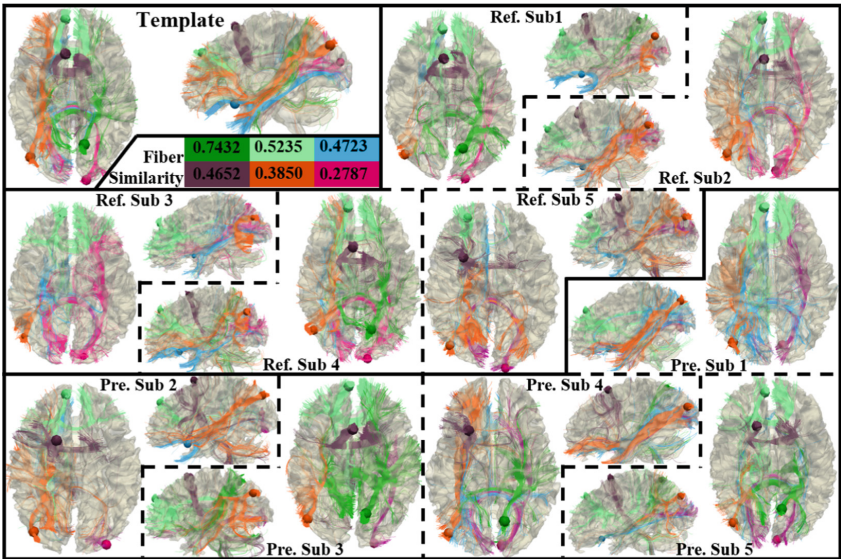


Fig. 4. Visualization of the corresponding fiber bundles of identified 3-hinge region.

In order to better demonstrate the structural consistency of these stable 3-hinges, in Fig. 4, we visualized six consistent 3-hinges on 11 selected subjects and the neural fiber modes across these 3-hinges. The stable 3-hinges and the corresponding nerve fibers are marked with the same color, and the similarity of the nerve fibers across the 3-hinge regions between the template and subjects is also marked with the same color. As shown in Fig. 4, the corresponding similarity of the 3-hinges in dark purple is close to the average similarity, and the corresponding nerve fibers are also similar between populations. This verifies the structural consistency of the identified 3-hinges.

From the functional perspective, the average similarity of activation intensity of consistent 3-hinges in a functional network based on multi-modal data between template and subject is 0.441, while the similarity based on structural data is 0.366. This indicates that

the addition of functional data analysis does greatly improve the functional consistency of the identified 3-hinges.

In general, in this section, we verify that the consistency of the identified 3-hinges is significantly stronger than that of the methods based on structural data.

3.3 Comparative Analysis on the Consistent 3-hinges Based on Structural Data and Multimodal Data

As mentioned in Sect. 2.4, we analyze the distribution and corresponding functions of structural-based and functional-based consistent 3-hinge regions in the cerebral cortex. In Fig. 5, the distribution of these three hinges on the brain surface is measured by the AAL template. Next, we count the function of the brain regions with more 3-hinge regions in the two groups. In this step, the regions with fewer 3-hinge regions in both groups are ignored. The consistent 3-hinge regions based on multimodal data have more distribution in CAL (22), CUN (23), LING (24), SOG (25), MOG (26), IPL (31) and ANG (33). These areas are more relevant to visual function. This indicates that the introduction of functional data analysis has played a great role in analyzing the group consistency of the 3-hinge regions in the visual functional region. The consistent 3-hinge regions based on the structural data are more distributed in PreCG (1), SFGdor (2), ORBsup (3), IFGoperc (6), SFGmed (12), HIP (19), PoCG (29), PCL (35), and MTG (43). These regions are more related to motor and memory functions, suggesting that the 3-hinge regions have stronger structural stability in these functions.

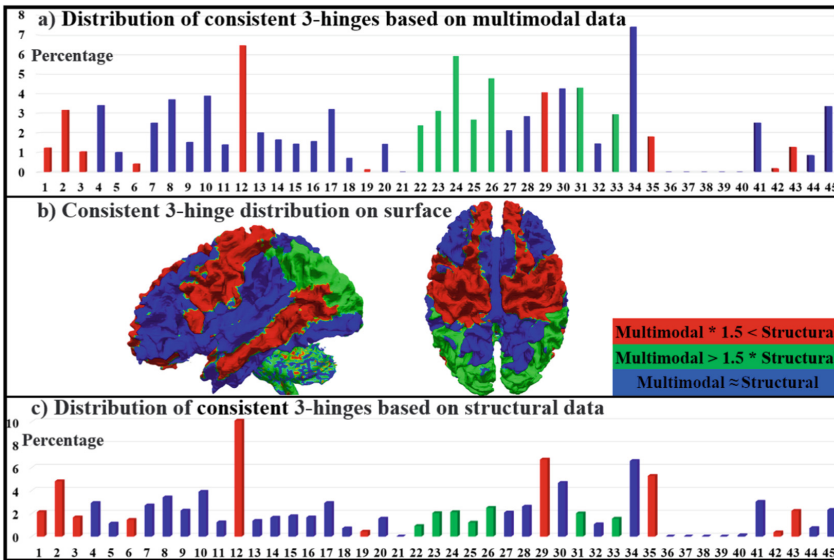


Fig. 5. Distribution of consistent 3-hinges in AAL brain regions based on structural and multimodal data

4 Conclusion

In this work, we propose a joint representation of functional and structural profiles in a data-driven approach for identifying consistent 3-hinges. We use functional network representation and fiber connectivity pattern of the DICCCOL system to obtain functional and structural consistency, respectively. And combine these two consistencies to identify 38 functionally and structurally consistent 3-hinge regions. Compared with the single-modal method with DICCCOL only, the results obtained by our proposed multi-modal method have a more consistent 3-hinge pattern across subjects. And we further analyze that consistent 3-hinge regions based on multimodal data are closer to visual functions, while 3-hinge regions based on structural data are closer to memory and motor function.

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