A graph matching-based sulcal pattern analysis: Application to the study of twin brains

K. Im[1], R. Pienaar[1], J-M. Lee[2], J-K. Seong[3], Y. Choi[2], K. Lee[4], and P. E. Grant[1]

[1]Children's Hospital Boston, Boston, MA, United States, [2]Hanyang University, [3]Soongsil University, [4]Chosun University

Introduction

Gyral folding has long fascinated scientists, as the character of gyral folding is related to functional compartmentalization. There is a large variability in the pattern of gyral folding across individuals and in genetic disorders but without means of quantifying these differences, it is difficult to define their functional significance or better understand their genetic/epigenetic etiology. Visual classification schemes lack the necessary dynamic range and reproducibility. Curvature measures can capture local properties of gyral folding, but they do not allow characterization of the spatial relationship between gyri or sulci. In this study we explore the potential of a novel method where the gyral pattern is represented as a sulcal pit-based graph and automatically compared between different brains using a spectral-based matching algorithm. Our method allows characterization of the positioning, arrangement, number and size of sulcal segments and their interrelationship. We applied this method to a twin study to investigate the genetic effect on the sulcal patterns.

Methods

Two T1-weighted images were acquired and averaged for each subject. The images were processed to extract cortical surfaces using the FreeSurfer pipeline. The sulcal pattern is represented with a graph structure using sulcal pits as the nodes. Sulcal pits are defined as the deepest local regions of sulci, and show relatively invariant spatial distribution, which may be closely related to functional areas under tight genetic control (Im et al., 2010; Lohmann et al., 2008). Sulcal pits and their corresponding sulcal catchment basins were automatically identified on the white matter surface using a watershed algorithm based on sulcal depth map. Each sulcal pit corresponds to a node in the graph representation. If sulcal basins met, sulcal pits in those basins were connected with an undirected edge (Fig. 1). We used 3D position (x, y, z) and sulcal depth of the node and area of sulcal basin for sulcal geometry. We also used the number of connections with 1st neighborhood nodes (the number of edges) on each node and the paths between nodes in the graph for graph topology to reflect sulcal arrangement and patterning. We adapted a spectral matching technique (Leordeanu and Hebert, 2005) to determine the optimal match and compute the similarity value between them. This method exploits geometric features of nodes as well as their inter-relationships. A total of 48 young healthy twin volunteers were recruited, consisting of 14 female and 10 male monozygotic twin pairs,

Fig. 1. Extraction of sulcal pits and graph contruction

with ages ranging from 18.3 to 24.9 years (mean ± standard deviation: 20.7 ± 1.8 years). Sulcal graphs were constructed for the left and right hemispheres and lobar regions in twin data. We tested if the mean similarity between 24 twin pairs is significantly higher compared to the mean similarity of 24 unrelated pairs randomly taken from the same data pool. We carried out a permutation test based on 10,000 times set of random unrelated pairs.
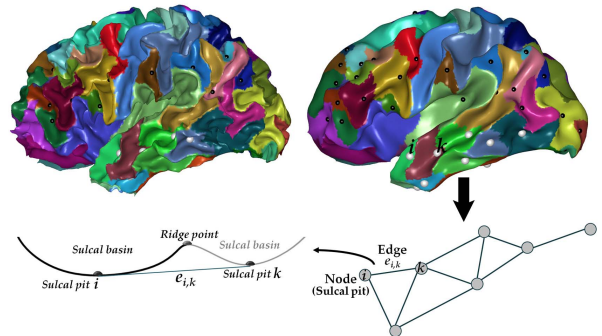
Results

The example of optimal sulcal pattern matching and similarity measure in the temporal lobe is shown in Fig. 2. In the pair having high similarity value, the geometric features of nodes and their relationship, as well as their sulcal arrangement are more similar (Fig. 2A). The results of our analysis showed that the similarity of monozygotic twins was significantly larger than the similarities of unrelated pairs for all regions (permutation test P values, both hemispheres: < 0.0001, left frontal and temporal lobes: < 0.0001, parietal lobe: 0.0036, occipital lobe: 0.0005, right frontal: 0.0002, temporal, parietal and occipital: < 0.0001). Fig. 3 shows the permutation distribution of the statistic, the mean similarity, from 10,000 resamples and the mean similarity from the twins for the left and right hemispheres.
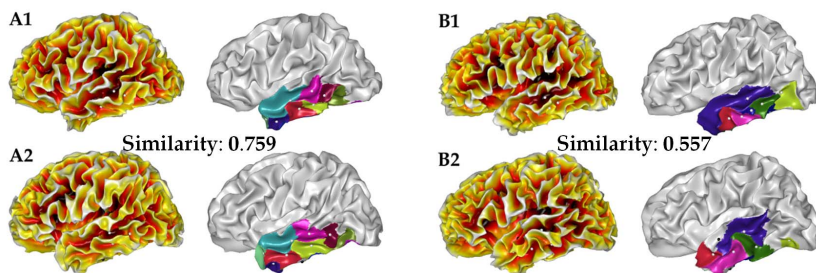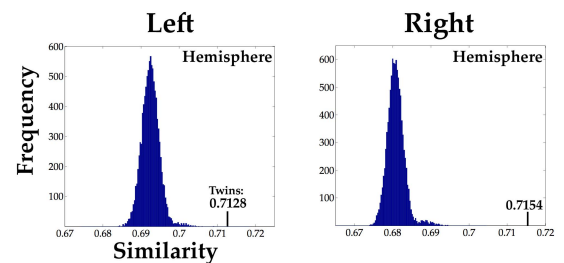

Fig. 2.

Fig. 3.

Discussion

We have developed a novel quantitative method to automatically compare and quantify differences in sulcal patterns between different brains. To the best of our knowledge this is the first quantitative comparison of this type. Our method provides comprehensive and quantitative analysis of sulcal patterns that captures not only simple connection/interruption and presence/absence of sulcal segments but also their arrangement and interrelationship based on geometric features and the topology of graph structure. We showed the statistically significant genetic impact on the sulcal pattern. This method can be applied to various genetic developmental disorders, to provide a quantitative and reliable comparison of gyral folding based on sulcal anatomy.

References

Im, K., Jo, H.J., Mangin, J.F., Evans, A.C., Kim, S.I., Lee, J.M., 2010. Spatial distribution of deep sulcal landmarks and hemispherical asymmetry on the cortical surface. Cereb Cortex 20, 602-611.

Leordeanu, M., Hebert, M., 2005. A spectral technique for correspondence problems using pairwise constraints. ICCV '05: Proceedings of the Tenth IEEE International Conference on Computer Vision. IEEE Computer Society,Washington, DC, USA, 1482-1489.

Lohmann, G., von Cramon, D.Y., Colchester, A.C., 2008. Deep sulcal landmarks provide an organizing framework for human cortical folding. Cereb Cortex 18, 1415-1420.