PARAMETRIC REPRESENTATION OF SULCAL AND GYRAL TREES

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Introduction Sulcal and gyral trees have shown to be important biomarkers for disease progression and cortical development. Due to the lack of one-to-one correspondence between trees at the node/edge level, building coherent statistical models has been a challenge for trees. The sulcal and gyral trees do not align well across subjects even after image registration. The problem is further compounded by the lack of *easy-to-use* algebraic representation for trees, which is the starting point of building statistical models. We address these problems using the weighted spherical harmonics (SPAHRM).

Methods The collection of sulcal and gyral curves wereobtained from the MRI scans in the Human Connectome Project (HCP) consisting of 268 females and 176 males. The white and pial surfaces were extracted using FreeSurfer. Sulcal/gyral curves were extracted and represented as graphs [2]. The sulcal and gyral trees were assigned value -1 and 1 respectively at the node level (Figure 1). All other parts of the surface mesh are assigned value 0. Then the trees are represented using the weighted-SPHARM Y_{lm} [1]:

$$Trees = \sum_{l=0}^{k} \sum_{m=-l}^{l} e^{-l(l+1)\sigma} f_{lm} Y_{lm},$$

where parameters f_{lm} are estimated in the least squares fashion [1]. The parameter σ determines the smoothness of the representation. The degree k expansion requires estimating more than $(k+1)^2$ coefficients. We used $k = 100$ with more than 10000 basis. The representation has the following properties. 1) If σ is chosen sufficiently small, we can reconstruct the sulcal/gyral trees with almost perfect accuracy. 2) Algebraic operations such as averaging, correlating and constructing test statistics can be done through the expansion coefficients.

Results The method is applied in localizing sulcal/gyral tree differences between males and females. The smoothing parameter $\sigma = 0.001$ was used in performing the two sample t-statistic. We obtained highly localized differences mainly in the temporal region (Figure 2). The *transposition test* was used to generate half million permutations, which took 40 min [3]. The t-stat. values larger than 4.48 and smaller than -4.27 gives p-value smaller than 0.05 (corrected). We mainly found the differences in the temporal lobe, especially in the superior temporal gyrus and sulcus.

[1]Matlab code: `http://www.stat.wisc.edu/~mchung/softwares/weighted-SPHARM/weighted-SPHARM.html`

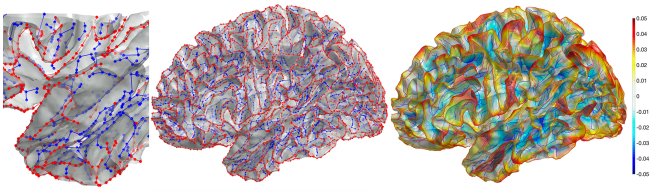

Fig. 1. Sulcal (blue) and gyral (red) trees are extracted. The left is the enlarged region of the temporal lobe. The weighted-SPHARM was used to represent the trees (right).

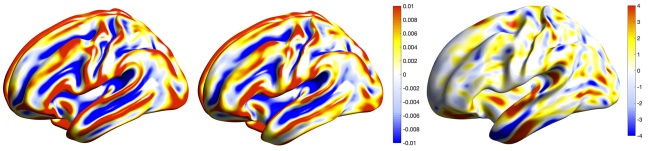

Fig. 2. The average diffusion maps of 274 females (left) and 182 males (middle) projected to the average surface template. The t-statistic map (right) shows localized sulcal and gyral pattern differences (female - male).

Conclusion We presented the parametric representation of trees that enable us to perform the statistical analysis at the node or edge level. The method enables us to construct the proper inner product space on the collection of trees and even compute the correlation between trees.

1. REFERENCES

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