Persistent Network Homology from the Perspective of Dendrograms

Submission No:

2210

Authors:

Hyekyoung Lee[1], Moo K. Chung[2,1], Hyejin Kang[1], Boong-Nyun Kim[1], Dong Soo Lee[1]

Institutions:

[1]Seoul National University, Seoul, Korea, Republic of, [2]University of Wisconsin, Madison, WI

Introduction:

The modular structure of brain connectivity helps to understand from the local module information to their global relationships of brain network [2,3]. Usually we select only one optimal modular network by maximizing the predefined metric such as a modularity. But the optimal network can be changed depending on the metric and it is not yet known which network is truly modular. In this study, we seek the evolutionary changes of modular structures by increasing the threshold in correlation matrix, rather than choosing a fixed modular structure. It can be directly related with the hierarchical clustering with the persistent property and visualized by a dendrogram. As an application, we constructed the brain networks using the FDG-PET data of 24 attention deficit hyperactivity disorder (ADHD), 26 autism spectrum disorder (ASD) children and 11 pediatric control (PedCon) subjects. The difference between the changes of the modular structures was compared by the distance measure between dendrogram, known as Gromov-Hausdorff distance [1].

Methods:

Given a set X of point cloud data, Rips complex $R(X,\varepsilon)$ is generated by connecting two points i and j if the distance $d(i, j)$ is smaller than ε. A sequence of Rips complexes for increasing ε is called a Rips filtration and satisfies $R(X,\varepsilon1)\subset R(X,\varepsilon2)$ for $\varepsilon1<\varepsilon2$. If we define the distance $d(i,j)$ as $1\text{-}corr(i,j)$ where $corr(i,j)$ is the correlation between i and j, the constructed Rips complex with filtration value ε is equivalent to the thresholded network with correlation cutoff value ε [4]. Thus, we define the sequence of networks as a persistent network.

The connected components of the Rips complex are called the 0th persistent homology groups or persistent clustering [3]. The topological changes of modular structures of network are also the persistent clustering. Since the persistent clustering is directly connected with the agglomerative hierarchical clustering with single linkage, we can visualize the changes of module structures and their relationships of brain network using a dendrogram without choosing one fixed modular structures.

Results:

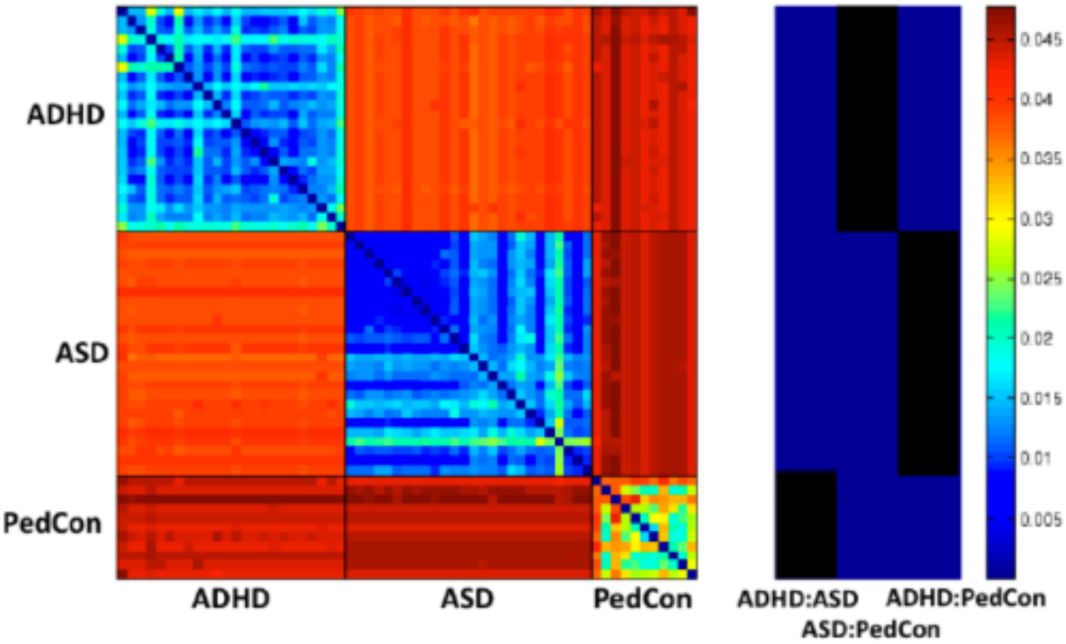
All PET scans were obtained from ECAT EXACT 47 (Siemens-CTI, Knoxville, USA) PET scanner with an intrinsic resolution of 5.2 mm FWHM. PET images were preprocessed using Statistical Parametric Mapping (SPM) package. After spatial normalization to the standard template space, mean FDG uptake within 97 regions of interest (ROIs) were extracted. The values of FDG uptake were globally normalized to the individual's total gray matter mean count.

We illustrated dendrograms which visualize the modular structures of ADHD, ASD and PedCon when increasing distances from 0 to 0.7 in Fig. 1. All ROIs of PedCon network are connected faster than ADHD and ASD. In ADHD network, the ROIs between lobes, frontal, limbic, subcortical, parietal, temporal and occipital lobe and cerebellum are highly disconnected [5]. For ASD, the ROIs in frontal and parietal lobes are separated for a longer duration that PedCon [6].

The distance between dendrograms can be measured by Gromov-Hausdorff distance. We generated the different datasets of each group using the leave-one-out cross-validation and constructed 24 ADHD, 26 ASD and 11 PedCon dendrograms. After estimating the distance between dendrograms, we performed Wilcoxon rank sum test between three pairs of (ADHD and ASD), (ASD and PedCon) and (ADHD and PedCon) as shown in Fig. 2. The dendrograms, constructed by dataset of different groups, are always different with the significance level 0.05.

Conclusions:

We look at the topological changes of modular structures varying the correlation threshold. It is same with the agglomerative hierarchical clustering which has the persistent property. The results of ADHD, ASD and PedCon can be visualized by dendrograms and they are significantly different.



(a) Gromov-Hausdorff distances between dendrograms **(b) p-value**

Figure 2. (a) Gromov-Hausdorff distances between ADHD, ASD and PedCon dendrograms and (b) p-value of differences of distances between ADHD and ASD, ASD and PedCon and ADHD and PedCon. We constructed 24 ADHD, 26 ASD and 11 PedCon dendrograms using datasets obtained by leave-one-out cross validation and measured their distance by Gromov-Hausdorff distance. The distances within a group are small in blue-colored regions and the distances between groups are large in red-colored regions in (a). By Wilcoxon rank sum test, we measured their significances between each pair of groups in (b).

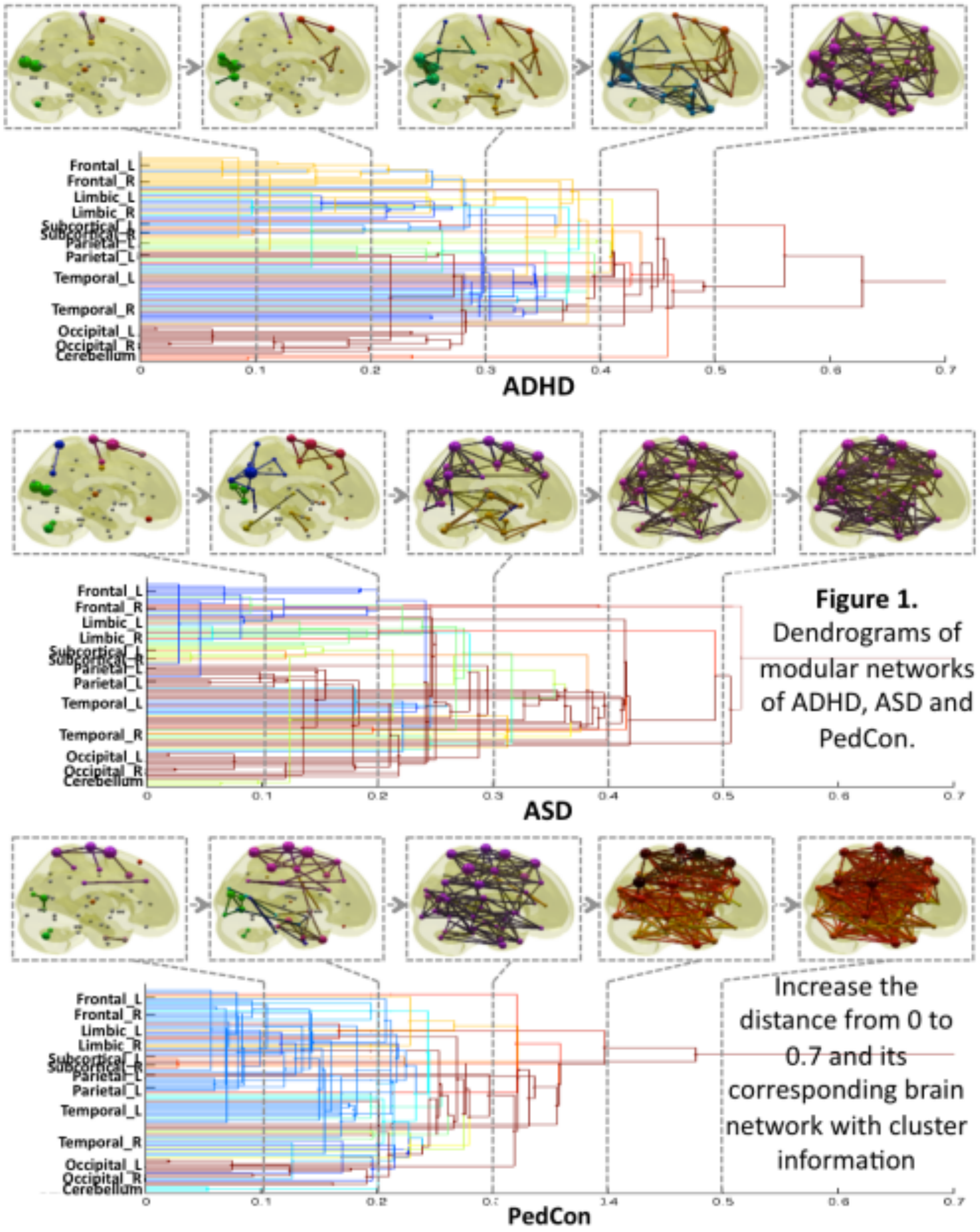


Figure 1. Dendrograms of modular networks of ADHD, ASD and PedCon.

Increase the distance from 0 to 0.7 and its corresponding brain network with cluster information

Modeling and Analysis Methods

PET Modeling and Analysis

Abstract Information

References

[1] Bassett, D. (2006), 'Small-world brain networks', The Neuroscientist, vol. 12, pp. 512-523.
[2] Chen, Z.J., He, Y., Rosa-Neto, P., Germann, J. and Evans, A.C. (2008), 'Revealing Modular Architecture of Human Brain Structural Networks by Using Cortical Thickness from MRI', Cerebral Cortex, vol. 18, pp. 2374-2381.
[3] Calrlsson, G. and Memoli, F. (2010), 'Characterization, stability and convergence of hierarchical clustering methods', Journal of Machine Learning Research, vol. 11, pp. 1425-1470.
[4] Lee, H., Chung, M.K., Kang, H., Kim, B.-N. and Lee D.S. (2010), Discriminative persistent homology of brain networks', IEEE International Symposium on Biomedical Imaging (ISBI), submitted.

[5] Cubillo, A. and Rubia, K. (2010), 'Neuroimaging of adult ADHD', Expert Review of Neurotherapeutics, vol. 10, pp. 603–620.
[6] Minshew, N.J. and Williams, D.L. (2007), 'The new neurobiology of autism: Cortex, connectivity, and neuronal organization', Archives of Neurology, vol. 64, pp. 945–950.