**Obtaining functional dynamic brain networks with contiguous co-clustering**

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**Introduction:** Contiguous co-clustering is a data mining technique useful for discovering co-occurring coherent patterns in simultaneous time series. For contiguous co-clustering, time-series are stacked to form a matrix, each series becoming a row, and each time point, a column. This matrix is then looked for co-clusters: groups of rows presenting simultaneous coherent patterns — occurring in the same columns. This method has been successfully applied to extract useful information from gene expression data, suggesting that application to other biological series is promising [1]. We applied this algorithm to brain fMRI time series. In this scenario, co-clustering allows the identification of co-functional regions, i.e., regions presenting coherent spatio-temporal activity patterns. This information can be exhibited in a dynamic functional brain network, for visualization purposes and also for helping to discriminate different groups of brain activity.

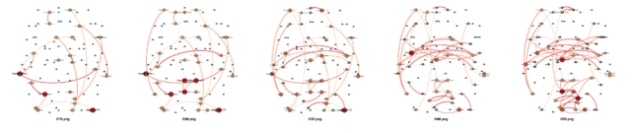
**Methods:** fMRI data was collected on 19 controls and 19 patients suffering from a motor disorder. Subjects were asked to perform a motor task (finger tapping), following a rest/movement block protocol. Images were pre-processed and segmented in 90 regions. Averaging over the voxels of each region yields their corresponding time-series. Contiguous co-clustering was applied to the individual series and also to the average series of each group (controls and patients). The co-functionality information given by the co-clusters was used to define a functional network, with 90 nodes representing the brain regions, and edges between them indicating their co-activity, i.e. that they were present in the same co-cluster during that specific period of time. Edges were weighted by the correlation between the two regions. Two paths were followed: generation of a group network from the combination of individual networks, and also from the average series of the group.

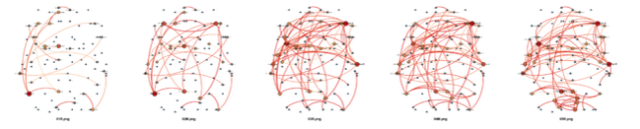
**Results:** Table 1 shows the quantity of co-clusters found in the individuals of each group (on average) and on the average series. Figure 1 shows snapshots of the networks generated from the average series for controls (top) and patients (bottom). Bigger nodes in red represent more connected regions. The snapshots correspond to the first 2 rest/movement blocks. Similar results were obtained from the combination approach, but networks with more edges are generated.

*Table 1: Quantity of co-clusters*

|  |  |  |
| --- | --- | --- |
| Group | Group avg. | Avg. series |
| Control | 107 ± 28 | 100 |
| Patients | 115 ± 32 | 162 |

*Figure 1 Network snapshots*



**Discussion:** A reasonable amount of patterns could be found, and the average quantity of patterns found for individual subjects is close to that found in the group average series. Networks derived from this method are clearly distinctive between controls and patients. However, the rest movement blocks do not appear to be clearly characterized, as the movement (and rest) periods are distinct.

**Conclusion**: Contiguous co-clustering appears to be a promising method for generating dynamic brain networks. In our experiment, networks obtained are clearly distinct between controls and patients, although no clear pattern arose corresponding to the rest movement blocks. As future work, it might be interesting to calculate the temporal evolution of topological metrics in the network, in order to verify its capability to characterize both the blocks of experiments and the groups of subjects.

**References:** [1] Madeira et al., IEEE/ACM Trans. Computat. Biol. Bioinf. 7(1): 153-165, 2010.

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