Multi-Level Parcellation of the Cerebral Cortex Using Resting-State fMRI

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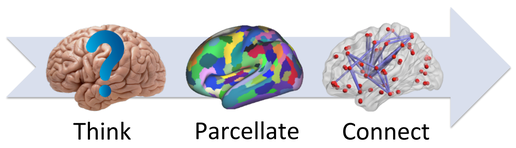
Highlights

- A three-layer parcellation framework which uses a different clustering strategy at each layer, attacking different problems.
- Resting-state fMRI is used to capture the functional organization of the entire cortex.
- Segregates the cortex into highly reproducible and functionally homogeneous parcels at different resolutions.
- More effective than the state-of-the-art approaches at single-subject and group levels.

Introduction

The analysis of the human connectome provides a better understanding of the functional organization of the brain as well as helps explore its evolution through aging and in neurological disorders (such as Alzheimer's disease) [1]. In a whole-brain connectivity analysis, a critical stage is the computation of a set of network nodes that can effectively represent functional subregions.



Despite the attempts at developing parcellation algorithms using rs-fMRI [5, 6, 7], there still remain challenges, such as generating **reproducible** and **functionally consistent** parcellations at both single-subject and group levels.

Data Acquisition and Processing

- We evaluated our approach with a set of 100 subjects from the Human Connectome Project [2].
- We conducted our experiments on the rs-fMRI datasets, containing scans from 100 different subjects (54 female, 46 male adults, age 22-35).
- For each subject, gray matter voxels were mapped to the native cortical surface and registered onto the 32K standard triangulated mesh to establish correspondences [3].
- Each time series was temporally normalized to zero-mean and unit-variance.

Step 1: Supervertex Clustering

Inspired by the superpixels [4], each vertex is iteratively clustered into a *supervertex* as per their distance, computed with a Euclidean function in the form of:

$$D = \sqrt{\left(\frac{d_c}{N_c}\right)^2 + \left(\frac{d_g}{N_g}\right)^2} \qquad (1)$$

where d_c corresponds to the functional distance, measured by the **Pearson's distance transformation** and d_g corresponds to the spatial distance, measured by the **geodesic distance** along the cortical surface, approximated as the length of the shortest path between the nodes. N_c and N_g refer to the **normalization factors**.

Algorithm 1: Supervertex Clustering

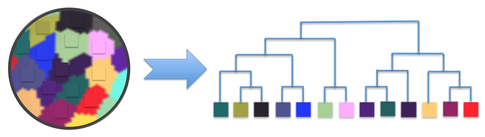
```
/* k initial supervertex centroids are
   selected by uniform sampling.          */
foreach vertex v do
    labels(v) ← 0
    distances(v) ← ∞
repeat
    changed ← false
    foreach supervertex centroid S_k do
        /* Distance calculated only for
           vertices within a range.       */
        foreach vertex v within R mm of S_k do
            D = distance between S_k and v
            if D < distances(v) then
                distances(v) ← D
                labels(v) ← k
                changed ← true
    Compute the new supervertex centroids
until changed ≠ true
```

Step 2: Single-Level Parcellation

We join adjacent *supervertices* into spatially contiguous parcels using **agglomerative hierarchical clustering** with a bottom-up strategy, in which pairs of clusters are merged if their similarity is the maximal among the other pairing clusters.

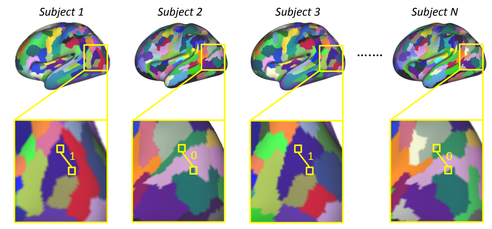
- **Linkage Criterion:** Ward's linkage rule.
- **Similarity Metric:** Pearson's correlation distance.

The output is a dendrogram, in which the leaves represent the *supervertices* and the root represents an entire hemisphere.



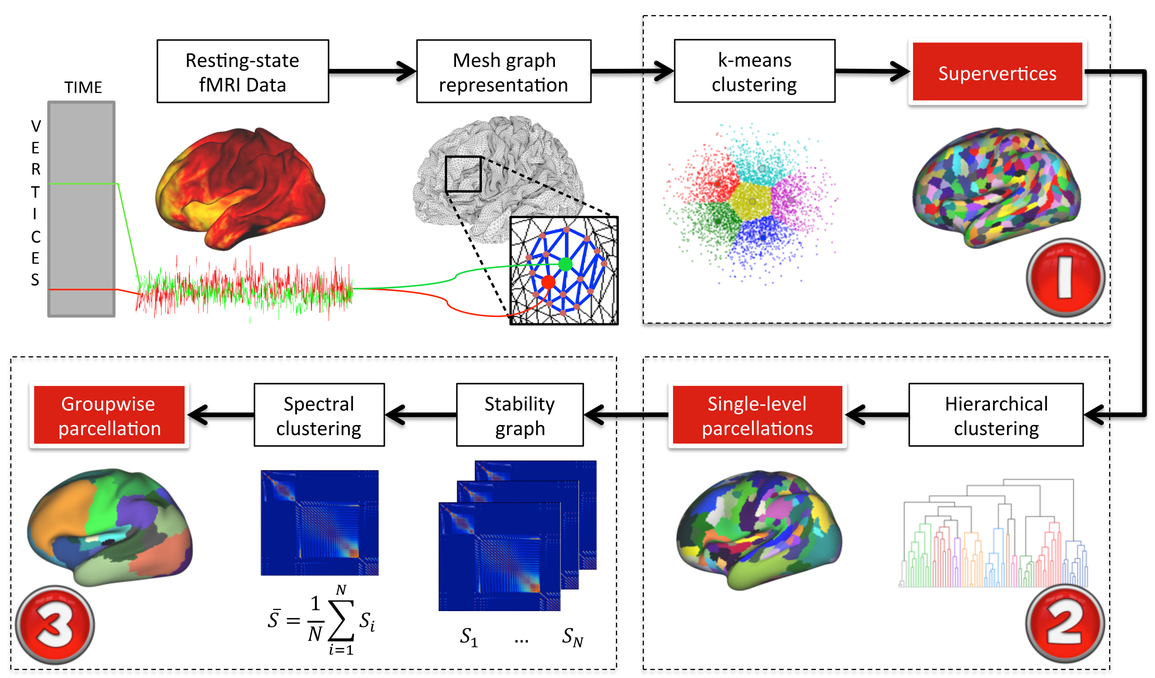
Step 3: Groupwise Parcellation

We compute a fully-connected, undirected graph of the parcel stability for each individual parcellation [5], in which edges $e_{ij} = 1$ if vertices i and j are in the same parcel and $e_{ij} = 0$ otherwise. The graphs are averaged across the whole population and subdivided by spectral clustering with normalized cuts [6] into pre-defined number of subregions.



$$w = \frac{1 + 0 + 1 + \cdots + 0}{N}$$

3-LAYER Parcellation Pipelines



Comparison Methods

- **RG-HC:** A single-subject parcellation method composed of region growing and hierarchical clustering [7].
- **NCUT:** Spectral clustering with normalized cuts directly applied on the cross-correlated affinity networks obtained from each subject separately [6].
- **MEAN:** The average affinity network is parcellated via n-cut spectral clustering [6] (only applies to the groupwise experiments).

Performance Measures

- **Reproducibility:** Parcel overlaps are computed with a two-pass Dice score-based method [7].
- **Functional Homogeneity:** The average pairwise correlations within each parcel [6].
- **Functional Segregation:** Silhouette width is defined by combining within-parcel homogeneity H and inter-parcel separation S as follows:

$$S_{width} = \frac{H - S}{max\{H, S\}} \qquad (2)$$

Quantitative Results

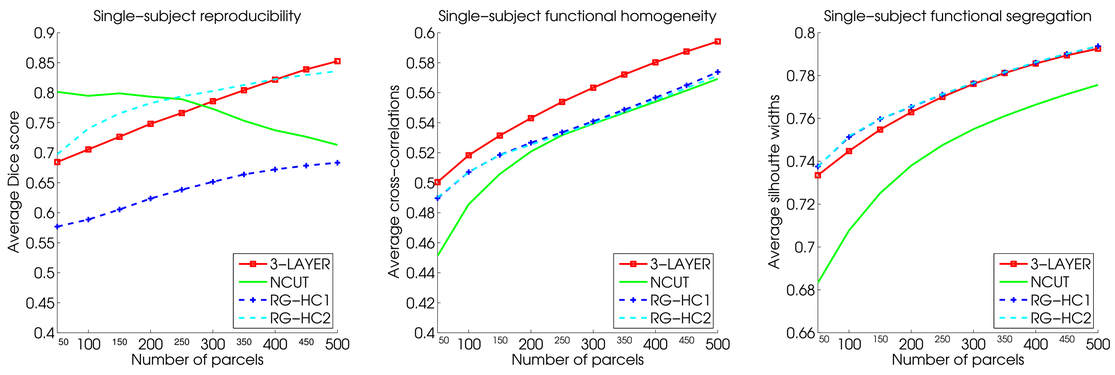


Figure 1: Single-subject reproducibility (left), functional homogeneity (middle), and functional segregation (right) results.

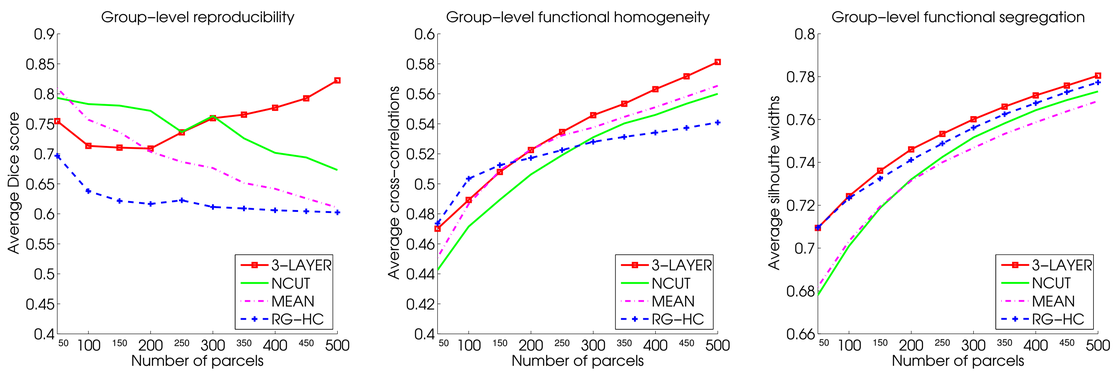


Figure 2: Group-level reproducibility (left), functional homogeneity (middle) and functional segregation (right) results.

Visual Results

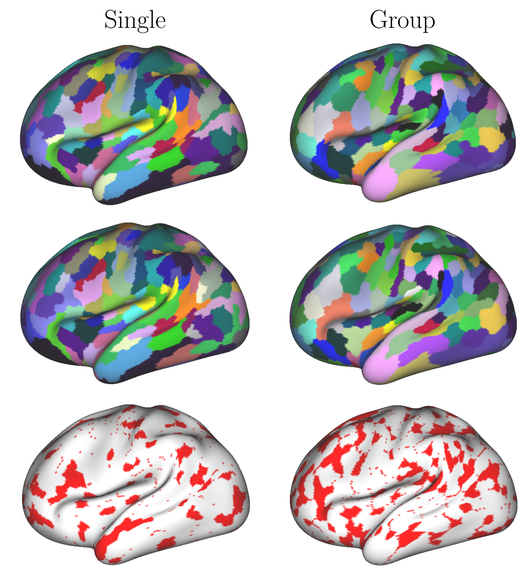


Figure 3: Individual and groupwise parcellations obtained by the proposed method for 200 parcels. Single-level and groupwise parcellations in the first two rows were derived from different rs-fMRI datasets of the same subject and from different subgroups of the population, respectively. The third row shows the differences between the first and second parcellations.

Functional Connectivity

- Proposed method segregates the cortex into functionally distinctive parcels as shown below.
- Sharp transitions in the correlation patterns are significantly aligned with the parcellation borders.

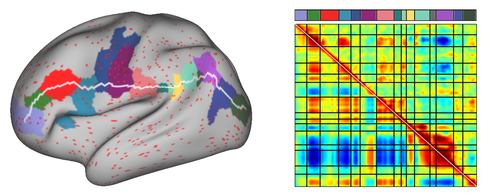


Figure 4: *Left:* A path drawn on the cortical surface, crossing the parcellation borders at a right angle. *Right:* The correlation (upper triangle) and connectivity (lower triangle, as measured to the vertices marked in red) profiles derived from the vertices along the path. Black lines indicate the parcellation borders.

Acknowledgments

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HUMAN Connectome PROJECT
EPSRC
Developing Human Connectome Project

References

[1] Sporns et al., "The Human Connectome: A structural description of the human brain," 2005.

[2] Van Essen et al., "The WU-Minn Human Connectome Project: An overview.," 2013.

[3] Glasser et al., "The minimal preprocessing pipelines for the Human Connectome Project," 2013.

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[5] van den Heuvel et al., "Normalized cut group clustering of resting-state fMRI data," 2008.

[6] Craddock et al., "A whole brain fMRI atlas generated via spatially constrained spectral clustering," 2012.

[7] Blumensath et al., "Spatially constrained hierarchical parcellation of the brain with resting-state fMRI," 2013.

Contact

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Source codes goo.gl/GNkxqw

Video youtu.be/zDWdgtfzOvo