

Highlights

- A k -means based approach to cluster the rs-fMRI data.
- Can be used for dimensionality reduction and/or pre-parcellation of the cortex in network analysis.
- Sub-divides the cortex into relatively large number of functionally homogeneous parcels with high reproducibility.
- Evaluated with a set of 100 subjects from the Human Connectome Project.

Introduction

Cortical parcellation constitutes a key step to identify the functional connections within the brain. Parcellation methods usually start with clustering the low-level rs-fMRI data into functionally homogeneous and non-overlapping subregions and build network models based on this abstraction with the following benefits:

- It reduces the dimensionality of the data, thus decreases the computational cost.
- It improves the SNR levels within subregions.

We propose a k -means algorithm inspired by superpixels [1] to address this problem and compare it with the existing approaches based on region growing (RG) [2], Ward's hierarchical clustering (HC), and spectral clustering with normalized cuts (NCUT) [3].

Data

We conducted our experiments on the rs-fMRI datasets, containing two 30-minute scans from 100 different subjects (54 female, 46 male adults, age 22-35); acquired, pre-processed and de-noised as part of the Human Connectome Project (www.humanconnectome.org). For each subject, gray matter voxels were mapped to the native cortical surface and registered onto the 32k standard triangulated mesh with no topological defects to establish correspondences. Each time series was temporally normalized to zero-mean and unit-variance.

Supervortex Clustering

Our *supervortex* clustering algorithm is different from the classical k -means in two aspects:

- We limit the cluster search range to reduce the number of distance calculations, thus improve the computational performance.
- We define a hybrid distance function which is capable of matching highly correlated vertices with each other, while enforcing spatial continuity within a cluster.

We cluster the cortical vertices into *supervortices* with respect to their functional similarity and spatial proximity. The approach is summarized in Algorithm 1.

Algorithm 1: Supervortex Clustering

```
/*  $k$  initial supervortex centroids are selected by uniformly sub-sampling the cortical mesh. */
```

```
foreach vertex  $v$  do
```

```
   $labels(v) \leftarrow 0$ 
```

```
   $distances(v) \leftarrow \infty$ 
```

```
repeat
```

```
   $changed \leftarrow false$ 
```

```
  foreach supervortex centroid  $S_k$  do
```

```
    foreach vertex  $v$  within  $R$  mm of  $S_k$  do
```

```
       $D =$  distance between  $S_k$  and  $v$ 
```

```
      /* Distance calculations performed only for vertices within predefined search range  $R$ . */
```

```
      if  $D < distances(v)$  then
```

```
         $distances(v) \leftarrow D$ 
```

```
         $labels(v) \leftarrow k$ 
```

```
         $changed \leftarrow true$ 
```

```
    Compute the new supervortex centroids
```

```
  until  $changed \neq true$ 
```

Distance Function

Each vertex is iteratively associated with a cluster with respect to their distance, computed with an Euclidean function in the form of

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

where d_c and d_g correspond to the functional and spatial distance measures, respectively. **Functional similarity** is measured by the Pearson's distance transformation. **Spatial proximity** is 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**.

Quantitative Results

Evaluation is performed in terms of scan-to-scan reproducibility and functional homogeneity at two resolutions ($k = 1000$ and 2000). Reproducibility is obtained by computing Dice scores after matching two parcellations of each subject and averaging across the whole cortex. Homogeneity is measured by computing the average cross-correlations between rs-fMRI time series within each cluster (after applying Fisher's z -transformation). Results are given in Fig. 1 and summarized below.

- **Reproducibility:** Robust parcellations are generated with an average Dice score of $0.94 (\pm 0.04)$ and $0.93 (\pm 0.04)$ achieving at least 14.4% and 8.7% better reproducibility than the existing approaches for $k = 1000$ and 2000 , respectively.
- **Functional Homogeneity:** Our parcellations are at least as homogeneous as those of the other approaches and, on average, surpassing RG1, RG2, and NCUT for $k = 2000$.
- **Functional Connectivity:** Functional connectivity profiles computed on a set of *supervortices* are shown in Fig. 2.
- **Visual Results:** Parcellations of one subject obtained by each method are demonstrated in Fig. 3.

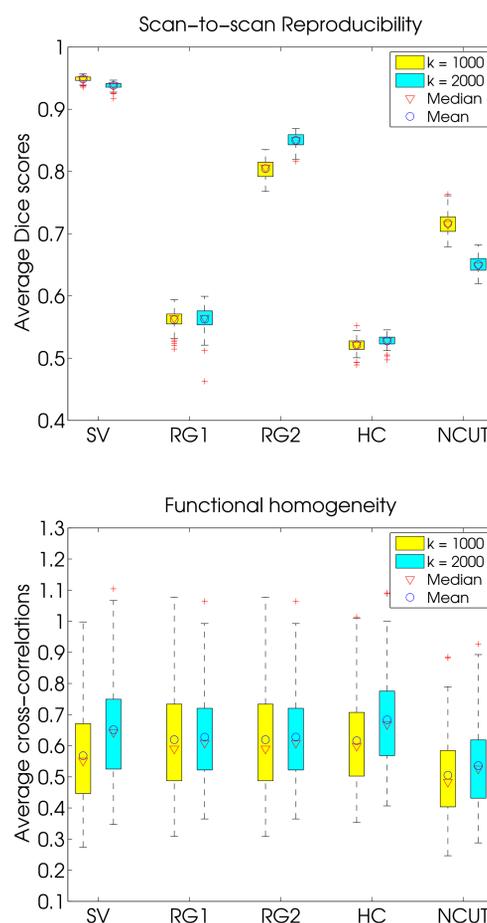


Figure 1: Reproducibility (top) and functional homogeneity (bottom) results. Each method was run with 1000 and 2000 clusters. Boxes indicate the range within the whole group of subjects. See the text above for the experimental setting.

Connectivity Results

- *Supervortices* within the same cortical area show similar functional connectivity patterns.
- There is a sharp transition in the connectivity patterns where *supervortices* cross the border between two cortical areas.

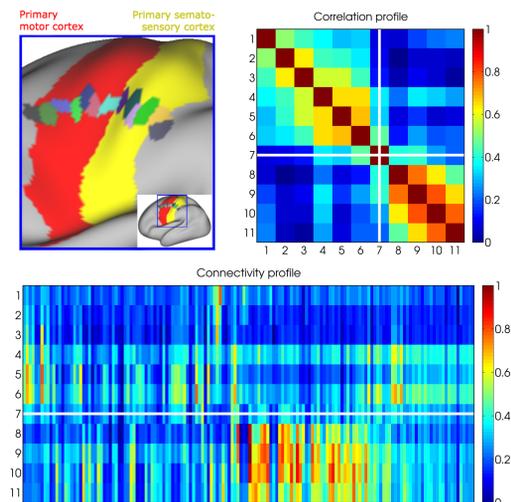


Figure 2: **Top Left:** A set of *supervortices* spanning across the primary motor (red) and primary somato-sensory (yellow) cortex, delineated from an anatomical atlas [4]. **Top Right:** Correlation profile, computed by cross-correlating the average time series within the *supervortices*. **Bottom:** Connectivity profile, computed by correlating the average time series of the highlighted *supervortices* with the average time series of the other *supervortices* across the yellow and red cortical areas (not shown).

Acknowledgments

LaTeX poster template modified from *Jacobs Landscape Poster* version 1.1.



References

- [1] Achanta et al., "SLIC superpixels compared to state-of-the-art superpixel methods," 2012.
- [2] Blumensath et al., "Spatially constrained hierarchical parcellation of the brain with resting-state fMRI," 2013.
- [3] Craddock et al., "A whole brain fMRI atlas generated via spatially constrained spectral clustering," 2012.
- [4] Desikan et al., "An automated labeling system for subdividing the human cerebral cortex into gyral based ROIs," 2006.

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Visual Results

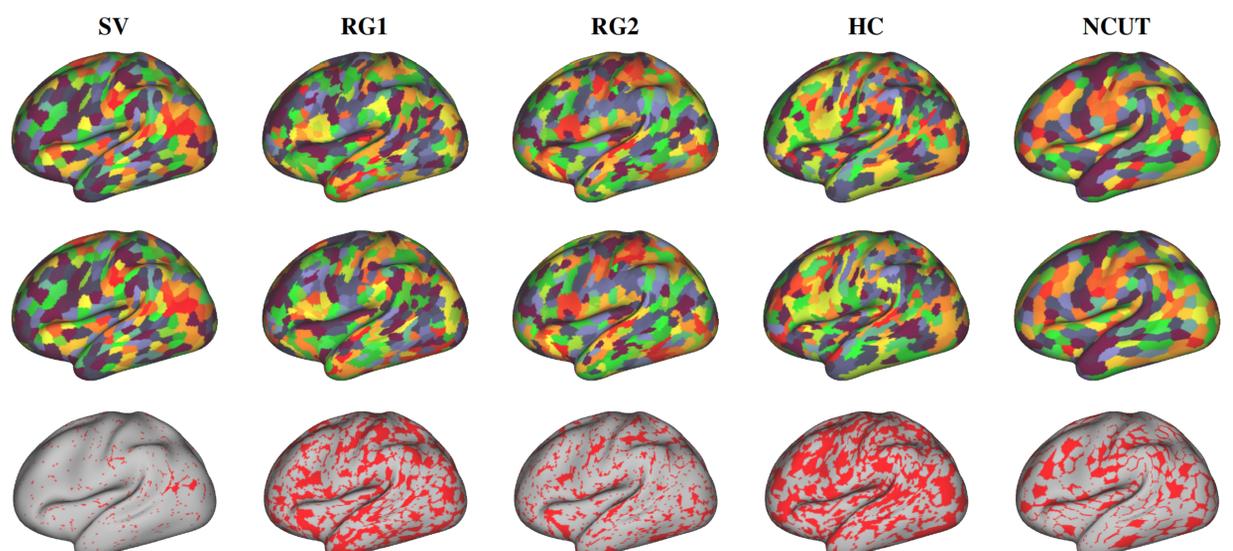


Figure 3: Pre-parcellations derived by the proposed method (SV), region growing (RG) [2], Ward's hierarchical clustering (HC), and normalized cuts (NCUT) [3] for $k = 1000$ clusters. The parcellations in the first and second row were obtained from different scans of the same subject in order to evaluate scan-to-scan reproducibility. Parcel colors were matched for better visualization and easier comparison. The last row shows the non-matching clusters. RG1 and RG2 refer to the region growing approach run with different seed sets per scan and using the same seeds for both scans of the same subject, respectively.