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Subject-specific Structural Parcellations Based on Randomized AB-divergences

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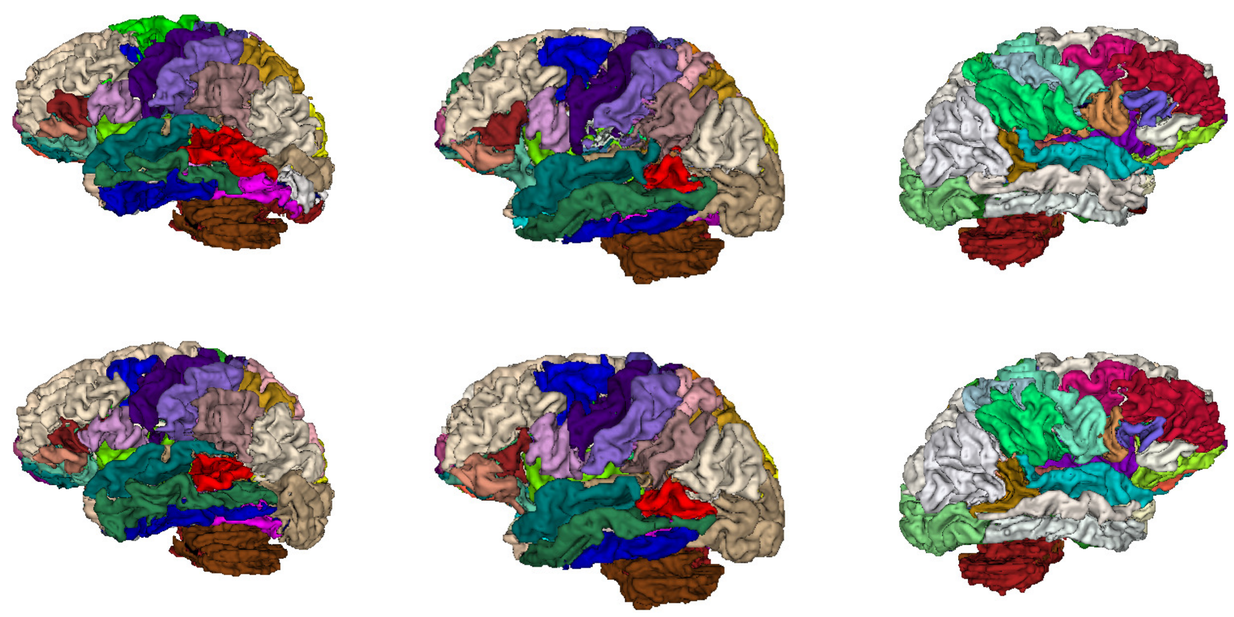
Introduction

Brain parcellation provides a means to approach the brain in smaller regions. It also affords an appropriate dimensionality reduction in the creation of connectomes. Most approaches to creating connectomes start with registering individual scans to a template, which is then parcellated. Data processing usually ends with the projection of individual scans onto the parcellation for extracting individual biomarkers, such as connectivity signatures. During this process, registration errors can significantly alter the quality of biomarkers.

In this paper, we propose to mitigate this issue with a hybrid approach for brain parcellation. We use diffusion MRI (dMRI) based structural connectivity measures to drive the refinement of an anatomical prior parcellation. Our method generates highly coherent structural parcels in native subject space while maintaining interpretability and correspondences across the population. This goal is achieved by registering a population-wide anatomical before individual dMRI scan and generating connectivity signatures for each voxel. The anatomical prior is then deformed by re-parcellating the brain according to the similarity between voxel connectivity signatures while constraining the number of parcels. We investigate a broad family of signature similarities known as AB-divergences and explain how a divergence adapted to our segmentation task can be selected. This divergence is used for parcellating a high-resolution dataset using two graph-based methods. The promising results obtained suggest that our approach produces coherent parcels and stronger connectomes than the original anatomical priors.



Methods

In this work, we parcellate the cortex according to the similarity between connectivity signatures derived from a tractography analysis. We propose to measure the similarity between signatures by computing an AB-divergence. The parameter of this divergence was set by measuring the sensitivity of the parcellation to random noise injection. Once the parameter selected, we compared three parcellation methods: tessellations, a parcellation based on a MRF framework (sGrasp) and random parcellations. We measured parcellations coherence, and we counted the tracks connecting different brain regions obtained when re-running the tractography with the novel parcellations.

Connectivity Signatures

- 9 subjects, 3 scans per subject
- anatomic prior atlas: Fressurfer used to parcellate the brain into 86 regions of the Desikan atlas [5]
- tractography using **probtrackx** (5000 seed per voxel)

final connectivity signature of each voxel p:
a vector p_i of 86 components such that:

$$\sum_{i=1}^{86} p_i = 1 \qquad p_i \geq 0 \quad \forall i$$

(likelihood to reach each region from p)

AB-divergences

The AB-divergence proposed by Cichocki et al. generalize Alpha, Beta, and Kullback-Leibler divergences [1] ($\alpha, \beta, \alpha+\beta \neq 0$)

$$D_{AB}^{(\alpha,\beta)}(p||q) = \frac{-1}{\alpha\beta}\sum_i \left({p_i}^{\alpha}{q_i}^{\beta} - \frac{\alpha}{\alpha+\beta}{p_i}^{\alpha+\beta} - \frac{\beta}{\alpha+\beta}{q_i}^{\alpha+\beta} \right)$$

We considered only the symmetric AB-divergences, for $\alpha = \beta$:

$$D_{AB}^{(\alpha,\alpha)}(p||q) = \frac{1}{2\alpha^2}\sum_i \left({p_i}^{2\alpha} + {q_i}^{2\alpha} - 2{p_i}^{\alpha}{q_i}^{\alpha} \right) = \sum_i \left(\frac{{p_i}^{\alpha}}{\alpha\sqrt{2}} - \frac{{q_i}^{\alpha}}{\alpha\sqrt{2}} \right)^2$$

We measured them in a unified way by computing squared Euclidean distance after projecting the connectivity signatures by the following function ψ_α:

$$\psi_\alpha : (p_1, ..., p_n) \mapsto (\overline{p_1}, ..., \overline{p_n}) \quad \texttt{where} \quad \overline{p_i} = \frac{{p_i}^{\alpha}}{\alpha\sqrt{2}}$$

Parcellation reproducibility

- noise injected by compressing the projected signatures by Random Projections [2]
- similarity between the parcellation measured by aRI
- for a given α:
  small similarity = parcellation driven by the signatures
  (and not by cortical geometry)

input: data X of size $N \times T$, parameter t and number of power iteration q
1. form the $N \times t$ matrix Ω by sampling from Gaussian distribution $\mathcal{N}(0,1)$
2. $U \leftarrow (X^T X)^q X^T \Omega$
3. get W by orthonormalizing the columns of U with Gram-Schmidt process
4. $Y \leftarrow XW$ **0.5em**

output: projected data Y, of size $N \times t$

Random projection for data compression [2].
$q = 3$ produced the best results.

Tessellations/Parcellations

- center of the anatomical atlas (and their signature)
- tessellation: shortest geodesic distance to the center
- parcellation: considers also similarity to the center [3]

Random Parcellations

- parcel center randomly selected inside each anatomical region
- 20 parcellation were generated for each scan

Parcellation Coherence

- each parcel pa, correlation of the connectivity signatures Σ_{pa}
- **coherence** measured by the ratio between the largest eigenvalue and the Frobenius norm of Σ_{pa}:

$$c(pa) = \max_i \left[|\sigma^i_{pa}| / ||\Sigma_{pa}||_2 \right]$$

- parcellation coherence: avg. of parcels coherence, weighted by parcel volume:

$$\mathcal{C} = \sum_{pa} vol(pa)c(pa) / \sum_{pa} vol(pa)$$

Parcellations Comparisons

adjusted Rand Index (aRI), computed from the mismatch matrix **m** between two parcellations X and Y. **m** measures the overlap between the parcels of X and Y:

$$aRI = \frac{\sum_{k,l}\binom{m_{k,l}}{2} - \left[\sum_k \binom{a_k}{2}\sum_l \binom{b_l}{2}\right] / \binom{N}{2}}{\frac{1}{2}\left[\sum_k \binom{a_k}{2} + \sum_l \binom{b_l}{2}\right] - \left[\sum_k \binom{a_k}{2}\sum_l \binom{b_l}{2}\right] / \binom{N}{2}}$$

where $a_k = \sum_l m_{k,l}$ and $b_y = \sum_k m_{k,l}$

Results

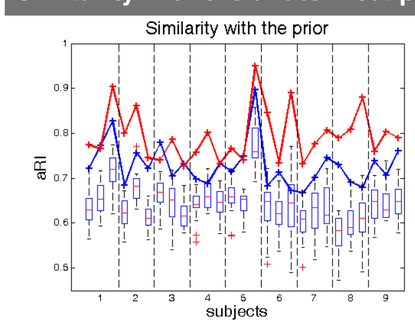
AB-divergence parameter setting

n	$\alpha = 0.25$	$\alpha = 0.5$	$\alpha = \mathbf{0.75}$	$\alpha = 1.0$	$\alpha = 2.0$	$\alpha = 4.0$	$\alpha = 8.0$	correlation
6	**0.31**±0.008	0.34±0.007	0.34±0.011	0.38±0.016	0.55±0.023	0.75±0.017	0.88±0.009	0.73±0.012
8	0.42±0.010	0.43±0.006	**0.41**±0.011	0.43±0.016	0.59±0.022	0.78±0.017	0.90±0.008	0.77±0.010
10	0.48±0.011	0.48±0.007	**0.45**±0.011	0.47±0.016	0.62±0.021	0.80±0.015	0.91±0.007	0.80±0.009
12	0.54±0.010	0.52±0.007	**0.47**±0.011	0.50±0.016	0.64±0.020	0.81±0.014	0.92±0.007	0.82±0.009
14	0.56±0.011	0.56±0.007	**0.50**±0.011	0.52±0.015	0.66±0.021	0.82±0.014	0.92±0.007	0.84±0.008
16	0.59±0.010	0.58±0.007	**0.52**±0.011	0.53±0.015	0.67±0.02	0.83±0.013	0.92±0.007	0.85±0.008
20	0.63±0.010	0.61±0.008	**0.55**±0.010	0.56±0.014	0.69±0.019	0.84±0.012	0.93±0.006	0.87±0.007
25	0.67±0.009	0.64±0.007	**0.57**±0.010	0.58±0.014	0.70±0.018	0.84±0.012	0.93±0.006	0.89±0.006
av.	0.526	0.520	**0.475**	0.495	0.639	0.811	0.914	0.82

Average pairwise aRI ± SEM, for all AB-divergences and number of random projections n (avg. over the 27 scans of the 45 pairwise aRI measured for each scan).

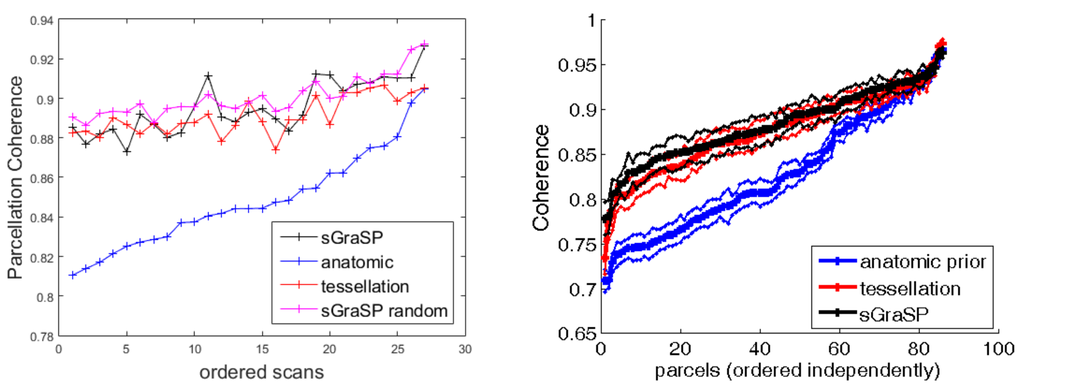
- most sensitive parameter: $\alpha = 0.75$ (for most number of random projections)
- most AB-divergences are more sensitive to noise injection than the standard Pearson correlations

Similarity with the anatomical prior



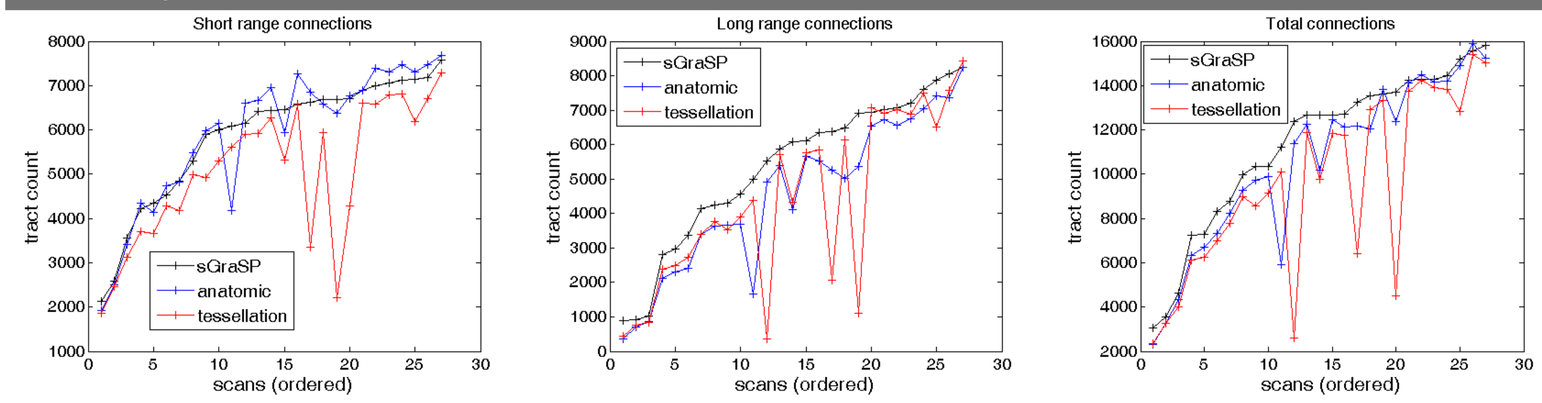
similarity with the anatomical prior, for tessellations (red), sGraSP parcellations (blue) and twenty random sGraSP parcellations (boxplots)

Parcellation coherence



(1) parcellation coherence (2) Average parcel coherence (± SEM).

Connectivity



After signatures update (1) number of tracts linking adjacent regions ("short range" connections) (2) long range connections. (3) total, sorted by sGraSP counts.

Conclusion

- tessellations very similar to the prior (less update of the prior)
- tessellation and parcellation very coherent
- stronger connectivity after tractography update for the parcellation, in particular for long range connectivity

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