

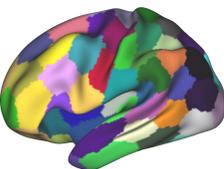
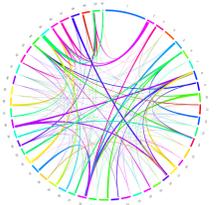
Introduction

Context

- ▶ Brain connectivity studies can provide key insight into the brain's organisation
- ▶ Parcellation of the cortical surface is essential for the construction of connectivity networks
- ▶ Parcellation evaluation is very challenging due to the absence of ground truth

Highlights

- ▶ Two **quantitative** brain parcellation evaluation measures
- ▶ Evaluate group consistency and fidelity to the connectivity matrix
- ▶ Tested on 5 different methods
- ▶ Measures follow what is expected intuitively



Database

Data

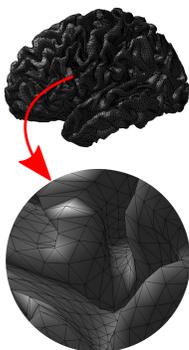
- ▶ 50 different subjects of the Human Connectome Project database [1]
- ▶ Cortical surfaces represented as 32k vertices meshes
- ▶ Sulcal mesh registration yields vertex correspondences across subjects

Tractography matrix

- ▶ Obtained from FSL's bedpostX and probtrackX [2]
- ▶ A row of the matrix describes how a vertex is connected to the rest of the cortical surface: **Connectivity profile**
- ▶ Affinity between vertices: Pearson's correlation between connectivity profiles

Parcellation methods

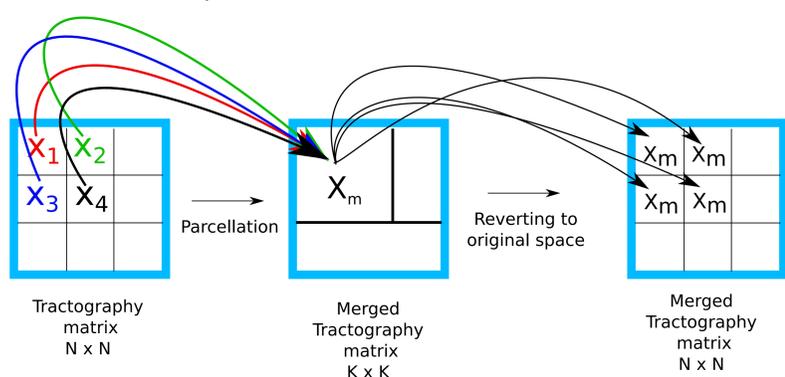
- ▶ Connectivity independent
- ▶ Connectivity driven: regroup vertices with a high affinity



Information Loss: Kullback-Leibler Divergence

Connectivity Matrix Merging After Parcellation

- ▶ Assign a merged connectivity profile to each parcel by averaging the parcels' vertices' connectivity profiles
- ▶ For N vertices and K parcels:



Kullback-Leibler Divergence

- ▶ Evaluate the **information loss** caused by approximating the tractography matrix χ with the merged matrix χ_m reverted to the original $N \times N$ space.
- ▶ Compute the KL divergence between χ and χ_m , normalised to be probability mass functions.
- ▶ The KL divergence should be **minimal** when the parcellation is the most faithful to the data

Group Consistency: Sum of Absolute Differences

- ▶ Inspired from the **Minimum Description Length** concept
- ▶ Single-subject parcellations matching based on the number of shared vertices
- ▶ Compute a **group average** merged tractography matrix
- ▶ Compute the SAD between each subject's merged tractography matrix and the average
- ▶ Evaluates how close the group is to the average representation
- ▶ Compares **network similarity** rather than parcel boundaries

Results

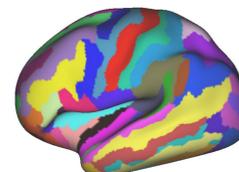
Compared methods

Connectivity independent:

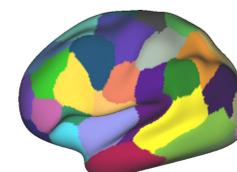
- ▶ Anatomical parcellations (Destrieux atlas [5])
- ▶ Poisson disk sampling random parcellations

Tractography driven:

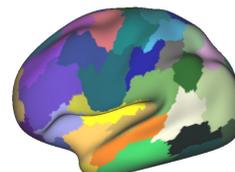
- ▶ Hierarchical clustering
- ▶ Multi-scale spectral clustering
- ▶ Group-wise multi-scale spectral clustering



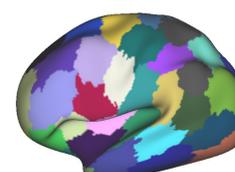
Anatomical



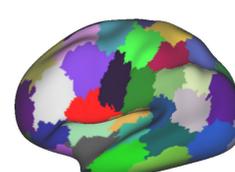
Random



Hierarchical



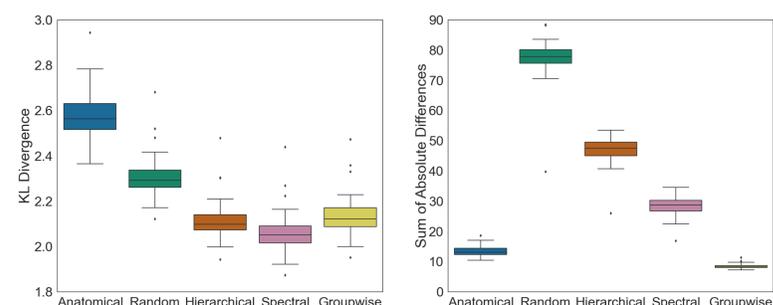
Spectral



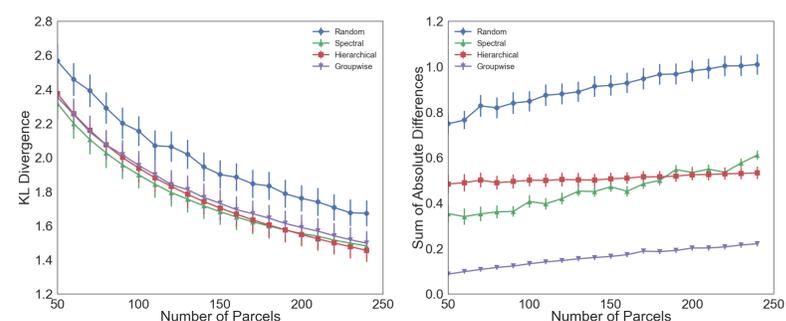
Groupwise

Quantitative results

- ▶ Boxplot comparison of all methods:



- ▶ Evolution of the two measures with respect to the number of parcels:



Acknowledgements

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References

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- [2] Behrens, T. (2007): Probabilistic diffusion tractography with multiple fibre orientations: What can we gain? *NeuroImage*, vol. 34, no. 1, pp. 144-155
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