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Transcriptomic parcellation of the human brain reflects structure and function

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Transcriptomics parcellation of the cortex best reflects cytoarchitectonic divisions.

INTRODUCTION

- Traditional parcellations of the human cortex represent neuroanatomy and cytoarchitectonic organization
- Recent atlases were derived from neural activity at rest or during tasks, i.e., functional organization
- Gene expression is variable across the human cortex [1]
- Regional gene expression reflects the regional composition of cell types
- Here we derive a transcriptomic parcellation of the human cortex

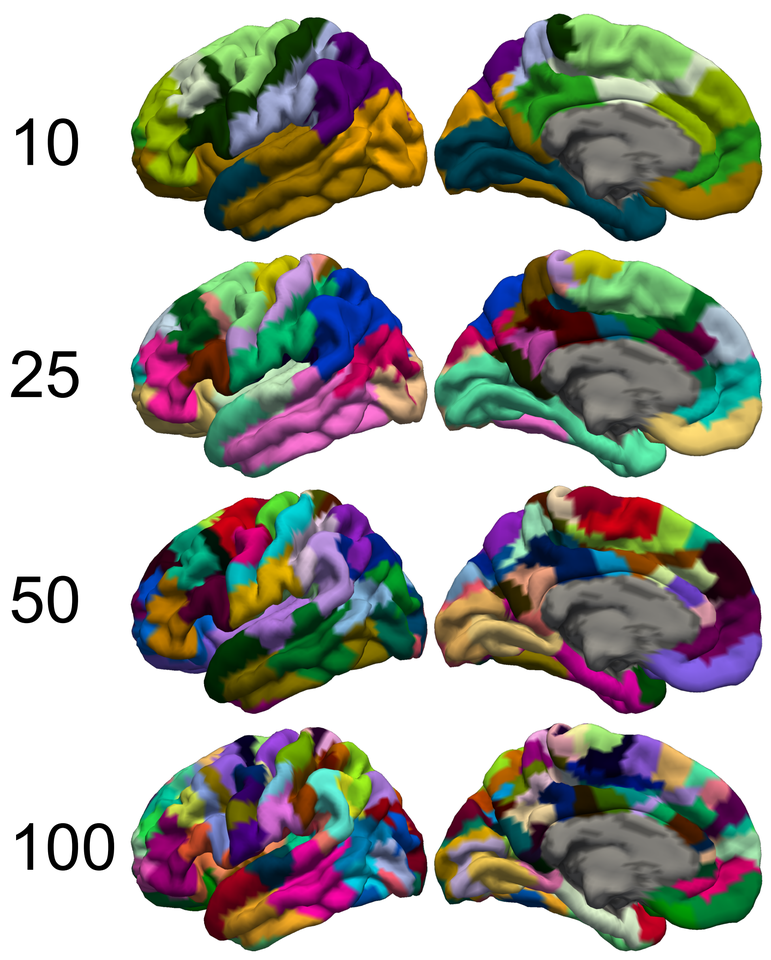
METHODS

1. Microarray gene expression data from the Allen Institute [1].
2. Each gene represented by one probe (max. variance)
3. Compute top 100 principal components (PCs) and select PCs representing brain cell types (22 selected).
4. Expression of the selected PCs interpolated across the cortical surface.
5. Hierarchical clustering (complete linkage) for k=10, 25, 50, 100.
6. Test overlap with existing atlases using spin-test [2] with 1,000 permutations.

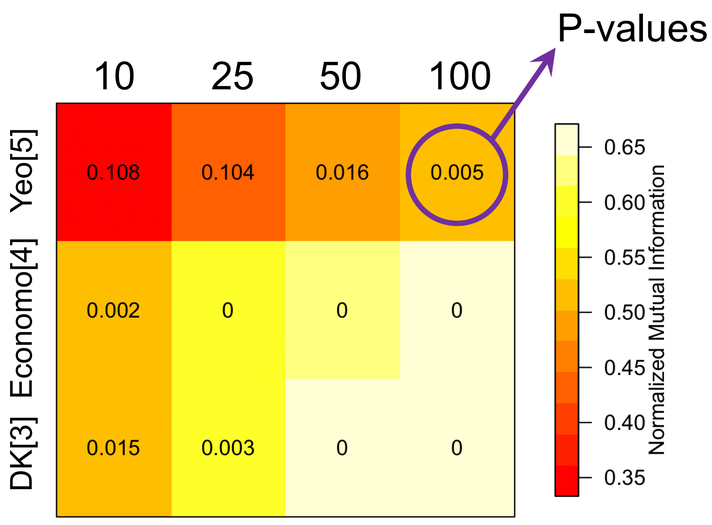
Get the atlas:
https://github.com/andrealtmann/transcriptomics_parcellation

RESULTS

Transcriptomic parcellation of the cortex



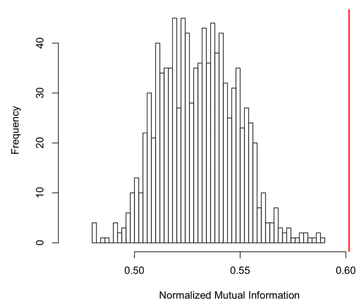
Significant overlap with structural and functional parcellations.



ADDITIONAL INFORMATION

- 3,702 gene expression samples in the Allen Atlas from six donors
- Each measures 58,692 gene probes
- After quality control and sample selection (cortical samples in the left hemisphere) 1221 cortical gene expression samples were retained
- Each gene is represented by a single gene expression probe
- Computed the top 100 principal components (PC)
- We selected components that represented brain cell-types (neurons, microglia, astrocytes, oligodendrocytes, endothelia).
- For each of the selected components we interpolated the eigen gene-expression across the entire surface of the left hemisphere using kernel density-based smoothing and geodesic distances along the pial surface.
- Finally, we used hierarchical clustering with complete linkage (with k=10, 25, 50, 100) to assign each vertex on the surface to a cluster.

- The resulting parcellations were tested for their spatial overlap with structural (DK[3] and ECO[4]) and functional parcellations (YEO[5]) using the spin-test[2] with 1,000 permutations and normalized mutual information (NMI), and a mask for the medial wall.



Normalized Mutual Information (NMI) between permuted ECO and the transcriptomic parcellation with K=25. The red line marks the NMI of the unpermuted atlas.

References:

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