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Julich-Brain GapMaps parcellation based on structural connectivity using Constellation

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The release of the Julich-Brain[1] has broadened the horizons of brain mapping, especially in the field of cytoarchitectonics. This meticulous work of 25 years proposes a 3D probabilistic atlas of areas distributed across the cortex and subcortical nuclei. Among these areas some have a special status: because the cytoarchitectonic mapping of these areas in the postmortem histological brains is still in progress, they were regrouped under the labelling GapMaps, to provide a whole-brain consistent parcellation. Thus, GapMaps study is a work-in-progress in the spirit of the Julich-Brain as an atlas in continuous evolution.

To contribute to the segregation of these particular regions, which are among the most complex from the architectonics point of view, we have adapted Constellation[2], an algorithm used to produce structural-connectivity-based parcellations from tractography data. From a predetermined group of subjects of the HCP 1200S dataset, with a point-to-point matching between their cortical meshes[3] and their pre-processed individual tractographies[4], an averaged connectivity profile to the whole cortex is computed for the surface projections of each GapMap[5]. This mean profile is then used to determine, with a watershed algorithm, basins corresponding to highly connected regions of the profile. Each such basin is supposed to correspond to a specific cortical area. The dimension of the connectivity matrix of each subject of the group is reduced using these basins and an average matrix is computed. Based on the latter, a pairwise distance is calculated between the reduced connectivity profiles of the vertices of the GapMap. From this pairwise distance, groupwise clusterings are computed using a K-medoid algorithm, with a degree of freedom on the number of clusters allowed, from 2 to 12 clusters. Finally, from these various clusterings and using a predefined criterion, we determine the optimal number of areas, resulting in a sub-parcellation of each GapMap [Figure 1].

The determination of the number of areas constituting each GapMap is a real challenge as, currently, there is no widely accepted ground truth. Thus, the comparison of these parcellations with their cytoarchitectonic counterparts is of high interest both to link computational and anatomical realities, and to integrate two different modalities of brain mapping.

Finally, Constellation may also be used to project an atlas on individual subjects in order to obtain individual connectivity matrices and parcellations[6]. Thereby, it will be used to provide connectivity matrices to simulations of the brain dynamics using parcels of homogeneous sizes[7]

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