Hierarchical parcellation using discrete Morse theory of whole-brain high-resolution resting-state 7T fMRI data

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Target audience: Neuroscientists, engineers and clinicians interested in brain parcellation using resting-state fMRI at ultra-high field.

Purpose: With the recent development of fast acquisition sequences at ultra-high-field (7T), high spatial resolution resting-state fMRI (rs-fMRI) can now be collected from the whole-brain with improved temporal resolution for the study of the haemodynamic fluctuations underlying functional connectivity[1]. Parcellation of the brain into functionally meaningful regions is a crucial step in studies of brain connectivity using complex network analysis. A method for obtaining individual brain parcellations based on rs-fMRI has recently been proposed, which grows a set of stable seeds into an initial detailed parcellation that is then further clustered using a hierarchical approach that enforces spatial contiguity of the parcels[2]. Although excessive smoothing is avoided, 2.35mm FWHM Gaussian kernel smoothing of the stability maps is nevertheless used to remove spurious features before the growing step, which precludes the exploration of the ultra-high spatial resolution of our data. Here, we present a modification of this method based on discrete Morse theory that circumvents stability map smoothing, hence allowing finer parcellations of ultra-high resolution rs-fMRI.

Methods: 9 healthy subjects were studied on a 7T whole-body scanner with a 32-channel receive RF coil. 2x5min of rs-fMRI data were collected using a GE-EPI sequence with TE=32ms, TR=2.5s, FA=75º, GRAPPA factor = 3, simultaneous-multi-slice factor = 3, nominal echo spacing = 0.82ms, whole-brain coverage by 123 sagittal slices and 1.1mm isotropic resolution. A T_1-weighted structural image was also acquired using multi-echo MPRAGE, with 1mm isotropic resolution[3]. Data analysis was carried out using Matlab, FSL and SPM tools. Pre-processing included: motion correction; slice time correction; physiological noise correction using an extended RETROICOR based on simultaneous cardiac and respiratory data[4]; minimal spatial smoothing with a 1.5mm FWHM Gaussian kernel; tissue segmentation of structural images; and co-registration between functional, structural and MNI images.

Brain parcellation is performed based on each rs-fMRI dataset, in a gray matter mask including cortex, deep gray matter, brainstem and cerebellum, with the following steps. 1) A stability map is computed as the root mean square error between all time-series in a 3mm radius ROI and its mean time-series, which reflects the suitability of each voxel to be representative of its neighborhood[2]. 2) An initial partition is performed by assigning each voxel to a stable basin surrounding a local minimum, using discrete Morse theory[5]. The stability map is modelled as a cubical complex, K, whose vertices are the voxels of the image. A discrete gradient vector field, V, is then built from K[6], and the partition of the image is defined by considering the voxels in the stable set of each minimum[5]. 3) A hierarchy of parcellations with successively finer levels of detail is obtained by an iterative procedure that simplifies V based on the concept of cancellable closest points[5]. These are pairs of critical cells in K that have a single V-path between them in the Morse chain complex and that are the closest to each other in terms of persistence. This measure determines the order of cancellation, thus preserving the most significant structural features of the image. The intra-subject reproducibility of the proposed method was measured by computing the Dice similarity between matching parcels in the parcellations of the two datasets from each subject. Parcels were matched between parcellations by using a minima tracking procedure based on the respective gradient vector fields[7].

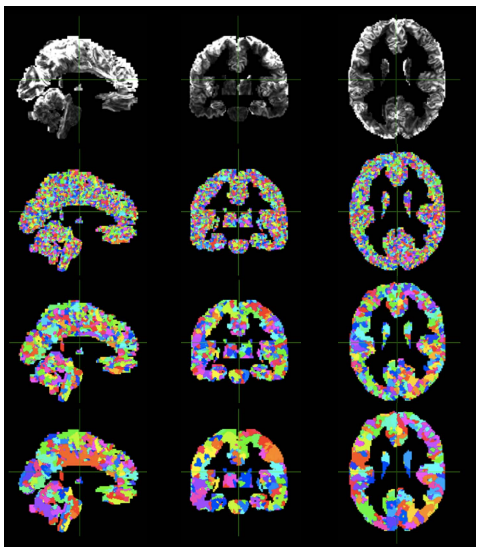

Fig.1. Stability map (top) and parcellations at different levels of detail (80k, 10k and 3k parcels, from top to bottom), for one example dataset.

Results: The stability map, initial parcellation and subsequent parcellations at different levels of detail, are shown for one representative dataset, in Fig.1. The parcellations intra-subject reproducibility is shown in Fig.2, for the different levels of detail: Dice coefficients increase from 0.82 to 0.96 between 3k and 20k parcels and then stabilize with a trend to decrease slightly towards the highest levels of detail.

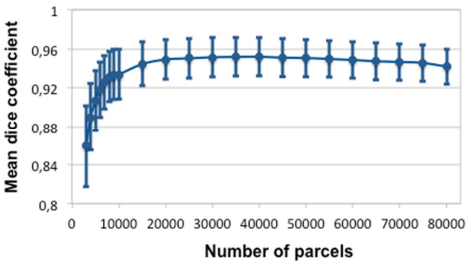

Fig.2. Intra-subject reproducibility of parcellations at different levels of detail, measured as the group mean dice coefficient (error bars represent SD).

Conclusion: The proposed method produced brain parcellations of whole-brain, ultra-high-resolution 7T rs-fMRI data at levels of detail of up to 80k parcels, with excellent intra-subject reproducibility. The significance of such fine brain parcellations should be investigated in future studies. The parcel matching approach that is implicit in our method, and is used here for within subject comparison, should allow the extension of the method to group parcellations. These results open up new possibilities for complex network analysis of whole brain connectivity with ultra-high spatial resolution.

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References: 1. Wald et al., Neuroimage 2012, 62(2): 1221-9 **2.** Blumensath et al., Neuroimage 2013, 76: 313–24. **3.** van der Kouwe et al., Neuroimage 2008, 40(2): 559-69. **4.** Jorge et al., Magn Reson Imag 2013, 31(2): 212-20. **5.** Delgado-Friedrichs et al., TPAMI 2014, doi:10.1109/TPAMI.2014.2346172. **6.** Robins et al., TPAMI 2011, 33(8): 1646–58. **7.** Reininghaus et al., TVCG 2012, 18(9): 1563-73.