Individual brain parcellation based on single subject ICA

E. van Oort[1], and D. Norris[1]
[1]MR Techniques in Brain Function, Radboud University Nijmegen, Donders Institute, Nijmegen, Gelderland, Netherlands

Introduction:

Standard brain atlases are commonly used in neurological applications of MRI, particularly fMRI studies. This abstract describes research attempting to develop a method to create an individual parcellation based on a single subject Independent Component Analysis (ICA). It uses high quality multi echo resting state fMRI data from 47 subjects. The goal is to develop a method that can create an atlas tailored to the individual subject, to account for inter-subject variability.

Data and Methods:

rs-fMRI data were acquired at 3T from 47 healthy subjects on a Siemens Magnetom Trio system using a 32 channel head coil The resting state scan used a five echo multi echo EPI with acquisition parameters: TR = 2000 ms, TE = 6.9, 16.2, 25, 35 and 44 ms, flip angle 80°, 39 slices, 3.5 mm isotropic resolution, 1030 volumes, scan time 35 minutes, GRAPPA factor 3, 6/8 partial Fourier. rs-fMRI preprocessing involved realignment, merging of the five echoes, and spatial normalization to MNI space using functions from SPM5 (Wellcome Department of Imaging Neuroscience, University College London, UK). Non-brain regions were removed using the Brain Extraction Tool from FSL (fMRIB's Software Library, http://www.fmrib.ox.ac.uk/fsl). The data were filtered in the temporal domain with a 6th order Butterworth band pass filter.

Damoiseaux *et al.* showed that it is possible to find at least ten different resting state networks on a group level, using ICA techniques.[1] The current work used a very long resting state scan, 35 minutes, to have enough information for a detailed single subject ICA. MELODIC was set to obtain 75 Independent Components (ICs). A tool was developed to discard the ICs containing artifacts, white matter or regions outside the brain, so only components relating to anatomical grey matter structures remained. This tool also applies a spatial filter to remove small clutter from the components that are selected for further processing.

The remaining ICs were used to parcellate the brain for every subject. ICs were split up into their constituent regions. Some of these regions will overlap. For an atlas-like parcellation it is necessary to have a single label for every location, so this overlap has to be resolved. In the case of a small overlap, like a sliver of overlap from both parent regions, the voxels of the overlap were assigned to the neighbouring region with which it had the highest correlation. With a larger overlap (n>100 pixels), the overlapping region is removed from both neighbours and becomes a new region. In the case of a large overlap which constitutes the major part of both parents, the parents are joined and become one larger region. This strategy was applied iteratively until all overlaps were resolved. The resulting regions were used to parcellate the brain. The quality with respects to the AAL template was checked visually, and by using it for a graph analysis, using resting state partial correlations between regions, similarly to work by van den Heuvel *et al.*[2] The networks resulting from both the AAL template and the parcellation were examined for small-world properties, and are shown in Fig 1.

Results:

The brain parcellation was successfully performed for every subject. Figure 2 shows slice number 36 from the first 9 subjects (i.e. not specially selected), together with a 3D rendition of the parcellation of subject 1. On average, this resulted in a parcellation containing 218 regions. The parcellations were visually inspected viewing slices and 3D renders. There are several similarities to the regions of the AAL template. The regions were also used as a basis for a graph analysis. Figure 1 shows the graphs showing the small-world factor as a function of threshold. Both networks have a small-world factor higher than one, and this increases as a power law function with increasing threshold. This shows that the network defined by the parcellation method is organized as a small-world network.

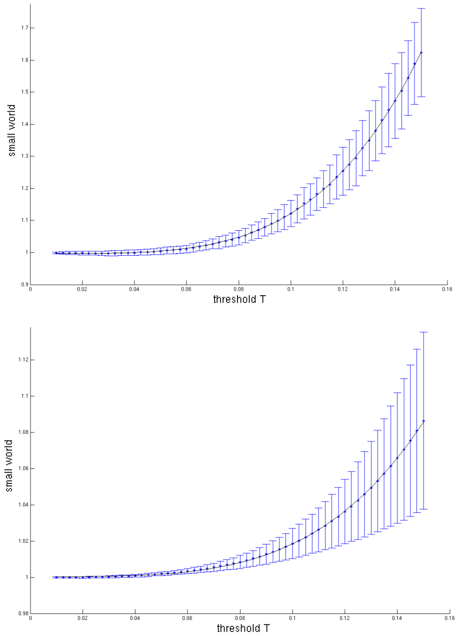

Figure 1, small-world AAL (top) and parcellation (bottom)

Conclusion and Discussion

The parcellation method described in this abstract shows promise in providing a tailored atlas for an individual subject, based on resting state fMRI and ICA techniques. There is still a large degree of variability between subjects, but the resulting parcellations also seem quite similar to the AAL template. The 3D renditions in particular show the structure of the parcellation. Several anatomical features are easily recognizable, all based on the ICA analysis without using any prior information.

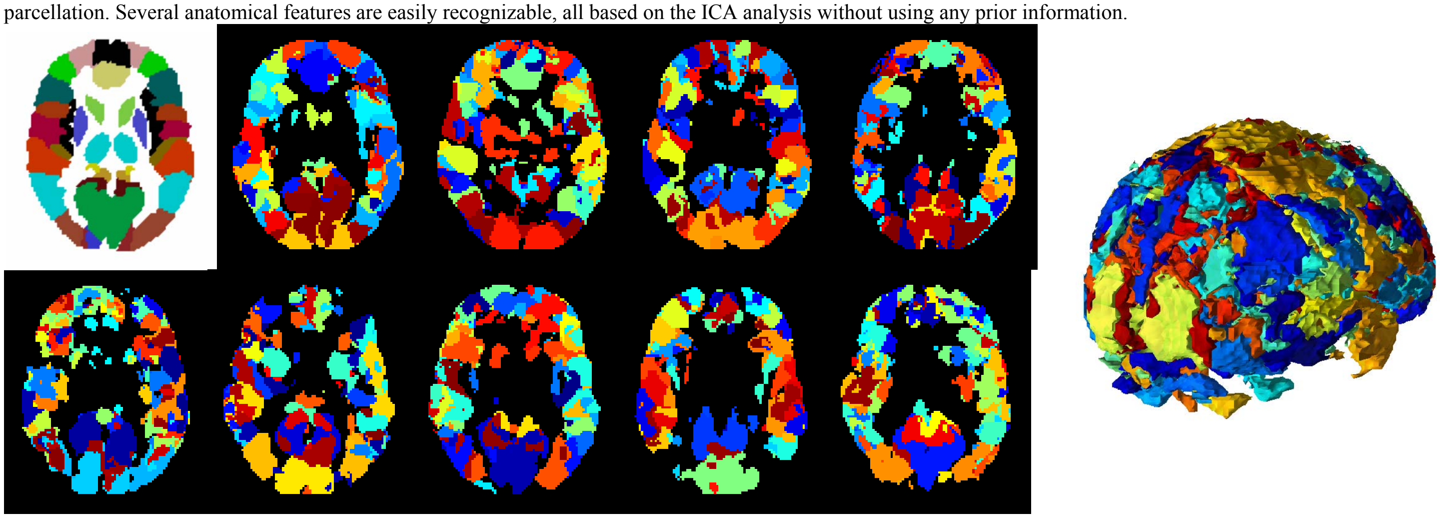

Figure 2, slice 36 of the AAL template and of the parcellation of subjects 1 to 9, and a 3D rendition of the parcellation of subject 1

References:

[1] J.S. Damoiseaux *et al.,* Consistent resting-state networks across healthy subjects, *PNAS* September 2006

[2] van den Heuvel *et al.*, Small-world and scale-free organization of voxel-based resting-state functional connectivity in the human brain, *NeuroImage 2008*