Atlas-based analysis of resting state functional connectivity MRI

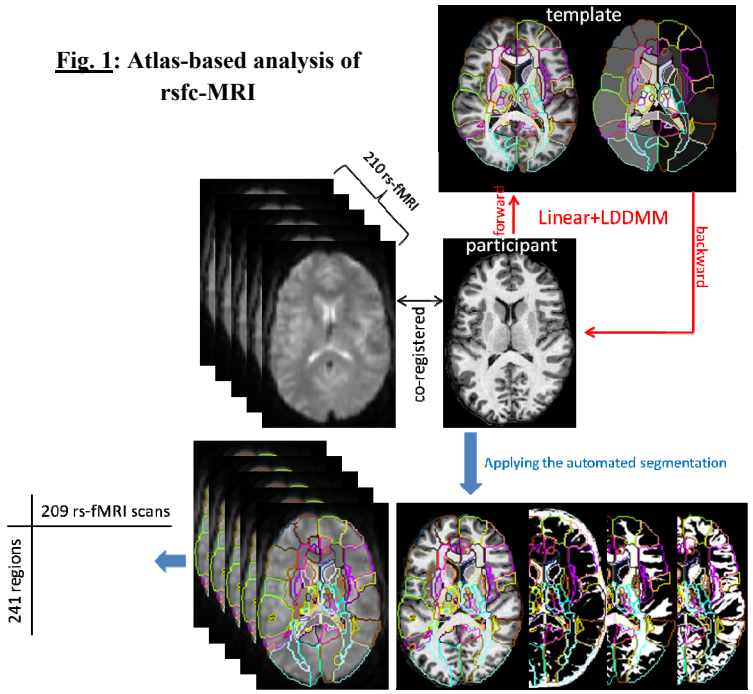
A. V. Faria[1,2], S. Joel[1,3], X. Tang[4], P. vanZijl[1,3], M. Miller[4], J. Pekar[1,3], and S. Mori[1]

[1]Radiology, Johns Hopkins University, Baltimore, MD, United States, [2]Radiology, State University of Campinas, Campinas, SP, Brazil, [3]FM Kirby Research Center for Functional Brain Imaging, Kennedy Krieger Institute, Baltimore, MD, United States, [4]Biomedical Engineering, Johns Hopkins University, Baltimore, MD, United States

Introduction: Resting state functional connectivity MRI (rsfc-MRI) is becoming widely-used for neuroscience studies. This approach is particularly important in patient populations who would have difficulty with paradigms used in task-related fMRI. Studying diseases in clinical populations is challenging due to two factors. First, identification of corresponding cortical areas across subjects is not straightforward. Secondly resting state connectivity is usually assessed from pixel-to-pixel time-domain correlation, which is inherently very noisy[1,2]. A widely used approach is to average over voxels by applying Gaussian filters that cannot reflect biological and anatomical local particularities. We propose, as an alternative, an Atlas-Based Approach (ABA) to functional connectivity, where an automated 3D segmentation is applied in each individual. The automated segmentation works as an anatomical filter, reducing the dimensionality of the data from hundreds of thousands of voxels to a vector of hundreds of regions. In this study we report on initial findings in functional brain connectivity and inter-session intra-subject reproducibility of the results.

Methods: High resolution anatomical images (T1-WI) and rsfc-MRI data were acquired in two sessions in each 21 normal volunteers (data available at http://www.nitrc.org/projects/multimodal/). The rsfc-MRI data were slice-time corrected, motion-corrected, and a component based-method (CompCor)[3] was used for the reduction of physiological noise. As shown in Fig. 1, the T1-WI were co-registered with the rsfc-fMRI scans and normalized to a single subject template that was segmented into 185 3D regions of interest (ROIs)[4], using large-deformation diffeomorphic metric mapping (LDDMM)[5]. Using the deformation fields from LDDMM and the inverse linear matrix, we warped the segmentation map from our template to each subject space. This process was done using the software DiffeoMap (www.mristudio.org). Peripheral white matter and cortex were separated individually using Statistical Parametric Mapping (SPM) segmentation. As a result, we obtained a matrix of 241 regions and 209 time-domain rsfc-MRI values for each participant. From these matrices we extracted the correlations between the rsfc-MRI time-courses of each ROI, for each participant.

Fig. 1: Atlas-based analysis of rsfc-MRI



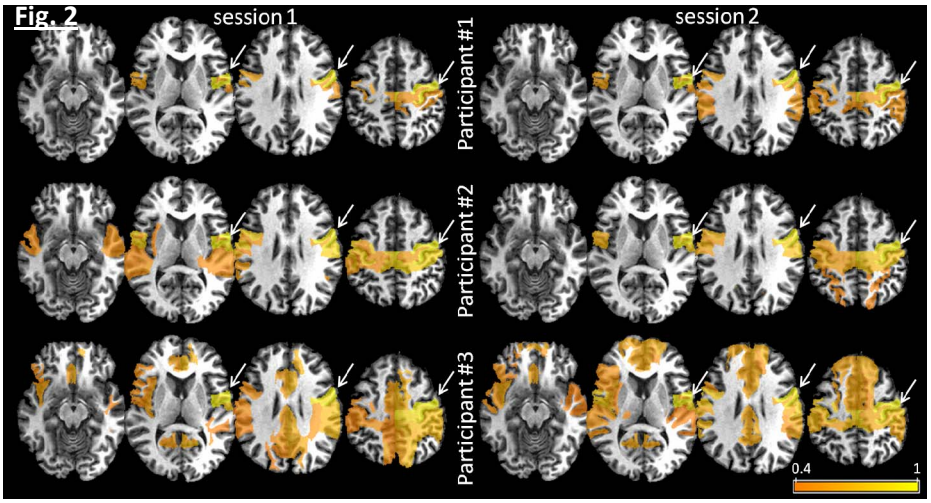


Table 1: Reproducibility of rsfc-MRI. Average of regional inter-session and inter-subject correlation coefficients. Highest correlations (red) were found inter-session.

		Participant #1		Participant #2		Participant #3	
		session 1	session 2	session 1	session 2	session 1	session 2
Part. #1	session 1	1					
	session 2	0.66	1				
Part. #2	session 1	0.37	0.36	1			
	session 2	0.34	0.33	0.56	1		
Part. #3	session 1	0.33	0.34	0.37	0.34	1	
	session 2	0.39	0.37	0.45	0.38	0.67	1

Results and Discussion: Figure 2 shows, as an example, the result for the correlation of one of the 241 ROIs (left pre-central gyrus, arrows) in three participants, for the two sessions. Regions highly correlated with this area (correlation coefficient >0.4) are color-coded. Left pre-central gyrus was highly correlated with the homologous gyrus as well as with post-central gyri, superior temporals (in participants #2 and #3), and cingullum (participant #3). The correlation maps of the left pre-central gyrus with other areas were more similar inter-subject (between scans 1 and 2) than inter-subject (correlation coefficient = 0.69 and 0.4, respectively). Similar results were found for other regions (table 1), indicating the reproducibility of the inter- and intra-subject rsfc-MRI using ABA.

Each parcel can be individually analyzed or can be combined with others to study previously defined resting state networks. Additionally, the investigation of the interactions among these regions can reveal novel networks. In the future, because we are using a highly accurate normalization-based whole brain analysis, we may use results from voxel-by-voxel analysis to refine the automated segmentation, particularly in cortical areas, thereby improving its capability to map functional relevant connections.

Bibliography: **1.** Shehzad Z, et al. 2009. Cereb Cortex, 19(10):2209-29; **2.** Damoiseaux JS, et al. 2006. PNAS, 12;103(37):13848-53. **3.** Behzadi Y, et al. 2007. *NeuroImage*, 37(1):90-101; **4.** Oishi K, et al. *NeuroImage*, 46(2):486-99. **5.** Miller MI, et al. 2005. *PNAS*, 102(27):9685-690.