# Reliable amygdala segmentation using clustering of multimodal data at 7 Tesla.

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**Introduction:** The amygdala has a typical volume of 1500 $mm^3$. Its location next to the sphenoidal sinus results in a variety of MR image artifacts, which increase with field strength. However, brain scanning at 7T provides considerable improvement of SNR and CNR, and thus it has the potential for *in vivo* parcellation of amygdala images into neurologically significant subdivisions that may improve interpretation of fMRI-based neuropsychological studies. The analysis and clustering techniques we have developed for this purpose may assist parcellation of other deep brain structures.

**Methods:** 9 healthy subjects underwent structural scanning on a 7 Tesla Magnetom MRI system (Siemens, Erlangen) with an 8-channel head array coil (RAPID, Rimpar). MP-RAGE images with full brain coverage were obtained (TR=3000 ms, TE=2.95 ms, TI=1100 ms, voxel (1.2 mm)³, flip angle=6°, iPAT=2). These were used for localization and as inputs for the clustering procedures used. Additionally, fully flow-compensated spoiled GRE was used to obtain 30 coronal slices encompassing the amygdala with isotropic voxel size of 1.2 mm (no gap) (TR=2000 ms, TE=20.2 ms, flip angle=70°). Scans of the same slices with the same resolution were performed using a TSE sequence (TR=9130 ms, TE=22 ms, flip angle=60°). Total scan time was 40 min. To assess replicability of the results, each sequence was repeated at each session, and subjects were scanned a second time a week later.
To improve clustering we used the strategy of combining images having different contrast mechanisms. We manually delineated the amygdala in order to exclude the extraneous tissue which is generally included by automatic tools such Freesurfer or FSL atlas [1]. Finally, we used the well-established method of spectral clustering [2,3] to identify subregions. Multivariate feature vectors containing the image intensities for the GRE and TSE acquisitions were utilized. Cluster numbers (k) of 3, 4 and 5 were investigated, using the value of Cramer's V [4] as a guide to the optimum number. To assess replicability, correlations of voxels within the amygdala between all acquisitions were computed.

**Results and discussion:** The amygdala has been previously segmented with the use of DTI data at 3 T [5]. This study shows its first structural segmentation at 7 T. TSE and GRE sequences provided specific contrast information, while the MR-RAGE data did not add any additional feature (Fig. 2). After applying spectral clustering, when Cramer's V was computed across both sessions, good consistency was found with k = 3 for 6 out of 9 subjects. This number is consistent with a broad classification of the 13-15 amygdaloid nuclei that is generally accepted in histological studies [6] (Fig. 1). The remaining 3 subjects showed larger values of Cramers V when k = 5. The spatial distribution of the clusters found within the amygdala was topologically similar to the groups of nuclei shown in histology-based maps, but their sizes did not show the same consistency [7]. These discrepancies should be seen as a challenge for further research for *in vivo* methods. The high correlation of image intensity across weeks (0.70 for TSE and GRE) confirms the robustness of the data acquisitions and clustering techniques used. Furthermore, since spectral clustering uses a matrix formed from image intensities produced by both sequences (Fig. 1), the resultant clusters are common to both contrasts while artifacts are specific to each contrast. In conclusion, the increased CNR available at 7 T enables segmentation of the amygdala, and may be used to investigate brain areas with similar tissue characteristics and feature complexity to assist *in vivo* anatomical and functional studies.

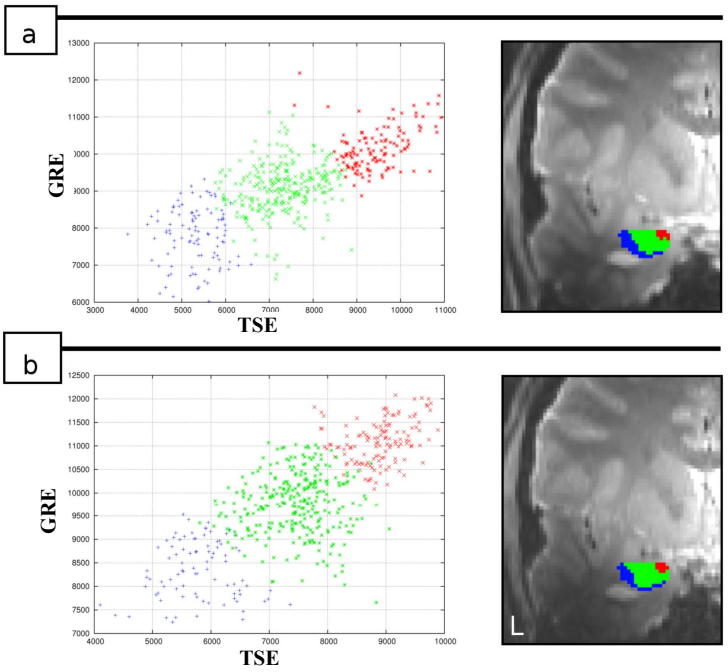


**Fig.1.** Single data left temporal lobe. (**a**) first week session (with the acquisitions repeated) (**b**) second week session. (**a-b left**) 2D histogram of all voxels within the amygdala. Each voxel shows two contrasts intensity. Spectral clustering is shown in colours representing the resultant clusters from both TSE and GRE grey values. (**a-b right**) Coronal view. Resultant clusters from both contrasts on each week superimposed into a TSE image. Clusters show high correspondence across weeks.

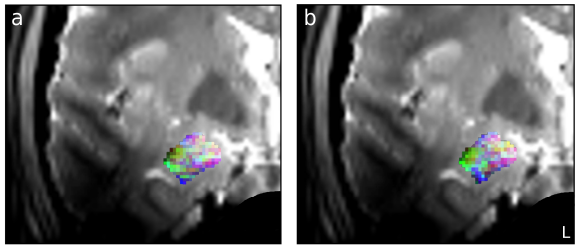


**Fig.2.** False colour images (FCI) of the left amygdala represent the weight of each sequence contribution to the contrast. Single subject coronal view (**a-b**) all acquisitions on a single session (1 $mm)^3$. After contrast enhancement, TSE has the red colour channel, GRE green, MP-RAGE blue. Figures show tissue heterogeneity within the amygdala consistent across weeks.

**References:** **[1]** Hanson *et al* 2009, Proc OHBM 15:360 SA-PM. **[2]** Ng *et al* 2002, Proc. Neural Information Processing Systems (NIPS), 14:849-856. [**3**] Lohmann *et al* 2009, Proc ISMRM 17:695. **[4]** Cramer 1946, Princeton University Press, Princeton, NJ. **[5]** Solano-Castiella *et al* 2008, Proc ISMRM 16:1835 T-AM. **[6]** Sah *et al* Physiol Rev 2003;83(3):803-834. **[7]** Amunts *et al* 2007, Anat Embryol. 210:343-352.