Quantification of whole brain T1 and T2 relaxation times - Automated grouping of similar regions to define cortical areas

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Introduction: The recent development of rapid volumetric relaxometry methods enables determination of T1 and T2 relaxation times for whole brain with high resolution (1 mm³ isotropic voxels) and in a reasonable acquisition time (~15 minutes). The aims of the present study were to use such methods to (1) quantify T1 and T2 values in specific cortical grey matter (GM) regions for healthy volunteers at 1.5T and (2) aggregate regions showing statistically dependent relaxation times to define cortical areas.

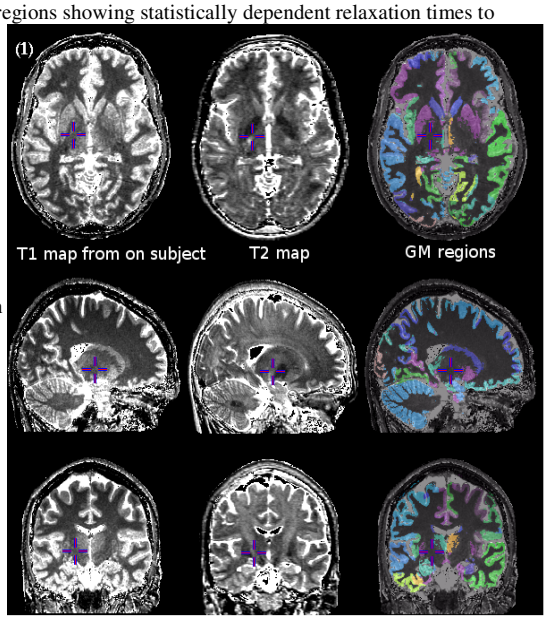
Methods: Twenty (10 males, 10 females) healthy young (29.6±4 years, range 24-37y) subjects were enrolled in the study, which was conducted on a Siemens Sonata 1.5T system using a quadrature head coil. The following whole-brain data sets were acquired: 4 T1-weighted (3D spoiled GRE scans, 1 mm^3, TR = 22 ms, TE = 9.2 ms, $\alpha = 30°$), 1 T1-weighted (same parameters except $\alpha = 10°$), 4 T2-weighted (2D multi-slice fast spin echo scan with 2 mm slices and 1*1 mm in-plane resolution, TR = 3300 ms, TE = 104 ms) and 4 PD-weighted (as for T2w, but with TE = 15 ms).

3D T1 and T2 maps: An average of the four T1-weighted scans with $\alpha 2=30°$ and the T1-weighted scan with $\alpha 1=10°$ were first registered [1] and resampled in the average brain space [2]. T1 was then calculated from the 3D spoiled GRE images acquired with constant echo time, repetition time and varied flip angles ($\alpha 1=10°$ and $\alpha 2=30°$) [3].

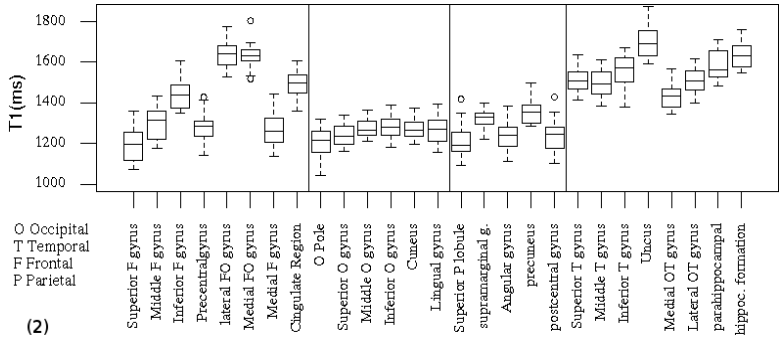
An average of the four T2 and PD-weighted scans were registered [1] and resampled in the average brain space [2]. T2 was estimated from the 2D multi-slice FSE scan (T2 and PD-weighted data) with constant repetition time (TR = 3300 ms) and varied echo time (TE1=15ms and TE2=104ms).

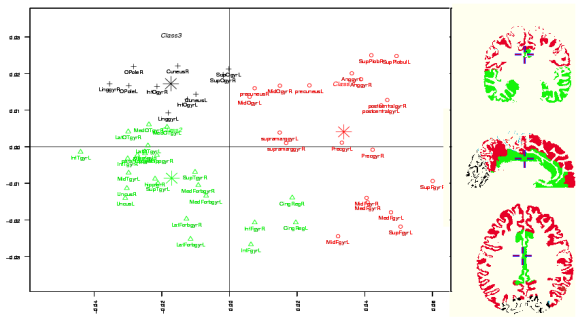
Region segmentation and relaxation quantification: Intensity non-uniformity correction [4] was applied individually to all four native T1- ($\alpha 2=30°$), T2- and PD-weighted MR images. All were registered [1], resampled in the Talairach-like MNI brain space [2], intensity normalized and averaged to create T1-, T2- and PD-weighted average volumes, respectively. Fuzzy Bayesian classification was used to classify voxel intensities from T1W, T2W and PDW average volumes into GM, white matter (WM) and cerebro-spinal fluid. A digital atlas was mapped onto the GM class, using a non-linear registration algorithm to automatically extract the different anatomical regions as defined in [5]. T1 and T2 relaxation times are estimated on a voxel-by-voxel basis [3]. For each subject, the mean T1 and T2 relaxation times within each GM region (limited to fuzzy GM values above 95%) are used for analysis.

Multivariate group analysis using correspondence analysis (CA) and hierarchical clustering (HC): This multivariate analysis is based on the analysis of a contingency table organized as follows: table's rows correspond to the subjects, table's columns correspond to the regional relaxation times described above. CA is a non-centered principal component analysis associated with a Chi-square metric that extracts relationships between row profiles or between column profiles. Within the signal subspace selected by the first two components of CA (66 and 68% of total variance for T1 and T2 respectively), ascending hierarchical clustering (HC) was applied to extract clusters of anatomical regions showing homogeneous patterns of T1 or T2 values.



Results: Figure (1) shows the average T1 and T2 images for one subject along with an overlay of the segmented regions. The distributions of the T1 relaxometry values in each cortical GM region from the 20 subjects are represented using a boxplot in Fig. (2). The projections of the GM regions on the first two principal components of T1 relaxometry CA are shown in Fig. (3) with 3 clusters extracted from HC. Anatomical representations of the clusters are also presented (colors match between projection and anatomical regions). Interestingly, all frontal and parietal regions are grouped together. The temporal structures are merged with the cingulum. The occipital structures are also grouped together. Similar results are found with T2-based analysis (not shown).





(3) Projections of the grey matter regions on the first two principal components performed on T1

Discussion: We used an automated operator-independent segmentation procedure to identify regions for quantification of relaxation times, avoiding partial volume effects errors due to inter-rater variability. Comparison to previously published GM relaxation times at 1.5T is difficult as a wide range of T1 and T2 values are reported in the literature (T1: 998-1304ms; T2: 77.9- 93.3ms) [6-9]. Our values (in Fig. 1) are a bit higher than these reports. However, our GM:WM ratio of 1.85 is within the range of previously reported values (1.49-2.13). The combination of CA and HC has identified groups of structures that are related statistically and these correspond to large cortical regions that have been previously defined anatomically. Our future work will involve combining T1, T2 and PD maps as input to the CA and comparing the resulting regions to those defined by cytoarchitectonics [10].

Conclusions: We have proposed a method to study the spatial statistical dependencies seen in cortical GM relaxation times from a homogeneous population of subjects. The method combines standardized anatomic segmentation, correspondence analysis and ascending hierarchical clustering to identify antomical regions.

References : [1] Collins et al., JCAT 18,192–205,1994.[2] Evans et al., IEEE NSS 813–1817, 1993. [3] Deoni et al., Magn Reson Med 53(1):237-41,2005 [4] Sled et al. IEEE TMI 17,87–97, 1998. [4] Collins et al, IPMI 210–223, 1999. [5] Breger et al. Radiology 171,273:276,1989. [6] Whittall et al., MRM 37:34-43,1997 [7] Henderson et al., MRI 17:1163-1171, 1999 [8] Vymazal et al., Radiology 211:489-495,1999 [9] Srinivasan et al., AJNR 24:58-67,2003. [10] Zilles et al., Adv Neurol 70,29-43, 1996.