Exploring cortical cytoarchitecture in high resolution R1 maps

José P. Marques[1] and Rolf Gruetter[2,3]

[1]*CIBM, University of Lausanne, Lausanne, Vaud, Switzerland,* [2]*LIFMET - Laboratory for Functional and Metabolic Imaging, EPFL, Lausanne, Vaud, Switzerland,* [3]*Department of Radiology, University of Lausanne and Geneva, Lausanne, Switzerland*

Introduction

In recent years there has been a wide interest in studying in vivo the cyto-architectonic properties and myelin distribution within the animal and human cortex. Different contrasts, such as ratios between T_1-w and T_2-w images [1] or quantitative T_1 maps [2, 3], have shown suggestive similarities with the known myelin distribution through-out the human cortex and ex-vivo histological myelin staining [4,5]. In this abstract, R_1 maps obtained at 7T with high-resolution (0.65mm isotropic) will be used to study variation of R_1 values throughout the cortex and at different cortical depths.

Methods

Data from 7 subjects (41±12) were acquired in a 7T MR scanner (Siemens Medical Solutions, Erlangen, Germany) using a 32-channel head coil (Nova Medical Inc). The following sequences were acquired: (a) MP2RAGE sequence [6]: $MP2RAGE_{TR}/TI_1/TI_2$= 6/0.8/2.7s, α_1/α_2=7/5 degrees, res=0.65mm isotropic, T_{acq}=10min; (b) Sa2RAGE sequence [7]: $Sa2RAGE_{TR}/TD_1/TD_2$ = 2.4/0.052/1.8s, α_1/α_2= 4/11 degrees, resolution 2x2x2.5mm^3 resolution, T_{acq}=2.30 min;

The Sa2RAGE image and MP2RAGE image were co-registered using FLIRT (www.fmrib.ox.ac.uk/fsl). Quantitative R_1 maps were computed [8] and were used for brain segmentation using freesurfer (http://surfer.nmr.mgh.harvard.edu). 6 equally spaced layers were generated and the corresponding R_1 maps were smoothed with a 2mm kernel. The pial layer was not considered in the analysis (due to the contamination of CSF partial volume and the inaccurate estimation of CSF R_1's). Regions where the segmentation failed were automatically removed from the analysis by the following protocol: if, in any of the surfaces, the R_1 data at any point from each **subject deviates more than 4 standard deviations** from the average of the same subject within that surface, this column is not considered for further processing; Finally, the surfaces from the 6 subjects were averaged on a common freesurfer space.

The correlation between R_1 values in each surface and the curvature was regressed out [3]. The R_1 cortical variations in different brain regions were evaluated: (a) using ROI analysis in different Brodmann areas; (b) using a PCA decomposition of the R_1 decay from WM surface to CSF through all surface points (the two hemispheres were evaluated separately to rule out segmentation errors and evaluate the consistency of the findings).

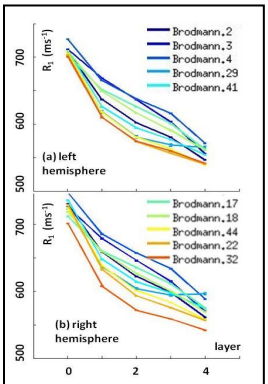

Figure 1 Plots of average R1accross subjects as a function of layer number for the left (a) and right (b) hemisphere. Different lines correspond to different Brodmann areas.

Results

Figure 1 shows plots of the R_1 variation in different cortical areas (sensory BA2-3, motor BA4, auditory BA41, visual BA17-18, Brocca BA44 and BA Wernicke 22) as a function of the layer number. Good agreement can be observed between the curves in the left (Fig 1a) and right hemisphere (Fig 1b). A PCA decomposition of the R_1 dependence on the layer number allowed to observe: **1st component** (explaining 97% of the R_1 variance) decays from the wm layer to pial layer (Fig 2.c), in which primary sensory, motor, audio and visual areas are clearly emphasized (Fig 2a,b), is in good agreement with histological myelin and with previous reports of the average myelination [1,3]; a **2nd component** that shows hump on the middle layers (Fig 2.f) allows a clearer separation of V1 fom auxiliary visual areas (Fig. 2d,e)– this observation could be associated with the presence of the highly myelinated stria of Gennari; a **3rd component** which emphasizes the cingulum and insula cortical areas. Asymmetries between left and right hemisphere are visible on the 1st component throughout most brain regions but in the mid frontal areas (ex. BA32) brain regions (Fig 1a,b Fig 2a,b). The only close to statistically significant left-right asymmetry observed in the 2nd component was that associated with the Brocca area (BA44). The independent observation of the same spatial features (Figs 2a,d,g vs Figs 2b,e,h) and layer dependence (Fig 2c,f,i) on the left and right hemisphere suggests that this could be a robust method to extract cortical information. These patterns were also observable in individual subjects (data not shown).

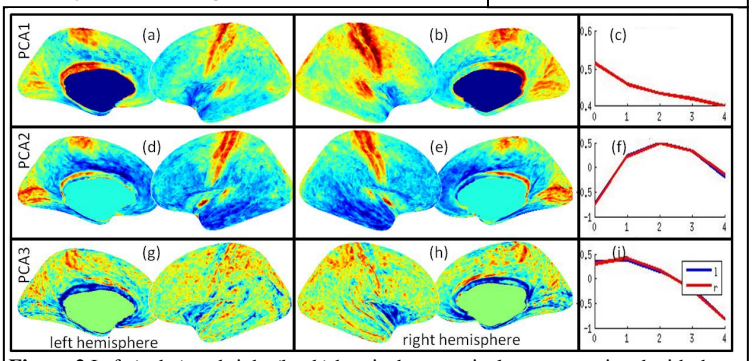

Figure 2 Left (a,d,g) and right (b,e,h) hemisphere cortical maps associated with the first 3PCA components characterizing the R1 values from the white matter to the pial surface. Plots of the left (blue) and right (red) principal components through cortex variation can be observed for PCA 1, 2 and 3(c,f,i).

Conclusions

High-resolution (0.65 mm isotropic) R_1 maps can be obtained in ~12 mins showing both a good differentiation between grey and white matter and within grey matter. It was possible to observe a widespread asymmetry between left and right hemispheres (in agreement with previous literature [10]). New spatial patterns arise when looking at different PCAs – clear separation of V1 from auxiliary visual areas (PCA-2), cingulate cortex (PCA-3) suggesting that different Brodmann areas could be segmented through clustering.

References

[1] Glasser M.F. et al J. of Neuroscience, 2011; [2] Weiss M. et al Annual Meeting HBM 2010; [3] Sereno M.I. et al Cereb. Cortex, 2013; [4] Bock et al, J. Neurosci., 2009; [5] Geyer et al, Frontiers in Neuroscience, 2011; [6] Marques JP et al Neuroimage, 2010 ; [7] Eggenschwiler F. et al MRM, 2011; [8] Marques JP et al Proc. ISMRM, 2012; [9] Marques JP et al Proc. ISMRM, 2012; [10] Wansapura J et al, JMRI, 1999