Segmentation of the frontal lobe using inversion recovery cortical layers imaging

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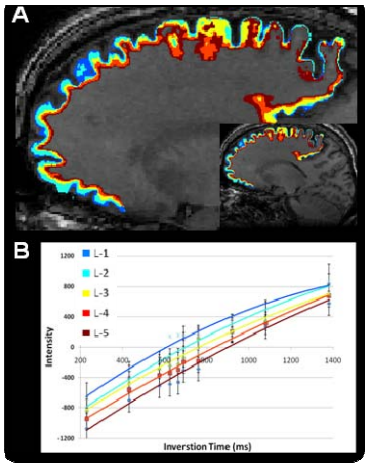
Introduction

The human cerebral cortex has an organized cyto-architecture of six distinct layers, which was the basis for the brain parcellation into neuro-anatomical regions (1). Cytoarchitectonical brain mapping is a powerful tool for localization of activated brain regions in functional neuroimaging and for neurosurgical navigation and brain mapping research. Recently novel histological approaches are developed to map the brain architecture quantitatively. Hence the ability to identify the cortical layers has a key role in brain segmentation; however, currently there is no in vivo imaging modality to visualize neuronal cell structures mainly due to resolution and contrast limitations. The identification of the brain cyto-architecture relays on histological procedures therefore suffers from its known limitations (work on post mortem tissue, artifacts of fixation, tissue disintegration and shrinkage). Magnetic resonance imaging (MRI) is the non-invasive, in-vivo imaging modality that provides the best anatomical details on the human brain. Previous studies of shown (2,3,4) that there is correlation between the architecture of the cortical layers and the longitudinal relaxation time, T1. Recently we have shown (5) that using our analysis framework (6) the cortex can be segmented into laminar sub-structures based on multi dimensional inversion recovery (IR) dataset both on human and rat brains. In this work, we further investigate the cortex segmentations among subjects and between different neuro-anatomical regions.

Fig 1: MRI clustering pattern of the frontal lobe and their relaxation curve



Materials and methods

MRI Experiments: Twelve subjects (aged 25-35) underwent MRI in a 3T scanner (GE). The protocol included 7 IR sequences with the following parameters: TR/TE=10000/8.4ms, matrix of 512x384 (reconstructed to 512x512) with final pixel size of 0.43x0.43 mm^2 and varied slice thickness covering the entire hemisphere in the sagittal plane. The inversion time (TI) varied for each experiment at the following values: 230, 432, 575, 760, 920, 1080, 1380, 2100ms. In addition conventional T1-SPGR was collected at similar resolution. The total MRI protocol lasted for 45 minutes.

Image Analysis: The multi dimensional-IR images were co-registered, and then were analyzed using a multi-spectral clustering framework (6) of the IR dataset. The T1 map of each subject was calculated using non-linear regression.

Statistical analysis: We extracted the fraction volume of the MRI clusters within different Brodmann's areas (BA) along the frontal lobe (Brodmann's areas 6, 8, 9, 10, 46, 47) of each subject. We performed factorial ANOVA of 6 (BA) X 5 (MRI clusters) for each subject, and post hoc analysis was done to check for significant interaction between each pair of regions (ANOVA with Bonferroni corrected significance level).

Results and Discussion

Fig 1A shows the MRI clustering analysis (k=5) focused on the frontal lobe in a representative subject, and the intensity (mean and std) of each cluster from the IR images from different subjects (Fig 1B). Note the laminar appearance of each MRI cluster along the cortex; each cluster has a distinct relaxation curve.. Fig 2 summarizes the relative volume of each MRI cluster at different BAs along the frontal lobe. From the statistical analysis (see methods) we conclude that there is an interaction between BA regions and MRI clusters ($p<0.001$). Of all possible 15 pairs of regions, 11 were found to be statistically significant. To validate our methodology, we applied it on the visual cortex in attempt to identify the stripe of Gennari which delineate between striate (BA17 and the extra striate (BA18) cortices (Fig 3): (A) a representative slice at TI of 760ms with the border of the cortex outlined in red. (B-D) An inset of the occipital region; where the border between striate (BA17) and extra-striate (BA18) cortices are given at different TIs (230 (B), 575 (C) and 760 (D)). It appears that the striate cortex is characterized by a dark stripe in the middle of the cortex at TI of 230 ms (yellow arrow in B) which turn to be brighter at bigger TIs (yellow arrow in C). This characteristic is absent at the extra-striate cortex. The border between the two regions is best seen at TI of 760 and marked by the yellow arrows. (E) Shows a multi-spectral analysis of the IR data, where the different colors represent regions with distinct T1 profile (i.e. has distinct relaxation curve similar to Fig 1B). It should be noted that one cluster is apparent in the area of the striate cortex (the brown cluster) that is marginally apparent elsewhere. (F) Shows specific T1 histograms of the striate and extra-striate cortices. Note that there is a larger portion of pixels with low T1 in BA17 than in BA18.

Fig 2: The fractional volume of each cluster at different Brodmann's areas along the frontal lobe

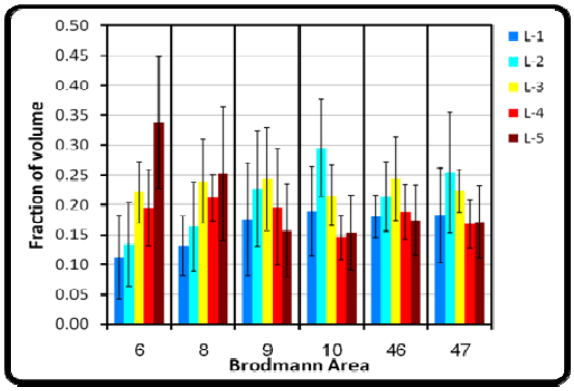


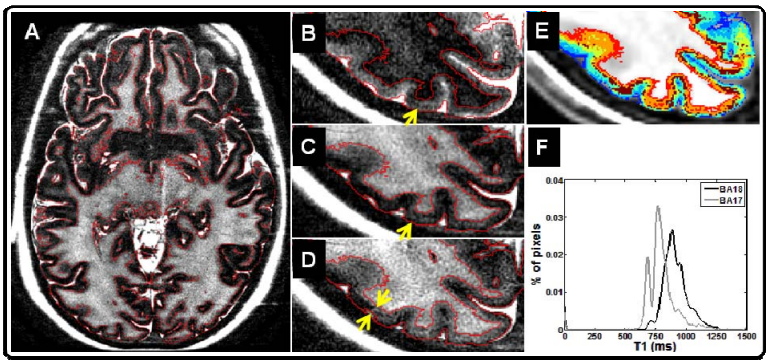
Figure 3B-D shows an inset of the visual cortex of multi-spectral IR images. (The stripe of Gennari is marked in yellow arrow). Fig 3E-F shows the MRI clusters of that region (k=6) and normalized T1 histogram of areas 17 and 18. Note the differences in the T1 histogram where BA17 has a bigger peak at lower T1 relative to BA18, which match a heavily myelinated region like the stripe of Gennari.

Conclusion

Inversion recovery provides a unique contrast that enables characterization of the laminar segmentation of the cortex. In this study we found that each of the MRI clusters has its own relaxation curve, and their composition at different BAs is statistically significant.

Moreover we applied our methodology at the striate and extra striate cortices and managed to identify the stripe of Gennari and characterize its T1 histogram differences.

Fig 3: Inversion Recovery Lamination Pattern of the Striate and Extra-Striate Cortex



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