COMPUTING AVERAGE CORTICAL PROFILES AT 3 TESLA

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Introduction: Psychiatric diseases such as schizophrenia are characterized by non-focal cortical thinning of several brain regions [1]. Current analysis methods do not provide any information on which cortical layers are implicated because the resolution of images acquired routinely using conventional MRI field strengths (e.g. 3T) is considered to be too low. One solution is to increase imaging resolution by using ultra-high field MRI (e.g. 7T) [2, 3]. But ultra-high field MRI is often not readily available and performing large cohort studies (needed because the effect sizes for psychiatric diseases are typically very small) at 7T is complicated. Here we propose a new automatic analysis method that extracts detailed cortical profile information from conventional whole brain T1-weightd scans acquired at 3T, part of a standard scan protocol. This method exploits the fact that aberrations found in psychiatric diseases are non-focal in nature.

Methods: To assess its feasibility we used the 3D FFE T1-weighted images (acquired on a 3 Tesla Philips Achieva; TR/TE 10 ms/4.6 ms; flip-angle=8°; FOV= 240x240 mm; 200 slices, 0.75 isotropic voxel size; total scan duration 602 s) from 5 healthy subjects who participated in a previous study and for which written informed consent was obtained prior to scanning.

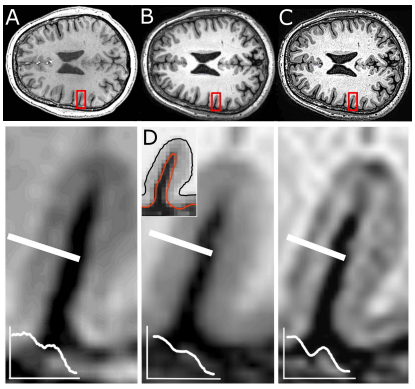

Figure 1:T1-weighted image acquired at 7T (A). T1-weighted image of same subject acquired at 3T (B). Image B after 3D deconvolution (C). White bars denote cross-sections and corresponding profiles shown in lower row. Automatic cortical delineation computed on original 3T (B) image shown in D.

In the first step, Freesurfer [4] was used to automatically delineate the inner (white matter), the outer (pial) boundaries and the curvature of the cerebral cortex allowing us to measure cortical profiles at every cortex position. Next, the resolution of the original T1-weighted image was upsampled by a factor of 2 (in all 3 directions) after which parallel iterative 3D deconvolution [5] (Wiener filter preconditioned landweber method; 3 iterations; normalize PSF; anti-ringing step; divergence detection; gamma = 0) was applied. This step enhances image details but also substantially reduces signal-to-noise ratio. Then for each subject and each cortical region (assuming the same cytoarchitecture within a single region, e.g. Brodmann areas (BA)) the deconvoluted data was sampled along all cortical profiles. Next, to increase homogeneity, only profiles were selected for which the absolute curvature of the cortex was < 0.1 and the length (before normalization) deviated < 10% from the median profile length for the specific area. Finally, these selected profiles were aligned (scaling and translation) and averaged (increasing SNR again) yielding one average cortical profile per region (per subject).

Results: Figure 2 (left panel) shows the mean cortical profiles computed for 4 different Brodmann areas. The right panel shows the profiles (averaged over all 5 subjects) created without the application of the additional selection step (i.e. all profiles found for one Brodmann area).

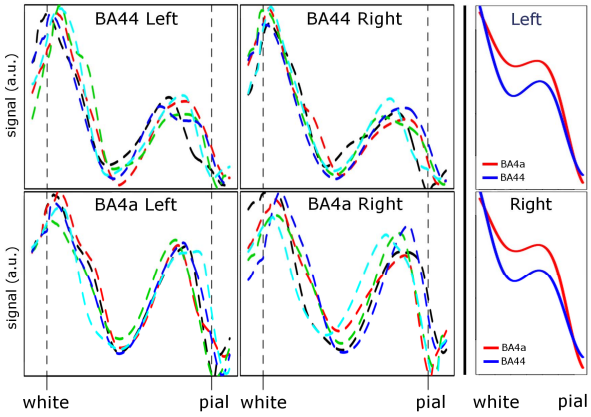

Figure 2: average cortical profiles computer for 4 different Brodmann areas from 5 healthy subjects (left panel). average profiles (averaged over all subjects) without additional selection on curvature and length (right panel) .

Discussion: These initial results show (left panel) that for each of the 4 Brodmann areas the average cortical profiles of the 5 subjects are in good agreement. Moreover, the results clearly show that the average profiles are more similar between homologue Brodmann areas than between different Brodmann areas (e.g. the height of the maximum near the pial surface) indicating that this method is sensitive enough to detect interregional differences. Additional selection using curvature and profile length (left panel) results in more pronounced profiles compared to no selection (right panel) and may allow for a better detection of subtle group differences. This method is not limited to T1-weighted images (as used in this example) but can be used with any type of contrast provided that accurate cortical delination is possible. Future work includes relating the differences found between average cortical profiles of the different Brodmann areas to known differences in cyto/myelo-architecture for these areas.

Conclusion: The results of these initial experiments suggest that this automatic analysis method can be used to extract detailed information on cortical configuration from existing large datasets acquired with conventional MRI scanners. The application of this method is not limited to psychiatric diseases but it can also be used to study for instance cortical changes during brain development.

References: [1] Garey (2010) J Anat, 217, 324 ff. [2] Wachnert et al. (2013) Proc Intl Soc Mag Reson Med., 21, 270. [3] Zwanenburg et al. (2012) Radiology, 262, 995 ff. [4] http://surfer.nmr.mgh.harvard.edu. [5] http://fiji.sc/Parallel_Iterative_Deconvolution.