How much resolution is needed for in-vivo analysis of cortical myeloarchitecture?

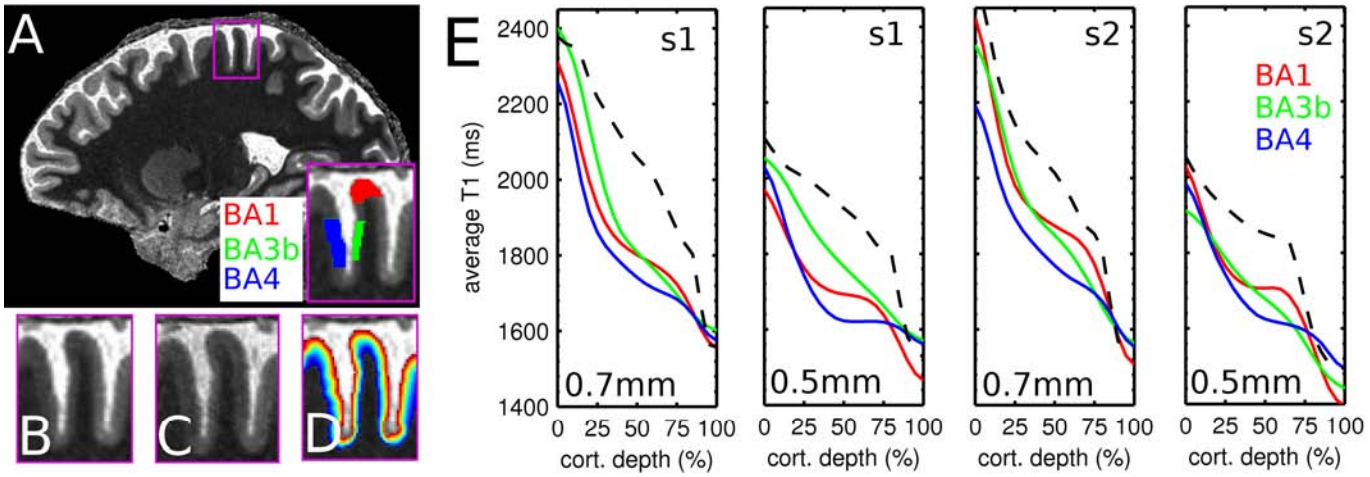
Miriam Waehnert[1], Juliane Dinse[1,2], Christine Tardif[1], Andreas Schäfer[1], Stefan Geyer[1], Pierre-Louis Bazin[1], and Robert Turner[1]
[1]*Department of Neurophysics, Max-Planck Institute for Human Cognitive and Brain Sciences, Leipzig, Germany,* [2]*Faculty of Computer Science, OvGU Magdeburg, Magdeburg, Germany*

Introduction: Recent studies have demonstrated that T1 contrast exhibits intra-cortical variations that reflect myeloarchitecture in the living human brain ([1], [2], [3]). In histological ex-vivo studies on two-dimensional sections, a semi-automated method for cortical profiling has been widely used for detection and mapping of cortical areal boundaries [4]. Such cortical profiles can now be constructed in-vivo, in 3D, using MR images. However, histological resolution is better than 5 µm, whereas the resolution of standard structural MRI is typically 1mm. Here we explore the effect of spatial resolution on the distinguishability of cortical architecture using cortical profiles from quantitative T1 maps at 7T.

Materials and methods: Two human subjects were scanned on a 7-T MR system. The MP2RAGE sequence was used to obtain quantitative T1 images of the whole brain at 0.7 mm isotropic resolution (TI1/TI2=900/2750ms, TR=5s, α_1/α_2 =5°/3°, GRAPPA=2, BW=250Hz/Px, partial fourier in phase encoding direction 6/8) and of the left and right hemispheres at 0.5 mm isotropic resolution (same imaging parameters as for 0.7 mm resolution but with no acceleration).

The three volume images were co-registered into MNI space at an isotropic resolution of 0.4 mm, and an image fusion algorithm was used to generate a whole brain image from the two hemispheric 0.5 mm images. Next, the brain image with 0.7 mm resolution was segmented and the cortical surface was reconstructed [5]. Cortical profiles were obtained with our novel volume-preserving stratification method [6] (Fig. D). Finally, guided by accepted landmarks, we manually selected regions of interest (ROI) in the left hemisphere of the 0.7 mm resolution image within Brodmann Areas (BA) 1, 3b and 4 (Fig. A inset). Average profiles were computed for these ROIs (which each included 2500 to 9500 voxels), and for the entire cortex, both from the 0.5 mm resolution data and the 0.7 mm resolution data. All image processing was performed with in-house software based on MIPAV.

Results: Average profiles of the BAs and the entire cortex are shown in Fig. E for the 0.7 mm data and the 0.5 mm data of each subject. The average T1 values in the 0.5 mm data profiles are somewhat lower than those from the 0.7 mm data, mainly due to reduced partial voluming in the outer- and innermost laminae. Qualitatively, even at 0.7mm the cortical T1 profiles in the targeted BAs are well separated from that of the entire cortex, but their shapes are similar (Fig. E). More pronounced variation in shape is found in the 0.5 mm profiles: BA 3b has a relatively linear average T1 profile, while the average profile of BA 1is flatter in the middle third of the cortex, and the T1 profile of BA 4 dips rapidly from the GM/CSF surface and remains low through half the cortical depth. This is consistent with the fact that BA 4 is heavily myelinated as far as layer II, while the two bands of Baillarger are quite indistinct [7].



BA	s1, 0.7	s1, 0.5	s2, 0.7	s2, 0.5
1	95	89	78	56
3b	113	107	89	70
4	87	85	74	77
cortex	190	171	211	184

Fig.: (A) T1 map with cortex of manually segmented BAs; zoomed-in ROIs at 0.7 mm (B) and 0.5 mm (C) isotropic resolution; (D) volumetric stratification to give cortical depths; (E) average profiles of BAs and the whole cortex (black dashed line) sampled from 0.7 mm and 0.5 mm T1 maps from subject 1 (s1) and subject 2 (s2); for clarity average standard deviations were not plotted but are given in the table.
Table: standard deviations in milliseconds per BA, subject and resolution.

Discussion and conclusions: Volume-preserving layering (stratification) of cortex enables realistic profiles to be measured, which differ by cortical area. At the highest resolution of 0.5 mm, the striking differences in cortical profiles should enable their assignment to distinct cortical areas using automatic classifiers that take into account the profile shape. Inter-subject variability, small GM/WM segmentation errors and partial voluming make the general modeling of individual profiles a continuing challenge. Isotropic spatial resolution of 0.5 mm or better is vital for accurate cortical parcellation.

References: [1] Geyer et al. (2011), Front. Hum. Neurosci.; 5, 1 ff. [2] Glasser et al. (2011), J. Neurosci.; 31, 11597 ff. [3] Bock et al. (2009), J. Neurosci. Methods; 185, 15 ff. [4] Schleicher et al. (1999), NeuroImage; 9, 165 ff. [5] Bazin et al. OHBM 2012 #883 [6] Waehnert et al. OHBM 2012 #898 [7] Vogt and Vogt 1919 J. Psychol. Neurol. 25, 278 ff.