Fine details of cortical and sub-cortical anatomy revealed in-vivo by ultra-high resolution quantitative T1 mapping

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Introduction

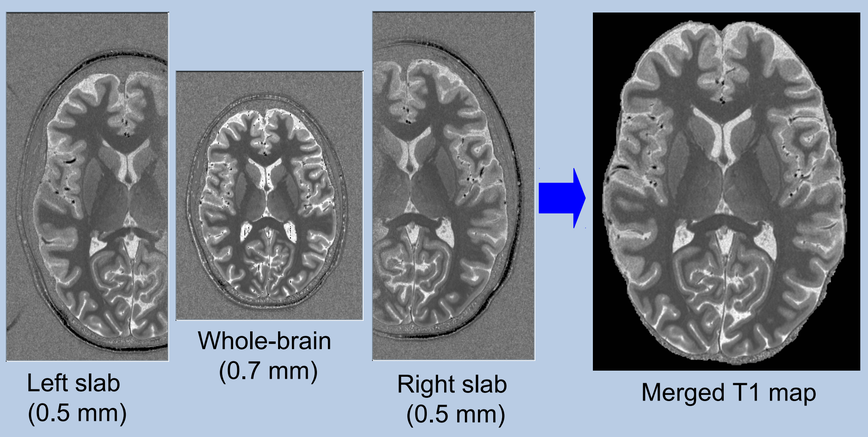
With the increased SNR of 7 Tesla MRI, the resolution of anatomical brain images acquired in-vivo can move toward resolutions well below the millimetre.

We present here an imaging methodology pushing the limits of in-vivo anatomical quantitative MRI at 7T, which produces ultra-high resolution maps of T1 at an unprecedented isotropic resolution of 0.5 mm over the whole human brain.

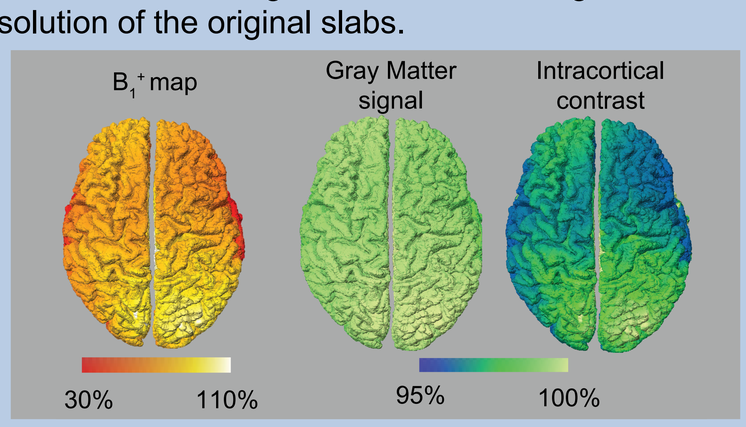
On these high resolution images, we can see many fine details of neuroanatomy at the single subject and group level, including intra-cortical T1 variations indicative of microarchitecture.

Methods

Structural brain MR images were acquired for 12 healthy volunteers at 7T (Siemens Magnetom) using the MP2RAGE sequence (TR=5000 ms, TI1=900 ms, TI2=2750 ms) [1,2] in three steps: first a sagittal whole-brain image was acquired at 0.7 mm isotropic resolution (with a GRAPPA acceleration factor of 2, 10:57 min), then two sagittal image slabs covering the left and right hemisphere separately were acquired at 0.5 mm isotropic resolution (no acceleration, 28:02 min).



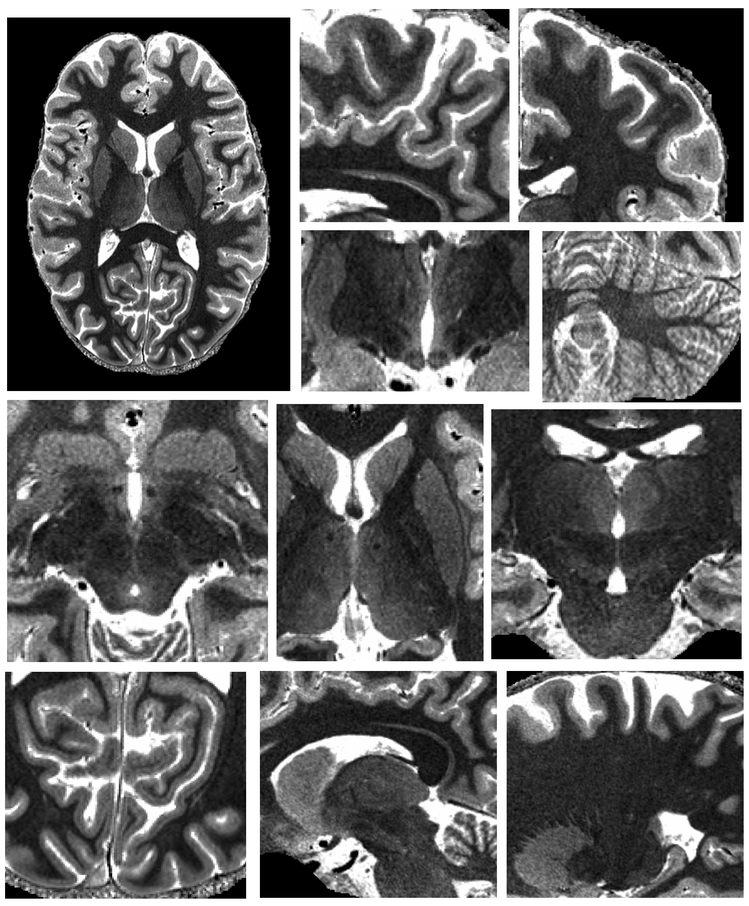
The three images were merged as follows: first, the whole-brain image was normalized into MNI space at 0.4 mm isotropic resolution, then both hemisphere slabs were co-registered to the whole-brain image. The extra-cranial tissues were then removed with the CBS Tools [3] on the whole-brain image. The estimated quantitative T1 values of the slab with highest resolution and acquired second inversion signal were selected at each voxel in order to fuse the image data while retaining the full resolution of the original slabs.



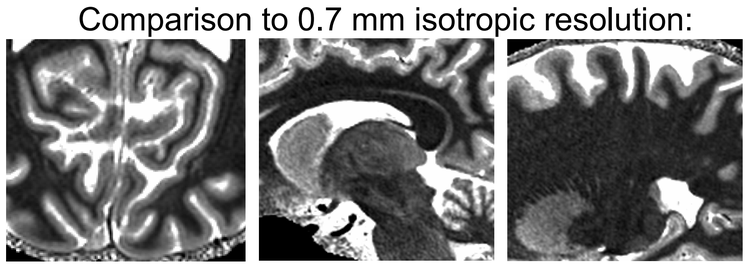
To assess the quality of the T1 maps, we also acquired a whole brain B_1^+ in one subject [5] and simulated the effect of B_1^+ variation on the MP2RAGE ratio-image signal in Matlab based on analytical equations for the MP2RAGE [1,6] and MR tissue values at 7T [7]. Despite large B_1^+ variations, the estimated gray matter signal and intracortical contrast was very homogeneous.

Results

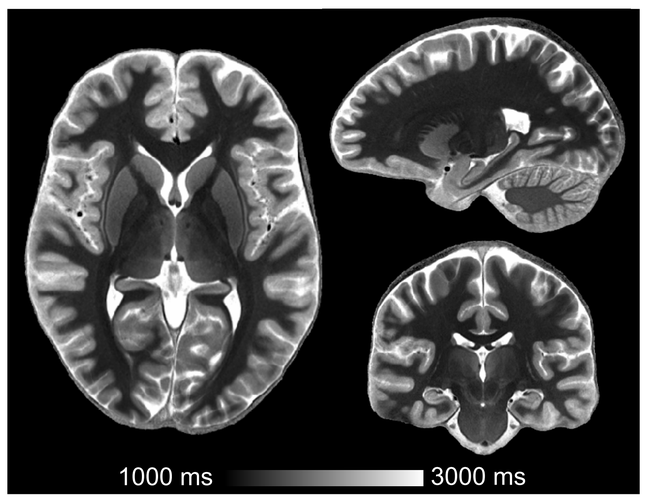
1 Single subject T1 anatomical details at 0.5 mm



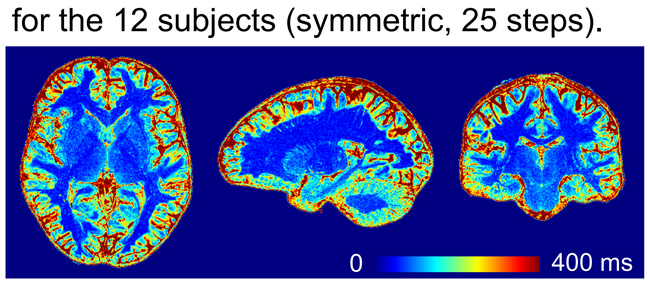
Comparison to 0.7 mm isotropic resolution:



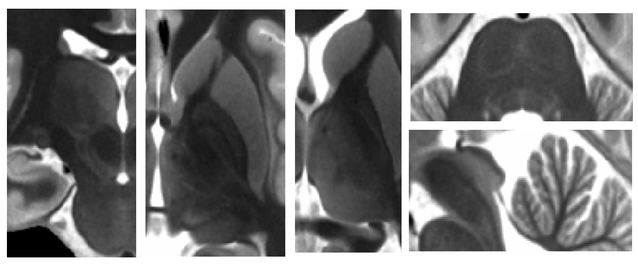
2 Average T1 anatomy atlas at 0.4 mm



Groupwise average obtained with SyN [4] for the 12 subjects (symmetric, 25 steps).



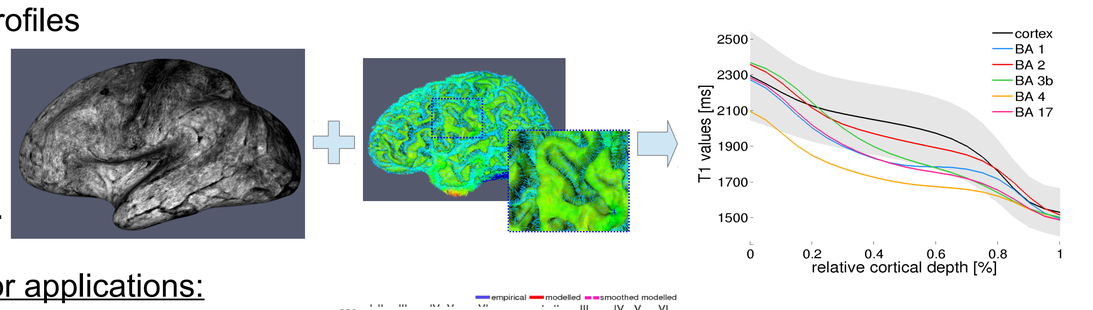
Standard deviation of groupwise T1.



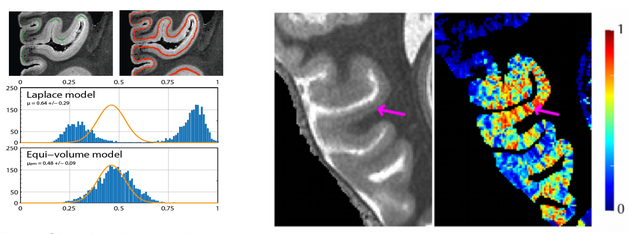
Details of sub-cortical anatomy.

3 Cortical maps and profiles

With the CBS Tools [3], we extracted high-resolution cortical surfaces and profiles [3].

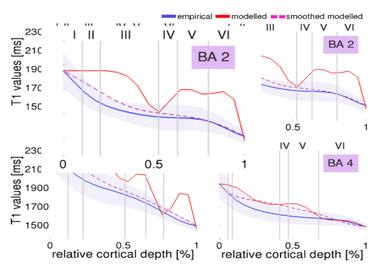


See our other posters for applications:

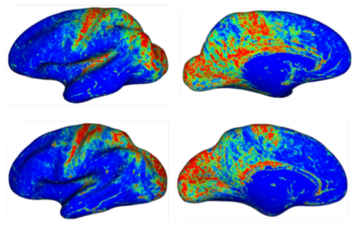


Realistic Laminae
#3819 W-Th

MT/V5 Mapping
#3817 W-Th



Generative T1 model
#3811 W-Th



Heavily Myelinated Areas
#3816 W-Th

Conclusions

Ultra-high resolution quantitative mapping of T1 at 7 Tesla reveals a rich brain anatomy in individual subjects within reasonable acquisition times. The proposed approach yields high quality images at a resolution of 0.5 mm, fine enough to differentiate small nuclei and cortical areas. Combined with ultra-high resolution processing methods, these images will provide fine-level anatomical information in-vivo to combine directly with functional activity in the same subject.

Get our processing tools online:

http://www.cbs.mpg.de/institute/software/cbs-hrt/
http://www.nitrc.org/projects/cbs-tools/

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