A 7T Human Brain Microstructure Atlas by Minimum Deformation Averaging at 300µm

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Model: www.imaging.org.au/7T-Human **Online View: www.tissuestack.org**

Introduction

Digital MRI atlases serve to integrate data from differing modalities, stereotactic localisation, automated region identification, automated segmentation and direct comparisons between individuals [1]. While paper atlases can provide exquisite detail of delineated structures, they are typically based upon an individual subject's histology and as such make it difficult to identify structures in novel subjects in an automated fashion. Here we generate a minimum deformation average (MDA) from a population of subjects based upon high resolution 7T MR imaging.

Method

All data was acquired on a 7 T whole-body Magnetom research scanner (Siemens Healthcare, Erlangen, Germany) with a gradient strength of 70 mT/m, slew rate of 200 T/m/s and 32-channel headcoil (Nova Medical, USA).

MP2RAGE: 48 (16 female, 31.1±8.6yr) individuals were imaged using a prototype MP2RAGE sequence with a range of resolutions: 0.5mm (18 indiv.), 0.75mm (21), 1.0mm (8) and 1.3mm (1). TR= 4330ms, TI1/TI2=750/2370ms, TE=2.8ms, flip angle=5,6, and GRAPPA = 3. The image matrix was typically 256x300x320 or 420x378x288 but was dependent upon coverage and FOV. The MP2RAGE denoised images [6, 7] were intensity-normalised using a histogram clamping technique.

QSM: 29 (14 female, 26.6±3.8yr) individuals were imaged using a multiple echo gradient recalled echo 3D whole brain dataset. TR=25ms, TE=4.4,7.25,10.2,13.25,16.4, 19.65,23ms flip angle=13, FOV 210x181.5x120mm, matrix=280x242x160, GRAPPA=2. The phase data was combined using COMPOSER [8] and susceptibility processing was performed using total generalized variation (TGV) [9], which incorporates phase unwrapping, background field removal and dipole inversion in a single step.

TSE: 26 (13 female, average age 26.8±3.9) individuals were imaged using 3 repetitions of a 2D Turbo Spin Echo (TSE) sequence covering a slab orthogonally to the axis of the hippocampus with a resolution of 0.2x0.2x0.8mm, flip angle 134, TR 10.3s. Before the atlas creation, we averaged the three TSE acquisitions per participant to one dataset to increase SNR and reduce the amount of data to be processed. Then we resampled the TSE data to an isotropic voxel size of 0.4 mm.

A probabilistic model of all modalities was created using the method in Janke et al [2] and Grabner et al [4]. In the present case, the fitting strategy consisted of 2 linear fits to the evolving internal model followed by a hierarchical series of non-linear grid transforms. These transforms started with a step size of 32mm followed by 16mm, 12mm, 8mm, 6mm, 4mm, 2mm, and finished with 1.5mm. These fitting steps use progressively de-blurred data with a 3D kernel FWHM of half the current step size. Twenty iterations at each fitting stage were performed using the ANIMAL algorithm [5]. As the step size decreased the resolution of the evolving model to which data was being fit was increased, starting with a step size of 1.0mm and finishing with a resolution of 0.3mm. Given the multiple overlapping samples it is possible to increase the resolution to this point without suffering from a lack of information at any point. Our technique differs from Fonov et al's [3] during the intermediate model generation in that a robust averaging process is used to reduce the effect of artefacts and small handling tears in the brain. The averaging technique is a “winner takes all” approach and as such places a lower weight on data at each voxel that is greater than two standard deviations from the current model. This increases the likelihood that a single minimum is achieved for the entire model. The fitting process took approximately two weeks on a 250 core commodity Debian GNU/Linux cluster.

Results

Representative views demonstrate the contrast that can be achieved in a 7T MDA model. Note in particular the substructures emerging in the Hippocampus, deep brain stem/pons, and the thalamus, which commonly shows very little internal structures on T1 weighted MRI.

Conclusion

The increase in resolution and signal from the modelling process means that we can now readily identify multiple thalamic and neocortical nuclei that are not visible in individual subjects. In the future, we plan to release a complete multi-modal model including segmentations and tissue density maps. Code is available as part of MINC in the volgenmodel package and the model will be available for download.

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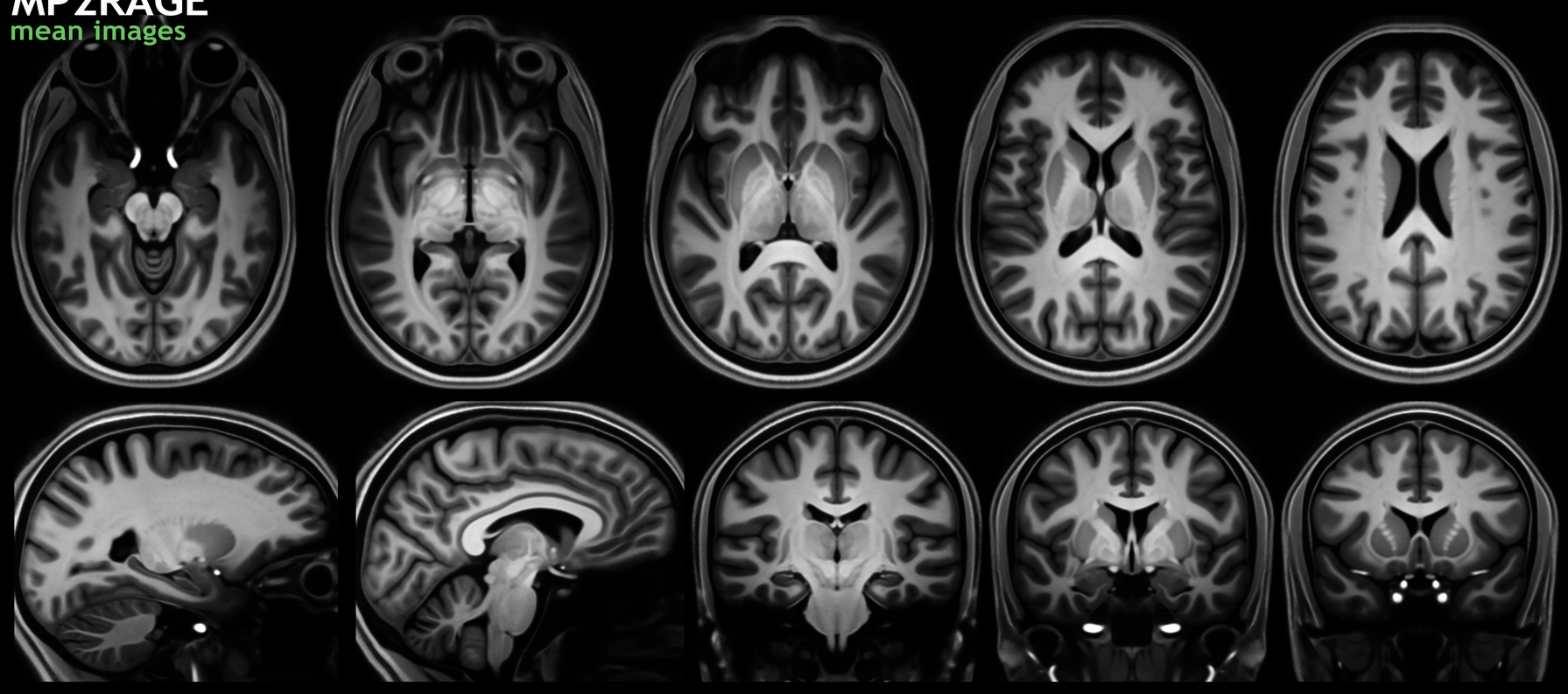
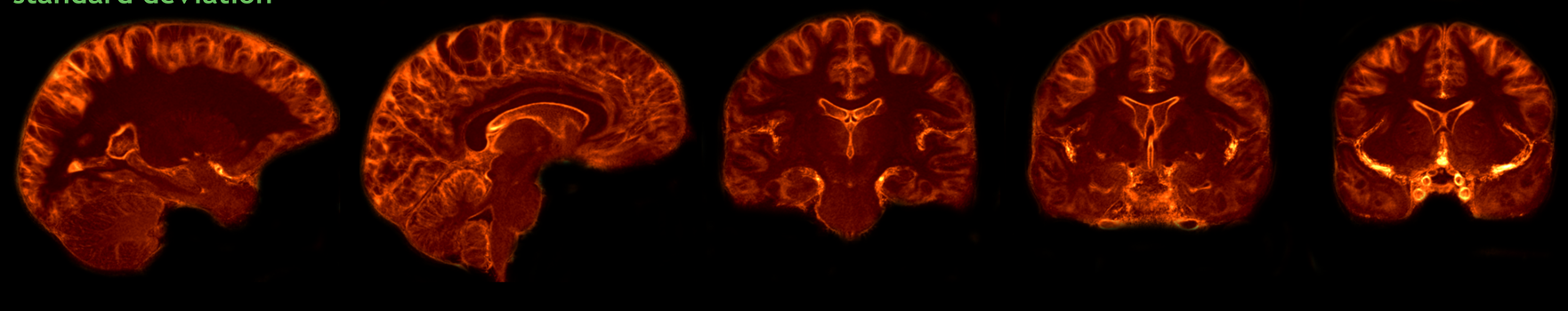
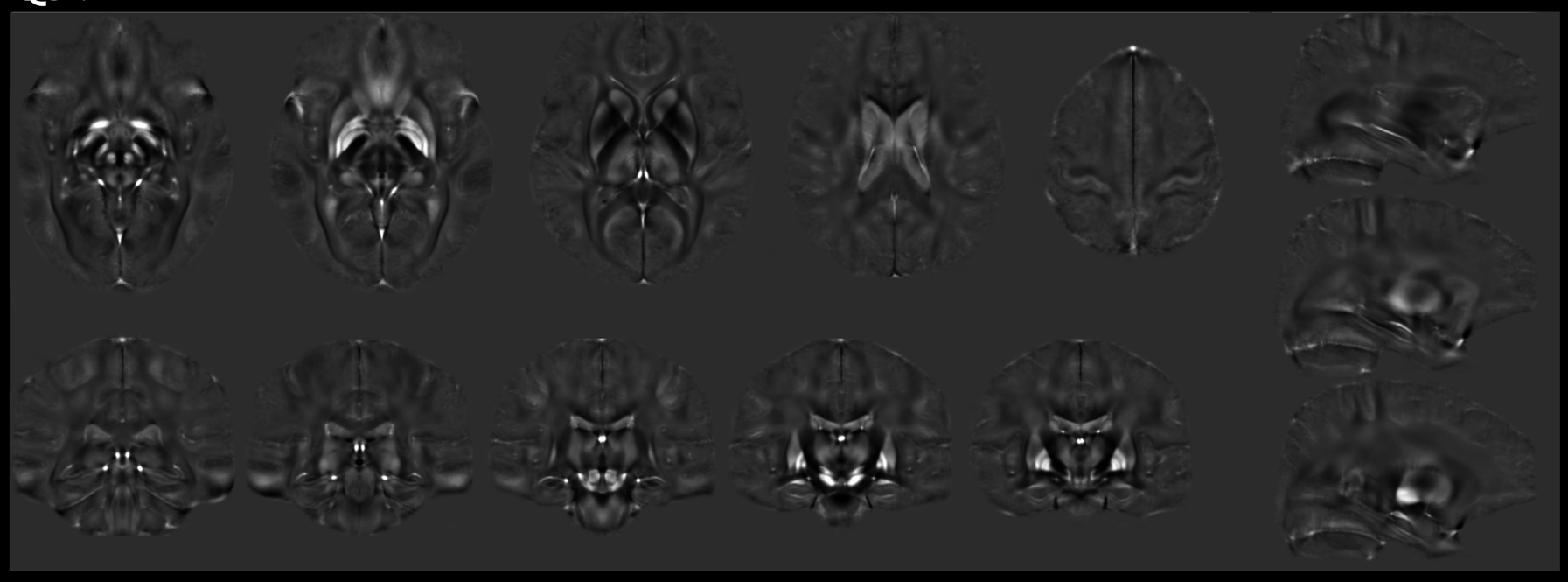
MP2RAGE
mean images



standard deviation



QSM



TSE