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

Andrew Janke¹ <andrew.janke@cai.uq.edu.au>, Kieran O'Brien¹,², Steffen Bollmann¹, Tobias Kober³, Lars Marsteller¹ and Markus Barth¹

¹. Center for Advanced Imaging, University of Queensland, Australia.
². Siemens Healthcare Pty Ltd, Brisbane, Queensland, Australia
³. Advanced Clinical Imaging Technology (HC CIMA SUI Dr RAI PI), Siemens Healthcare AG, Lausanne, Switzerland

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 comparison between subjects [1]. While paper atlases can provide an exact description of detailed structures, they are typically based upon an individual'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 MRI 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/ms and 31 mT/m/ms pulse (Nova Medical, USA).

MP2RAGE: 48 (16 female, 31-16.8y) individuals were imaged using a prototype MP2RAGE sequence with a range of resolutions: 0.5mm (18 Ind) [4], 0.25mm (21), 0.125mm (8) and 1.0mm (6). TR: 2500ms, TE: 2.24ms, flip angle:5°, and GRAPPA 2. The image matrix was typically 334x334x170 or 668x332x85 but was dependent upon coverage and FOV. The MP2RAGE-deposited images [6,7] were intensity-normalised using a histogram clipping technique.

QSM: 79 (24 female, 26 63.8y) individuals were imaged using a multiple echo gradient recalled-echo 3D whole brain dataset. TR:2500ms, TE:4.72,7.5,10.7,13.9,16.4, 20.4,23.3, 30.7, flip angle:11, FOV: 210x181x120mm, matrix:256x256x192, GRAPPA 2. The global data was corrected using COMPOSER [8] and susceptibility-inversion was performed using total generalized variation (TGv) [9], which incorporates phase unwrapping, background field removal and double inversion in a single step.

TSE: 26 (13 female, average age 26 63.8y) individuals were imaged using 3 repetitions of a 2D Turbo Spin Echo (TSE) sequence covering a slab approximately to the size of the hippocampus with a resolution of 0.2x0.2x0.6mm, flip angle 120°, TR 19.5ms. 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 0.4mm.

A probabilistic model of all modalities was created using the method in Janke et al. [10] and Graber et al. [11]. In the present case, the fitting strategy consisted of 7 linear fits to the evolving template model followed by a hierarchical series of non-linear grid transforms. These transforms started with a step size of 30mm followed by 16mm, 12mm, 8mm, 6mm, 4mm, 2mm and finishing with 1mm. These fitting steps used progressively better blurred data with a 3D kernel. For the current step, intensity iterations at each fitting stage were performed using the ANIMAL algorithm [12]. As the step size decreased, the resolution of the evolving model to which data was being fitted was increased, starting with a step size of 15mm 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 Forey et al. [3] during the intermediate mode progression in that each averaging process is used to reduce the effects of artefacts and signal handling in the brain. The averaging technique is a "whites lasers all" technique 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. In particular, the substructures emerging in the hippocampus, deep brain structures, and the thalamus with high contrast show very little internal structures on 7T weighted MRI.

CONCLUSION

The increase in resolution and signal from the modelling process means that we can now readily identify multiple thalamic and necortical 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 MNC in the repo mentioned above and the model will be available for download.

References