15µm³ Average mouse models in Waxholm space from 16.4T 30µm³ images

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Model: http://www.imaging.org.au/AMBMC **TissueStack: http://github.com/NIF-au/TissueStack**

Introduction

Atlases allow stereotaxy, automatic segmentation and comparison between individuals. While paper atlases[1,2] can provide exquisite detail of delineated structures, they are typically based upon an individual. This makes automated structure identification in a novel individual difficult.

Improvements in field and gradient strength have led to an increase in the number of segmented regions in MRI atlases. Arguably, the best current mouse atlas is that of Dorr et al in 2008[3], acquired at 7T with a final resolution of 32um^3 and 62 segmented structures.

The data in this MRI atlas was acquired at **16.4T** and created using a specific adaptation of a nonlinear averaging technique. The final resolution is **15µm^3** which is nearing histological clarity. Further detail of structure segmentation is given in poster **#1286 (Prog #1075)**.

Method

18 animals were perfused and fixed with 4% paraformaldehyde and 0.1% Magnevist®. Brains were extracted and incubated in 0.1% Magnevist/PB for 4 days, placed in Fomblin and imaged on a 16.4T (89mm) Bruker micro-imaging system using a 15 mm SAW coil. MRI was acquired using a 3D gradient echo sequence **TR/TE/FA= 50ms/12ms/30°**, 82 KHz spectral bandwidth and 8 excitations with an acquisition time of 5h 15mins to produce T1/T2*-weighted images at 30µm^3 isotropic resolution.

Images were B0 corrected using N3 and intensity normalised using a histogram clamping. A probabilistic model was created using a method very similar to that of Fonov et al[5] and Grabner et al[6]. The fitting strategy consisted of 3 linear fits to the evolving internal model followed by a hierarchical series of non-linear grid transforms. These transforms used millimetre step sizes of **1.067, 0.533, 0.267, 0.2, 0.133** and **0.06**. The fitting uses smoothed data with a 3D FWHM of half the step size. 20 iterations at each fitting stage were performed using the ANIMAL algorithm.

Our technique differs from Fonov et al's 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 places a lower weight on data at each voxel that is greater than 2 standard deviations from the current model. The fitting process took **~3 weeks** on a **50core** commodity Debian GNU/Linux cluster.

Results

This model exhibits fine detail in structures not seen before, especially with regards to the thalamic nuclei. 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 the overlaid histology will be released along with matching segmented MRI data. Code is available as part of MINC in the volgenmodel package.

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