

Image Registration of Whole-body Mouse MRI

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Introduction. In recent years, much effort has been focused on creating new mouse models of human disease. When studying mouse models, phenotyping is the main bottleneck in the workflow. It has already been demonstrated that whole-body MRI can accelerate the acquisition of anatomical data [1, 2], but automated image analysis is required to rapidly analyze the data. In this project, a labelled atlas was generated by manually segmenting 12 organs in one image of a whole, fixed mouse. This atlas was then registered to the other whole mouse images and the organs were automatically labelled.

Materials and Methods. Sixteen C3H mice were perfusion fixed with formalin and 10 mM Magnevist with ultrasound guidance [3]. Imaging was performed on a 7-T magnet with a four-channel Varian^{INOVA} console (Varian Inc., Palo Alto, CA) multiplexed to 16 coils for parallel imaging. A spin echo sequence was used: TR/TE = 650/15 ms and $(100 \mu\text{m})^3$ voxels with an imaging time of 13 h. A free-form, deformation-based non-linear registration [3] was employed using a multi-resolution grid approach to register the atlas to the other mice. The registration consisted of an affine and non-rigid component and the resulting transformation was used to propagate the labels from the atlas to each animal's native space. The volumes of organs were measured by counting the number of voxels associated with each organ. Due to noisy data, the segmented organs in the atlas were propagated to only 12 animals in the data set. The segmented organs are listed in the Table. An average volume was determined for each organ with the standard deviation used to roughly indicate the performance of the registration. More formally, the brain, heart, kidney and lungs in 5 consecutive coronal slices in 9 animals were manually segmented. The manually segmented labels were compared with propagated label slices using Dice similarity index (SI).

Results and Discussion. In Figure 1, the average image (right) is more blurred than the single image (left), but the major organ outlines are still easily discernible. The top panel of Figure 2 shows the organs that were manually segmented for the atlas rendered in 3D and the bottom panels are the automatic label propagations. The table shows the average volume of the organs from the 13 mice. The standard deviation is expressed as a percentage and the organs are ranked from lowest to highest standard deviation. The brain, bone, spinal chord and liver have very low standard deviations and upon visual inspection, there are only very minor errors in registrations at the boundary. This can be expected as these organs have very well defined outlines in the images. Correspondingly, the SI for the brain is very high at 0.98. The eye, heart (SI 0.98), kidney (SI 0.94), stomach and lung (SI 0.94) have a comparatively larger standard deviation and correspondingly,

larger errors occurred at the boundaries. These organs have much more freedom to deform as the body cavity constrains their shape less rigidly. The colon and bladder have very large standard deviations but this can be expected, as the mice were not controlled for water or food intake. The spleen was typically not well registered, and visual inspection revealed that this organ varies appreciably in size and position from mouse to mouse.

Conclusions. We have developed a reliable phenotyping tool in which we can automatically segment 12 organs in an MR image of a whole mouse. Future work will entail using this tool to find anatomical anomalies in disease models.

References

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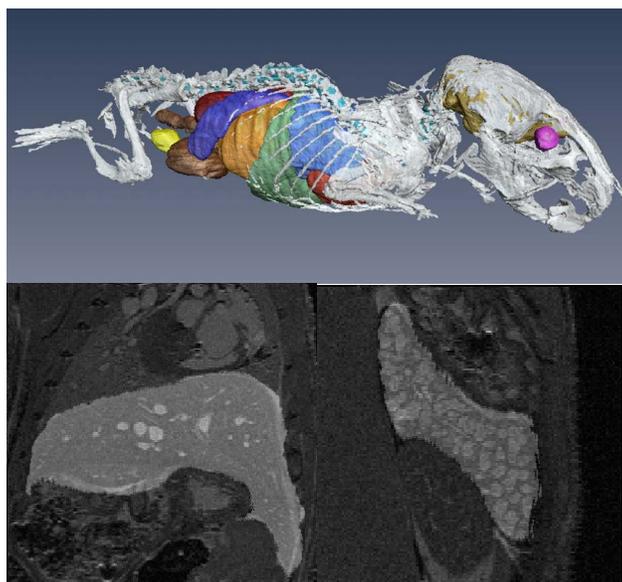


Figure 2. The top image is a 3D rendering of the manually labelled volumes in the atlas. The bottom two images show the propagated liver label (left) and spleen label (right) onto a different mouse.

	Avg. of 13 (mm ³)	Std Dev (%)
Brain	508	6
Bone	881	6
Sp. chord	150	7
Liver	1310	7
Eye	18	9
Heart	306	9
Kidney	348	14
Lung	455	14
Stomach	367	19
Colon	245	29
Spleen	85	35
Bladder	44	46

Table: The average volumes of the automatically obtained segmentations ordered according to the standard deviation.