Multi-atlas label propagation for accurate anatomical segmentation of rat brain images

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PURPOSE: Various quantitative imaging strategies rely on the capability to segment regions of interest (ROIs) that have distinct structural or functional properties. Accurate image registration that enables comparisons within and between subjects and determination of how regions are affected by pathological or physiological processes remains a challenge.
Automated multi-atlas based approaches have been proposed for the human brain. They provide highly accurate structural segmentations by propagating manual delineations from multiple atlases and consolidating them in the space of a target image[1,2].
The aim of this work was to develop a method for automatically defining ROIs on MR images of normal and atrophic rat brains. We adapted the MAPER (multi-atlas propagation with enhanced registration) algorithm[2] for the purpose.
METHODS: All images were acquired on a Bruker BioSpec 7T (Bruker Biospin, Ettlingen, Germany) under isoflurane anaesthesia. Target images were acquired from male Sprague Dawley rats (n=8), 298±76 g body weight. T2 weighted structural images were acquired using a RARE spin echo sequence with the following parameters: TE/TR=69.1/13445.8ms, FOV=3x1.5cm^2, matrix dimension 256x128, slice thickness 0.4mm (75 slices), RARE factor=8. Status epilepticus was induced in the target rats using pilocarpine injection after baseline scanning. Follow-up scanning was performed after 6 and 35 days, yielding a total of 24 target images. A database of seven atlases, each consisting of a structural MR scan of a healthy adult rat with similar acquisition parameters, paired with a corresponding manual segmentation into 29 regions[3], was used as label sources.
Tissue classification on the seven atlas and 24 target images was performed using the "Segment" module in SPM8. Templates from Tohoku University[4] were used as priors with a low (10e-6) background value added to tissue probability maps to avoid zero prior probability for enlarged ventricles. The resulting individual tissue probability maps were summed and smoothed with a 0.5 mm^3 3D FWHM Gaussian kernel to avoid sharp transitions, and used for brain extraction.
Each target image was processed in turn, using all seven atlases as input. Using the NiftyReg registration algorithm[5], coarse registration was performed with tissue probability maps as inputs. The resulting transform was used as the starting point for the fine registration step, where the T2-weighted images were paired and aligned. For the coarse registration, the control point spacing was 10mm and the similarity criterion was the sum of squared differences; for the fine registration, the control point spacing was 1mm and the similarity measure was normalized mutual information. After propagating all seven atlas label sets into the space of the target image, the resulting individual segmentations were consolidated into a consensus label set using vote-rule based decision fusion.
RESULTS: Visual assessments confirmed the success of the segmentation method on healthy as well as on pathologic MR rat brain images (Fig.1). Volumetric ROI changes matched expectations: for example, the right ventricles increased by 46%±43 at D0+6 and by 82%±64 at D0+35. The high standard deviations are explained by the variability between subjects relative to the affection of the brain after SE.
DISCUSSION: Although the proposed method performed well in this study, its accuracy depends on the accuracy of the tissue classification. Extensive structural changes over time, such as those in the ventricle regions, meant that the prior templates were less representative for the follow-up images, limiting the accuracy of the prealignment (Fig.1, arrow). While this weakness remains to be addressed, the method holds promise in that it eliminates the time and effort required for manual segmentation, as well as its interrater variability.
CONCLUSION: The adaptation of the MAPER method to rodent data sets is suitable for creating accurate segmentations including in pathology, and facilitates image quantification in longitudinal and intersubject studies.
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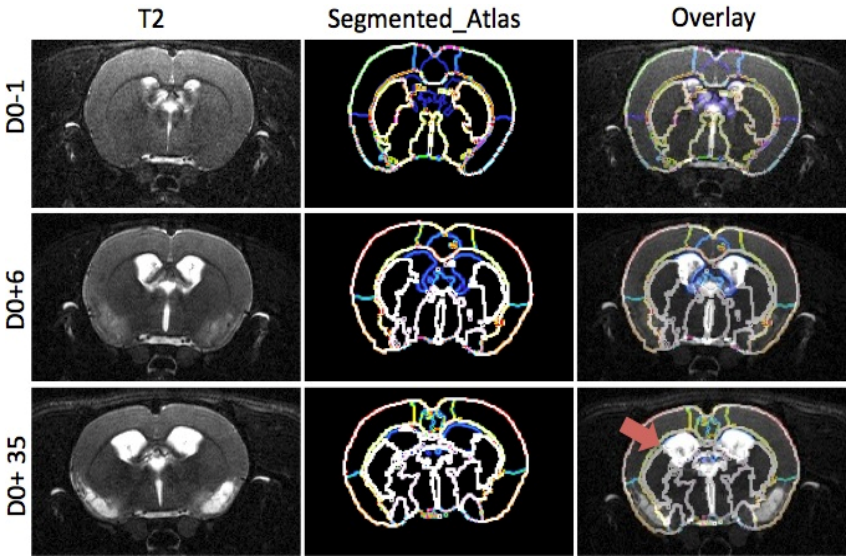

Fig.1: Image of the same rat acquired at three time points. Left column: intensity-based images. Middle: Corresponding segmentations. Right: Overlay. Label outlines are superimposed on coronal sections selected to show ventricles. D0-1 are baseline images, D0+6/D0+35 images were acquired 6 and 35 days after SE induction. The arrow shows a region where prealignment was not perfect.