Multi-atlas propagation with enhanced registration – MAPER

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Abstract. To address the challenge of applying expert anatomical knowledge captured in brain atlases to unseen brain images, we previously proposed "MAPER" (multi-atlas propagation with enhanced registration).

The approach is based on a pairwise image registration procedure that incorporates tissue class information to obtain a robust anatomical correspondence estimate, even when the target brain is distinctly differently configured from the atlases. Multiple segmentations obtained by propagating individual atlas label sets are combined using a simple procedure (vote-rule decision fusion).

We participate in the "MICCAI 2012 Grand Challenge and Workshop on Multi-Atlas Labeling" with a procedure that remains unchanged in principle from our previous publications. Only at the detail level was the method adapted to the particularities of the challenge.

1 Introduction

The advent of large, publicly available repositories of images of the human brain (ADNI, AIBL, Predict-HD, IXI, OASIS etc.) has changed the playing field for image analysis. Whereas smaller-scale projects could rely on visual review of images by a trained expert, this traditional approach does not scale well to the requirements of data analysis in large multi-centre studies. To extract the information required to answer a defined research question, automatic anatomical segmentation methods are among the most promising and widely applicable avenues.

An established approach for achieving automatic segmentation is to exploit expert knowledge contained in manual segmentations pertaining to magnetic resonance (MR) images. A variety of algorithms have been proposed. Multiatlas label propagation, followed by a consolidation (fusion) step has repeatedly been shown to be accurate and robust.

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We apply here a label propagation method where expert labels are warped into the target space using a geometric transformation determined through pairwise nonrigid image registration. To increase the robustness of the image registration step against large discrepancies that can arise from, e.g., atrophy, initial global and coarse transformations are calculated from pairs of tissue probability maps, rather than native T1 signal maps. Multiple segmentations resulting from processing multiple atlases with a single target set are consolidated in the space of the target using vote-rule decision fusion [1]. We previously described performance characteristics of the underlying multi-atlas method [2] and the tissue-probability based enhancement ("MAPER") [3]. MAPER-generated segmentations of the baseline and screening images acquired by ADNI are publicly available [4].

2 Method

2.1 Material

We downloaded the data for the "MICCAI 2012 Grand Challenge and Workshop on Multi-Atlas Labeling", consisting of 35 images in total, originating from the OASIS project (http://oasis-brains.org). T1-weighted images of 15 subjects had been labelled as training data and supplied with corresponding label sets, which had been generated by manual delineation of 138 regions¹. Testing data consisted of 20 T1-weighted images of 16 subjects. Label sets for the testing data were hidden from the contestants.

2.2 Image registration

Probabilistic classification of intracranial voxels into tissue classes (grey matter, white matter, and cerebrospinal fluid) was performed on the atlas and target images. The partial volume estimates from the tissue classification were combined into a multispectral image volume, with each channel of the image representing a partial volume estimate for one of the three tissue classes. The atlas and target images were then aligned using affine and coarse nonrigid (20 mm control point spacing, CPS) registration. As a departure from our previous implementations, we did not use the summed cross-correlation as the similarity measure to maximize. Instead, we minimized Kulback-Leibler divergence across all channels of the multi-spectral image volume.

The resulting transformation was then used as a starting point for a more detailed registration (10, 5, and 2.5 mm CPS), where normalized mutual information (NMI) between the signal intensities of a T1 image pair is maximized. Displacements were applied to the atlas image via a lattice of control points and blended using B-spline basis functions [5]. At each resolution level, the output transformation of the previous stage was used as the starting point.

¹ Label sets were provided by Neuromorphometrics, Inc. (http://neuromorphometrics.com/) under academic subscription.

2.3 Label fusion

Each pairing of an atlas with a target set yields a label set that uniquely assigns an anatomical label to each target voxel. To consolidate these multiple label sets, the per-voxel modal value of all label assignments was chosen as the final unique assignment (vote-rule decision fusion [1]). In the case of multiple modes, the final label was chosen at random from the tied label values.

2.4 Parameter modifications

To generate tissue probability maps, we subsampled the input images to a resolution of $2 \times 2 \times 2$ mm before applying FSL FAST. This led to an acceleration of the global and coarse registration steps without loss of accuracy.

2.5 Software toolkits

Tissue probability maps were obtained using FAST from the FSL suite [6] and combined using "fslmerge".

The tools used for affine ("reg_aladin") and nonrigid ("reg_f3d") registration were obtained from the Nifty Reg toolkit, an efficient implementation of B-spline warping [7].

Vote rule decision fusion was applied using "combineLabels" from IRTK (www.doc.ic.ac.uk/~dr/software/).

3 Discussion

Its characteristics predestine the MAPER method for certain application scenarios. For example, using normalized mutual information as a similarity metric in the high-dimensional registration steps entails robustness against acquisition differences. MAPER is thus particularly suitable if atlas and target (training and testing) images have been acquired differently, ie. on different scanners, at different centres, or using different sequences. Using tissue probability maps for coarsely aligning atlas and target images relaxes the usually strict requirement that the atlas set be anatomically representative of the target set. Consequently, MAPER performs better than other approaches when target images with severe atrophy are to be segmented with atlases of young, healthy subjects [3]. Neither of these strengths is relevant in the Grand Challenge. Nevertheless, we participate with this method for two reasons. First, the enhancements have been developed with the stated objective of avoiding sacrifices of accuracy in "easy" application scenarios, so we expect its performance on the Grand Challenge data to be reasonable. Second, MAPER output can serve further development, both as a foundation and as a lower-bounds benchmark: for testing sophisticated segmentation combination strategies, it delivers individual segmentations, plus the result from vote-rule fusion to indicate the level of accuracy that any newly developed method should be able to beat. A separate entry to the Grand Challenge, provided by co-author CL, will use MAPER in this way.

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