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Learning-Based 3T Brain MRI Segmentation with Guidance from 7T MRI Labeling

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Abstract

Brain magnetic resonance image segmentation is one of the most important tasks in medical image analysis and has considerable importance to the effective use of medical imagery in clinical and surgical setting. In particular, the tissue segmentation of white matter (WM), gray matter (GM), and cerebrospinal fluid (CSF) is crucial for brain measurement and disease diagnosis. A variety of studies have shown that the learning-based techniques are efficient and effective in brain tissue segmentation. However, the learning-based segmentation methods depend largely on the availability of good training labels. The commonly used 3T magnetic resonance (MR) images have insufficient image quality and often exhibit poor intensity contrast between WM, GM, and CSF, therefore not able to provide good training labels for learning-based methods. The advances in ultra-high field 7T imaging make it possible to acquire images with an increasingly high level of quality. In this study, we propose an algorithm based on random forest for segmenting 3T MR images by introducing the segmentation information from their corresponding 7T MR images (through semi-automatic labeling). Furthermore, our algorithm iteratively refines the probability maps of WM, GM, and CSF via a cascade of random forest classifiers to improve the tissue segmentation. Experimental results on 10 subjects with both 3T and 7T MR images in a leave-one-out validation, show that the proposed algorithm performs much better than the state-of-the-art segmentation methods.

1 Introduction

Magnetic resonance (MR) imaging is a powerful tool for in vivo diagnosis of brain disorders. Accurate measurement of brain structures in MR image is important for studying both brain development associated with growth and brain alterations associated with disorders. These studies generally require to first segment structural T1-weighted MR images into white matter (WM), gray matter (GM), and cerebrospinal fluid (CSF). Thus MR image segmentation is a key processing step in medical image analysis, such as morphometry, automatic tissue labeling, tissue volume quantification and image registration,

and has considerable importance to the effective use of medical imagery in clinical and surgical setting. Although this diversity of processing applications promotes the development of various automatic segmentation techniques, accurate automated tissue segmentation still remains a difficult task.

So far, many learning-based techniques have been applied for tissue segmentation, including support vector machines (SVM) [1], artificial neural networks (ANN) [2], deep convolutional neural networks (CNNs) [3], and random decision forests [4, 5]. The performance of learning-based segmentation methods is largely dependent on the quality of the training dataset. In general, training datasets were most commonly generated by manual labeling of 3T MR images, which typically exhibit insufficient signal-to-noise ratio (SNR) and intensity contrast. The inaccuracy and unreliability of these manual delineations affect image segmentation and subsequent quantitative statistical analysis.

By the end of 2010, more than 20 ultra-high field MR scanners, mainly 7T, have been in operation in the world for human medical imaging [6]. 7T scanners give images with significantly higher intensity contrast, greater SNR [7], and more anatomical details [8]. The utilization of higher field strengths allows the visualization of brain atrophy that is not evident at lower field strength, promoting better understanding of neurological disorders, cerebrovascular accidents, or epileptic syndromes [9].

In this paper, we present an automatic learning-based algorithm for segmentation of 3T brain MR images by introducing the segmentation information obtained from their corresponding 7T MR images. Specifically, to integrate information from multiple sources, we harness the learning-based multi-source integration framework (LINKS) strategy [5], which is based on random forest and has been applied to accurate tissue segmentation of infant brain images. In particular, image segmentation is achieved by automatically learning the contribution of each source through random forest with an auto-context strategy [10, 11]. By iteratively training random forest classifiers based on the image appearance features and also the context features of progressively updated tissue probability maps, a sequence of classifiers is trained. Specifically, the first random forest classifier provides the initial tissue probability maps for each training subject. These tissue probability maps are then further used as additional input images to train the next random forest classifier, by combining the high-level multi-class context features from the probability maps with the appearance features from the T1-weighted MR images. Repeating this process, a sequence of random forest classifiers can be obtained. In the application stage, given an unseen image, the learned classifiers are sequentially applied to progressively refine the tissue probability maps for achieving final tissue segmentation.

2 Materials and Methods

10 volunteers (4 males and 6 females) with age of 30 ± 8 years were recruited for this study. All the participants were scanned at both 3T Siemens Trio scanner and 7T Siemens ultra-high field MR imaging scanner with a circular polarized head coil. The 3T T1-weighted images were obtained with 144 sagittal slices using two sets of parameters: (1) 300 slices, voxel size $0.8594 \times 0.8594 \times 0.999 \text{ mm}^3$; and (2) 320 slices, voxel size $0.8594 \times 0.999 \times$

0.8594 mm³. The 7T T1-weighted MR images were acquired with 192 sagittal slices using two sets of parameters: (1) 300 slices, voxel size $0.80 \times 0.80 \times 0.80$ mm³; and (2) 320 slices, voxel size $0.6 \times 0.6 \times 0.6$ mm³. The 7T MR images were linearly registered to the spaces of their corresponding 3T MR images.

Standard image preprocessing steps were performed before tissue segmentation, including skull stripping, intensity inhomogeneity correction, histogram matching, and removal of both cerebellum and brain stem by using in-house tools. Specifically, the segmentations of 7T MR images were obtained by first using the publicly available software, FSL [12], to generate a relatively accurate segmentation, and then performing necessary manual corrections by an experienced rater via ITK-SNAP (www.itksnap.org).

2.1 Proposed Algorithm

Brain tissue segmentation is carried out using a cascade of random forest classifiers, which will be trained using *the appearance features* obtained from 3T MR images and the *ground truth segmentation labels* obtained by semi-automatic delineation of corresponding 7T MR images. The main motivation for using segmentation information from 7T MR images is because of their greater contrast and details compared with 3T MR images, as illustrated in Fig. 1. An overview of our proposed algorithm is shown in Fig. 2, in which a series of classifiers are trained with both T1-weighted MR images and tissue probability maps of WM, GM and CSF as input. Specifically, the first classifier is trained by only the appearance features from the T1-weighted MR images. When training the subsequent random forests, the context features of WM, GM, and CSF probability maps, generated in the previous iteration, are used as additional input for training. Note that the context features capture information of voxel neighborhood and thus improve classification robustness. This training process is repeated and finally a series of random forests are constructed with progressively refined probability maps. In the testing stage, each voxel of an unseen T1-weighted MR image goes through each trained random forest sequentially. Each classifier will produce a set of GM, WM, and CSF tissue probability maps, which together with the T1-weighted MR image are used as input to the next trained classifier for producing the improved GM, WM, and CSF tissue probability maps.

In our work, we employ the random forest to train the classifiers. The random forest (RF) is an ensemble of decision trees that is based on bagging and random decision forests. Based on the decisions given by all the trees, the class of input feature vector is determined using majority voting. The random forest is able to capture complex data structures and is resistant to both over-fitting (when trees are deep) and under-fitting (when trees are shallow) [13]. Each tree classifier $h(X, \Theta_k)$ is constructed using the feature vectors of a random subset of training voxels X . Each element of the feature vector corresponds to a feature type. At each node of the tree, splitting is based on a small randomly selected group of feature elements. The random generated vector Θ_k determines both the voxel subset and the nodal feature subsets associated with the tree. Its randomness promotes diversity among the tree classifiers [14].

2.2 Appearance and Context Features

In this paper, we use 3D Haar-like features to compute both appearance and context features, due to computational efficiency. Specifically, for each voxel x , its Haar-like features are computed as the local mean intensity of any randomly displaced cubical region (R_1), or the mean intensity difference over any two randomly displaced, asymmetric cubical regions (R_1 and R_2) [5]:

$$f(x, I) = \frac{1}{R_1} \sum_{u \in R_1} I(u) - b \frac{1}{R_2} \sum_{v \in R_2} I(v), R_1 \in R, R_2 \in R \quad (1)$$

where R is the region centered at voxel x , I is the image under consideration, and parameter $b \in \{0, 1\}$ indicates whether one or two cubical regions are used. Within R , the intensities are normalized to have unit L_2 norm. For each voxel, a large number of features can be extracted.

3 Experiments

In this study, we train a sequence of 10 random forest classifiers, each consisting of 20 forests with maximal depth of 100. A number of 30,000 voxel samples, randomly selected from the brain region of each training subject, were used to train the decision trees in each random forest, with the voxel neighborhood size of $9 \times 9 \times 9$, minimum 8 samples for each leaf node, and 100,000 random Haar-like features for each tree. Example results, shown in Fig. 3, indicate that the tissue probability maps are progressively improved and increasingly consistent with the ground truth, by using the sequential random forest classifiers.

3.1 Comparison with Other Methods on 10 Subjects

We compared our method with other segmentation methods provided in the following software packages: FSL and Medical Image Processing, Analysis, and Visualization (MIPAV). The leave-one-out cross-validation based Dice ratios for the 10 training subjects are reported in Table 1. The results indicate that the proposed method outperforms other methods for all three tissue types in most cases. Specifically, for the average Dice ratio of all 10 subjects, our method performs much better than any other comparison methods. For example, compared to the best method, our method improves about 7% for GM, >3% for WM, and >12% for CSF.

Qualitative results for visual inspection are also shown in Figs. 4, 5 and 6. From Fig. 4, we can observe that our method, compared with FSL, MIPAV and SPM, produces results that are significantly consistent with the ground-truth segmentations. WM surfaces generated by the ground truth and different methods are shown in Fig. 5. Figure 6 shows the differences of the label maps with respect to the ground-truth segmentations, indicating that the proposed method produces better segmentation with less false positives and false negatives.

4 Conclusion

In this paper, we presented a method for robust and accurate segmentation of 3T T1-weighted MR images by introducing the segmentation information from their corresponding 7T MR images (with high image quality). The proposed algorithm could combine the T1-weighted MR images with the tentatively estimated tissue probability maps to progressively refine the tissue probability maps by using the sequential random forest classifiers.

Comparison results demonstrate the advantage of the proposed method in terms of accuracy.

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Fig. 1.

Comparison between 3T and 7T T1-weighted MR images.

Fig. 2.

Method overview. The appearance features from the T1-weighted MR images and the context features from the WM, GM, and CSF probability maps are used for training a sequence of random forest classifiers.

Fig. 3.

The first column shows the original image, the segmentation results obtained by the proposed algorithm, and the ground truth segmentation. Subsequent columns show the tissue probability maps of GM, WM, and CSF output by the sequential random forest classifiers. The last column shows the ground-truth tissue probability maps.

Fig. 4. Comparison of segmentation results by different methods on a typical subject. Each row shows the results on a representative slice.

Fig. 5.
Comparison of WM surfaces generated by ground truth and different methods.

Fig. 6. Label differences with the manual segmentation. The first column shows the segmentation results by different methods. The next three rows show the differences of the GM, WM and CSF label maps with the ground-truth. Black and white denote false negatives and false positives, respectively.

Table 1

Comparison of tissue segmentation performance in terms of Dice ratio.

	Dice (%)	Sub.1	Sub.2	Sub.3	Sub.4	Sub.5	Sub.6	Sub.7	Sub.8	Sub.9	Sub.10	Mean (±STD)
GM	Proposed	87.54	88.81	88.78	87.94	86.33	92.62	90.72	90.31	91.38	90.45	89.49 ± 1.83
	FSL	83.39	81.85	81.32	83.09	81.03	81.07	78.75	83.07	82.13	77.57	81.33 ± 1.80
	MIPAV	84.31	81.74	81.66	80.56	81.92	83.89	79.70	84.47	83.43	83.85	82.55 ± 1.58
	SPM	77.39	77.58	79.71	77.75	79.53	78.81	79.60	78.01	84.63	70.21	78.32 ± 3.36
WM	Proposed	93.80	94.18	94.26	93.25	93.45	95.90	95.27	94.07	95.62	95.36	94.52 ± 0.90
	FSL	94.15	87.96	88.60	89.98	85.17	95.29	90.13	95.00	92.76	95.87	91.49 ± 3.46
	MIPAV	92.82	87.49	88.69	86.85	86.76	92.32	90.33	94.37	92.02	94.90	90.66 ± 2.91
	SPM	82.08	79.78	81.41	81.25	80.26	83.21	87.30	83.46	84.82	84.22	82.78 ± 2.18
CSF	Proposed	79.85	78.18	76.34	77.09	73.29	88.11	86.15	80.50	77.58	82.62	79.97 ± 4.32
	FSL	64.79	60.46	60.75	63.12	49.70	77.48	69.73	64.94	66.29	70.72	64.80 ± 6.99
	MIPAV	64.69	59.65	59.89	61.51	48.34	75.14	69.67	70.75	63.80	69.59	64.30 ± 7.21
	SPM	67.77	63.32	51.76	69.70	51.90	78.32	73.43	77.83	75.15	61.91	67.11 ± 9.28