

Brain Tissue Segmentation in MRI by Supervised Classification and Regularization

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Abstract. Segmentation and volumetry of brain tissues from MRI has interesting clinical and neuroscience applications. We report about a fully automatic brain segmentation method, which is based on voxel-wise feature extraction and tissue classification using decision forests with subsequent spatial regularization in a conditional random field context. Evaluation has been performed on two different image datasets, namely the IBSR and MRBrainS, using different similarity metrics. The average Dice coefficients for cerebrospinal fluid, gray matter and white matter range from 0.69 to 0.86. Computation time is between 2 and 3 minutes, with 1 additional minute required for skull-stripping. The segmentation tool is publicly available from our website.

Keywords: Brain tissue segmentation, MRI, decision forest, conditional random field

1 Introduction

Accurate segmentation of brain tissues from magnetic resonance images (MRI) is an important task in many clinical applications and also in neuroscience research. There exists a large body of literature, describing many different fully- or semi-automatic approaches for brain tissue segmentation, a review can be found in [2]. The quantification of brain tissue volumes based on segmentations has applications in neurodegenerative diseases [8], multiple sclerosis [10] and also in brain tumors [5].

The aim of this contribution is not to propose a new approach for brain tissue segmentation. In fact, decision forests for brain tissue segmentation have been introduced before, e.g. in [13]. Our goal is rather, to evaluate and report about the accuracy of a previously published method for segmenting tumor-bearing brain images [4,9]. This method segments 4 tumor sub-compartments and it also segments the remaining healthy tissues, consisting of cerebrospinal fluid (CSF), gray matter (GM) and white matter (WM). Until now, only the accuracy of the tumor segmentation has been evaluated [7]. Here we would like

to give insights into the accuracy of the segmentation of the healthy tissues. For this, we have slightly adapted the existing code, to consider only 3 different tissues classes (CSF, GM, WM) and a background class.

2 Methods

In a first pre-processing step, we extract the brain of the patient in order to simplify the segmentation problem. This is done in a fully automatic way using a publicly available ITK filter for skull-stripping [3]. For the tissue segmentation, we adapted an existing method for brain tumor segmentation [4] to perform segmentation of healthy tissues only in brain MR images. The method is a combination of supervised classification using a decision forest classifier and subsequent spatial regularization by minimizing the energy of a conditional random field. The decision forest uses a high-dimensional voxel-wise feature vector that combines intensity information with texture and gradient statistics, plus localization information. The complete segmentation pipeline is fully automatic and does not require user intervention at any point. More details about the segmentation method can be found in [4].

3 Results

We report results on two different datasets: the IBSR data [11] and the MRBrainS data [6]. The IBSR data consists of T1-weighted MR images (at 1.5T) from 18 different subjects. The MRBrainS data contains multi-sequence scans at 3T (T1-weighted, T1-weighted with inversion recovery and T2-FLAIR), with 5 datasets being available for training and 15 datasets for testing.

Our evaluation has been performed separately on both datasets: on the IBSR, we performed 6-fold cross-validation and on the MRBrainS we performed leave-one-out cross-validation on the training data. The results on the MRBrainS test data will be reported on the website. For the IBSR we used only one modality (T1), while for the MRBrainS data we used all 3 available image modalities (T1, T1-IR, T2-FLAIR) simultaneously for segmentation.

Some example results are shown in figure 1 for IBSR patient 1 and in figure 2 for MRBrainS testing patient 1. While both segmentation results look acceptable, it can be observed that due to inaccuracies in skull-stripping, part of the cortical gray matter of MRBrainS patient 1 was not correctly segmented.

We report 4 different similarity metrics for evaluating segmentation accuracy (see e.g. [1] for an explanation of the metrics): the Dice coefficient for measuring the overlap with the ground-truth, the Hausdorff distance to give an idea of the surface distance compared to the ground-truth and the absolute volume error as well as the relative volume error because the volume is clinically the most relevant measure. Results for the IBSR data are shown in table 1 and results for the MRBrainS training data in table 2.

On a standard PC, average computation time for segmentation is approximately 3 minutes for the IBSR images and approximately 2 minutes for the

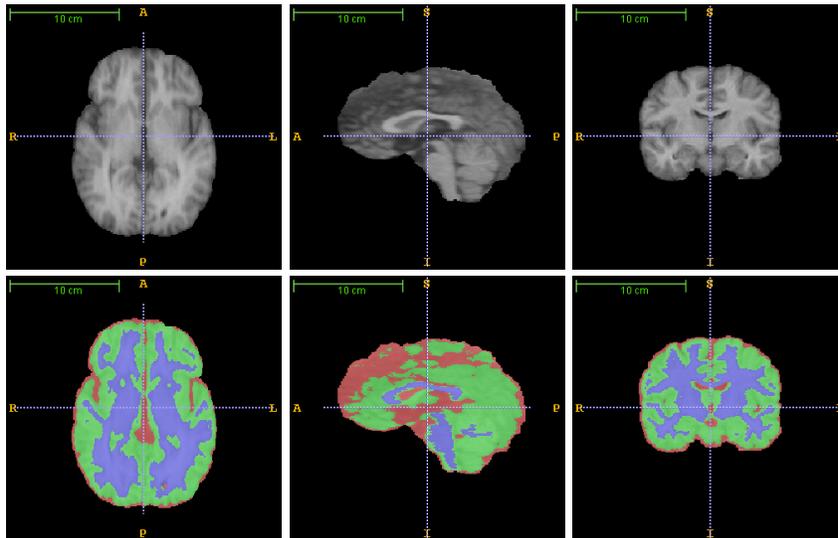


Fig. 1. Patient 1 from the IBSR dataset. First row from left to right: original skull-stripped T1-weighted image in axial, sagittal and coronal view. Second row from left to right: overlay of the segmentation result produced by our method (color code: CSF=red, GM=green, WM=blue) in axial, sagittal and coronal view.

Table 1. Similarity metrics on IBSR data

	CSF	GM	WM
Dice coefficient	0.69 ± 0.08	0.86 ± 0.02	0.86 ± 0.02
Hausdorff distance [mm]	2.5 ± 0.8	2.3 ± 0.5	2.5 ± 0.7
absolute volume error [ml]	65.9 ± 31.2	103 ± 68.6	40.3 ± 27.1
relative volume error [%]	34.6 ± 15.5	13.2 ± 8.8	8.0 ± 5.3

MRBrainS images. The difference in computation time is due to the difference in image resolution. Approximately 1 additional minute is required for skull-stripping.

4 Discussion and Conclusion

We have presented a fast and fully automated method for segmentation of healthy brain tissues in magnetic resonance images. The framework is flexible, it can be applied to different datasets, even containing different modalities. For this, it is necessary that training of the supervised method is performed on the same set of modalities, which should be used for segmentation later.

The accuracy of the segmentations in terms of Dice overlap, surface distances and volume errors is comparable to other state of the art methods for brain tissue segmentation, but the computation speed is faster than most other methods.

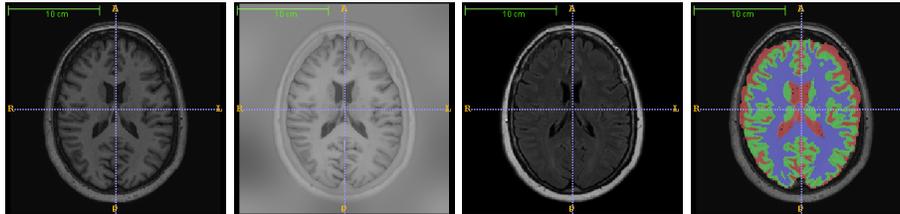


Fig. 2. One axial slice of MRBrainS patient 1 from the testing dataset. From left to right: T1-weighted image, T1-weighted image with inversion recovery, T2-FLAIR image, and an overlay of the segmentation result produced by our method (color code: CSF=red, GM=green, WM=blue).

Table 2. Similarity metrics on MRBrainS training data

	CSF	GM	WM
Dice coefficient	0.86±0.01	0.79±0.02	0.84±0.03
Hausdorff distance [mm]	2.0±0.6	1.8±0.2	2.8±0.1
absolute volume error [ml]	41.8±18.0	46.3±25.3	23.3±13.8
relative volume error [%]	10.4±5.8	8.6±4.3	7.0±5.2

For example, accuracy in terms of Dice coefficient on the IBSR dataset is similar to a number of currently available approaches, including FSL⁴ and SPM⁵, when comparing to the results reported in [12]. A major source of error, especially for the gray matter, can be caused by inaccuracies of the skull-stripping. Thanks to its objectiveness, the automated method has potential applications for clinical measurements of atrophy in patients with longitudinal follow-up scans. The segmentation tool is publicly available⁶.

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⁴ <http://fsl.fmrib.ox.ac.uk/fsl/fslwiki/>

⁵ <http://www.fil.ion.ucl.ac.uk/spm/>

⁶ A MS Windows command line tool can be downloaded from our website http://www.istb.unibe.ch/content/research/medical_image_analysis/software/index_eng.html

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