Automatic Segmentation of Multi-contrast MRI Using Statistical Region Merging

P. Dvorak[1, 2], K. Bartusek[2], and E. Gescheidtova[3]

[1]Department of Telecommunications, Faculty of Electrical Engineering and Communication
Brno University of Technology, Technicka 12, Brno 612 00, Czech Republic
[2]Institute of Scientific Instruments of the ASCR, v.v.i., Kralovopolska 147, Brno 612 64, Czech Republic
[3]Department of Theoretical and Experimental Electrical Engineering
Faculty of Electrical Engineering and Communication, Brno University of Technology
Technicka 12, Brno 612 00, Czech Republic

Abstract— Several methods have been developed for segmentation of MR images. Some of them are fully automated and some of them rely on an expert's assistance, such as determination of a starting point etc.. The fully automated methods are usually based on prior knowledge of a given object and can be used only for particular problem. The purpose of the proposed method is a fully automatic segmentation for general MR images independent on the number of tissues present. The proposed method is based on Statistical Region Merging (SRM) algorithm developed by Richard Nock and Frank Nielsen in 2004. The suitable MR contrasts for this algorithm, as it was confirmed during the test phase, are T1, T2 and FLAIR images. The segmentation process divides to image into regions according the properties in the area, but it does not consider the unconnected areas. For this reason, the algorithm is repeated for created segments without a joint border condition. The algorithm was tested on 5000 axial images with resolution 256×256 pixels. In 2256 slices, the tumor was present. Since the proposed method is fully automatic and independent of image intensities, each image of the database can be considered as unique and independent of others. The Dice coefficient for tissue segmentation varies for particular tissues. The best average result was achieved for grey matter, where the dice coefficient reached value 0.84. The results show the suitability of SRM method for multi-contrast MRI segmentation.

1. INTRODUCTION

This paper focuses on automatic segmentation of magnetic resonance images, which belongs to the general problem of image segmentation. Since the MR technique is becoming more popular due to its non-invasive principle, the imaging of biological structures by MR equipments is a routine investigating procedure today [1]. For this reason, the automatic processing of this kind of images is getting more attention and can lead to automatic evaluation of tissue properties [2] or pathology detection [3].

General image segmentation is still an unsolved problem, therefore specific methods have to be applied for particular types of images. General method that could be applied for all kinds of images has not been developed so far and in the near future the situation will probably remain the same. For MR image segmentation, the classic techniques such as thresholding, region growing, active contour, etc. can be used [4]. Another type of segmentation used in MRI is pixel classification into several classes. This can be either supervised using algorithms such as SVM [5] used e.g., in [6], or unsupervised using clustering algorithms. Such algorithms can be based on data space division such as k-means algorithm [7] or they can respect the noise distribution such as Gaussian Mixture Model using the Expectation-Maximization algorithm for determination of model parameters [8].

The method proposed in this paper does not involve any a priori knowledge about the input image, such as reference image, training process or defined number of tissues. Hence, the technique can be labeled as a fully automatic and unsupervised segmentation algorithm of MR brain images.

2. METHODOLOGY

The segmentation process consists of three main steps: Preprocessing, Segmentation and Segment merging. At first, the preprocessing is performed. This step consists of general preprocessing algorithms used in MR processing works. The preprocessing is followed by the segmentation, which is carried out by Statistical Region Merging algorithm, which was developed by Nock and Nielsen in 2004 [9]. When the image is segmented, the regions are merged to detect occurrences of particular tissues in several locations.

2.1. Preprocessing

As in every kind of image processing, the preprocessing is an important step for image analysis. The preprocessing here consists of Region of Interest (ROI) definition, noise reduction, and inhomogeneity compensation. In case of multi-contrast segmentation, the registration of particular images is desired. Since the aim of this work is the segmentation itself, the preprocessing process is described roughly and several techniques are recommended.

Several techniques for ROI definition (Brain extraction) such as the algorithm proposed in [10] have been developed. This step also decreases the run-time since the image can be cut to the smallest necessary size. The noise reduction is carried out by Wiener filter [11], which uses a statistical approach and makes the tissues more compact and reduces the noise with borders preserved, which is the advantage compared to, e.g., widely used Gaussian filter. For the inhomogeneity compensation purpose, the algorithm Histogram matching, which is implemented in 3D Slicer (http://www.slicer.org/) can be used. The multi-contrast registration can be done by algorithm for multi-modal brain images, the new technique described in (bi-modal) is suitable.

Nevertheless, the images of the testing database are already co-registered and skull-stripped. Thus, the aim of this work is the segmentation technique and the registration and skull-stripping are not performed here.

2.2. Segmentation

The segmentation uses the Statistical Region Merging (SRM) algorithm. Here, the method was adapted to multi-contrast MR images, where the algorithm can work with any number of contrasts. The reason has been described above.

The only input of Statistical Region Merging Algorithm, except the image itself, is a parameter Q, which according to [9] "allows quantifying the statistical complexity of the image, the generality of the model, and the statistical hardness of the task." The larger Q, the more smaller segments are created. In our case of MRI segmentation with image size about 200×200 px, this parameter was firmly set to value 256 according to experiments. Since the Segment Merging is carried out afterwards, the slight oversegmentation is appropriate here. Since the SRM is primarily designed to RGB image segmentation, where each channel is represented by 8 bits, the intensities in every MR contrast are normalized into the range $\langle 0; 255 \rangle$.

The SRM algorithm starts with splitting the input image into small segments with the size just of one pixel. In 4-connexity, every pixel creates 4 or less adjacent pairs. The pairs of adjacent pixels are sorted according to the similarity between these two pixels. The neighboring pixels are joined into segments if they meet the similarity condition. The set of adjacent pixels is traversed only once, which makes the algorithm very fast. The detailed information about the SRM algorithm can be found in [9]. The advantage of this method, compared to segmentation techniques based on boundary detection, such as active contours [12], is its performance in areas where no clear border are visible, which is also the case of brain MR images. Another advantage, as already mentioned, is its speed.

2.3. Segment Merging

The segmentation process divides the image into regions according to the properties in the area, but it does not consider the unconnected areas. For this reason, the postprocessing step consisting of segments unification has to be performed.

The unification process is similar to the segmentation algorithm and it is also mentioned in [9]. In SRM, each pixel is considered to be a unique region at the beginning and only adjacent pixels can be merged during this process. Here, each segment created during SRM can be merged with any other segment. In SRM, each pixel creates no more than 4 pairs. Every segment creates $N-1$ pairs, where N denotes the number of regions in segmented image. All of these pairs enter the same computation as pairs in SRM algorithm. According to the experiments, the Q in this process is reduced to value 128 to avoid the repetition of the oversegmentation.

The result of the Segment Merging is a labeled image, where one label does not need to create a connected region, which means that more locations of particular tissue were detected.

3. EXPERIMENTS AND RESULTS

3.1. Datasets

Brain tumor image data used in this work were obtained from the MICCAI 2012 Challenge on Multimodal Brain Tumor Segmentation (http://www.imm.dtu.dk/projects/BRATS2012) organized by

B. Menze, A. Jakab, S. Bauer, M. Reyes, M. Prastawa, and K. Van Leemput. The challenge database contains fully anonymized images from the following institutions: ETH Zurich, University of Bern, University of Debrecen, and University of Utah.

The test database consists of simulated T1, T2, and FLAIR images. From each case, 100 slices in each plane were taken. 25 subjects of high-grade and 25 subjects of low-grade glioma were available, which means that the algorithm was tested on 5000 images with resolution 255×255 px. In 2256 slices, the tumor was present. Since the proposed method is fully automatic and independent of image intensities, each image of the database can be considered as unique and independent of others.

All the simulated images are in BrainWeb space [13]. The information about the simulation method can be found in [14].

3.2. Evaluation Criteria

For the evaluation of region segmentation, Dice Coefficient and Accuracy were used. The Dice Coefficient (DC) (DICE), in some works called Similarity Index, is computed according to the equation

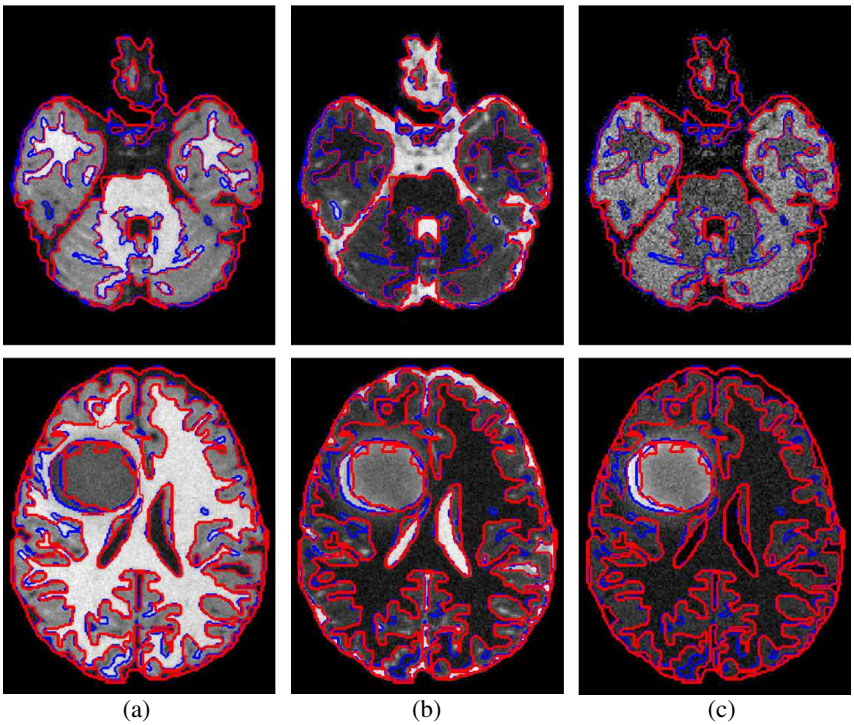
$$\mathrm{DC} = \frac{2\,|A \bigcap B|}{|A| + |B|}, \tag{1}$$

where A and B denotes the ground truth and the result masks of the segmentation, respectively. This criterion compares the intersection of two sets with their union. The range of values of DC is $\langle 0; 1\rangle$, where the value 1 expresses the perfect segmentation. According to [15], the DC $> 0,7$ indicates an excellent similarity.

Another measure widely employed for segmentation evaluation is Accuracy (A), used e.g., in [6] and defined by the equation:

$$A = \frac{TP + TN}{TP + FP + TN + FN}, \tag{2}$$

where TP, FP, FN and TN stand for "True Positive", "False Positive", "False Negative", and "True Negative", respectively. Both measures are in the same range as DC and the higher value indicates the better performance as well.



(a) (b) (c)

Figure 1: Results of the segmentation of healthy slices with and without a tumor for different subjects. (a) T1-weighted images. (b) T2-weighted images. (c) FLAIR images, Red: result of segmentation, Blue: ground truth.

Table 1: Segmentation evaluation by dice coefficient and accuracy for both planes.

	Dice		Accuracy	
	Median	Average	Median	Average
WM	0.87	0.84 ± 0.13	0.91	0.91 ± 0.05
GM	0.87	0.85 ± 0.06	0.87	0.86 ± 0.05
CSF	0.81	0.78 ± 0.16	0.95	0.94 ± 0.03
Tumor	0.59	0.47 ± 0.31	0.96	0.92 ± 0.17
Edema	0.56	0.49 ± 0.34	0.97	0.95 ± 0.95

3.3. Results

The summary of the segmentation process results is in Table 1.

In average, the number of detected tissues in images was 1.4 more than the true number. This was due to inaccurate segmentation of small regions. The average size of such redundant region was about 11.8% of the brain size. This was mostly due to unclear border between adjacent tissues and created regions in between.

The results are visualized in Fig. 1, where the ground truth segmentation (blue) is compared with the result of the proposed algorithm (red) on all T1, T2 and FLAIR contrast that were used for the segmentation. The results for healthy brains and brains with tumor are shown.

4. CONCLUSION

The purpose of this work is to show a fully automatic segmentation technique for multi-contrast MRI. This method works also for one-contrast MRI but with less precision, since not all tissues could be well separated according to intensities in one image. The future work will cover an improvement in segment merging process, the automatic tissue determination according to properties, and extension into 3D.

The big advantage compared to other state-of-the-art methods is its independence of the number of segmented tissues. The algorithm can automatically segment both healthy and afflicted brains and could be used also for other parts of the body.

ACKNOWLEDGMENT

The described research is funded by projects SIX CZ.1.05/2.1.00/03.0072, project GACR 102/12/1104, and project COST CZ LD14091.

REFERENCES

1. Gogola, D., A. Krafck, O. Strbak, and I. Frollo, "Magnetic resonance imaging of surgical implants made from weak magnetic materials," *Measurement Science Review*, Vol. 13, No. 4, 165–168, 2013.
2. Mikulka, J., E. Gescheidtova, P. Marcon, K. Bartusek, and A. prlkov, "Evaluation of tissue properties in MR images," *PIERS Proceedings*, 339–342, Moscow, Russia, Aug. 19–23, 2012.
3. Dvorak, P., W. Kropatsch, and K. Bartusek, "Automatic detection of brain tumors in MR images," *36th International Conference on Telecommunications and Signal Processing (TSP)*, 577–580, 2013.
4. Zhang, H., J. E. Fritts, and S. A. Goldman, "Image segmentation evaluation: A survey of unsupervised methods," *Computer Vision and Image Understanding*, Vol. 110, No. 2, 260–280, 2008, [Online] Available: http://www.sciencedirect.com/science/article/pii/S1077314207001294.
5. Cortes, C. and V. Vapnik, "Support-vector networks," *Mach. Learn.*, Vol. 20, No. 3, 273–297, Sep. 1995, [Online] Available: http://dx.doi.org/10.1023/A:1022627411411.
6. Mikulka, J. and E. Gescheidtova, "An improved segmentation of brain tumor, edema and necrosis," *PIERS Proceedings*, 25–28, Taipei, Mar. 25–28, 2013.
7. MacQueen, J. B., "Some methods for classification and analysis of multivariate observations," *Proceedings of 5th Berkeley Symposium on Mathematical Statistics and Probability 1*, 281–297, 1967.
8. McLachlan, G. and D. Peel, *Finite Mixture Models*, John Wiley & Sons, Inc., 2000.
9. Nock, R. and F. Nielsen, "Statistical region merging," *IEEE Transactions on Pattern Analysis and Machine Intelligence*, Vol. 26, No. 11, 1452–1458, 2004.

10. Uher, V., R. Burget, J. Masek, and M. Dutta, "3d brain tissue selection and segmentation from MRI," *36th International Conference on Telecommunications and Signal Processing (TSP)*, 839–842, 2013.
11. Lim, J. S., *Two-dimensional Signal and Image Processing*, Prentice Hall, 1990.
12. Mikulka, J., E. Gescheidtova, and K. Bartusek, "Soft-tissues image processing: Comparison of traditional segmentation methods with 2d active contour methods," *Measurement Science Review*, Vol. 12, No. 4, 153–161, 2012.
13. Prastawa, M., E. Bullitt, and G. Gerig, "Simulation of brain tumors in MR images for evaluation of segmentation efficacy," *Medical Image Analysis*, Vol. 13, No. 2, 297–311, 2009. [Online] Available: http://www.sciencedirect.com/science/article/pii/S1361841508001357.
14. Cocosco, C. A., V. Kollokian, R. K.-S. Kwan, G. B. Pike, and A. C. Evans, "Brainweb: Online interface to a 3d MRI simulated brain database," *NeuroImage*, Vol. 5, 425, 1997.
15. Zijdenbos, A. and B. Dawant, "Brain segmentation and white matter lesion detection in MR images," *Critical Reviews in Biomedical Engineering*, Vol. 22, 401–465, 1994.