Multi-parametric Segmentation of MR images of the Brain

[1, 2]P. Dvořák, [2]K. Bartušek

[1]Dept. of Telecommunications, Faculty of Electrical Engineering and Communication, Brno University of Technology, Brno, Czech Republic,
[2]Institute of Scientific Instruments of the ASCR, v.v.i., Brno, Czech Republic
Email: pavel.dvorak@phd.feec.vutbr.cz

Abstract. *This work deals with segmentation of magnetic resonance images. For better distinguishing between particular tissues, particular properties of tissues and their manifestation in different types of imaging are used. Specifically, T1 and T2 images are used. The segmentation is based on the approximation of more dimensional histograms. Since the noise distribution in MR images is close to Gaussian distribution for large signal-to-noise ratio, the approximation is done by Gaussian Mixture Model, where the number of components is determined using Bayesian Information Criterion and Elbow method.*

Keywords: GMM, Image Segmentation, MRI, Multi-parametric Image Segmentation, Tissue Classification.

1. Introduction

This paper focuses on automatic segmentation of magnetic resonance images, which belongs to the general problem of image segmentation. 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 remain the same.

For MR image segmentation, the classic techniques such as thresholding, region growing, active contour, etc. can be used [1]. These methods work only with one type of image. If more types of images such as T1-weighted, T2-weighted or Diffusion weighted are present, it is useful to take advantage of all of them. The advantage can be seen in Fig. 1. It is obvious in this figure that tissues, which have similar intensities in one type of image, can be distinguished on another type and vice versa.

The proposed method is related to MR images with large signal-to-noise ratio, because they can meet the condition of approximately Gaussian distribution of noise. Here, images acquired by Spin Echo and Turbo Spin Echo sequence are used. All processed images were acquired in the Faculty Hospital in Brno Bohunice by the Philips Achieva MRI system ($B_0 = 1.5$ T).

2. Noise in MR Images

The noise in real and imaginary MR images can be described by Gaussian distribution [2]. Since the magnitude images are created by non-linear operation, the distribution of noise in this type of image is no longer Gaussian. Here, the noise distribution is Rician. The Rician distribution is described by Eq. 1 [3].

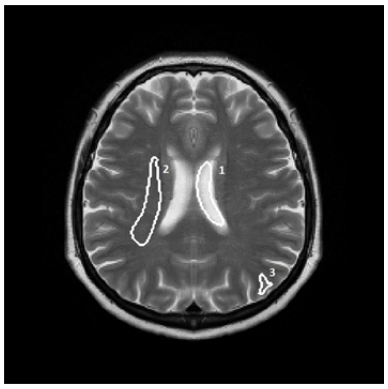
$$p_M(M) = \frac{M}{\sigma^2}\exp\left(\frac{-\left(M^2 + A^2\right)}{2\sigma^2}\right) I_0\left(\frac{AM}{\sigma^2}\right) \qquad (1)$$

where σ is the standard deviation of the Gaussian noise in the original real and imaginary images. They are assumed to be the equal. I_0 denotes the modified zeroth order Bessel

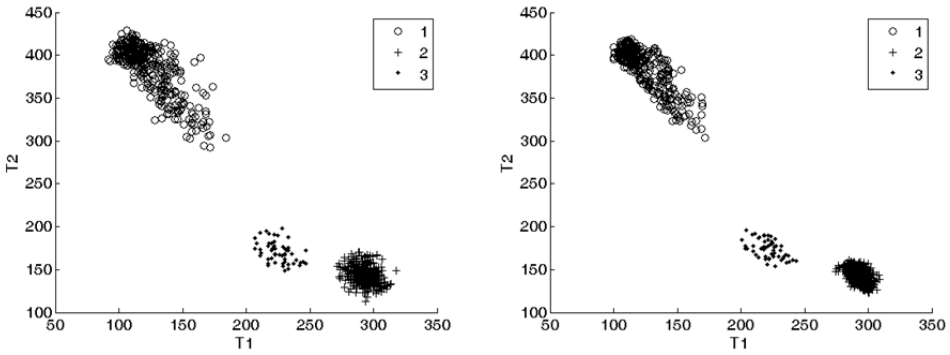
function of the first kind. A and M mean the pixel intensity in the absence of noise and the measured pixel intensity, respectively.

The Rician distribution for large signal-to-noise ratio is comparable to Gaussian distribution. Since the input images of brain, which are used in this work, meet the condition of large signal-to-noise ratio, the noise is approximated by the Gaussian distribution. The Gaussian distribution is described by Eq. 2 [2].

$$p_M(M) = \frac{1}{\sigma\sqrt{2\pi}} \exp\left(\frac{-(M-A)^2}{2\sigma^2}\right) \tag{2}$$



(a)



(b) (c)

Fig. 1. Distribution of pixel intensities of lateral ventricle (1), white matter (2) , and grey matter (3) in T1-T2 space. (a) selected regions, (b) distribution of pixels in original image, (c) distribution of pixels in filtered image.

3. Segmentation

The proposed method is based on unsupervised classification of particular pixels into several groups. At first, the N-dimensional histogram is approximated by a mixture of Gaussians, where the N denotes the number of modalities. Here, we use 2 different modalities – T1- and T2-weighted images. Then, all pixels of the brain are classified as a pixel of particular Gaussian, which depends on the probability density function of every Gaussian in particular point in the N-dimensional space. Only the pixel intensity in every image type is considered for the classification. No relations between neighbour pixels are considered. The post processing step consists of the operations with the resulting image. Before the segmentation itself, only the brain is extracted from the image according to method described in [4]. Then

the image is filtered by Gaussian filter to make particular parts of the brain more consistent. The comparison is shown in Fig. 1.

Histogram Approximation

The approximation of *N*-dimensional histogram is based on the assumption that the distribution of the noise in magnitude MR image is approximately Gaussian [2]. The histogram of the brain area is approximated by a mixture of Gaussians. The method is based on Gaussian Mixture Model (GMM) [5], which is one of the unsupervised learning and its typical use is for the clustering. It is a statistical probability model. The computation is based on the probability density of all pixels in the data space. The algorithm tries to find a statistical model of the density function that minimizes the square error of probability function of the model and the true data.

The GMM algorithm uses an algorithm called Expectation Maximization (EM) [5], which is an iterative algorithm searching for the maximum likelihood estimation of the statistical model. This iterative process leads to the local optima.

For the component number estimation of the mixture model, the Akaike Information Criterion (AIC) [6] or Bayesian Information Criterion (BIC) [7] are commonly used. Their comparison can be found in [8]. On the other hand, the algorithm can work under the assumption of knowledge of the image and the number of tissues. Here, we use the BIC with the so-called Elbow method. The idea behind this method is to choose a number of components so that adding another one does not improve the results significantly. The dependence of BIC on the number of components is shown in Fig. 3.

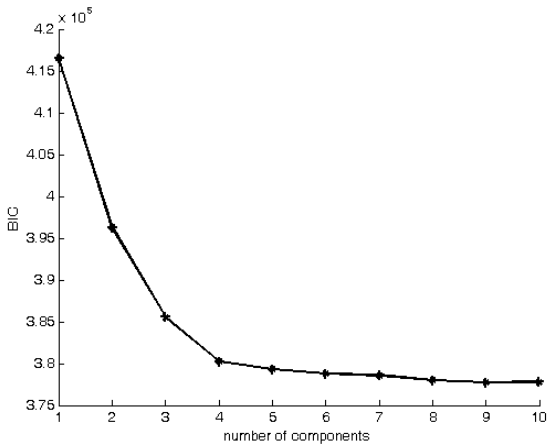


Fig. 2. Dependence of the Bayesian Information Criterion on the number of components.

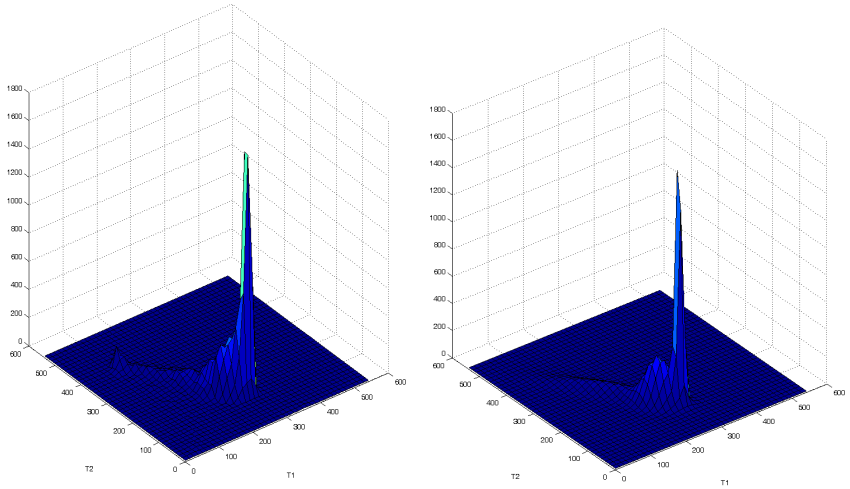
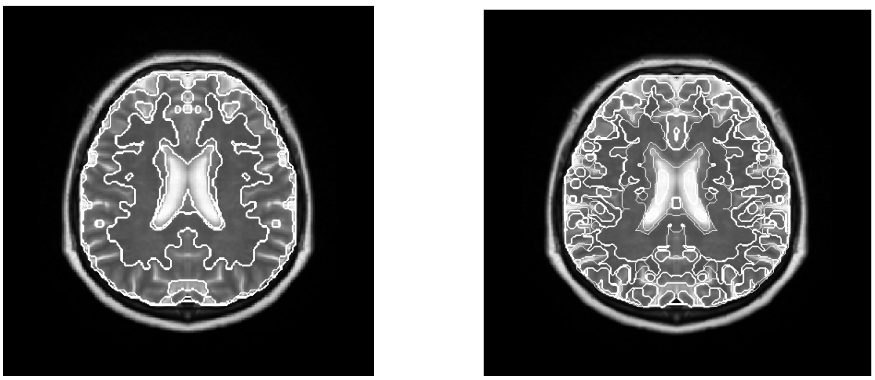


Fig. 3. Approximation of a 2-dimensional histogram by different numbers of mixture components. (a) original histogram, (b) approximation by 4 Gaussians, (c) approximation by 10 Gaussians.

The output of the described process is a probability density function. This denotes the probability of the pixel value of every tissue in the *N*-dimensional data space. In Fig. 2, one can see the approximation of a 2-dimensional histogram by 4 Gaussians.

4. Results

The results of the proposed method can be seen in Fig. 4, where the comparison of different number of components is shown. Despite the fact that the BIC penalize the larger number of components, the coefficient is still lower than for smaller number of components. But this could lead to oversegmentation, as can be seen in Fig. 4b. For this reason, the Elbow method is used and the result of segmentation with Elbow method is in Fig. 4a.



(a) (b)

Fig. 4. Segmentation of brain by GMM with (a) 4 components and (b) 10 components.

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