UNSUPERVISED SEGMENTATION OF DUAL-ECHO MR IMAGES BY A SEQUENTIALLY LEARNED GAUSSIAN MIXTURE MODEL

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ABSTRACT

This paper proposes a method for unsupervised segmentation of brain tissues from dual-echo MR images without any prior knowledge about the number of tissues and their density distributions on each MRI echo. The brain tissues are described by a Finite Gaussian Mixture Model (FGMM). The FGMM parameters are learned by sequentially applying the Expectation Maximization (EM) algorithm to a stream of data sets which are specifically organized according to the global spatial relationship of the brain tissues. Preliminary results on actual MRI slices have shown the method to be promising.

1. INTRODUCTION

Quantitative measurements of brain tissues from multi-echo MR images can be used to diagnose many brain diseases [5, 7, 15, 14, 4] and to trace brain development through ageing [6]. For example, in comparison with normal people, patients with Alzheimer dementia have higher total cerebrospinal fluid (CSF), total ventricular and third ventricular CSF volumes, and lower brain volumes; while schizophrenic patients have significantly smaller brain volumes, but similar CSF volumes. Furthermore, a decrease in brain size and concurrent rise in CSF percentage are associated with normal ageing.

Segmentation is the first and also the most crucial step towards the automatic quantitation of brain tissues from MR images. Currently, most segmentation methods for multi-echo MR images use pattern recognition techniques [12, 1, 3, 13]. Each pixel of the MR images is considered as a pattern, and the pixel density in each echo image is considered to be one feature component of the pattern. For instance, the p echo MR images of size $N \times M$ can be described by $N \times M$ patterns, each pattern having p features. Each pattern can be represented as a p dimensional vector $\mathbf{x}_i = (x_{i1}, x_{i2}, \cdots, x_{ip}) \in \Re^p$, where, $i = 1, 2, \cdots, N \times M$; x_{ij} is the density of the ith pattern on the jth echo.

In general, segmentation techniques for MR images consist of three major steps:

- *Pixel classification:* The pixels or patterns are classified into a certain number of classes. Normally the number of classes is equal to the number of tissues so that the relationship between pixel classes and tissue types is one to one. The commonly used methods are those based on Finite Gaussian Mixture Models (FGMM) [2, 8, 9, 10], Fuzzy C-Means (FCM) [1, 3] or Artificial Neural Networks (ANN) [3, 13].
- *Correction:* It is inevitable that there will be some misclassification of pixels since most classification techniques only employ the density information of tissues. The partial volume effect, inhomogeneities of the RF and gradient magnetic fields, and imaging noise generate widely scattered and overlapped density distributions of the tissues. This step tries to correct the misclassification by incorporating spatial constrains on the class of a pixel and the classes of its neighbours. Some possible methods are $n \times n$ majority-filter, Markov Random Field [10] or atlas-based approaches.
- *Tissue labelling:* Every class of pixels is assigned an unique tissue name or label in order to measure the volume of a specific tissue. This can be accomplished interactively or according to an a-prior density-tissue relationship or by using an anatomical atlas knowledge base.

Obviously, the pixel classification is of predominant importance to the accurate quantitative measurement of brain tissues. This paper focuses on this problem. An unsupervised FGMM-based pixel classification method

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is presented for proton density weighted (PDW) and spin-spin relaxation time weighted (T2W) dual-echo MR images of human brains.

2. PIXEL CLASSIFICATION

It is assumed that there is a finite number of tissues in the image, say g, and each tissue can be modelled by one Gaussian. Furthermore, each pixel is considered to be an independent data point and represented by a two dimensional feature vector, $\mathbf{x} = (x_1, x_2)$, where x_1, and x_2 are the densities of the PDW, and T2W images respectively. With this assumption, the whole image can be modelled by a mixture of g component Gaussian distributions in some unknown proportions $\pi_i, i = 1, 2, \cdots, g$. The p.d.f of a data point $\mathbf{x}$ will be

$$f(\mathbf{x} \mid \Psi) = \sum_{i=1}^{g} \pi_i f(\mathbf{x}, \mu_i, \Sigma_i) \quad (1)$$

where, $0 \leq \pi_i \leq 1$, $\sum_{i=1}^{g} \pi_i = 1$, Ψ is a vector containing parameters π_i, μ_i, Σ_i for $i = 1, 2, \cdots, g$. Hence,

$$f(\mathbf{x}, \mu_i, \Sigma_i) = \frac{1}{2\pi} \mid \Sigma_i \mid^{-\frac{1}{2}} e^{-\frac{1}{2}(\mathbf{x}-\mu_i)^t \Sigma_i^{-1} (\mathbf{x}-\mu_i)} \quad (2)$$

describes the $i'th$ component Gaussian distribution with mean μ_i, $\mu_i \in \Re^2$, and covariance Σ_i, a 2 x 2 matrix.

In this mixture framework, the posterior probability that a pixel $\mathbf{x}_j$ belongs to the $i'th$ tissue is given by

$$\tau_{ij} = \pi_i f(\mathbf{x}_j, \mu_i, \Sigma_i) / f(\mathbf{x}_j) \quad (3)$$

A pixel can thus be classified as belonging to the tissue to which it has the maximum posterior probability (Bayesian decision).

The fit of a model to the data can be measured by the total log likelihood of the data

$$L(\Psi) = \sum_{j=1}^{N} \log f(\mathbf{x}_j \mid \Psi) \quad (4)$$

where, N is the total number of data points.

Now, in order to classify a pixel as one tissue to which its posterior probability is maximum of all tissues, the parameter $\Psi = \hat{\Psi}$ should be firstly found to maximize the total log likelihood. The Expectation Maximization (EM) algorithm can be used to find such an estimation of the parameter $\hat{\Psi}$ [11]. However, it has been noticed that results of the EM algorithm are generally very sensitive to the initial values of the parameters because of local maxima for the total likelihood in the parameter space.

A simple method to learn the parameters of the mixture model is to use the EM algorithm with a predefined number of Gaussians (tissues) and some initial means and covariances [8, 9, 10]. For example, the number of tissues can be defined according to the contents of the images to be segmented (known a-priori); initial means can be chosen manually by visual inspection of the feature space; and the initial covariances are selected as very small values.

Exploring the global structure of a transaxial image of human brains, it is found that along the saggital direction from left to right, background (BG) and tissues fat (or skin), bone, grey matter (GM), white matter (WM), and cerebrospinal fluid (CSF) appear in sequence. This suggests that if the data points are presented into the EM algorithm in this sequence, it would be possible to learn Gaussians one after another, and hence the number of Gaussians can be calculated directly from the content of the image.

With this observation, the data points are divided into a sequence of subsets. Each subset consists of data points coming from c columns of a transaxial slice of the images along the saggital direction, where $c = 1, 2, 3, \cdots$, as shown in Figure 1(a). All subsets of the data are input and processed one by one. The learning procedure can be described as follows.

Step 1 Initialize the number of Gaussians as zero, and an empty processing data set, choose the *criteria* (discussed latter) for judging unclassified data points.

Step 2 Input a subset of data into processing data set.

Step 3 Classify the current subset of data with previously learned Gaussians. Label and count the unclassified data. If the number of Gaussians is zero, label the entire subset of data as unclassified.

Step 4 If the number of unclassified data points is greater than some *threshold*, add one Gaussian with the initial mean equal to the center of all the unclassified data points.

Step 4 Use the EM algorithm to estimate parameters for the current Gaussians from the current processing data set.

Step 5 If all subsets of data are processed, stop. Otherwise, go to **Step 2**

Here, the *criteria* for judging if a data point can be classified or not are set according to the Mahalanobis distance [11] between the data point and each of the Gaussians. If a point $\mathbf{x}_j$ satisfies

$$(\min_{i=1 to g} d_{ij}) \geq d_0 \quad (5)$$

it is labeled as unclassified. Where, g is the current number of Gaussians, d_0 is a Mahalanobis distance threshold, and d_{ij} is the Mahalanobis distance from $\mathbf{x}_j$ to the $i'th$ Gaussian.

$$d_{ij} = (\mathbf{x}_j - \mu_i)^t \Sigma_i^{-1} (\mathbf{x}_j - \mu_i) \quad (6)$$

This sequential learning framework can not only detect the number of Gaussians automatically, but also solve the initialization problem of the EM algorithm.

3. RESULTS AND DISCUSSION

A pair of actual spin-echo (SE) MR images were chosen to test the proposed methods. The first echo is a PDW image scanned at TR=1800 and TE=20; the second echo is a T2W image scanned at TR=1800 and TE=80. The image resolution is 256 × 256 pixels. The results are presented in Figure 1.

Each subset of data contains 16 continuous columns of pixels, i.e. 16 × 256 pixels. The *criteria* d_0 was chosen as 2.5 and the *threshold* of unclassified patterns was 7% of the total patterns in each subset. In total, seven Gaussians, as shown in Figure 1(b), were learned. Visual examination shows that they correspond to BG, skull, skin (or fat), GM, partial volume of GM and CSF, CSF and WM respectively. The number of each ellipse is the learning order of the Gaussians. It is quite consistent with the spatial relationship of these tissues.

The advantages of the proposed sequential method to learn a FGMM are obvious. It doesn't need any prior information about the number of tissues and their density distribution in the feature space and can not only detect the number of Gaussians, but also provide an efficient way to obtain the initial means. Although the method was proposed for our dual-echo MR images, in fact, it has nothing strictly connected with them. Therefore, the method can be applied to any multi-echo or multi-spectral transaxial MRI brain images.

The proposed method uses some heuristic knowledge about the spatial distribution of head tissues on transaxial MR images and naturally organizes the data subsets in columns. A more intuitive scheme to obtain data subsets would be to use regions which are generated from an oversegmentation of the MR images by using K-means, vector quantization, or some other simple image segmentation technique. Although this scheme would require more computation for the initial oversegmentation, better final results could be expected for the MR images. Furthermore, it is a more general approach and can thus be applied to MR images scanned in other directions, such as saggital and verticofrontal directions, or indeed to other kinds of images.

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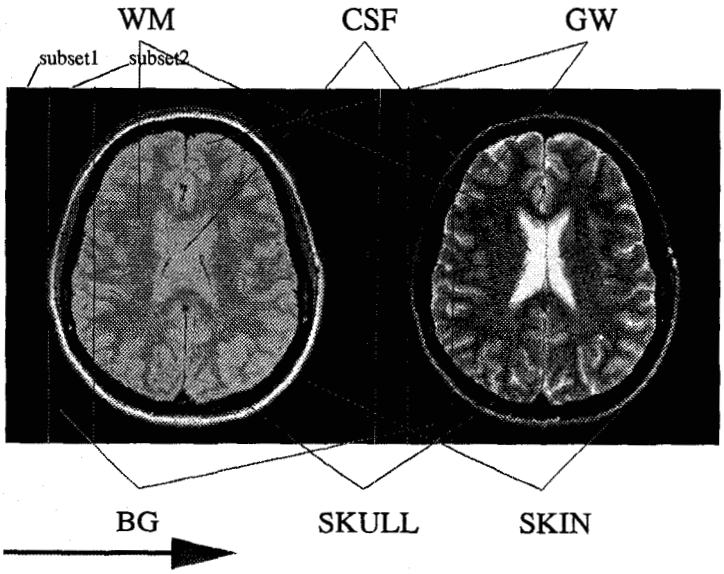

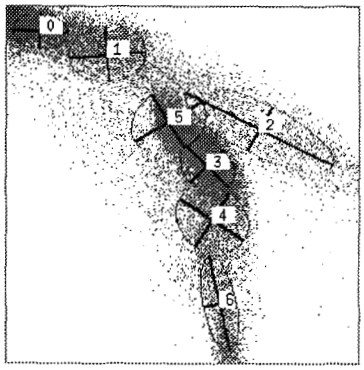

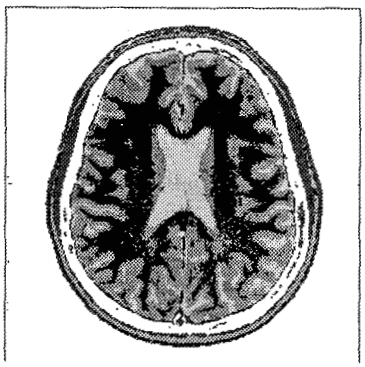

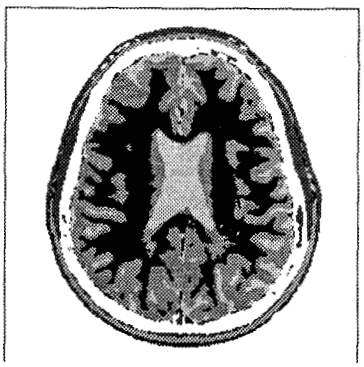

Figure 1: (a) An actual transaxial dual-echo MR images, PDW (left) and T2W (right); and the spatial distribution of tissues. (b) Gaussian ellipses of the sequentially learned FGMM on the feature space. (c) Classification of the pixels by the FGMM. (d) Segmentation after correction of (c) with a 3×3 majority-filter.

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