

Modified Expectation Maximization Algorithm for MRI Segmentation*

Ramiro Donoso, Alejandro Veloz, and Héctor Allende

Departamento de Informática, Universidad Técnica Federico Santa María,
Valparaíso-Chile

rdonoso@inf.utfsm.cl, avelozb@inf.utfsm.cl, hallende@inf.utfsm.cl

Abstract. Magnetic Resonance Image segmentation is a fundamental task in a wide variety of computed-based medical applications that support therapy, diagnostic and medical applications. In this work, spatial information is included for estimating parameters of a finite mixture model, with gaussian distribution assumption, using a modified version of the well-know Expectation Maximization algorithm proposed in [3]. Our approach is based on aggregating a transition step between E-step and M-step, that includes the information of spatial dependences between neighboring pixels.

Our proposal is compared with other approaches proposed in the image segmentation literature using the *size and shape test*, obtaining accurate and robust results in the presence of noise.

Keywords: Expectation Maximization algorithm, Finite Mixture models, spatial information, Magnetic Resonance Imaging segmentation.

1 Introduction

Magnetic Resonance Imaging (MRI) has a special interest in computer-based biomedical applications due to the inherent high definition, contrast and resolution of soft tissues. In this sense, image segmentation techniques make possible computer-based quantitative analysis methods able to support diagnosis and decision making in clinical settings, thus improving medical outcomes (see, e.g., [1], [6] and [8]).

This work is focussed in the segmentation of brain anatomical structures on MRI for which a wide variety of methods have been proposed. Parametric statistical approaches are employed commonly for labeling pixels that are assigned according to probability values determined by the intensity distribution of the image. With a suitable assumption about the underlying distribution of the image regions, statistical approaches attempt to solve the problem of estimating the associated class label, given only the intensity of each pixel. In this sense, maximum *a posteriori* (MAP) or maximum likelihood are two widely used criteria for estimating the class or label of a pixel.

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Finite mixture models that assume gaussian distributions for the mixture components, are one of the commonly used models for image segmentation. However, being this method a histogram-based approach, spatial information is not taken into account for estimating model parameters because the pixel intensities are considered to be independent samples drawn from a given gaussian random variable that represents a tissue type. This approach produces unreliable results in most MR images due to noise and to artifacts as the partial volume effect and bias field distortion (see [10]).

In order to address this problem, spatial dependences between pixels can be implicitly introduced by using the pixels coordinates as an extra feature. Also, Markov Random Fields (MRF) have been employed to take into account spatial dependences between pixels, but these approaches introduce a high computational cost for parameter estimation. Other approaches include spatial relationships between pixels for estimation the mixture model parameters. In [2] a modification of the well-know Expectation Maximization (EM), called Neighborhood EM (NEM), is proposed. In this approach, the spatial information is incorporated penalizing the log-likelihood function. Similar approaches are proposed in [10], where prior probabilities of the image classes from a mixture model are modeled as a random variable given by a MRF. In [5] Hybrid EM (HEM) algorithm is introduced based on both EM and NEM algorithms. The latter is used for fine tuning of the finite model parameters.

In order to address the segmentation of high amount of MRI images generated from patients in most medical centers, a simple method for estimating the parameters of a gaussian finite mixture model is proposed in this work. This method is based on the EM algorithm, and is called ETM algorithm, where spatial information is considered from neighboring pixels for the MRI segmentation. The ETM algorithm includes a transition step (T-step), between E-step and M-step, that increases the likelihood for certain pixels based on local relationships in a predefined neighborhood. The E-step is performed without changes and a modified M-step is derived form the T-step.

This work is organized as follows. In section 2 the mixture-model-based approach for image segmentation and the proposed method, called ETM algorithm, are presented. In section 3 a comparison between the proposed ETM algorithm and other segmentation methods are presented using the *sizes and shapes test* applied in [11]. The methods considered here for comparison are the classical EM algorithm [7], Neighborhood EM (NEM) [2], Hybrid EM (HEM) [5], Fuzzy C-Means (FCM) and Modified Fuzzy C-Means (FCMM) [9]. Finally, some discussions and conclusions are reported in section 4 and 5, respectively.

2 Methodology

2.1 Mixture Model-Based Image Segmentation

Let $I = \{\mathbf{x}_i \in \mathbb{R}^p | i = 1, \dots, n \text{ and } p \in \mathbb{N}\}$ be the set of pixels forming an image. Each pixel value is a realization of random variable X , which density function is determined by the weighed sum of K components. Each one of these components

correspond to the density functions of the K regions from which it is suspected that the image is composed. Let $R_k = \{\mathbf{x}_j \in \mathbb{R}^p | j = 1, \dots, n_k \text{ and } p \in \mathbb{N}\}$ be the set of pixels that compose the k -th region of the image; these pixels are a realization of a random variable $X_k, k = 1, \dots, K$, whose probability density function is denoted by $g_k(X_k | \theta_k)$. In this sense, the density function of random variable X is given by:

$$f(x_i | \phi) = \sum_{k=1}^K p_k * g_k(x_i | \theta_k) \quad (1)$$

where $\phi = \{p_1, \dots, p_K, \theta_1, \dots, \theta_K\}$ are the set of unknown parameters of the mixture model, that are estimated in such way that the (log)likelihood function represented by the joint probability of having a particular set of pixel values $\{\mathbf{x}_1, \dots, \mathbf{x}_n\}$ is maximized, given the set of parameters ϕ , i.e., $L(\mathbf{x}_1, \dots, \mathbf{x}_n | \phi) = \prod_i f(\mathbf{x}_i | \phi)$. There is no requirement that the components $g_k(x_i | \theta_k)$ should all belong to the same parametric family, but in most MRI segmentation approaches the same functional form for each region but with different parameters is assumed (see, e.g., [10]). In this work, a multivariate gaussian distribution with parameters $\theta_k = (\mu_k, \Sigma_k)$ for $g_k(x_i | \theta_k)$ is assumed.

The maximum likelihood estimate (MLE) of ϕ can be found numerically using various optimization algorithms. A very important approach widely used in mixture modeling is the Expectation Maximization (EM). This is an iterative method for optimizing the likelihood function when some information is missing. In our case, the missing information is the region to which pixels belong. The MLE of ϕ using EM algorithm is obtained iterating two steps until convergence. In the first step (E-step) the posterior probability that a pixel \mathbf{x}_i belong to each region is computed using the Bayes formula. In the second step (M-step), the parameters of the mixture model are estimated by maximizing the likelihood function. For instance, assuming a normal mixture the mean vector μ_k , the covariance matrix Σ_k and the weight p_k for the normal mixture component of the k -th region of the image should be estimated.

2.2 ETM Algorithm

In this work a modified Expectation Maximization algorithm is proposed. This modification is based on increasing the likelihood of the mixture model for pixels that are homogeneous within the region with higher probability. These pixels have a better fit to its underlying probability distributions, and therefore increase the likelihood of the mixture model. The increment of the likelihood is achieved by weighting *free* or *homogeneous* pixels, during a step of transition (called T-step) that is performed between E-step and M-step. In the T-step, *free* pixels have a higher weight than the pixels that are not. The steps of the proposed ETM algorithm are explained below.

E-step (expectation): As suggested in the classical EM algorithm [7], in this step the expected value of the likelihood is obtained. For this purpose the following formula is used:

$$Pr(\theta_k | \mathbf{x}_i) \equiv c_{ik} = \frac{p_k * g_k(\mathbf{x}_i | \theta_k)}{\sum_{l=1}^K p_l * g_l(\mathbf{x}_i | \theta_l)} \quad (2)$$

where the value c_{ik} is an element of a matrix C and represents the probability that the pixel $\mathbf{x}_i \in I$ belongs to the region k in the image.

T-step (transition): In this step the probability of assigning a pixel \mathbf{x}_i in the class k is modified. Let PA be a matrix of size $n \times K$, whose elements are given by:

$$pa_{ik} = \frac{c_{ik} + \sum_{\mathbf{x}_j \in N_8(\mathbf{x}_i)} c_{jk} * v_{ij}}{1 + \sum_{\mathbf{x}_j \in N_8(\mathbf{x}_i)} v_{ij}} \quad (3)$$

where v_{ij} takes a value $\alpha > 0$ if $\mathbf{x}_j \in N_8(\mathbf{x}_i)$, and 0 otherwise, i.e., v_{ij} represents the influence of the neighbor \mathbf{x}_j on \mathbf{x}_i , and pa_{ik} is calculated as the weighted average of the probabilities of membership of the 8-neighbors $\mathbf{x}_j \in N_8(\mathbf{x}_i)$ of \mathbf{x}_i . It is clear that pa_{ik} represents the modified probability that a pixel \mathbf{x}_i belongs to the class k taking into account the influence of all neighbors. After this calculation, the elements of the probability matrix C are updated by replacing the value c_{ik} by pa_{ik} if \mathbf{x}_i is a *non-free pixel*. A pixel \mathbf{x}_i is considered a *free pixel* if the class assigned to c_{ik} , i.e., $\arg \max_k [c_{ik}]$ is the same class obtained according the matrix pa_{ik} , i.e., $\arg \max_k [pa_{ik}]$.

With the updated probability matrix C , the weight for each pixel of the image is calculated in order to increase the likelihood of the mixture model for *free pixels*. In this sense, a higher weight is assigned to *free pixels*, respect to *non-free pixels*. We propose to do this using two variants, a crisp weighting (see equation (4)) and a fuzzy weighting (see equation (5)).

$$ph_i = \begin{cases} 1 & \text{if } \mathbf{x}_i \text{ is a free pixel} \\ 0 & \text{otherwise} \end{cases} \quad (4) \quad ph_i = \frac{\max_k [c_{ik}]}{\max_k \left[\frac{\sum_{\mathbf{x}_j \in N_8(\mathbf{x}_i)} c_{jk} * v_{ij}}{\sum_{\mathbf{x}_j \in N_8(\mathbf{x}_i)} v_{ij}} \right]} \quad (5)$$

where the values v_{ij} have the same behavior as in equation (3). In the equation (5) the element ph_i , i.e., the weight of the pixel \mathbf{x}_i , takes values greater than 1 if the higher probability of assignment of this pixel in certain class is greater than the weighted average of the probabilities of membership of all of their 8-neighbors in each class. In this sense, pixels that better fit to its underlying class, have a higher influence (i.e., higher weight) in the mixture model parameter estimation process.

M-step (maximization): In this step, the mixture model parameters are calculated. For this purpose the likelihood function is used including the weights for each pixel calculated in the previous step. Therefore, the set of parameters of the mixture model is obtained using a modification formulae presented in [7], which are shown below:

$$\hat{p}_k = \frac{\sum_{i=1}^n c_{ik} * ph_i}{\sum_{i=1}^n ph_i} \quad (6) \quad \hat{\mu}_k = \frac{\sum_{i=1}^n c_{ik} * \mathbf{x}_i * ph_i}{\sum_{i=1}^n c_{ik} * ph_i} \quad (7)$$

$$\hat{\Sigma}_k = \frac{\sum_{i=1}^n c_{ik} * ph_i * (\mathbf{x}_i - \hat{\mu}_k)(\mathbf{x}_i - \hat{\mu}_k)'}{\sum_{i=1}^n c_{ik} * ph_i} \quad (8)$$

3 Results

To make an appropriate evaluation of the segmentation algorithms, the *Sizes and Shapes Test* [11] was implemented. This test consists in segmenting a group of 12 synthetic images with different intensities of background and objects, where the first 8 images correspond to circles of different sizes (referred as *Set of Sizes*) and the last 4 correspond to ellipses with different eccentricities but maintaining approximately the same area (referred as *Set of Shapes*). In addition, with the purpose to make the images more realistic, a low-pass filter was applied and a gaussian additive noise component was introduced to the P percents of pixels of the image.

In order to measure quantitatively the performance of the proposed ETM algorithm, we calculate the accuracy, the RUMA index (relative ultimate measurement accuracy of object area [11]), the *Total Difference (TD)*, the *Low Segmentation (LS)* or false negatives, and the *Over Segmentation (OS)* or false positives. These indices are given by:

$$\text{Accuracy} = \frac{\text{Area}(O \cap \bar{O})}{\text{Area}(O)} * 100 \quad \text{RUMA} = \frac{|x_r - x_s|}{x_r} * 100$$

$$\text{TD} = \text{LS} + \text{OS} \quad \text{LS} = \frac{\text{Area}(O \setminus \bar{O})}{\text{Area}(O)} \quad \text{OS} = \frac{\text{Area}(B \setminus \bar{B})}{\text{Area}(O)}$$

where, O and B represent the region of the object and the background in the reference image, respectively. Analogously, \bar{O} and \bar{B} represent the same regions in the segmented image. The terms x_r and x_s correspond to the intensity value of the pixels in the reference image and the segmented image, respectively. Finally, the operation $R_1 \setminus R_2$ is defined by $R_1 \setminus R_2 = p \setminus p \in R_1, p \notin R_2$.

The ETM algorithm was compared with the EM, NEM, HEM, FCM and FCMM algorithms in 3 configurations of the *sizes and shapes test* and 3 experimental runs for each of these configurations, obtaining the mean and standard deviation of each index previously explained. The configurations used are defined by the intensity I_f of the background, the intensity I_o of the object, the diameter D or eccentricity e which defines a circle or ellipse respectively, the percentage P of pixels corrupted by gaussian noise and the standard deviation σ of this noise. The results for the 3 configurations used are presented below, in table 1.

Experiments with real T1-weighted MR images (with contrast agent *gadolinium*) were also conducted in a set of 32 MRI images with Brain Tumor, also used in [8]. These image data set were segmented with the ETM, EM, NEM, HEM, FCM, FCMM, region growing (RG) [8] and Genetic Algorithms (GA) [4] with 4 regions or classes defined a priori (tissues types in the image). The comparison of the results were performed using the Gold Standard (GS) of the image data set, provided by Carlos Van Buren Hospital of Valparaíso-Chile. We performed 5 experimental runs for each algorithm, obtaining the median and mean of the accuracy, the mean of the false positive (FP) and false negative (FN) errors and the mean of the time (in seconds) needed to produce the segmented image (see table 2). All indexes are shown with their respective standard deviations. In figure 1 2 instances of segmented MR images are shown as example.

Table 1. Results obtained with synthetic images

Configuration 1 with $I_f = 20$, $I_o = 102$, $D = 128$, $P = 25\%$ and $\sigma = 40$.					
Algorithm	LS (sd)	OS (sd)	TD (sd)	RUMA (sd)	Accuracy (sd)
ETM	0 (0)	0,0225 (0,0001)	0,0225 (0,0001)	7,2903 (0,0086)	100 (0)
EM	0,0156 (0,0004)	0,1662 (0,0013)	0,1818 (0,0015)	26,6559 (0,0155)	98,4426 (0,0385)
NEM	0,0126 (0,0002)	0,1362 (0,0021)	0,1488 (0,0019)	22,5671 (0,0035)	98,7382 (0,0229)
HEM	0,0157 (0,0004)	0,1647 (0,0012)	0,1804 (0,0015)	26,3491 (0,0154)	98,4273 (0,0385)
FCM	0,037 (0,001)	0,0744 (0,0038)	0,1114 (0,0028)	11,7085 (0,0053)	96,2988 (0,0994)
FCMM	0,0373 (0,001)	0,074 (0,0038)	0,1113 (0,0029)	11,8891 (0,0023)	96,2708 (0,1038)
Configuration 2 with $I_f = 182$, $I_o = 130$, $e = 0.7$, $P = 10\%$ and $\sigma = 80$.					
Algorithm	LS (sd)	OS (sd)	TD (sd)	RUMA (sd)	Accuracy (sd)
ETM	0,001 (0,0003)	0,0017 (0,0001)	0,0028 (0,0003)	1,2695 (0,0001)	99,8977 (0,0251)
EM	0 (0)	0,2124 (0,0005)	0,2124 (0,0005)	3,9775 (0,0002)	100 (0)
NEM	0,028 (0,0005)	0,0543 (0,0027)	0,0823 (0,0027)	2,7221 (0,0006)	97,1974 (0,0536)
HEM	0,0312 (0,0043)	0,0583 (0,009)	0,0895 (0,0132)	2,8962 (0,0022)	96,8763 (0,4278)
FCM	0,0363 (0,0004)	0,0651 (0,0022)	0,1014 (0,0026)	2,1042 (0,0005)	96,3719 (0,0436)
FCMM	0,0364 (0,0004)	0,0648 (0,0022)	0,1012 (0,0026)	3,083 (0,0006)	96,3576 (0,043)
Configuration 3 with $I_f = 20$, $I_o = 223$, $e = 0.9$, $P = 10\%$ and $\sigma = 80$.					
Algorithm	LS (sd)	OS (sd)	TD (sd)	RUMA (sd)	Accuracy (sd)
ETM	0 (0)	0,0359 (0,0008)	0,0359 (0,0008)	13,3558 (0,0032)	100 (0)
EM	0 (0)	0,278 (0,0018)	0,278 (0,0018)	70,0654 (0,0035)	100 (0)
NEM	0,0005 (0,0002)	0,1374 (0,0011)	0,1379 (0,0012)	41,4617 (0,0025)	99,9508 (0,0201)
HEM	0,0011 (0,0003)	0,1417 (0,0005)	0,1428 (0,0008)	42,7161 (0,0009)	99,8871 (0,0347)
FCM	0,0115 (0,0006)	0,0279 (0,0019)	0,0395 (0,0024)	13,1291 (0,0048)	98,8475 (0,0578)
FCMM	0,0115 (0,0006)	0,0281 (0,0018)	0,0396 (0,0024)	16,11 (0,0041)	98,8533 (0,0602)
Resume of the three configurations.					
Algorithm	LS (sd)	OS (sd)	TD (sd)	RUMA (sd)	Accuracy (sd)
ETM	0,0003 (0,0006)	0,0200 (0,0172)	0,0194 (0,0234)	7,3052 (6,0432)	99,9659 (0,0591)
EM	0,0052 (0,0090)	0,2189 (0,0562)	0,2452 (0,0464)	33,5663 (33,5815)	99,4809 (0,8992)
NEM	0,0137 (0,0138)	0,1093 (0,0476)	0,1101 (0,0393)	22,2503 (19,3717)	98,6288 (1,3800)
HEM	0,0160 (0,0151)	0,1216 (0,0560)	0,1162 (0,0377)	23,9871 (20,0148)	98,3969 (1,5056)
FCM	0,0283 (0,0145)	0,0558 (0,0246)	0,0705 (0,0438)	8,9806 (5,9973)	97,1727 (1,4509)
FCMM	0,0284 (0,0146)	0,0556 (0,0243)	0,0704 (0,0436)	10,3607 (6,6466)	97,1606 (1,4666)

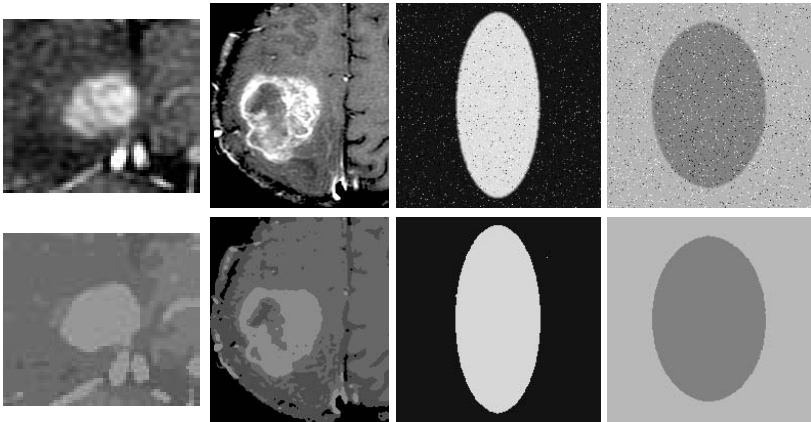
**Fig. 1.** Examples of segmented synthetic and real MR images (original images (upper row) and their corresponding segmented images (bottom row))

Table 2. Results obtained with real MR images with 4 classes

Algorithm	Median	Mean (sd)	FN (sd)	FP (sd)	Time (sd)
ETM	97,6031	95,1324 (10,36)	4,8676 (10,36)	9,5436 (7,89)	1,6435 (0,74)
EM	97,1843	94,3037 (10,99)	5,6963 (10,99)	6,8459 (6,62)	1,0957 (0,38)
NEM	95,3293	88,8553 (20,8)	11,1447 (20,8)	2,9788 (2,24)	2,3603 (1,15)
HEM	96,1029	93,2426 (12,29)	6,7574 (12,29)	5,358 (5,22)	1,2006 (0,53)
FCM	91,4426	86,6887 (17,33)	13,3113 (17,33)	2,8059 (4,79)	0,8612 (0,22)
FCMM	91,5879	87,6018 (14,17)	12,3982 (14,17)	2,6723 (3,33)	0,688 (0,13)
GA	94,3389	89,8554 (13,72)	10,1446 (13,72)	4,8939 (9,25)	1,1288 (0,11)
RG	97,6669	92,8924 (13,27)	7,1076 (13,27)	9,1703 (15,63)	0,6821 (0,09)

4 Discussion

As shown in Table 1 the proposed ETM algorithm succeeds in obtaining the lowest value for the TD index (only 1,9%) respect to other algorithms, which indicates that in most cases the ETM algorithm performs a more appropriate segmentation, with the lowest error respect to other segmentation techniques. As shown in resume of table 1, ETM algorithm obtains an accuracy of 99,96% without an important over segmentation (the ETM algorithm never gets more than 3.6% for OS , compared to other EM-based methods that get more than 10%).

Moreover it is observed that generally the RUMA rate obtained by the ETM algorithm is always one of the lowest, except in configuration 3 of Table 1, which means that the segmentation performed by this algorithm in terms of intensity, sometimes does not match the original image. However, since the proposed algorithm was designed primarily for the purpose of segmenting MRI, we aim to obtain a segmentation of homogeneous regions as connected as possible.

As shown in figure 1 for synthetic images, the proposed algorithm is robust to noise, mainly because the ETM algorithm includes spatial information of pixels when calculating the mixture model parameters, that is why we recommend using this method on images with high noise (see Configuration 1) and low contrast (see Configuration 2).

The ETM algorithm gets the best results for segmentation of the 32 real MR images, obtaining 95,13% of accuracy with a standard deviation of 10,36 (see Table 2). Moreover, with the ETM algorithm the lowest rates of false negatives were obtained, and also the lowest standard deviation, compared to the other approaches. Nevertheless, the false positives errors were not that good, but comparable with other approaches considered in this work.

With the inclusion of T-step, the ETM algorithm is more efficient compared with other techniques including spatial information data, because this modification does not increase the complexity significantly. ETM, EM, NEM and HEM have the same complexity in M-step, $O(nK)$. As for E-step complexity, ETM and EM is $O(nK)$, NEM is $O(mn^2K)$ (m is the number of iterations of E-step), HEM is $O(nK)$ in selective hard EM and $O(n^2K)$ in later NEM [5]. In T-step, ETM have a complexity of $O(8nk)$. The fastest is EM, closely followed by HEM and ETM, and NEM is the worst. This is corroborated by *a posteriori* temporal efficiency obtained in Table 2.

5 Conclusion

In this work, we introduced a modified Expectation Maximization algorithm to estimate mixture model parameters in a very simple way, taking into account spatial relationships between pixels. The proposed method outperforms other approaches proposed in the literature and constitute a reliable approach to segment MR images of the brain.

Further work is needed in order to provide more flexibility in the spatial relationships dependences modelling or to incorporate the bias field estimation to correct or compensate the intensity inhomogeneities introduced during the acquisition process in MRI. The proposed ETM algorithm is intensity-based, but incorporating spatial dependences between pixels, hence the segmentation do not depend on the region size as is the case with region-based approaches, so it could be applied to segment other brain anatomical structures, such as White Matter or Gray Matter, without requiring additional time.

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