Full Automatic Framework for Segmentation of MR Brain Image

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ABSTRACT

Magnetic Resonance Imaging is one of the most important medical imaging techniques for the investigating diseases of the human brain. A novel method for automatic segmentation Magnetic resonance brain image framework is proposed in this paper. This method consists of three-step segmentation procedures step. The method first uses level set method for the non-brain structures removal. Second, the bias correction method is based on computing estimates of tissue intensity distributions variation. Finally, we consider a statistical model method based on bayesian estimation, with prior Markov random filed models, for Magnetic resonance brain image classification. The algorithm consists of an energy function, based on the Potts model, which models the segmentation of an image. The algorithm was evaluated using simulated Magnetic resonance Images and real Magnetic resonance brain images.

Keywords: MRI; Bias correction, level set method, Markov Random Field, maximum a posteriori, Segmentation.

1. INTRODUCTION

Magnetic resonance image segmentation has been proposed for a number of clinical investigations of varying complexity. Automatic segmentation of MR scans is very useful for research and clinical study of much neurological pathology. The accurate Segmentation of MR images into different tissue classes, especially gray matter (GM), white matter (WM) and cerebrospinal fluid (CSF), is an important for the diagnosis and prognosis of certain illnesses. Moreover, regional volume calculations may bring even more useful diagnostic information. Among them, the quantization of gray and white matter volumes may be of major interest in neurodegenerative disorders such as Alzheimer disease, in movements disorders such as Parkinson or Parkinson related syndrome, in white matter metabolic or inflammatory disease, in congenital brain malformations or perinatal brain damage, or in post traumatic syndrome.

The automatic segmentation of brain MR images, however, remains a persistent problem. The major MR image segmentation problem when MR image is the corruption with a inhomogeneity bias field. Several approaches have been proposed to address this limitation of intensity-based classification. Numerous MRI segmentation methods have been reported. The brain atlas can be used as spatial priors for segmentation [1,2,3]. The template-moderated segmentation proposed by Warfield et al. [4] clearly demonstrates the strength of the use of a spatial prior sinces regions that overlap in intensity space but are spatially disjoint can be separated. Brain tissue segmentation based on fractional voxel properties has been developed by Shattuck et al. [5]. Motivated by the need to improved tissue segmentation in the presence of pathological regional changes.

The aim of this study is to introduce a new MR image segmentation framework. This framework combines the level set method, the bias correction scheme by Wells et al. [1], and the MRF algorithm by Geman et al. [7]. In contrast to most other brain segmentation schemes, our new segmentation methods integrates bias correction, non-parametric classification. We have developed a three-step segmentation method for fully automatic segmentation of the brain in 3-D MR images. The method is an extension and combination of previous techniques, and consists of the following processing steps: (1) the introduction of level set method [6] model to deal with non-brain structures removal problem. (2) the introduction of spatially distributed model estimation and classification to deal with spatially non-uniformity correction problem. (3), it uses a statistical model including Bayesian distributions for brain tissues intensities and Markov random filed (MRF) based spatial contiguity constraints for tissue classification. This algorithm consists of an energy function, based on the Potts model, which models the segmentation of an image. The energy function provides efficient strategy for MR Image segmentation. To find the optimal segmentation, this energy function is minimized using ICM algorithm. The statistical model accounts for the piecewise

contiguity of brain regions, in a certain amount, for intensity non-uniformity without being dependent upon any specific initialization. Extensive experiments using MR images generated by the BrainWeb simulator [9] and real MR data have been used to evaluate the proposed method. The results show that the proposed method can produce good segmentation performance.

2. SEGMENTATION FRAMEWORK

We propose the automatic MRI brain image segmentation framework.. The segmentation algorithm consists of a sequence of processing steps are shown in flow diagram form in Fig. 1 and include: (1) Input the MRI image data; (2) Removal of non-brain tissue (3) radio frequency (RF) inhomogeneity correction; (4) MRF brain tissue segmentation.

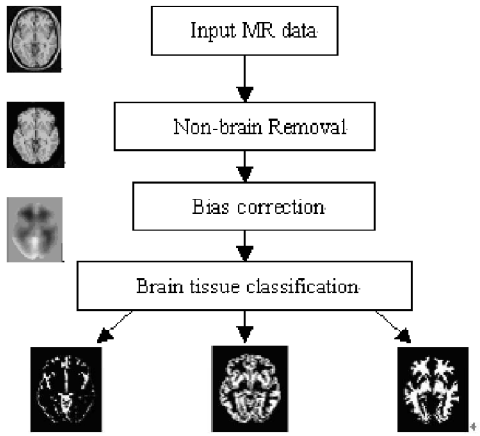


Fig.1 The flow chart of the MRI image segmentation

2.1. Removal of non-brain tissue

The Skull-stripping of MR brain image has important applications in neuroimage analysis as a preliminary step, for instance, the analysis of spatial distribution of gray matter and the quantification of the cortical morphology. In general, the skull-stripping algorithms can be classified into automated or semi-automated method according to the degree of user intervention. In this work, we use level set method to remove all non-brain tissue from brain image. The level set method was devised by Osher and Sethian [3], The main idea in the level set method is to describe a closed curve Γ in the image plane as the zero level set of a higher dimensional function $\phi(X,t)$ in R^3.

$$S(t) = \{X \in R^3 \mid \phi(X,t) = 0\} \tag{1}$$

The function ϕ describes a 4D surface defined by $\phi(X,t) = d$, where d is traditionally the signed distance from X to the front S .The evolution rule for ϕ can be expressed as:

$$\frac{\partial \phi}{\partial t} + F|\nabla \phi| = 0 \tag{2}$$

where F is a scalar velocity function depending on local properties of front. The 4D surface ϕ deforms iteratively according to F, and the position of the 3D front $S(t)$ is deduced from ϕ at each iteration by the relation $\phi(X(t),t) = 0$. The hypersurface ϕ^{n+1} at each $n+1$ is computed from ϕ^n at step n using the ralation:

$$\phi^{n+1}(X) = \phi^n(X) - \Delta t \cdot F|\nabla \phi^n(X)|, \quad \forall X \in R^3 \tag{3}$$

$$F = P(I)(1 - \varepsilon k) \tag{4}$$

where, $0 < \varepsilon < 1$ is a constant, I is the image intensity and k is the curvature, obtained from divergence of the gradient of the normal vector to the front, $p(I)$ is the data consistency term and acts as a stopping criterion at the location of the desired boundaries; it is defined according to intensity I of the input image data. The process can be shown in Fig.2.

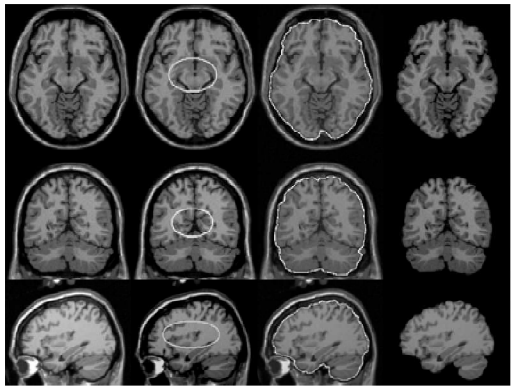


Fig.2 Remove non-brain tissue from brain image process. (a)Input image (b) initial process (c) brain tissue contour(d) final result.

2.2. Bias Correction

Inhomogeneneity in magnetic fields during image acquisition and magnetic susceptibility variations in scanned subjects cause intensity non-uniformities, also described as bias fields. These artifacts prevent characterization of voxel tissue content based solely on image intensity. As a result, segmentation as well as

quantitative studies of MR images require compensation for these non-uniformities. The method we implement is due to Wells [1].

Let Y be the observed image, X the ideal image, B the inhomogeneity, and N the noise present in the image. The interactions between those fields can be described as :

$$Y = X \times B + N \tag{5}$$

The noise is considered negligible. Taking the logarithm of Eq.5 gives:

$$\log(Y) = \log(X) + \log(B) \tag{6}$$

Assuming that the pixel intensities of a tissue type are normally distributed ,the probability for a pixel to belong to a class, in absence of inhomogeneities, can be expressed as :

$$p(y_i / x_k) = \frac{1}{\sqrt{2\pi\sigma_k}} \exp(-\frac{1}{2}(\frac{y_i - \mu_k}{\sigma_k})^2) - G_{\sigma_k}(y_i - \mu_k) \tag{7}$$

where y_i represents the intensity of image pixel, k number of a single class, μ_k mean of class k, σ_k represents the standard deviation of class k. In the presence of inhomogeneities, and according to Eq.6 and Eq.7, the same probability can be expressed as:

$$p(y_i / x_k, \beta_i) = G_{\sigma_k}(x_i - \mu_k - \beta_i) \tag{8}$$

where β_i is the inhomogeneity at this i_{th} pixel location. To estimate the inhomogeneity, the residual term R_i is computed for each pixel:

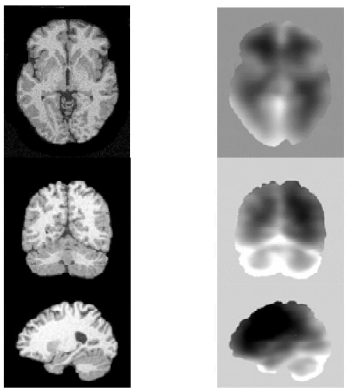
$$R_i = \sum_k p(x_k / y_i) \frac{y_i - \mu_k}{\sigma_k} \tag{9}$$

The inhomogeneity at the i_{th} pixel location, β_i ,is the average of the R_i in a 3×3 neighbourhood of pixel i.

Fig.3 presents the results of the estimated bias field. The method consists two steps:

1: Estimation of the tissue type for all the pixel y_i of the image.

2:Estimation of the inhomogeneity $\beta_i = mean(R_j)$ at each location i in the image, and correction according to Eq.7.The method is iterative, and is initialized with inhomogeneities equal to zero.



(a) (b)

Fig.3. Illustration of estimation bias field MR slice . (a) input image(b)estimated bias field

2.3. Image Modeling Using Markov Random Field

Consider the 3D cubic lattice of the image space as a set, S , of n voxels indexed in some manner from $i = 1,2,\cdots,n$. Let the observed data y represent one set of data values on S , a particular realization of a random vector Y . The value y_i denotes the observed record at position i . A segmentation of y will be represented by a set x , a particular realization of a random vector X . The values x_i denotes the segmentation value at pixel i . Let x^* represent the true segmentation y . We can assume each Y_i has the same known conditional density function, $p(y_i \mid x_i)$, which is dependent only on x_i . So the conditional probability of the observed record y ,given x ,is determined by:

$$p(y \mid x) = \prod_{i=1}^{n} p(y_i \mid x_i) \tag{10}$$

The true segmentation x^* is a realization of a locally dependent MRF with distribution $p(x)$. A probability $p(x)$ is a MRF if the following condition holds:

$$p(x_i \mid \{x_{k \setminus i}\}) = p(x_i \mid x_{N_i}) \tag{11}$$

where $x_{k \setminus i} = \{x_k \mid k \neq i\}$, N_i indexes a neighbourhood system(see Fig.4) around pixel i ,but not including index i , and $x_{N_i} = \{x_j \mid j \in N_i\}$.

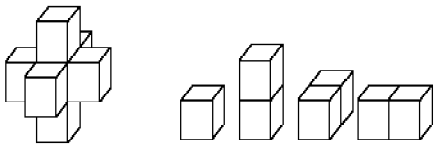


Fig.4 First order Neighbourhood system in 3D

Given the assumption that the image can be modeled by a MRF, the distribution, $p(x)$, is a Gibbs distribution with respect to x. That is, the probability that the system is in a particular state, x, is given by :

$$p(x) = \frac{e^{-\beta U(x)}}{Z} \tag{12}$$

where β is a parameter, $U(x)$ is an energy function and Z is a normalization factor, or partitioning function. $U(x)$ is a sum of functions, one of each pixel in x , which describes the interaction of each pixel with its neighbours. The normalization factor, Z , is the summation of $e^{-\beta U(x)}$ over all possible x , i.e.,

$$Z = \sum_{\omega} e^{-\beta U(x)} \tag{13}$$

where ω define the set of all possible configurations of x .We need to find the a posteriori probability, that is ,the probability given the observed data, y . Let $\hat{x}$ be the state that maximizes this probability. According to Bayes Theorem, maximizing this probability is equivalent to maximizing:

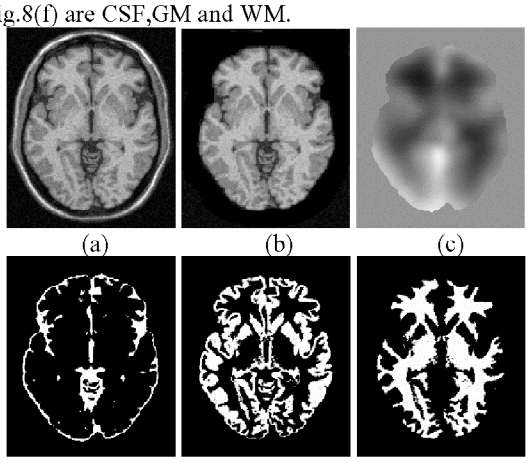
$$p(x \mid y) \propto p(y \mid x) p(x) \tag{14}$$

The state $\hat{x}$ is the maximum a posteriori(MAP) estimate of the true segmentation x^* and is the mode of the posterior distribution of x^*. Maximization of the posterior distribution gives us the maximum a posteriori estimate. Unfortunately, direct maximization of the $p(x \mid y)$ requires unrealistic computational effort. Therefore. Several algorithms for approximation of MAP were suggested [7]. We use the iterated condional models (ICM) algorithm proposed by Besag[8] to search for an optimal image labeling.

3. EXPERIMENTAL RESULTS

To evaluate the proposed our method, we performed two sets of experiments, one on simulated MR and another on real MR brain data. First, the brain tissue classification was evaluated using simulated MR images of the same brain generated by the BrainWeb simulator [9]. The BrainWeb site offers a large amount of different phantoms of MR brain images with different levels of noise and inhomogeneity. Test has been done on the T1-weighted images with 7% noise levels and 20% spatial inhomogeneity. We first stripped each skull using level set method, then corrected for inhomogeneity. Finally, classified using the MRF model. The brain tissue can be classified into white matter, gray matter, CSF.

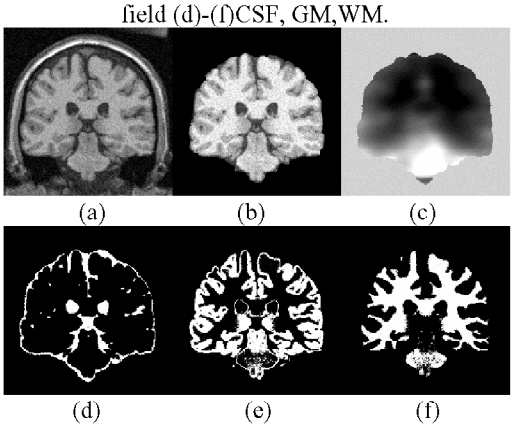
The classification of a single plane of the simulated T1 weighted BrainWeb image is illustrated in Fig.5 and Fig.6. Fig.5- Fig.6 (a) is the original image. Fig.5-Fig.6(b) is skull-stripped image.Fig.5-Fig.6(c) is estimated bias field. Fig.5-Fig.6(d)-(f) are CSF,GM and WM. Fig.8 and Fig.9 show one of Transverse and Coronal slice of the segmentation results for real T1 weighted MR images using the proposed method. Fig.8 (a) is the original image. Fig.8(b) is skull-stripped image.Fig.8(c) is the estimated bias field.Fig.8(d)-Fig.8(f) are CSF,GM and WM.



(a) (b) (c)

(d) (e) (f)

Fig.5 Transverse Slice segmentation results (a)original T1 images (b) skull-stripped image(c) estimated bias field (d)-(f)CSF, GM,WM.



(a) (b) (c)

(d) (e) (f)

Fig.6 Coronal Slice segmentation results.(a)original T1 images (b) skull-stripped image(c) estimated bias field (d)-(f)CSF, GM,WM.

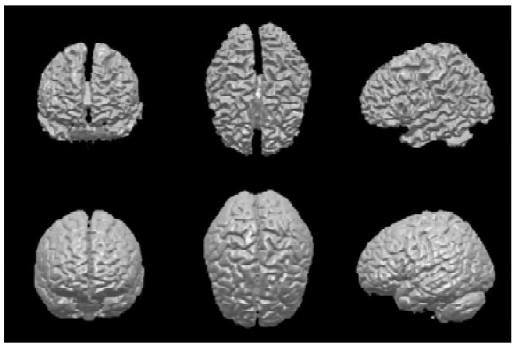
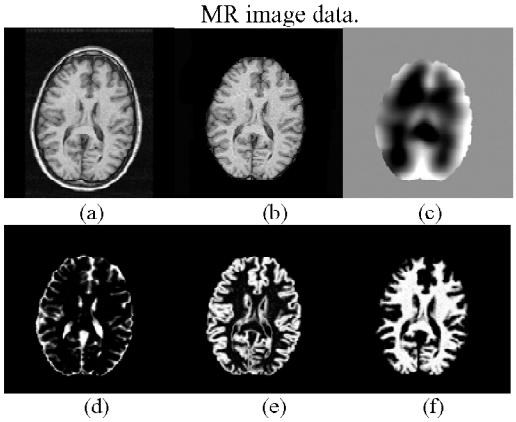


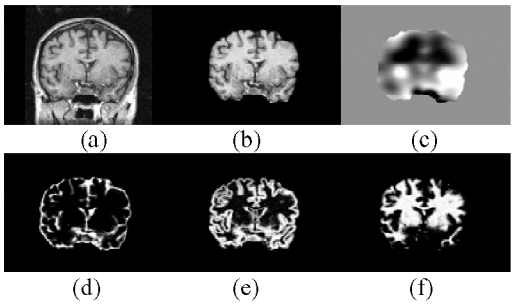
Fig.7 3D rendering of the white matter(Top) and gray matter(bottom) of a T1-weighted simulator MR image data.



(a) (b) (c)

(d) (e) (f)

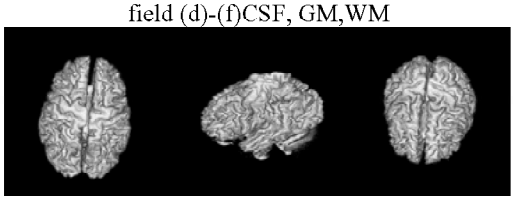
Fig.8 Real MR data Transverse slice segmentation. results (a) Original T1 images (b) skull-stripped image(c) estimated bias field (d)-(f)CSF, GM,WM.



(a) (b) (c)

(d) (e) (f)

Fig.9 Coronal Slice segmentation results.(a)original T1 images (b) skull-stripped image(c) estimated bias field (d)-(f)CSF, GM,WM



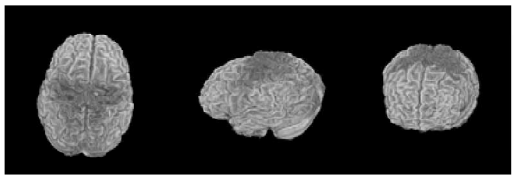


Fig.10 3D rendering of the white matter(top) and gray matter(bottom) of a real T1-weighted real MR image data.

Fig.7 and Fig.10 shows the final constructed 3D model of brain white matter and grey matter volume by our segmentation method.

The segmentation method can be improved by corrects global MR intensity inhomogeneity. The method also incorporation of contextual information in the classification procedure by modeling spatial interactions between neighboring pixels as Markov Random Field providing spatial regularization of the tissue maps which makes the segmentation less sensitive to noise.

4. CONCLUSIONS

This paper presents a fully automatic method for segmenting the brain from other tissue in a MR image of the human head. The method is an extension and combination of previous techniques. The proposed framework consists of a sequence of skull stripped, bias corrected and brain tissue classification. The proposed framework has been tested on both simulated and real MR image data. In the future, we are also planning on a large-scale clinical evaluation of this segmentation framework.

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