A new method of brain tissues segmentation from MRI with accuracy estimation

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Abstract

In this paper, a new concept has been incorporated using level set methodology for the specific segmentation of brain tissues in magnetic resonance imaging (MRI) brain images. In this segmentation, the normal tissues such as WM (White Matter), GM (Gray Matter) and CSF (Cerebrospinal Fluid) with other part of human head such as skull, marrow, and muscular skin are segmented. The segmentation has been done by using repeated level set method based on the condition sharp peak greater than three. The each segmented component is generating a hierarchical structure to make correct tissue segmentation. The performance of the segmentation method is estimated by different accuracy, sensitivity and error correction metric. The performance of segmentation process is analyzed using a defined set of MRI brain. From visualization and mathematical both point of measurement proposed gives very superior results on brain MR images.

Keywords: Brain Tissues, MRI of brain, Segmentation, Abnormality, Accuracy Estimation, Level Set, Performance Measurement.

1. Introduction

Databases surround hundreds of cross-sectional and longitudinal MRI which might require several hours per scan for correct manual segmentation. Such segmentation may have several error and exhibit nontrivial intra-expert inconsistency in the segmentation of huge databases over weeks which is known as “rater drift” [1].
Furthermore, manual segmentation using the transverse, coronal and sagittal views may result in uneven boundaries, which cause difficulties in character analysis. Hence, the fact that many applications depend on accurate, robust and cost-effective brain segmentation has inspired much work for developing automatic brain segmentation tools. The challenge in brain MRI segmentation is due to issues such as noise, non-uniform intensity, partial volume effect, shape complexity and natural tissue intensity variations. Under such conditions, incorporation of a priori medical knowledge, commonly represented in anatomical brain atlases by state-of-the-art studies is essential for robust and accurate automatic segmentation.

Several brain tissue segmentation approaches have been projected over the years. Some proposals attempt to use clustering techniques, being the Expectation Maximization a popular method. Some of those utilize Markov Random Fields to add perspective of the neighborhood of the voxel being labeled [2] [3]. In [2], an earlier probability atlas is engaged to initialize the EM method which gives spatial information. However, other authors have also proposed segmentation methods more besides CSF, GM or WM, like the basal ganglia, brainstem and others [4] [5]. Recently, discriminative semantic segmentation [6] method based on supervised decision forest to segment the brain tissues that achieving good results. Potential of diagnosing and differentiating diseases using MR images formulate them suitable in developing new pharmacotherapeutic methods [7-8]. Segmentation is a most important issue in processing and analyzing MR images which impress the ultimate results of analysis. Automatic segmentation of brain MR Images into its major tissues remains an inextricable problem in domain of medical image processing. First of all, noise may modify the gray value of pixels which uncertain the segmentation results. Moreover, inhomogeneities in MR Images modify the gray value of pixels belonging to one tissue increasingly and thus it makes difficult to their segmentation. Furthermore, the restriction on image resolution directed to partial volume effect in which one voxel may include parts from more than one tissue. Other imaging artifacts such as calibration parameters also make segmentation of MR Images more difficult [9]. The main limitation of existing segmentation to extract normal and abnormal tissue of brain and skull is the accuracy. We have found the problems which include: (a) the subcortical gray matter is underestimated, especially around the thalamus, the white matter fibers enter the gray matter structures, leading to poor contrast in the MR image. Accurate non-rigid alignment and segmentation are extremely difficult in this region. (b) The cortical gray matter is overestimated because segmenting the small folds of cortical gray matter correctly is more complicated with a probability atlas. Its smooth borders increase the likelihood of bridges or cavities across adjacent banks of a sulcus and influence the segmentation towards an overestimation of cortical gray matter [10]. (c) Over or under segmentation of normal brain tissue and non brain part are performed by the existing segmentation methodology. d) Increasing number of structures in the segmentation problem also increases the problem’s statistical complexity and likelihood of misclassified voxels.

The rest of the paper is organized as follows. In Section II, proposed method has been described briefly. Detailed results from proposed method are provided in Section III as results and discussion section. Finally we conclude our method in Section IV.

2. Proposed Method

We have to perform the three stage level set segmentation with three membership functions that clearly find out three regions. But for significant accurate segmentation of different tissues of brain and non brain part we use the repetitive level set segmentation method. The repetition of segmentation has been depends on the number of sharp peaks of the segmented region. We will repeat our three phase level set for peak greater than three for every segmented region. We have chosen peak value three because core module of our proposed method used concepts of three region segmentation.

The elementary conception of level set is to completely evolve a higher dimensional function $\Phi: \Omega \to R$ whose zero level set $C: \Phi = 0$ represents dynamic shapes on the surfaces. The growing curve $C$ partitions the image into two regions: $C_in$ region inside the curve, which is enclosed by $\Phi > 0$ and $C_out$, which is the region outside the curve, i.e., where $\Phi < 0$. Thus the entire idea behind [11] this steps is to represent the closed curve $C$ defined on the image domain can be represented by the zero level set $\Phi(x,y) = 0$ of a higher dimensional function called a Lipschitz function $\Phi: \Omega \to R$ such that
The curve \( C \) changes by
\[
\frac{\partial \Phi(x,y,t)}{\partial t} = \delta(\Phi) \left[ \mu \cdot d\nu \left( \frac{\partial \Phi}{\partial \nu} \right) - v + \sum_{i=1}^{M_1} w_i g((x,y)|\mu_i, \Sigma_i) \times P(C_{in}) 
\right] 
- \sum_{j=1}^{M_2} \sum_{i=1}^{M_1} w_j g((x,y)|\mu_j, \Sigma_j) \times P(C_{out})
\]
(2)

where \( w_i; i = 1, \ldots, M \) represent mixture weights or prior probabilities of each component satisfying summation of all weight equals to one for M pieces Gaussian densities. The initial outline is defined by \( \Phi(x,y,0) = \Phi_0(x,y) \). A Gaussian mixture model can be represented as a weighted sum of M pieces Gaussian densities,
\[
P(X|\lambda) = \sum_{i=1}^{M} w_i g(X|\mu_i, \Sigma_i)
\]
(3)

where \( X=\{x_1, x_2, x_3, \ldots, x_n\} \) is a set of N observations from a D dimensional space, \( w_i; i=1,2,\ldots,M \) represent mixture weights or prior probabilities of each module satisfying \( \sum_{i=1}^{M} w_i = 1 \). \( g(x_i|\mu_i, \Sigma_i) \) are D-variate Gaussian modules and denote the probability of observation \( x_i \) coming from the \( i^{th} \) component. Each Gaussian module can be represented as:
\[
g(x_i|\mu_i, \Sigma_i) = \frac{1}{(2\pi)^{D/2}|\Sigma_i|^{1/2}} \exp \left\{ -\frac{1}{2} (x_j - \mu_j) \Sigma_i^{-1} (x_j - \mu_j) \right\}
\]
(4)

where \( \mu_i, \Sigma_i \) are the representation mean and covariance matrices of individual modules. Hence, the parameters of the model are given by \( \lambda = \{w_i, \mu_i, \Sigma_i\}, i=1,2,\ldots,M \). The model parameters can be estimated by maximizing the overall likelihood of the observations \( X \) coming from the model \( \lambda \). Maximum likelihood phrase is a non-linear function of the parameters \( \lambda \) and, therefore, a closed form solution for direct maximization is not possible.

The histogram of a digital image with \( L \) of total probable intensity levels in the range [0,G] is defined as the discrete function:
\[
h(r_k) = n_k
\]
(5)

where \( r_k \) is the \( k^{th} \) intensity level in the interval [0,G] and \( n_k \) is the number of pixels in the image whose intensity level is \( r_k \). 255 is the maximum possible value for G for gray scale image. The process of peak calculation is made by choosing preceding three and next three neighbour positions for each gray value \( k \) in a circular manner into \((k-3)(k-2), (k-1), (k+1), (k+2) \) and \((k+3) \) respectively. If the frequency of a gray value \( k \) is larger than that of its three adjacent left and three adjacent right gray value frequencies then \( k \) is identified as a peak \( p_k \). Sharp peak
frequency is calculated from the total number of peaks value recorded from above divided by three. When segmentation method stopped after applying above method, we use expect maxima (EM) to extract maximum area between two connected regions of brain, and maximum area always appear as left child. If we consider a binary tree of root is the input image (BI) itself then we segment it into two regions BI1(contains WM, GM, marrow, and muscles skull) and BI2(contains GM, CSF, muscles skull). Inputted brain image is treated as level 0 and BI1 and BI2 treated as level 1. Number of sharp peak greater than 3 at level 1, so we repeat the segmentation and the segmented region of level 1 produce the level 2. Segmented part of level 2 does not have any sharp peak greater than 3 for normal brain. For the entire segmented region we place maximum area as left child. Region BI12 and BI21 both contains GM and muscles skull, so we add this segmented region to improve the accuracy. Region BI11 contains WM and marrow, and BI22 contains CSF and fats. Finally we segment WM, marrow, GM, muscles skull, CSF, and fats by using max area from left to right. If any abnormality present we can detect it in level 2, all steps are remain same except we use abnormality extraction methodology [14] and rest of the region are treated as normal segmented tissue.

3. Results and Discussion

We tested our method with a couple of MRI of brain images [15] from brainweb standard dataset. Our method correctly segment for different category of MRI of brain. The outputs of different steps of our proposed methodology with almost perfect segmentation for transverse type MRI has been describe here. It should be noted that all parameters that appear in the method have been set to fixed values, so all results shown here have been achieved with the same parameters. The results of different steps we used in our methodology shown in Fig. 1 below. Fig. 1(b) is the output generated by level set segmentation on Fig. 1(a) is test MRI of brain image. When we segment according to the level set method, it is very clearly visible to us that some of segmented parts are overlapped in each region of segmentation. To remove this problem we have incorporated the concepts of sharp peak on segmented image. That means we need to repeat the level set in each segmented region to produce better results or output. Thus reapply level set as segmented region has number of sharp peak greater than three to get better accuracy. Fig. 1(c) and Fig. 1(d) are the results of level set segmentation applied on segmented part of Fig. 1(b). Fig.1(c) consists of WM, some amount of GM, marrow, and few amount of muscle skin. Fig. 1(d) consists of CSF, some amount of GM, and muscle skin. Now, the number of sharp peaks of segmented parts of Fig. 1(c) and Fig 1(d) are not greater than three so we stop to repeat the segmentation process. We extract the outer region of Fig. 1(c) and Fig 1(d) by skull elimination algorithm [14]. Thus by using the concepts of maximum connected area we can extract WM from segmented part of Fig. 1(c) and the result has been shown in Fig. 1(e). Thus Fig. 1(e) fully consist of WM has been shown below. The rest of the brain tissues are collected from Fig.1 (c) and combined with maximum connected area component of Fig. 1(d) to produce GM. GM has been shown in Fig. 1(f). After extracting GM from segmented Fig. 1(d), rest of the brain tissue part is consider as CSF. Fig. 1(g) fully consist of CSF has been shown below. The similar way muscle skin and marrow as non tissue part of the brain has been shown in Fig. 1(h) and Fig. 1(i) below. Thus we able to segment different brain tissues with some other non-brain region very efficiently and truthfully. Fig. 1 shows all the segmented region of MRI of brain below.
Fig. 1. (a) Input MRI image; (b) three phase level set output performed on input image; (c) and (d) are the outputs of level set performed on segmented region of (b); (e) is the segmented white matter; (f) is segmented gray matter; (g) is segmented CSF; (h) is segmented muscle skin; and (i) is segmented marrow region of brain.

Our proposed method gives very good results for segmentation of different regions from the visualization point of reference. From the above figure it is easy to find out the area of each segmented region. The quantification and ratio of each segmented region such as WM, GM, and CSF has a great importance to identify the different type of brain disease. Different type abnormality has been also identified by their position on diverse brain tissues and dissimilar brain skull portions. Skull defect and appearances lesions may cause of skull meningeal and sulcal disease. Extracerebral masses and intracerebral masses can also been identified by our proposed method and abnormality detection [16] algorithm.

As segmentation may be biased visually thus we need to justify in terms of mathematical metric. Accuracy of a segmentation technique refers to the degree to which the segmentation results agree with the true segmentation. Although digital apparition can provide a level of recognized “ground truth or reference”, they are silently incapable to reproduce the full range of imaging characteristics and normal and abnormal anatomical variability observed in clinical data. First let AS be the automated segmented area and MS be the manual segmented area [16]. True positive TP is determine by the intersection pixel between automated (AS) and manual (MS) segmented area. False positive (FP) is determine by difference between AS and TP. False negative (FN) is determine by difference between MS and TP. The Jaccard index (J) between two areas is represented as follow:

\[ J(AS, MS) = \frac{|AS \cap MS|}{|TP + FN + FP|} \times 100\% \quad (6) \]

The relative area error (RAE) [16] for stroke region can be calculated as difference between ‘AS’ and ‘MS’ divided
Jacard Index measures the similarity measurement between two images and RAE measure the relative area error between two images. Thus greater Jacard index means better results and lesser RAE means better results. The performance of our proposed method for different region segmentation with above mentioned metric has been shown in table 1.

\[
RAE = \frac{(AS - MS)}{MS} * 100\%
\]  

(7)

From the above table it is clear that Jacard index always reached greater than 90% where average value is 97.44789. Thus greater Jacard index means better segmentation procedure. Average value of RAE is 3.172822984 which are very less value. Relative area error is also very less in our proposed method. Thus our proposed method
produces high accuracy with low error rate which is very essential for medical image segmentation. Our method has more truthful results than what can be acquired with its individual modules. To produce much more competent segmentation method our framework detains dissimilar types of features in each step that are of particular significance for MRI, i.e., allotments of tissue intensities, textural features, and connection with adjacent pixels or spatial features. A most important benefit of this method is the use of spatial information. The tissue probability of a pixel is determined by the signal intensities and by the location of the pixels. The method segments tissues that are heterogeneous in signal intensity. Although we also embrace the control of intensity correlated issues of other part of brain due to the spatial features and this method is less sensitive to noise for it. Thus our method correctly segment visually as well as metrically for different type of MR images with different tissues.

4. Conclusion

The experimental results signify that our proposed segmentation methods can increase the overall segmentation performance with each component individually. This is because the proposed method takes advantages of the categorization ability of segmentation method in addition to the MR intensity. Level set framework has been used for three phase segmentation with a fixed number of regions; we described a way how to reach accuracy of results by using peak calculation concept. All advantages of the level set framework are conserved, while its main problem related to accuracy has been solved. Robustness to noise, low error rate and high accuracy are the advantages of proposed framework. In order to examine the proposed segmentation method, it has been used for brain tissue segmentation using standard dataset. The experiments demonstrated that the segmentation results are much closer to ground truth.

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