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Contents:

(continued on inside back cover)

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Segmentation of Cerebrospinal Fluid and Internal Brain Nuclei in Brain Magnetic Resonance Images

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Abstract – *Brain tissue segmentation on structural Magnetic Resonance Imaging (MRI) has received considerable attention. Quantitative analysis of MR images of the brain is of interest in order to study the aging brain in epidemiological studies, to better understand how diseases affect the brain and to support diagnosis in clinical practice. Manual quantitative analysis of brain imaging data is a tedious and time-consuming procedure, prone to observer variability. Therefore, there is a large interest in automatic analysis of MR brain imaging data, especially segmentation of Cerebrospinal Fluid (CSF), Gray Matter (GM) and White Matter (WM). This paper presents a fully automated method for the segmentation of cerebrospinal fluid and internal brain nuclei from T1-weighted MRI head scans.*

The proposed methodology performs intensity based thresholding to get the boundaries between gray matter, white matter, cerebrospinal fluid and others. Combined with preprocessing techniques and incorporating mathematical morphology, we first perform the extraction of brain cortex. Subsequently, the cerebrospinal fluid is segmented by using orthogonal polynomial transform. Finally, the gray matter and the white matter regions in the MRI are segmented based on the intensity values. Experimental results show that the proposed method achieves reasonably good segmentation. The comparative analysis depicts that the proposed methodology shows better segmentation results with some other existing techniques like FAST, SPM5, k-nearest neighbor (k-NN) classifier, and a conventional k-NN. ***Copyright © 2013 Praise Worthy Prize S.r.l. - All rights reserved.***

Keywords: *Image Segmentation, Brain MRI, Skull Stripping, Cerebrospinal Fluid (CSF), Gray Matter (GM), White Matter (WM), Thresholding*

I. Introduction

Magnetic Resonance Imaging (MRI) is an advanced medical imaging technique providing rich information about the anatomy of human soft tissue [1]-[46]. MRI is used to visualize the anatomy and structure of a body organ for assistance in medical diagnostics of certain disease or conditions and to evaluate a particular disease [6], [7], [32], [46].

Obviously, the information that MRI provides has greatly increased knowledge of normal and diseased anatomy for medical research, and is a critical component in diagnosis and treatment planning [3].

Irrespective of its widespread use, the amount of data contained in MRI is far too much for manual interpretation and analysis, and this has been one of the biggest problems in the effective use of MRI. In the specific case of brain MRI, the problem of segmentation is particularly critical for both diagnosis and treatment purposes [23].

Image segmentation is one of the most important and critical tasks in the field of computer vision. It plays a vital role in biomedical imaging applications such as the quantification of tissue volumes diagnosis, localization of pathology study of anatomical structure, treatment planning, partial volume correction of functional imaging data, and computer integrated surgery [19], [26], [29].

Brain is one of the most complex organs of a human body and so it is a difficult problem to discriminate its various components and analyze it constituents. The majority of research in medical image segmentation pertains to its use for MR images, especially in brain imaging [44], [25].

The important problem in medical image analysis is the segmentation of anatomical regions of interest. Especially, the segmentation of tissue classes namely, cerebrospinal fluid (CSF), gray matter (GM) and white matter (WM). Tissue classification is also of importance in the study of neuro degenerative diseases such as Alzheimer's disease and multi-infarct dementia [2].

MRI is unique among diagnostic imaging modalities because it employs several independent parameters which determine the image scale [42].

The image intensity permits the detailed visualization of the internal anatomical structures in living human subjects. MR image parameters include tissue relaxation times: the spin-lattice relaxation time (T1) and the spin-spin relaxation time (T2), and the proton density (PD).

The goal of MR image segmentation is to accurately identify the principal tissue structures in these image

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volumes [23], [45]. The two most common segmentation methods include:

(1) Statistical methods: The first family of methods, which performs classification of brain tissues into different classes, based on intensity values (direct values of features computed from these values). Gray values thresholding is the most intuitive classification approach [15].
(2) Deformable models: The second family of segmentation methods deals with geometric deformable models, including active surfaces [25] and level-set-based deformable models.

Some of the segmentation methods available in the literature have managed to achieve desirable segmentation quality for brain MRI images [1], [35]. The main problems that affect the quality of MRI segmentation are noise, inhomogeneous pixel intensity distribution and blunt boundaries in the medical MR images caused by MR data acquisition process [26], [43], [36].

These problems do make manual quantitative analysis of brain imaging data a tedious and time-consuming procedure, prone to observer variability [27]. Hence, automation of the segmentation process is critical for applications in clinical research where the number of cases to process is large and the time available for experts to analyze the data is very limited. There are several typical MRI segmentation approaches as follows: 1. Threshold techniques, 2. Edge-based methods, and 3. Region-based segmentation [23]. Despite the existence of many MRI segmentation frameworks, brain MRI segmentation is still a subject requiring intensive exploration due to the numerous challenges[10], [24], [38], [39]. Here, we propose an automated segmentation method that performs skull stripping, and segmentation of cerebrospinal fluid and internal brain nuclei from T1-weighted MRI head scans. The brain is first extracted using a skull stripping algorithm (thresholding followed by light erosion, hard opening, and region-based methods). The skull stripping algorithm generates a brain mask that is applied to the original MRI data to mask out all non-brain-tissue voxels.

Regarding CSF and internal nuclei segmentation, we work with the assumption that, contrast exists between brain tissue (gray matter and white matter) and cerebrospinal fluid. Secondly, the cerebrospinal fluid is segmented effectively from the skull-stripped images with the aid of the orthogonal polynomial transform. Lastly, the gray matter and the white matter are segmented by 1) Smoothening, 2) Gradient computation and 3) Mathematical morphology. The output consists of the binary maps of the tissue classes of white matter, gray matter and cerebrospinal fluid. The experimental results and the comparative analysis demonstrate the effectiveness of the proposed method in segmenting brain MRI images.

The organization of the paper is as follows: A brief review of the existing works related to the proposed research is given in Section 2. A concise introduction about the brain tissue segmentation is presented in Section 3.

In Section 4, the proposed methodologies for segmentation are presented. The experimental results are shown in Section 5. The paper is concluded in Section 6.

II. Related Works

Numerous works in the literature dealing with brain MR image segmentation serve as the motivation for the proposed research. A brief review of some of those significant and related researches is given below:

Salih et al. [31] have evaluated the intensity of MR sequences known as T1-weighted images in an axial sliced section. Intensity group clustering algorithms are presented to achieve further diagnosis for brain MRI, which has been hardly studied. Subjective study has been suggested to evaluate the clustering group intensity in order to obtain the best diagnosis as well as better detection for the suspected cases. The technique makes use of image tissue biases of intensity value pixels to provide 2 regions of interest as techniques. Moreover, the original mathematic solution could still be used with a specific set of modern sequences. There are many advantages to generalize the solution, which give far more scope for application and greater accuracy.

Yang et al. [40] have introduced an automatic algorithm for segmentation of white matter lesions from volumetric MR images. The existing methods assumed that the different channel images have same resolution, which is often not available. Although their method is also based on T1 and T2 weighted MR images, they do not assume that they have the same resolution (Generally, the T2 volume has much less slices than the T1 volume). The method can be summarized as the following three steps: 1) Register the T1 image volume and the T2 image volume to find the T1 slices corresponding to those in the T2 volume; 2) Based on the T1 and T2 image slices, lesions in these slices are segmented; 3) Use deformable models to segment lesion boundaries in those T1 slices, which do not have corresponding T2 slices.

Dogdas et al. [13] have presented a technique for segmentation of skull and scalp in T1-weighted magnetic resonance images (MRIs) of the human head. The method uses mathematical morphological operations to generate realistic models of the skull, scalp, and brain that are suitable for electroencephalography (EEG) and magnetoencephalography (MEG) source modeling. They segment the brain using the Brain Surface Extractor algorithm; using this, they can ensure that the brain does not intersect the skull segmentation. They generated a scalp mask using a combination of thresholding and mathematical morphology. They find the inner and outer skull boundaries using thresholding and morphological operations.

Finally, they mask the results with the scalp and brain volumes to ensure closed and nonintersecting skull boundaries.

Drapaca et al. [14] have focused on the automated extraction of the cerebrospinal fluid-tissue boundary, particularly around the ventricular surface, from serial structural MRI of the brain acquired in imaging studies of aging and dementia. They examined a level set approach which evolves a 4D description of the ventricular surface over time. The 3D MR images of the entire brain are first aligned using global rigid registration.

They also followed the approach proposed by Chan and Vese which is based on the Mumford and Shah model and implemented using the Osher and Sethian level set method. For convergence they used region-based information provided by the image rather than the gradient of the image. Results on time sequences of 3D brain MR images were presented.

Gule et al. [16] have presented an image segmentation system to automatically segment and label brain MR images to show normal and abnormal brain tissues using self-organizing maps (SOM) and knowledge-based expert systems. The feature vector is used as an input to the SOM. SOM is used to over segment images and a knowledge-based expert system is used to join and label the segments. Spatial distributions of segments extracted from the SOM are also considered as well as gray level properties. Segments are labeled as background, skull, white matter, gray matter, cerebrospinal fluid (CSF) and suspicious regions.

Yeh and Fu [41] have proposed an optimization technique, a hierarchical genetic algorithm with a fuzzy learning-vector quantization network (HGALVQ), to segment multi-spectral human-brain MRI. Evaluation of the approach was based on a real case with human-brain MRI of an individual suffering from meningioma. The HGALVQ was verified by the comparison with other popular clustering algorithms such as k-means, FCM, FALVQ, LVQ, and simulated annealing. Experimental results show that HGALVQ not only returns an appropriate number of clusters and also outperforms other methods in specificity.

Chiverton et al. [11] have described an automatic statistical morphology skull stripper (SMSS) that uniquely exploits a statistical self-similarity measure and a 2-D brain mask to delineate the brain. The result of applying SMSS to 20 MRI data set volumes, including scans of both adult and infant subjects was also described.

Quantitative performance assessment was undertaken with the use of brain masks provided by a brain segmentation expert. The performance was compared with an alternative technique known as brain extraction tool. The results suggested that SMSS is capable of skull-stripping neurological data with small amounts of over- and under-segmentation.

Hore et al. [18] have introduced a fast, accurate and fully automatic method of segmenting magnetic resonance images of the human brain.

The approach is based on modifications of the soft clustering algorithm, fuzzy c-means, which enable it to scale to large data sets. The clustering algorithms coupled with inhomogeneity correction and smoothing are used to create a framework for automatically segmenting magnetic resonance images of the human brain.

The framework is applied to a set of normal human brain volumes acquired from different magnetic resonance scanners using different head coils, acquisition parameters and field strengths. Results are compared to those from two widely used magnetic resonance image segmentation programs, Statistical Parametric Mapping and the FMRIB Software Library (FSL).

Kong et al. [20] have presented a method for segmentation of brain tissues in MRI (magnetic resonance imaging) images. First, they reduce noise using a versatile wavelet-based filter. Subsequently, watershed algorithm is applied to brain tissues as an initial segmenting method. Normally, the result of classical watershed algorithm on grey-scale textured images such as tissue images is over-segmentation. The following procedure is a merging process for the over-segmentation regions using fuzzy clustering algorithm (fuzzy C-means). But there are still some regions which are not divided completely, particularly in the transitional regions of gray matter and white matter, or cerebrospinal fluid and gray matter. This motivated the construction of a re-segmentation processing approach to partition these regions. They exploited a method based on minimum covariance determinant (MCD) estimator to detect the regions needed segmentation again, and then partition them by a supervised k-nearest neighbor (kNN) classifier. The integrated approach yields a robust and precise segmentation.

Kuo et al. [21] have proposed a robust medical image segmentation technique, which combines watershed segmentation and the competitive Hopfield clustering network (CHCN) algorithm to minimize undesirable over-segmentation. A region merging method is presented, which is based on employing the region adjacency graph (RAG) to improve the quality of watershed segmentation. The relation of inter-region similarities was investigated using image mapping in the watershed and CHCN images to determine more appropriate region merging.

The performance of the proposed technique is evaluated through quantitative and qualitative validation experiments on benchmark images.

III. Brain Tissue Segmentation

Segmentation is a process of partitioning an image space into some non-overlapping meaningful homogeneous regions. In general, these regions will have a strong correlation with the objects in the image. The success of an image analysis system depends on the quality of segmentation. In the analysis of medical images for computer-aided diagnosis and therapy, segmentation is often required as a preliminary processing task. Medical image segmentation is a

complex and challenging task due to the intrinsically imprecise nature of the images. Fully automatic brain tissue classification from MR images is of great importance 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 task. Moreover, regional volume calculations may bring even more useful diagnostic information [30]. Brain MRI Segmentation" provides facility of segmenting the various brain tissues such as CSF, Ventricular, White Matter, and Gray Matter. These tissues are primarily extracted from the dual echo MRI slices at a position in axial plane about 7 to 8 cm from the top of the head. The brain MRI images visualize the anatomy and structure of brain and the segmentation of these medical images certainly play an important role in abnormality detection. Typically, segmentation can be defined as a fundamental and low-level operation for visualization and automated analysis and diagnosis of medical images. For years now, segmentation of MRI of the brain is an important problem in biomedicine; it has a number of applications including diagnosis, surgical planning and monitoring therapy.

The brain consists mainly of two tissue types: gray matter and white matter. About 40% of the human brain is made up of gray matter. Gray matter is made of neuronal and glial cells, also known as neuroglia that control brain activity. White matter fibers are myelinated axons which connect the cerebral cortex with other brain regions. White matter is responsible for communication between the various grey matter regions and between the grey matter and the rest of the body. The cerebrospinal fluid is also found within the brain and in the spinal cord that surrounds the brain and the spinal cord. The CSF consists of glucose, salts, enzymes and white blood cells.

This fluid circulates through channels (ventricles) around the spinal cord and the brain to protect them from injury.

IV. Proposed Methodology for Segmenting Brain MR Images

This section presents the proposed methodology for segmenting brain MRI images. Segmentation of MRI of the brain is an important problem in biomedicine; it has a number of applications including diagnosis, surgical planning and monitoring therapy.

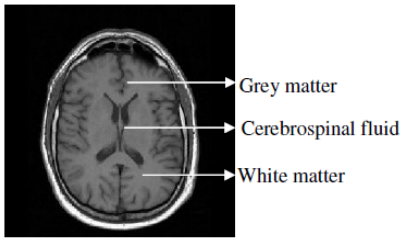


Fig. 1. Brain MR Image

The fundamental task in brain MRI segmentation is the classification of volumetric data into gray matter, white matter and cerebrospinal fluid tissue types.

But, it is not easy as it sounds, as there are some inherent difficulties associated with image segmentation; among them, are RF coil inhomogeneity, brain tissue susceptibility, and other systematic artifacts. Various preprocessing steps have been proposed to deal with some or all of these difficulties. Skull stripping is the first processing step in the segmentation of brain tissues.

Clearly, volumetric analysis of brain requires segmenting the cortical tissues from the non cortical tissues and the removal these non cortical tissues is termed as skull stripping. The skull removed MRI are used for further classification of the brain tissues into White matter, Gray matter and Cerebrospinal fluid. The following are the steps involved in the proposed methodology for brain MRI segmentation:

- Skull Stripping,
- CSF segmentation,
- Gray and White matter segmentation.

Fig. 2 presents an overview of the proposed methodology for segmenting brain MRI images.

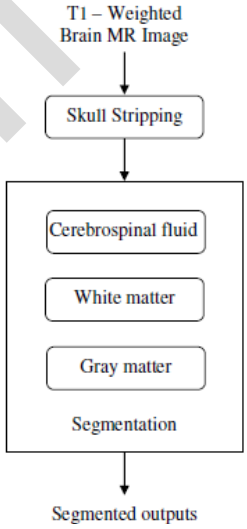


Fig. 2. Overview of the proposed methodology

IV.1. Skull Stripping

One of the important pre-processing steps in analyzing intracranial volumes is the extraction of the brain cortex from T1-weighted MRI head scans.

The subsequent analysis, tissue segmentation, is highly dependent on the robustness and precision of the brain masks generated in the brain extraction step. By accurately defining the brain cortex, one could essentially minimize errors for the analyses that follow. In the proposed method for skull stripping, we see the brain surface as a smooth manifold with relatively low curvature that separates brain from non-brain regions.

Also, the brain cortex can be visualized as a distinct dark ring surrounding the brain tissues in the T1 weighted axial MR images. The steps involved in the

proposed methodology for skull stripping are:

- Binarization via Thresholding,
- Morphological Operators,
- Region-based binary mask extraction.

Binarization via Thresholding: Binarization is the process that converts a grey-level image into a binary image I. The binarization process involves examining the grey-level value of each pixel in the enhanced image with the global threshold $Thres$, i.e.,

- If the pixel value (i, j) of the original image is lower than threshold , pixel (i, j) of binary image is black (value 0) ;
- If the pixel value (i, j) of the original image is higher than threshold, pixel (i, j) of binary image is white (value 1).

```
for i = 1 : n
    for j = 1 : m
        if I(i, j) < Thres
            imbinary(i, j) = 0
        else
            imbinary(i, j) = 1
        end
    end
end
```

Morphological Operators: The binary morphological operators are then applied on the binarized image. Elimination of any obstacles and noise from the image is the primary function of the morphological operators. The morphological operators namely, opening and closing are being employed in the proposed method.

Opening: An opening operation consists of an erosion followed by dilation with the same structuring element S:

$$I' = imopen(I, S)$$

Closing: A closing operation consists of a dilation followed by an erosion with the same structuring element S:

$$I' = imclose(I, S)$$

Erosion: Erosion operation on an image I containing labels 0 and 1, with a structuring element S, changes the value of pixel i in I from 1 to 0, if the result of convolving S with I, centered at i, is less than some predetermined value. We have set this value to be the area of S, which is basically the number of pixels that are 1 in the structuring element itself. The structuring element (also known as the erosion kernel) determines the details of how particular erosion thins boundaries:

$$I' = imerode(I, S)$$

Dilation: Dual to erosion, a dilation operation on an image I' containing labels 0 and 1, with a structuring element S, changes the value of pixel i in I from 0 to 1, if the result of convolving S with I', centered at i, is more than some predetermined value. We have set this value to be zero. The structuring element (also known as the dilation kernel) determines the details of how a particular dilation grows boundaries in an image:

$$I'' = imdilate(I', S)$$

Region-based binary mask extraction: Region-based extraction is done by examining the properties of each block that satisfy some criteria. We have used one of two criteria. One criterion is to look at the max-min difference and the other is to determine the mean values of the blocks. The process results with a brain mask that is then applied to the original MRI data. Consequently, we attain a brain MRI image with its brain cortex stripped.

IV.2. Segmentation of Cerebrospinal Fluid and Internal Brain Nuclei

After skull stripping, the next step is to segment the brain into its constituent issues such as White Matter, Gray Matter and Cerebrospinal fluid. The following are the processes involved in the segmentation of cerebrospinal fluid and internal brain nuclei.

IV.2.1. CSF Segmentation

Regarding CSF segmentation, we assume that there exists some contrast between brain tissue (gray matter and white matter) and cerebrospinal fluid, which separates the brain from the extra-cranial tissue. The segmentation methods we have seen so far can be roughly grouped into 2 categories: intensity based or surface based. Our method is an intensity based method and it does simple thresholding.

In order to segment the cerebrospinal fluid from the brain MRI image, we apply the orthogonal polynomial transform to the skull stripped image. While the theory of orthogonal polynomials is well developed, the practice of orthogonal polynomials is constructive, computational in several aspects.

Orthogonal polynomials of one variable defined by a non-negative measure on the real line have the image properties. Orthogonal polynomials are defined in terms of their behavior with respect to each other and throughout some predetermined range of the independent variable. Therefore the orthogonality of a specific polynomial is not an important notion. Indeed, by itself that statement does not make any sense. The notion of orthogonality implies the existence of something to which the object in question is orthogonal. Prior to transformation, the image S is blended using the formula:

$$S' = Sin\left(\frac{S_{(i)}{}^{3}}{100}\right)^{2} + \left(0.05 * rand\left(|S|\right)\right)$$

Orthogonal polynomial transform

Let $\left(p_l \,|\, l \geq 0\right)$ be a sequence of orthogonal polynomials on I with respect to some weight function $w(x)$, and let μ_l be defined [17], [34]. Let β_l be the leading coefficient of p_l.

We choose a value $m \geq 0$, and define $c_m = \beta_{m-1} / \left(\beta_m \mu_{m-1}\right)$. Then the following equation holds [28]:

$$\sum_{0 \leq l < m} \frac{1}{\mu_l} p_l(x)\, p_l(y) = \begin{cases} c_m \dfrac{p_{m-1}(y)\, p_m(x) - p_m(y)\, p_{m-1}(x)}{x - y} \\ x \neq y \\ c_m \left(p_{m-1}(x)\, p'_m(x) - p_m(x)\, p'_{m-1}(x)\right) \\ x = y \end{cases}$$

where p'_l denotes the derivative of p_l.

After applying the polynomial transform, the region corresponding to the CSF are segmented in the resultant image.

IV.2.2. White Matter and Gray Matter Segmentation

Following CSF segmentation, the next step is the segmentation of white matter and grey matter present in the brain MRI. The input to the process is the skull stripped image. The major steps used to segment the gray matter and white matter is given below:

The skull stripped input image S is smoothened by applying the 2-d Gaussian convolution filter to obtain another image S_I (Fig. 3).

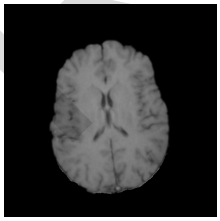
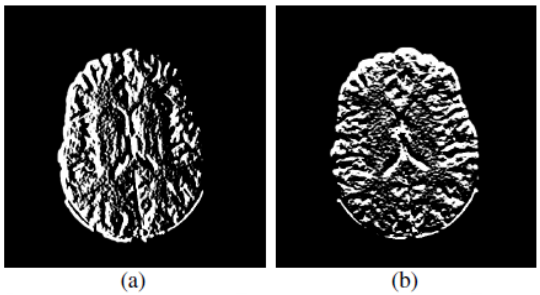


Fig. 3. Smoothening Results

Then, the x, y gradients of the smoothened image is computed (Figs. 4). The gradient of two variables x and y is defined by:

$$\nabla f(x,y) = \frac{\partial f}{\partial x}\hat{i} + \frac{\partial f}{\partial y}\hat{j}$$



(a) (b)

Figs. 4. (a) Gradient w.r.t x, (b) Gradient w.r.t y

Using the gradient values, the edges present in the image are marked using the following equations:

$$F = x_{(i)}^2 + y_{(i)}^2$$

$$E_I = \frac{1}{1+F}$$

The image E_I with the edges marked, is then subjected to binarization. The binarization process involves examining the grey-level value of each pixel in the enhanced image by means of global threshold T.

The global threshold T is determined by means of the function:

$$T = G_{Th}\left(E_I\right)$$

Then the binarized image BI is subjected to binary morphological operators *opening* and *closing*. The morphological operators are applied mainly for the purpose of removing any of the obstacles and noise from the image.

The white matter WM and the gray matter GM tissues in the brain MRI are finally segmented (thresholding) based on their intensity values:

$$R_{out} = \begin{Bmatrix} WM; & BI_i = 1 \\ GM; & BI_i = 0 \end{Bmatrix}$$

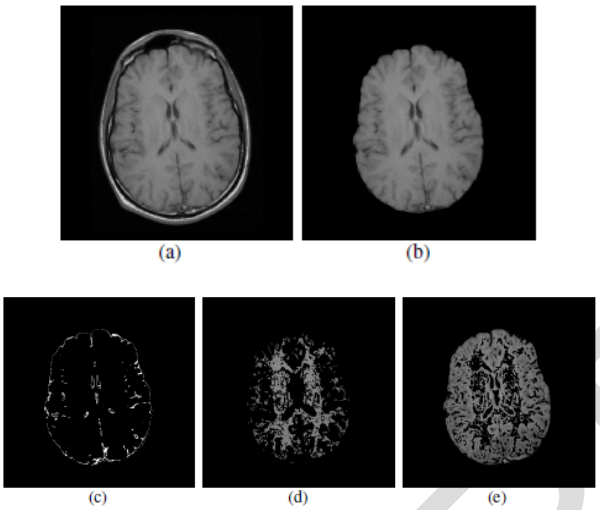
V. Results and Discussion

The experimental results of the proposed methodology for segmenting brain MRI images are presented in this section. The proposed methodology is implemented in Matlab (7.4). Here, we have tested our MRI brain segmentation using brain MRI images taken from the publicly available sources. As well, the performance of the proposed methodology is compared against the existing automatic MRI brain tissue segmentation methods [9] with FAST, SPM5, an automatically trained k-nearest neighbor (k-NN) classifier, and a conventional k-NN classifier by the similarity index SI based on a prior training set.

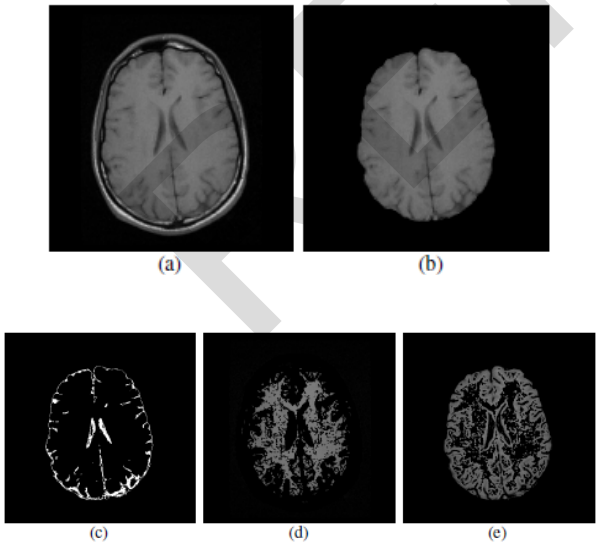
V.1. Experimental Results

The obtained experimental results are depicted in this section. The input to the proposed methodology is T1-weighted brain MRI images collected from publicly available databases. Regarding T1-weighting, every tissue in the human body has its own T1 and T2 value.

This term is used to indicate an image where most of the contrast between tissues is due to differences in the T1 value. The proposed methodology is based on Intensity Thresholding (IT), which is the easiest and fastest segmentation method, often adopted for preprocessing of medical images and preregistration problems. Here, segmentation of the three brain cortical tissues is performed via thresholding of voxel values within adjacent intervals.



Figs. 5. (a) Input Brain MRI Image, (b) Skull Stripped Image, (c) Segmented CSF, (d) Segmented WM, (e) Segmented GM



Figs. 6. (a) Input Brain MRI Image, (b) Skull Stripped Image, (c) Segmented CSF, (d) Segmented WM, (e) Segmented GM

The position of the interval bounds was initialized as follows: we used the skull stripped MRI data to compute the means of the three cortical tissues of interest. These mean values are then used to initialize the threshold values at the two interfaces CSF/GM and GM/WM. The sample results of brain MRI segmentation obtained using the proposed methodology is shown in the following figures.

The results show that the methodology can be considered as a promising platform for segmentation of anatomical structures.

V.2. Comparative Analysis

We have compared our proposed brain tissue segmentation method with the existing automatic MRI brain tissue segmentation methods [9] is presented in this section. The comparison is mainly done with the existing FAST, SPM5, an automatically trained k-nearest neighbor (k-NN) classifier, and a conventional k-NN classifier classification with the aid of the evaluation metric Similarity index, SI . The similarity index is used to express overlap between segmentations:

$$SI = \frac{2\left(s_1 \cap s_2\right)}{s_1 + s_2}$$

where, s_1 and s_2 denote the segmented volumes and $\left(s_1 \cap s_2\right)$ is the overlap of s_1 and s_2 .

The comparison techniques' details are given in a concise manner here. *FAST* [42] is a brain tissue segmentation method, which is part of FSL [43]. This method is based on a hidden Markov random field model and an associated expectation–maximization algorithm. *SPM5* contains a probabilistic brain tissue segmentation method [4].

A model, based on a mixture of Gaussians and tissue probability maps as deformable spatial priors, is fitted in an iterative procedure. A *k-nearest neighbor (k-NN)* brain tissue segmentation method, automatically trained on the subject itself using atlas registration, and extended with white matter lesion segmentation [12],[8] is the third method considered. The *conventional k-NN* brain tissue classifier is constructed from a prior training set of atlases using the T1w and PDw intensities as features [37]. Here, the proposed methodology is being compared by the similarity index SI of the brain tissues like Cerebrospinal fluid (CSF), White matter (WM) and (Gray matter) of the MRI image. The corresponding similarity index values of the proposed methodology and the existing technique is given in the following Table I. The results depicts that the proposed segmentation methodology shows better results in terms of similarity index value compared with other brain tissue segmentation methods. The proposed methodology's similarity value of the brain tissues like CSF, WM, GM shows better results compared with existing methods such as FAST, SPM5, k-nearest neighbor (k-NN) classifier, and a conventional k-NN.

TABLE I
ACCURACY (SI) VALUES OF THE BRAIN TISSUE SEGMENTATION METHODS

Brain tissue Segmentation methods	Similarity Index values		
	Cerebrospinal fluid(CSF)	White matter (WM)	Gray matter (GM)
Proposed methodology	0.84	0.94	0.91
FAST	0.75	0.94	0.88
SPM5	0.75	0.93	0.87
k-nearest neighbor (k-NN)	0.81	0.92	0.87
conventional k-NN	0.82	0.94	0.90

VI. Conclusion

In this paper, an automated, simple and efficient brain MRI segmentation method for classifying brain tissues has been presented. Initially, the cortex present in the brain MRI images is extracted by combining preprocessing techniques and incorporating mathematical morphology. Subsequently, the boundaries between gray matter, white matter, cerebrospinal fluid are marked on the preprocessed image by thresholding. The cerebrospinal fluid is then segmented by using orthogonal polynomial transform.

Lastly, the gray matter and the white matter regions in the MRI are segmented based on the intensity values.

Experimental results have showed that the proposed method does a reasonably good job in terms of segmentation. Obviously, the segmentation results enable the easy detection of the brain deformities like brain tumor, aging and more. As well, the proposed methodology shows better segmentation accuracy when compared with other existing techniques like FAST, SPM5, k-nearest neighbor (k-NN) classifier, and a conventional k-NN.

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