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Detection Techniques of Brain Tumour Segmentation: A Review

Mrs. Swati S. Sorte[1], Mrs. Manisha Khorgade[2]

Assistant Professor, Department of Electronics & Telecommunication, RGCER, Nagpur, MS, India [1, 2]

Abstract: Segmentation is the process to detect brain tumor. In the performance of the MRI image in terms of weight vector, execution time and tumor pixels detected, several methods in medical image have been processed and discussed based on requirements and properties of techniques in brain tumor detection .This paper is used to give more information about brain tumor detection and segmentation of HSOM with FCM is given. In this paper various step in detection of automatic system like (a) Image capturing (b) Edge detection (c) Image segmentation (d) Performance Evaluation are discussed.

Keywords: MRI, Correspondence, Morphometry.

1. INTRODUCTION

Magnetic resonance imaging (MRI) is advanced medical imaging technique, which is widely used in many medical applications because of its high spatial resolution and soft tissue contrast. With the increasing size and number of medical images, the use of computers in facilitating their processing and analysis has become necessary. MRI possesses good contrast resolution for different tissues and has advantages over computerized tomography (CT) for brain studies. Because of the advantages of MRI over other diagnostic imaging [3], the majority of researches in image segmentation pertain to its use for MRI images.

The task of image segmentation can be stated as the partition of an image into a number of non-overlapping regions, each with distinct properties. In general, the interesting tissues in brain are white matter (WM), gray matter (GM), and cerebral spinal fluid (CSF). Changes in the composition of these tissues in the whole volume or within specific regions can be used to characterize physiological processes and disease entities or to characterize disease severity [11]. Brain image segmentation of MRI means to specify the tissue type for each pixel or voxel in a 2D or 3D data set, respectively, on the basis of nformation available from both MRI images and the prior knowledge of brain. It is an important first step in many medical research and clinical applications, such as quantification of tissue volume, visualization and analysis of anatomical structures, multimodality fusion and registration, functional brain mapping, detection of pathology, surgical planning, and surgical navigation. It is also a complex and challenging task due to the intrinsic nature of the image. The brain image has a particularly complicated structure and it always contains artifacts such as noise, partial volume effects and intensity inhomogeneity.

In recent years, internal images of a human body can be easily analyzed by development of the medical imaging devices such as Computed tomography (CT), Magnetic Resonance Imaging (MRI), ultrasound imaging. In order to analyze the abnormalities, various imaging techniques have been introduced into medical fields which are the important tools for visual inspections by physician. Many related image processing techniques have accordingly been developed and reported in medical image processing fields. In most applications, however, they need certain a priori knowledge or manual operation by a user for analyzing. The various methods which are used for segmentation are described as follows:-

The first method to address sub problems in the area of MRI morphometry: 1) shape analysis and 2) segmentation. Firstly in this they have presented a method of analysing for group differences between irregular 2D contours. Using a novel dataset the shape analysis was applied and located a region of significant shape variation between patient and control groups. Secondly they explained the application of a deformable model to automatically segment structures and using a 4-fold cross validation presented a measure of its reliability (DICE scores).

1.1 Morphometry

Morphometry techniques applied to MRI have traditionally been a study of size, area and volume. Whilst these features are important, they represent crude measures that cannot express the complexity of anatomical shapes [5]. A typical morphometry study has the following steps:

1. MRI scans are acquired for two groups (patients and controls).
2. Segmentations (by an expert) are defined for a particular anatomical structure of interest.
3. Shape descriptors are extracted from the data.
4. Correspondences between descriptors are found.
5. Statistics are computed to identify significant differences between the groups. Within this methodology the goal is to identify shape features that may be used for discrimination between populations of controls (normal subjects) and patients

(Abnormal subjects). The underlying hypothesis is that shape variations are manifest as a result of a disease or abnormality. In the case of 2D shape variation there are many alternative shape representations such as distance transforms, medial axes, Fourier series, harmonic functions and deformation fields [5].

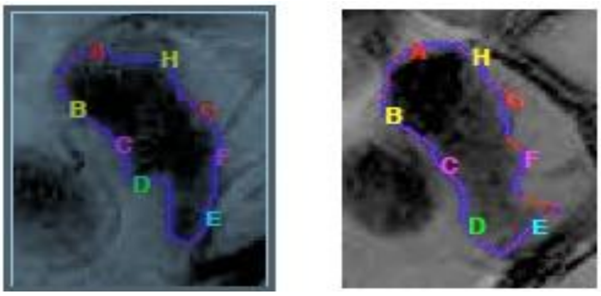

Figure1Shape context correspondence between two curves

Secondly, after correspondences are automatically obtained, a modified active appearance model is built. Using a novel transformation function the modified AAM is built to automate the segmentation of new data. The theory of appearance model fitting and the modified transform are applied. Both methods were applied to a high field MRI Parkinson's disease data set. Using the proposed shape analysis method a significant shape variation in the contour of their deep brain structure called the substantianigra was found. In addition, using the modified AAM a semi-automatic segmentation with a high level of overlap with human labeling was demonstrated. The contributions of this paper to the field of morphometry are two fold. Firstly, theyd address the shape analysis problem by computing correspondences from manually delineated data using a log-polar representation of contour points, called shape context. Using a novel re-sampling and line extraction method, statistical differences between contours are then found, this method is presented in section 2.

1.2 Shape Analysis

To extract meaningful information from the 2D structures, one would like to observe the variability of the outline (or mask) defining its structure. In a single slice (from a MR image) this forms a closed 2D contour which can be written as a function of its boundary coordinates. Importantly, the form of the function that defines the contour is otherwise unknown, and assumed to be highly variable among both patients and controls. In shape analysis it is the variability of the object contour that is important information for diagnosis. Clearly defining areas of high variability on contours across groups is a difficult to achieve. To do this empirically we examine a correspondence based approach where contour segments are analyzed after points are matched between patient and control contour groups. To do this they have first define a coarse set of corresponding points. Then sample the corresponding points uniformly to extract evenly spaced line segments. The line segments are then used to obtain a higher-resolution sample of the contour. Since the sampled points are in correspondence the resulting line segments are also in correspondence. Statistical differences between the line segments and their points can then be found using univariate t-tests.

1.2.1 Correspondence

Contour correspondences are computed using a well known shape descriptor, the shape-context introduced by Belongie et al. [3]. This descriptor can be used to compute correspondence without the need to minimize complex cost functions such as the minimum description length (mdl) methods [8]. Furthermore, shape-context is a highly descriptive representation of a contour function that is based on the distribution of relative contour positions. The term shape-context refers specifically to the joint histogram hi

$$hi(k) = \#\{q \mathrel{!=} pi : (q - pi) \# bin(k)\} \quad (1)$$

2. ALGORITHM BASED ON ANISOTROPIC DIFFUSION

Anisotropic diffusion was first introduced by Perona and Malik [6] as a multi-scale technique to detect edges. The algorithm is based on an anisotropic diffusion process that favours smoothing within continuous regions while it avoids smoothing across boundaries between regions. The filter is based on a constrained differential diffusion equation where pre-computed edges are viewed as locations with low diffusion coefficients by K as a scalar parameter, controlling the edge enhancement threshold. The diffusion equation is:

$$It = div(c(x, y, t)\nabla I) = c(x, y, t)\Delta I + \nabla c \cdot \nabla I \quad (2)$$

The operators div, ∇ and ∆ are the divergence, the gradient and the Laplacian operators respectively. I represents an intensity image while t is the process ordering parameter or diffusion time. The term c(x, y, t) is a scalar field controlling the diffusion strength. It has a monotonically decreasing function that is directly proportional to the initial magnitude of the gradient ∆I. At locations with large gradients, where
boundaries are assumed to happen, the initial value of
c(x, y, 0) is close to zero while it is a maximum at
locations with small gradients.

3. ALGORITHM BASED ON WAVELET ANALYSIS

Wavelets and multi-resolution analysis are intrinsically connected. Multi-resolution analysis with wavelets is based on two operations: dyadic dilations and integer translation [7]. The Wavelet transform has the advantage of being adaptable in both time and frequency to discontinuities in the signal. In the wavelet framework, a signal f(x) is represented as infinite combinations of a discrete wavelet at different scales and translations.

Magnetic resonance imaging (MRI) is a technique that uses a magnetic field and radio waves to create cross-sectional images of organs, soft tissues, bone, and virtually all other internal body structures.Several techniques have been developed for brain MR image segmentation]. In this paper, they have focussed our attention to image segmentation methods based on clustering. Clustering is the process of arranging data into groups having common characteristics and is a fundamental problem in many fields of science. Thus, image segmentation can be viewed as a special type of clustering. The most commonly used clustering algorithms have the K-means, the fuzzy c-means (FCM) algorithm, self-organizing map(SOM), and the finite mixture mode (FMM). Among these methods, FMM is a kind of statistical clustering method based on modeling of the probability density function (pdf), which could combine the advantages of the parameter estimation and non-parametric estimation. Furthermore, as a semi-parametric density estimation method, this model is only relevant to the complexity of solving problems but nothing to do with the size of the sample, so it has been applied widely in many areas.

One of the important characteristics is that the neighborhood pixels should be highly correlated in an image. In other words, the feature values of the neighboring pixels are more similar and the probability that they belong to the same cluster is greater. Unfortunately, the application of GMM to brain MR image segmentation is not take into account spatial information except intensity values, which will lead a misclassification on the boundaries and inhomogeneous regions with noises. In order to overcome this shortcoming, spatial smoothness constraints, generally applying an Markov random field (MRF) prior, had been imposed on the model. Such as, Sanjay-Gopal and Hebert firstly provides a modification of classical finite mixture model approach for pixel labeling, named with the partially variant finite mixture model (SVFMM).This model considers the pixel labels as random variables instead of parameters as the FMM and assumes a MRF prior on the data, this prior enforces spatially smoothness of the pixel labels and generates clusters that are spatially continuous.

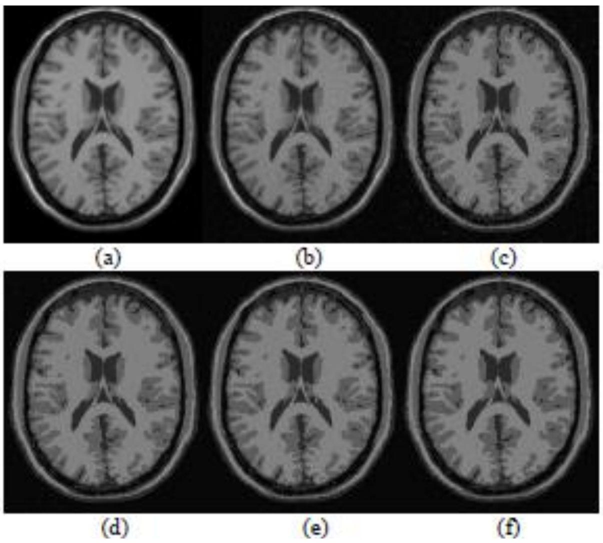

Fig. 2. The segmentation results of simulated brain image with 5% noise level by using four different methods method.(a) Simulated brain image, (b) image with 5% noise,(c) SVFMM,(d) CA-SVFMM, (e)WGMM,(f) Adaptive spatially information method.

But, there are some disadvantages using MRF prior as spatial smoothness constraints, such as, i)prior smoothness parameter which is rather inflexible; ii)the model do not provide closed form update equations ;iii) a large number of parameters more than the size of image pixels ;iv)not take into account the respective pixel such as edge pixel. For this reason, a number of modify models of the SVFMM were proposed. However, these modify models have not resolved the essence drawbacks of the SVFMM. In order to tackle above mentioned problems, we present a image segmentation method based on Gaussian mixture model with spatial information. In this model, an adaptive spatial information function is defined to contain the spatial information instead of MRF prior. Then, we design the weighted class probabilities of very pixels according to Bayesian rules and prove these probabilities to satisfy with two norms of polarity and spatial continuity [9]. The experiment results by synthetic MR brain image and real MR brain image demonstrate that the proposed modified model is not only effective to deal with noisy, but also reserve well edge property.

5. REGISTRATION

Registration is an important problem and a fundamental task in medical image analysis, computer vision, etc. In the medical image processing field, some image registration techniques are proposed to find a geometrical transformation that relates the points of an image to their corresponding points of another image.

There are two types of registration method which is obtained same modality or differential modality. In recent years, multi-modal image registration techniques are proposed for analyzing which obtained the different modal images. Especially, CT and MR imaging of the head for diagnosis and surgical planning indicates that physicians and surgeons gain important information from these modalities. It is because CT image can easily display the bone structure in detail, and MR imaging can shows information of soft tissue. In radiotherapy planning manual registration techniques performed on the head CT image and MR image. In general, in order to register the two images physicians segment the volumes of interest fi~om each set of slices manually. However, manual segmentation of the object area may require several hours for analyzing. It is because MDC Timages and MR images contain more than 100 slices. Therefore, manual segmentation and registration method cannot apply for clinical application in the head CT and MR images. Image registration technique in literature may be classified into two types; one is feature based, the other is direct method. In order to register the two types of images many automatic and semiautomatic image registration methods have been proposed. Fitzpatrick et al. [1] propose a visual assessment of accuracy of retrospective registration techniques. Ding et al. [2] propose the volume image registration by template matching. There is a registration method with similar level of the voxel [3]. Furthermore, many related registration methods with mutual information of CT and MR image are proposed [4-8]. But all of them require processing time for registration or manual operation.

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