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A Novel Image Segmentation and Volume Estimation method on MRI based Brain images

Dr K.M.Mohamed Sudheer

HOD, Govt Polytechnic College, Purapuzha, Thodupuzha, Kerala, India

Abstract: In this paper we present a novel approach for segmenting as well as estimating the volume of various brain tissues like white matter, gray matter, hippocampus Cerebro spinal fluid etc. In the study of brain morphometry, it is accepted that a relationship exists between brain structure and function, both normal and abnormal. One descriptor of morphometric structure is volume. Volumetric measures introduce a level of precision in the estimation of the size of white matter, grey matter, hippocampi and other tissues that is not available simply by visually inspecting a set of MR images. For that we need to perform MR image acquisition and image processing

Keywords: Threshold-based segmentation, Magnetic resonance, K-Means algorithm, Cavalieri's estimator

I. INTRODUCTION

1.Necessity of Volume Analysis-All real-world vision systems must deal with complicated and cluttered environments. Computer vision is a computational activity that involves constructing representations of an image at successive levels of abstraction. One starts at the pixel level and terminates at a symantically meaning symbolic description of the image. Image segmentation is the process that partitions the image pixels into non overlapping regions such that each region is homogeneous and connected [Bhandarkar and Zhang, 1999]. Volume estimation is also a classical problem in computer vision and of paramount importance to medical imaging. Accurate classification of magnetic resonance images according to tissue type at the voxel level is important in many neuro-imaging applications. Changes in the composition of gray matter (GM), white matter (WM), or cerebrospinal fluid (CSF) in the whole volume or within specific regions can be used to characterize physiological processes and disease entities or to characterize disease severity. The imaging techniques used for brain segmentation could be divided in the following groups [3] [4] [6] [32] [63]: threshold-based segmentation, statistical methods for brain segmentation and region growing methods. In the category of threshold-based segmentation was proposed the use of: iterative thresholding, histogram analysis and morphological operations. The region growing techniques applied to MRI images represents the final category. Abnormalities in brain morphology, including unilateral or bilateral volume loss are known to occur in Epilepsy, Alzheimer's disease, and in certain amnestic syndromes [4] [5] [56]. The objectives of magnetic resonance (MR)-based brain volume measurements are precise quantitation, identification of a normal range, and identification of the association between biologic variables and aberrations in this volumetric parameter. Brain volumes of subjects with a history of major depressive episodes but currently in remission and with no known medical co-morbidity were compared to matched normal controls by using volumetric magnetic resonance images. Subjects with a history of major depression had significantly smaller left and right hippocampal volumes [4] [5] [8] [27] with no differences in total cerebral volumes. These results suggest that depression is associated with hippocampal atrophy, perhaps due to a progressive process mediated by glucocorticoid neurotoxicity.

2.Analysis and diagnosis. Structural and functional brain imaging research is beginning to uncover significant neurobiological impairments in antisocial, violent, and psychopathic groups using functional magnetic resonance imaging, single photon emission computerized tomography (SPECT;) and positron emission tomography (PET).

MRI is a technique for determining which parts of the brain different types of physical sensation or activity such as sight, sound or the movement of a subject's fingers activates. MRI images of the subject's brain are taken and these set of images are analyzed. The raw input images from the MRI scanner require mathematical transformation (usually Fourier transformation) to reconstruct the images into real space so that images look like brains. The rest of the analysis is done using a series of tools to correct for distortions in the images, subject's movement's etc. Mesial temporal cortical abnormalities have been observed in antisocial and violent groups using PET [10] [59]. More specifically, abnormalities in the hippocampus have been reported in antisocial groups using PET, SPECT, and fMRI, whereas abnormal metabolism in the anterior amygdala-hippocampal complex has also been reported in repetitively violent offenders using magnetic resonance spectroscopy. Figure below shows the right-left hippocampal laterality scores for three group of subjects viz controls, unsuccessful psychopaths and successful psychopaths.

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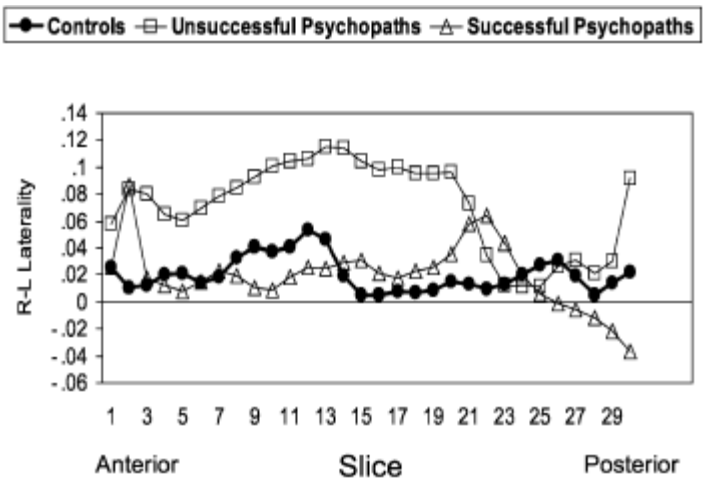

Right-left hippocampal laterality scores from interpolated slice volumes for the three groups. R, right; L, left.

Magnetic resonance (MR) imaging has been used in studies of the gray matter, white matter, hippocampal formation and in amygdala biometric studies for several years. The biometric data are useful for evaluating selective hippocampal atrophy in patients with intractable partial seizures [9] [11] [12] [13] [28] [36], Alzheimer-type dementia, amnesic syndromes, or schizophrenia. Different MR sequences have been used to evaluate the volume of the different tissue formations, and technical progress has allowed reduction of section thickness.

Method

In the specific case of MRI-based volume measurements the necessary operations can be summarized as follows:

a) Manipulation of the input images to achieve proper orientation and display of the segments
b) Segmentation of the Gray matter, White matter , Cerebro-spinal fluid, hippocampus etc from the remainder of the brain.
c) Estimating the volume of the different segmented parts of the brain.
In an idealized situation, these steps would occur instantaneously and automatically, i.e. without any interactive input. This is obviously not possible. . If the MR equipment used does not support the capability for acquiring 3-D gradient echo images in a non orthogonal plane, then the images should be reformatted perpendicular to the long axis of the part to be segmented. The first two steps outlined below address this reformatting issue. The current method of image processing includes the following steps

1.After loading orthogonal coronal 3-D gradient echo images (SPGR) into a workstation, the images are interpolated in the z-dimension to give cubic voxels.
2.The 3-D data set is then reformatted (transformation) for easier manipulation (i.e. rearrange the dimensions of multidimensional array)
3.The reformatted images are inspected, and their intensity distributions also are considered for further processing using the histogram display of the image.
4.The image is sent for displaying along with the intensity plot
5.Select the best threshold level to ignore certain parts of the data like the scalp, low-levels like cerebro-spinal fluid(CSF), air and other irrelevant soft and hard tissues of the brain
6.Segment out the different tissues like Gray-matter, White matter etc using an appropriate algorithm.
7.Having identified the different segments volume of these segments are found out using any one of the suitable method.

Segmentation Algorithm

K-means clustering algorithm is used to cluster each slice from a volume into a set of classes. The volumes used here consist of different separate slices. The ``center slice'' is chosen as the starting point because it has the best uniformity of signal within our MRI volume and also contains the most reliable anatomical information. Each MR slice is initially segmented by k-means clustering algorithm. Qualitative models of slices of brain tissue are defined and matched with their instances from imaged slices. If a significant deformation is detected in a tissue, the slice is classified to be abnormal

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and volume processing halts. Otherwise, the system locates the next focus-of-attention tissue based on a hierarchy of expected tissues. This process is repeated until either a slice is classified as abnormal or all tissues of the slice are labeled. If the slice is determined to be abnormal, the entire volume is also considered abnormal and processing halts. Otherwise, the system will proceed to the next slice and repeat the classification steps until all slices that comprise the volume are processed.

The K-Means algorithm for clustering has the drawback of always maintaining K-clusters. This leads to ineffective handling of noisy data and outliers. Noisy data is defined as having little similarity with the closest cluster's centroid. In K-means a noisy data item is placed in the most similar cluster, despite this similarity is low relative to the similarity of other data items in the same cluster with the centroid. In order to deal with the noisy data more effectively the idea is to first create a new cluster whenever data item has a distance with the most similar cluster's centroid beyond a threshold, and then place this data item in it. In other words the number of clusters K is expandable to accommodate the clustering of data items which contains noisy data.

The following is regular K-Means:

A. Select K data points as the initial representatives
B. For I =1 to N, assign item Xi to the most similar centroid (this gives K clusters).
C. For J = 1 to K, recalculate the cluster centroid Cj.
D. Repeat steps 2 and 3 until there is little or no change in clusters.

The expanding version of K-Means [8] is as follows:

1. Select K data points as initial representatives.
2. For I = 1 to N, assign item Xi to the most similar centroid (this gives K clusters).
3. For J = 1 to K, calculate the mean and standard deviation of similarity measure between every data item in cluster j and cluster centroid Cj.
4. For I = 1 to N, if the similarity measure between item Xi and it's cluster's centroid has a z-score < threshold, place item Xi in cluster K+1.
5. If step 4 was applied to any data item Xi, then reassign K=K+1.
6. For J = 1 to K, recalculate the cluster centroid Cj.
7. Repeat steps 2 to 6 until there is no change in clusters.

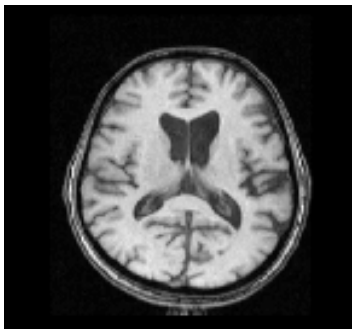

Fig (A)-MRI Brain image

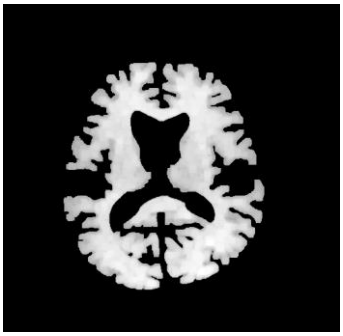

Fig (B) - Segmented Image

Brain Volume Estimation

Estimation of brain volume from serial sections typically involves using a rectangular, Cavalieri's, parabolic (Simpson's), or a trapezoidal rule. Cavalieri's estimator is most accurate since it's approach provides a better approximation of volume under some circumstances eventhough it requires equally-spaced sections.

Cavalier's Estimator of Morphometric Volume

Cavalieri's estimator of volume ($\mathbf{V_C}$) is a statistically unbiased form of the rectangular approach which requires systematic sampling.

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$$V_C = d\left(\sum_{i=1}^{n}(y_i)\right) - (t)y_{max}$$

IV. IMPLEMENTATION

Image Manipulation

The input image is an MRI based medical brain image (Axial T1) of size 256 X 256 or 512 X 512. The format of this image is dicom. Since the Axial T1 images are all of very big size of the order of 512 x 512 the image is resized to a convenient measure so that processing will be very faster. Moreover memory access speed will be high and there will be superfluous space also. The different slices are read one by one into 3-Dimensional array to explore the 3-D volume. The class type and size of the array are displayed for general information. The s interpolation to give 3-dimensional cubic voxels is done by populating the XYZ matrix (i.e. in all the three dimensions orientation of the voxels is calculated). In the x and y axes the inclination of the different slices are found out and they are manipulated to get the proper orientation. The dimensions of the multidimensional array are rearranged by permute–order method. The order is found by trial and error method. The input image is then squeezed so that all the singleton dimensions are removed. Singleton dimension means it will contain all the elements of the parent array but singleton dimensions get removed. After displaying the datas are reoriented for easier interpretation. Here the reorientation means the dimensions are flipped left to right such that the processing can be done on the third dimension without causing much damage to the read image. The 3-Dimensional volume is then explored on this rotated data. The intensity distribution of the histogram of the image is considered for pixel-by-pixel scanning and classification later in the segmentation process. The intensity distribution or the histogram of the image is then displayed. Later this is required for thresholding of the image and thereafter for segmentation also. The image is finally then rotated by 90 degrees to attain the vertical position.

Thresholding

Thresholding is done before segmentation. If the thresholding function does not return any value, then we say that the function shows non-blocking behaviour. Sometimes it may return some value, so we say that it shows blocking behaviour. The bins centers are calculated by finding the integer limits of the read digitized and rotated image. First we will try the direct indices first and then go for too many levels i.e the maximum range given. If the read digitized and rotated image is not an integer then we will try inferring discrete resolution first (i.e. we will input intensities which are often quantized). Next we will perform the gray thresholding by finding the norm values of the image intensities. Then apply some thresholding rules (simple global thresholding) to eliminate certain parts by using a threshold T. By selecting an appropriate threshold (40, 60 & 100) here a clean segmented result has achieved by eliminating. the shadows leaving only the objects. After that we go for segmentation

Segmentation

The segmentation is basically done to isolate the brain parts remove the soft tissues like cerebro-spinal fluid, brain scalp tissues and also to remove unnecessary datas like back ground air ,skull and other parts. The algorithm which is used here for segmentation is the k-means clustering algorithm. This non-hierarchical method initially takes the number of components of the population equal to the final required number of clusters. In this step itself the final required number of clusters is chosen such that the points are mutually farthest apart. Next, it examines each component in the population and assigns it to one of the clusters depending on the minimum distance. The centroid's position is recalculated every time a component is added to the cluster and this continues until all the components are grouped into the final required number of clusters. The choice of the selection of k different initial representatives is given to the user. Here the value of k is 3. These are the cluster centers or centroids. Each pixel will be placed in the cluster whose similarity measure is greater than or equal to a threshold. Recalculate the mean and standard deviation of similarity measure between every data item in cluster j and cluster centroid Cj. If similarity measure between item Xi and cluster centroid has a z-score < threshold, place item Xi in cluster K+1. Reassign K=K+1, then recalculate cluster centroid Cj. Repeat the above steps until there is no change in clusters. Later very small regions in the segmented image are merged into the adjacent ones closest in intensity using a region merging technique.

Erosion and Dilation Operations

Dilation and erosion are two fundamental morphological operations. Dilation adds pixels to the boundaries of objects in an image, while erosion removes pixels on object boundaries. The number of pixels added or removed from the objects in an image depends on the size and shape of the structuring element used to process the image. In the morphological

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dilation and erosion operations, the state of any given pixel in the output image is determined by applying a rule to the corresponding pixel and its neighbors in the input image

Volume calculation.

For estimating the volume of the brain and other segments we are using the Cavalieri's volume calculation method. It is a systematic sampling approach which requires equally spaced series of sections beginning with the first section. Here the numbers of sections chosen are ten. The Cavalieri's estimate of morphometric volume for equally spaced sections is determined by the following formula

$$V_C = d\left(\sum_{i=1}^{n}(y_i)\right) - (t)y_{max}$$

Where d is the distance between the sections that are being analyzed, t is the section thickness, y_i is the cross-sectional area of the i^{th} section through the morphometric region and ymax is the maximum value of y.

The different slices which are given as input in the first phase are again used here. The cross sectional area of each morphometric section is found by using a region of interest function. The slice thickness and section thickness are available from the information of the slice i.e. slice header file. From these available facts the volume of the brain is estimated. Similarly the same logic is applied for white and gray matter also.

The conventional method of volume estimation is also performed. Here the number of voxels in each slice of the brain is found out. Similarly the numbers of voxels in gray-matter, white mater etc are also found out. Later the product of the voxels and voxel-size (which is obtained from the metadata of the dicom information file) is found .to obtain the volume. This is applied to each slice of the image considered.

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BIOGRAPHY

DR.K.M MOHAMED SUDHEER IS CURRENTLY WORKING AS HEAD OF DEPARTMENT OF GOVT POLYTECHNIC COLLEGE, PURAPUZHA, THODUPUZHA, KERALA. HIS AREAS OF INTEREST ARE IMAGE SEGMENTATION, MOBILE ADHOC NETWORKING, SYSTEM ADMINISTRATION AND HARDWARE NETWORKING