Segmentation of Computed Tomography Brain Images Using Genetic Algorithm

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Abstract: Unlike research on brain segmentation of Magnetic Resonance Imaging (MRI) data, research on Computed Tomography (CT) brain segmentation is relatively scarce. We have begun to explore methods for soft tissue segmentation of CT brain data with a goal of enhancing the utility of CT for brain imaging. In this study, a novel method for automatic segmentation of Computed Tomography (CT) brain images has been presented. The method consists of two major phases. In the first phase, the original images are enhanced by using Selective Median Filter (SMF) and in the second phase the Genetic Algorithm (GA) is used to segment the image. The proposed method has been applied to real patient CT images and the performance is evaluated using Receiver Operating Characteristic (ROC) curve analysis. The result shows the superior performance of the proposed algorithm.

Key words: Selective median filter, CT brain images, segmentation, genetic algorithm, CT

INTRODUCTION

Image segmentation is the process of assigning labels to individual pixels in a volumetric data set, based on some criteria in the image. In medical image segmentation, pixels are labeled by tissue type. Image segmentation is required in many medical applications ranging from the education and assessment of medical students to image-guided surgery and surgical simulation.

Appropriate segmentation methods are highly dependent on image acquisition modality and the tissue of interest. For example, bone can be segmented in CT data using simple thresholding techniques because of the high contrast between bones and surrounding tissues. In contrast, soft tissues are not well differentiated in CT images and thresholding is inadequate.

Because, it provides superior contrast of soft tissue structures (Fig. 1), MRI is the method of choice for imaging the brain and most research on brain segmentation focuses on MRI. There are however, numerous situations when MRI is contraindicated and other alternatives, usually CT, need to be explored (Berquist et al., 2000). These situations include patients, who are too large for the MRI scanner, claustrophobic patients, patients with metallic or electrical implants and patients unable to remain motionless for the duration of the examination due to age, pain, or medical condition. Additional advantages of using CT include good
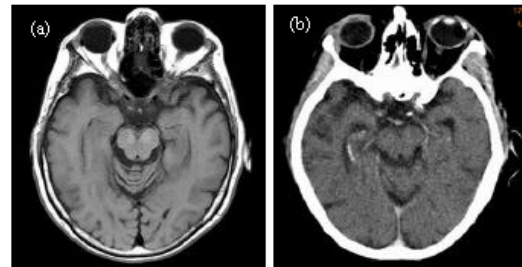

Fig. 1: Comparison between (a) MRI and (b) CT images of the brain. Gray and white matter are clearly distinguishable in the MRI image, but not in the CT image, while bone is easy to detect in the CT image

detection of calcification, hemorrhage and bony detail, plus lower cost, short imaging times and widespread availability. For these reasons, we have begun to explore methods for segmenting soft tissue in CT images. As a 1st step, we have evaluated the effectiveness of several segmentation methods developed for MRI for segmenting brain tissue in CT images.

The study on brain segmentation from MRI data is extensive and segmentation methods are well researched. Cuadra et al. (2001) gives an overview of the research on MRI brain segmentation. Laidlaw et al. (1994) used Bayesian classification to identify the distribution of different materials in MRI volumetric datasets of the brain.

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In this approach, voxels are allowed to contain >1 material and information from neighboring pixels is incorporated into the classification process. Several computer assisted methods have been proposed for the segmentation and quantification of brain tumors, ranging from manual or user-assisted outlining performed by a medical expert to fully automatic methods (Prastawa *et al.*, 2003). Common approaches include classification methods such as expectation-maximization or fuzzy connectedness (Liu *et al.*, 2005). The new use of dual energy CT for clinical applications has the potential of redefining the role of CT imaging for soft tissue segmentation. Dual energy CT scanners use two X-ray energy levels simultaneously (Ying *et al.*, 2006), allowing radiologists to better differentiate, characterize and isolate body tissues and fluid.

The FCM algorithm was used by Li *et al.* (1993) to segment MR brain images. Pham and Prince (1999) extended the traditional FCM to address the in homogeneities due to the MR acquisition process. Liu *et al.* (2006) a new algorithm, called an Alternative Fuzzy C-Mean (AFCM) is used for segmentation of medical images.

EM segmentation for MR brain images was first proposed by Wells *et al.* (1996). Wells *et al.* (1996) used EM algorithm to simultaneously estimate the classification of the image and a corrupting bias field characteristic to MR imaging. Pohl *et al.* (2006) presented a statistical model that combines the registration of an atlas with the segmentation of magnetic resonance images. We use an expectation maximization-based algorithm to find a solution within the model, which simultaneously estimates image artifacts, anatomical label maps and a structure-dependent hierarchical mapping from the atlas to the image space. The algorithm produces segmentations for brain tissues as well as their substructures.

Unlike study on brain segmentation for MRI, the study on brain segmentation on CT data is relatively sparse. The most common approaches use active contours (Maksimovic *et al.*, 2000), thresholding and region growing (Deleo *et al.*, 1985). However, all of these methods require manual input.

Hu *et al.* (2005) segmented brain matter from 3D CT images by first applying Fuzzy C-means and thresholding to 2D slices of the volume to create 2D masks and then propagating the 2D masks between neighboring slices. A method for automatic CT brain segmentation of Intracerebral brain Hemorrhage (ICH) is proposed by Loncaric and Kovacevic (1997). Five regions of interest (background, skull, brain, ICH and calcifications) were segmented using a combination of K-means clustering and neural networks.

MATERIALS AND METHODS

The method proposed in this study utilizes Genetic Algorithm (GA) to segment the brain image and the proposed research is compared with Bayesian classification and fuzzy C-means have been used on MRI data with good results.

Segmentation: Segmentation is a very commonly used and important step in medical image analysis and computer vision. The aim of image segmentation is to decompose an image domain into a number of disjoint regions so that the features within each region have visual similarity, strong statistical correlation and reasonably good homogeneity. Image segmentation techniques may be classified into a number of groups depending on the approach of the concerned algorithm. These include feature thresholding, contour based techniques, region based techniques, clustering, template matching, etc. Each of these approaches has its own merits and demerits in terms of applicability, suitability, performance, computational cost etc. and no one can meet all the demands. A gradient thresholding technique, for example, suffers from the problem of yielding contours with non-uniform thickness as well as discontinuities due to difficulty in selecting optimum threshold. The well-known watershed algorithm-a morphological instance of region based approach, apart from being computationally intensive, suffers from over or under-segmentation due to improper choice of marker points.

Recently, many researchers have focused their attention on a new class of algorithms, called metaheuristics. A metaheuristic is a set of algorithmic concepts that can be used to define heuristic methods applicable to a wide set of different problems. In this study, a metaheuristic algorithm called Genetic Algorithm (GA) is proposed to segment the brain images.

Enhancement: Image enhancement refers to attenuation, or sharpening, of image features such as edges, boundaries, or contrast to make the processed image more useful for analysis. In this study, a simple method aiming at improving the visibility of the loss of the gray-white matter interface in Computer Tomography (CT) brain images. The loss of the gray-white matter interface is one of the early signs of brain tumor diagnosis. The Selective Median Filter (SMF) is applied to reduce local noise with edges preserved in CT brain images. The SMF is a specially designed filter with adaptive size and shape depending on local pixel-value related to information surrounding the pixel of interest. The Fig. 2 shows, the original and enhanced image using SMF.
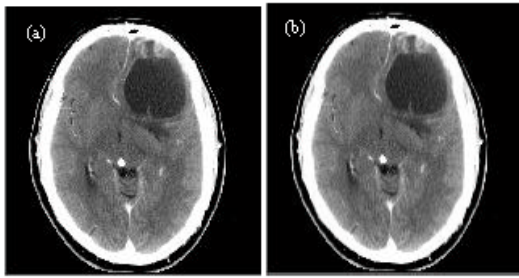
Fig. 2: a) Normal image and b) enhanced image

Genetic algorithm: A GA is a heuristic search or optimization technique for obtaining the best possible solution in a vast solution space. To apply a GA, an initial population is generated and the fitness of each member of the population is evaluated. The algorithm then iterates the following: members from the population are selected for reproduction in accordance to their fitness evaluations. The reproduction operators are then applied, which generally include a crossover operator that models the exchange of genetic material between the parent chromosomes and a mutation operator to maintain diversity and introduce new alleles into the generation or a combination of both to generate the offspring of the next generation. The fitness of the offspring is then evaluated and the algorithm starts a new iteration. The algorithm stops when either a sufficiently good solution is found or after a predetermined number of iterations.

Implementation: The parameters that control the GA can significantly affect its performance and there is no guidance in theory as to how to properly select them. The most important parameters are the population size, the crossover rate and the mutation probability. Researchers have commonly used these settings as either fixed or dynamic. In general, very good performance can be obtained with a range of parameter settings. Dynamic adaptive settings are advantageous to use over fixed settings, especially when the number of operators used is high. In this model, operators are given credit each time a better solution is found. A proportion of this credit is passed back to the parents of the created individual to assure operators are given credits for participating in creating the better solution. The Fig. 3 shows, the framework of the GA based segmentation.

The preprocessed images are considered for segmentation. Initially, the images are divided into kernels of size 10×10 pixels. The initial population of the GA is constructed by selecting the kernels at random. For each chromosome, two random numbers are generated, the

Original image

Enhancement using SMF

Divide the image into sub-images

Select 10 random sub-image

Convert the coordinates of sub-images into binary

Calculate the mean value of each sub-image as fitness value

Calculate the maximum fitness value (G_{max})

Apply genetic operators

Calculate the maximum fitness value in the new population (L_{max})

If $G_{max} < L_{max}$

$G_{max} = L_{max}$

Old population = New population
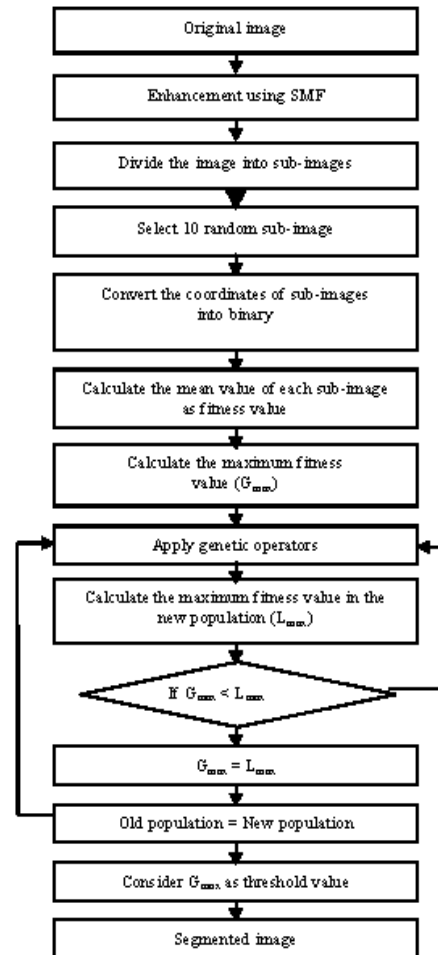
Consider G_{max} as threshold value

Segmented image

Fig. 3: Flowchart of GA based segmentation

numbers are considered as coordinates for selecting the kernel. Then the numbers are converted into binary to generate the chromosome. The size of the initial population is 10 and the mean feature value is calculated for each kernel as fitness value and the reproduction operator is applied to select the kernels having high probability based on roulette wheel selection and the crossover operator is applied on reproduced population with the probability of 0.6. Here, the parents are selected at random.

And the mutation operator applied to generate the new population with the probability of 0.03. From the new population the optimum fitness value is calculated. This optimum value is compared with the local optimum, if the local optimum is greater than the new one, then the local optimum is considered as global one and the next iteration is continued with the old population, otherwise, if the local optimum is less than the new one then the new population is copied into the old population and the new value is considered as global optimum and the next iteration is continued with the new population. This
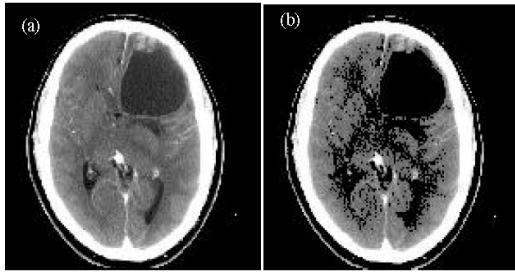
Fig. 4: a) Enhanced image and b) Segmented image

process will be repeated for 100 iterations and the global optimum from the last iteration is considered as threshold value to segment the brain images. The Fig. 4 shows, the result of segmented image from the proposed algorithem.

RESULTS

The Receiver Operating Characteristic (ROC) curve is a popular tool in medical and imaging research. It conveniently displays diagnostic accuracy expressed in terms of sensitivity (or true-positive rate) against (1-specificity) (or false-positive rate) at all possible threshold values. Performance of each test is characterized in terms of its ability to identify true positives, while rejecting false positives. The area under the ROC curve is an important criterion for evaluating diagnostic performance. Usually it is referred as the A_Z index.

The A_Z value of ROC curve is just the area under the ROC curve. The value of A_Z is 1.0 when the diagnostic detection has perfect performance, which means that TP rate is 100% and FP rate is 0%. The estimation of the A_Z value can be obtained with the trapezoidal rule that can underestimate areas under the curve. The A_Z value can also be computed by fitting a continuous binomial curve to the operating points.

In this research, the suspicious region extracted from the proposed algorithm is overlapped with a true abnormality as provided in the ground truth of the image is called a true positive detection.

An overlap means that at least 85% of the region extracted lies within the circle indicating a true abnormality. Suppose the overlap is <85% of the specified region and then the image is considered as false positive image. Figure 5 shows the ROC curves generated on the test set from the proposed algorithm compared with Bayesian classification and fuzzy C-means. The area under the ROC curve was found to be A_Z = 0.93 (93%), which shows the superior performance of the proposed algorithm.
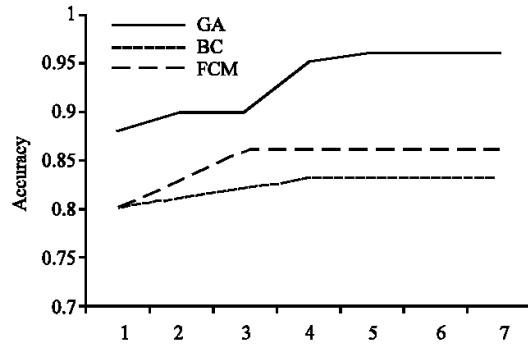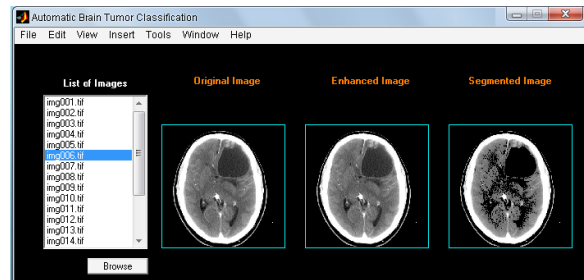

Fig. 5: ROC analysis

Fig. 6: Screenshot of the implementation

The proposed research is implemented with MATLAB® and the framework is shown in the Fig. 6.

CONCLUSION

In the study, two segmentation methods, Bayesian classification and Fuzzy c-Means were produced good results. In this study, the genetic algorithm is proposed for segmentation of CT brain images. And the results are compared with Bayesian classification and Fuzzy c-Means methods thorough ROC analysis. All three methods performed better than the existing methods and the proposed method has superior performance than the others.

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