

Image Segmentation and Classification of Mri Brain Tumors Based On Cellular Automata and Neural Network

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Abstract:

Cellular automata (CA) based seeded tumor segmentation method on magnetic resonance (MR) images, which uses Region of interest and seed selection. The region of tumor is selected from the image for getting seed point from abnormal region. This seed is selected by finding Co occurrence feature and run length features. Seed based segmentation is performed in the image for detecting the tumor region by highlighting the region with the help of level set method. The brain images are classified into three stages Normal, Benign and Malignant. For this non knowledge based automatic image classification, image texture features and Artificial Neural Network are employed. The conventional method for medical resonance brain images classification and tumors detection is by human inspection. Decision making is performed in two stages: Feature extraction using Gray level Co occurrence matrix and the Classification using Radial basis function which is the type of ANN. The performance of the ANN classifier is evaluated in terms of training performance and classification accuracies. Artificial Neural Network gives fast and accurate classification than other neural networks and it is a promising tool for classification of the tumors.

Segmentation of brain tissues in gray matter, white matter and tumor on medical images is not only of high interest in serial treatment monitoring of “disease burden” in oncologic imaging, but also gaining popularity with the advance of image guided surgical approaches. Outlining the brain tumor contour is a major step in planning spatially localized radiotherapy (e.g., Cyber knife, iMRT) which is usually done manually on contrast enhanced T1-weighted magnetic resonance images (MRI) in current clinical practice. On T1 MR Images acquired after administration of a contrast agent (gadolinium), blood vessels and parts of the tumor, where the contrast can pass the blood–brain barrier are observed as hyper intense areas. There are various attempts for brain tumor segmentation in the literature which use a single modality, combine multi modalities and use priors obtained from population atlases. Using gray scale, spatial information and thresholding method, region growing was applied to segment the region. The region of tumor is selected from the image for getting seed point from abnormal region. This seed is selected by finding Co occurrence feature and run length features. Seed based segmentation is performed in the image for detecting the tumor region by highlighting the region with the help of level set method.

I. Introduction

Ultrasound image segmentation is a critical issue in medical image analysis and visualization because these images contain strong speckle noises and attenuation artifacts. It is difficult to properly segment the interested objects with correct position and shape. In addition, poor image contrast and missing boundaries is a challenging task. Large numbers of different methods was proposed on ultrasound medical image segmentation. Some of them use a semi automated approach and need some operator interaction. Others are fully automatic and the operator has only a verification role. These methods can be represented by threshold based technique, boundary based methods, region based methods, mixture techniques that combined boundary and region criteria and active contour based approaches. Threshold technique uses only gray level information and do not consider the spatial information of the pixels and do not manage well with noise or poor boundaries which generally encountered in ultrasound images. Boundary based methods use the gradient of pixel values at the boundary between adjacent regions. In these methods an algorithm searches for pixels with high gradient values that are usually edge pixels and then tries to connect them to produce a curve which represents a boundary of the object. But to convert the edge pixels into close boundary is difficult for the ultrasound image segmentation. Region based segmentation is based on the principle that neighboring pixels within the one region have similar value. FCM algorithm is best known region based category for the segmentation. These methods affect the results due to speckle noises in ultrasound images. Another method is active contour method which is suitable for finding edges of a region whose gray scale intensities are significantly different from the surrounding region in the image. To segment homogenous regions, the semi automatic region growing methods first requires users to identify a seed point. In this paper, A full automatic region-growing segmentation technique is proposed. First we found the seed automatically using textural features from Co-occurrence matrix (COM) and run length features. Then using gray scale, spatial information and thresholding method, region growing was applied to

segment the region. With the advances in imaging technology, diagnostic imaging has become an indispensable tool in medicine today. X-ray angiography (XRA), magnetic resonance angiography (MRA), magnetic resonance imaging (MRI), computed tomography (CT), and other imaging modalities are heavily used in clinical practice. Such images provide complementary information about the patient. While increased size and volume in medical images required the automation of the diagnosis process, the latest advances in computer technology and reduced costs have made it possible to develop such systems. Blood vessel delineation on medical images forms an essential step in solving several practical applications such as diagnosis of the vessels (e.g. stenosis or malformations) and registration of patient images obtained at different times. Segmentation algorithms form the essence of medical image applications such as radiological diagnostic systems, multimodal image registration, creating anatomical atlases, visualization, and computer-aided surgery.

2. Automatic Selection Seed Point

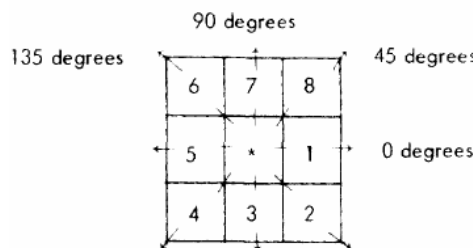
In this section we describe the method for automatic selection of abnormal region from ultrasound image using Co occurrence matrix probability feature and run length method

3. Co-Occurrence Matrix Probability Feature

A Co-Occurrence Matrix (COM) is square matrices of relative frequencies $P(i, j, d, \theta)$ with which two neighboring pixels separated by distance d at orientation θ occur in the image, one with gray level i and the other with gray level j “Fig. 1” [6]. A COM is therefore a square matrix that has the size of the largest pixel value in the image and presents the relative frequency distributions of gray levels and describe how often one gray level will appear in a specified spatial relationship to another gray level within each image region. Fig 3.1. Co occurrence matrix with its orientations There are 14 features that may be extracted from COM matrix, but usually 4 or 5 features are more interested ones. In this paper 2 textural features were calculated from the COM for direction h values of 0° and a distance d of 1. The matrix was normalized by the following function:

$$p(i, j, d, \theta) = \frac{P(i, j, d, \theta)}{R} \tag{1}$$

R is the normalized function, which is usually set as the sum of the matrix.



For example; with an 8 grey-level image representation and a vector t that considers only one neighbor, we would find [1]:

1	2	1	3	4
2	3	1	2	4
3	3	2	1	1

Fig 3.2 Image example

	0	1	2	3	4	5	6	7
0	0	0	0	0	0	0	0	0
1	0	1	2	0	0	0	0	0
2	0	1	0	2	0	0	0	0
3	0	0	1	1	0	0	0	0
4	0	1	0	0	1	0	0	0
5	0	0	0	0	0	0	0	0
6	0	0	0	0	0	0	0	0
7	0	0	0	0	0	0	0	0

Fig 3.3 Classical Co-occurrence matrix

In this work the co-occurrence features energy and entropy which can easily differentiate non-homogeneous region from homogeneous region are considered. Energy is called Angular Second Moment. It is a measure the homogeneity of the image and can be calculated from the normalized COM. It is a suitable measure for detection of disorder in texture image. Higher values for this feature mean that less changes in the image amplitude or intensity result in a much sparser COM. The energy is formulated by the following equation:

$$J = \sum_{i=1} \sum_{j=1} (p(i, j))^2$$

Entropy gives a measure of complexity of the image. Complex textures tend to have higher entropy. Entropy is represented by the following equation

$$S = -\sum_{i=1} \sum_{j=1} p(i, j) \log(p(i, j))$$

The value of energy and entropy are high for homogeneous regions and low for non-homogeneous regions. The abnormal region in the ultrasound images appears to be homogeneous. So these parameters can identify a seed pixel from the abnormal regions. Some cases the seed pixel is selected from the normal region which appears to be homogeneous. This drawback can be avoided by the calculating run length features that will describe in next section.

4. Gray Level Runlength Features

Run length features are based on computation of continuous probability of the length and gray level of the primitive in the texture. After the selection of seed pixel from co-occurrence features, we can check whether the selected seed pixel belongs to abnormal region or not. This can be checked by calculating the Run length features. These features are calculated from the Run length matrix $P(i, j)$ which describes the number of times that the image contains a run of length j in a given direction consisting of points having gray level i .

The following two features that give the good difference between homogeneous and non-homogeneous regions are considered.

Long run emphasis

$$\frac{\sum_{i=1}^G \sum_{j=1}^R j^2 p(i, j)}{\sum_{i=1}^G \sum_{j=1}^R p(i, j)}$$

Run length Non Uniformity

$$\frac{\sum_{i=1}^G \sum_{j=1}^R j p(i, j)^2}{\sum_{i=1}^G \sum_{j=1}^R p(i, j)}$$

That $P(i, j)$ is run length matrix, G denotes number of gray levels and R is longest run. The long run length emphasis is high for homogeneous region and low for non homogeneous region and the run length non uniformity is low for ,homogeneous and high for non homogeneous. The run length features have been calculated around the points selected by co occurrence features. If all the run length features of selected point and its neighborhood points are equal then the point is considered as a seed point.

5. CA ALGORITHM BASED ON SEED BASED SELECTION

A cellular automata is basically a computer algorithm that is discrete in space and time and operates on a lattice of cells. Since it was first proposed by Von Neumann and Ulam, Cellular Automata has attracted researchers from various fields in both physical and social sciences because of its simplicity, and potential in modeling complex systems. Each individual cell is in a specific state and changes synchronously depending on the states of some neighbors as determined by a local update rule. They are parallel, local and homogeneous, since the state of any cell depends only on the states of the local neighbors at the previous time step and the update rules are same for every cell.

Formally, a cellular automaton (CA) is a triple $A=(S, N, \delta)$, where S is a nonempty set, called the state set, N is the neighborhood, and $\delta: S^N \rightarrow S$ is the neighborhood; S^N , which is the argument of, indicates the states of the neighborhood cells at a given time, while, which is its value, is the state of the central cell at the next time step. Although the usual definition for “Cellular Automata” is in favor of a finite state set (discrete and bounded), continuous state sets in which the states are real numbers are also used in CA literature under the name “Continuous CA” or “Coupled Map Lattices”. A detailed discussion and some of the issues that can arise while using a continuous state set on a finite machine. There are various attempts of using CA in image processing problems including: image enhancement (sharpening and smoothing), image filtering, edge detection and image segmentation (Grow-cut). Grow-cut method uses a continuous state cellular automaton to interactively label images using user supplied seeds. The cells are corresponding to image pixels, and the feature vector is RGB or gray scale intensities. The state set for each image pixel consists of a “strength” value in a continuous interval $[0,1]$, a label and an image feature vector. The automata are initialized by assigning corresponding labels at seeds with a strength value between 0 and 1 where a higher value reflects a higher confidence in choosing the seed. Strengths for unlabeled cells are set to 0.

Where g is a pixel similarity function bounded to $[0, 1]$ depending on the image features i.e.,

$$g(x) = 1 - \frac{x}{\max \|\vec{C}\|_2}$$

Where the argument x is for instance, the absolute difference between the intensities of two neighboring pixels. The surprising success of this simple algorithm, especially on medical images, motivated us to further analyze the algorithm. We showed that the result of the iterations of this algorithm converges to that of the shortest paths algorithm by modifying the similarity function used: $g(x) =$. We note that, the original similarity function used in Grow-cut is a first order approximation to the one we utilized. In connecting shortest paths to cellular automata framework, maximizing the product of the edge weight ω_{ij} was shown to be equivalent to minimizing the sum of the $-\log \omega_{ij}$'s, i.e., $\|_{ij}\|$'s resulting in the shortest path between a seed node to any non seed node in the graph over the negative logarithm edge weights.

These weights can be interpreted similarly to the reciprocal weight ω_{ij} defined in Sinop and Grady, which was shown to infer a connection between the shortest path algorithm and the general seeded segmentation optimization with L_∞ norm minimization. Simultaneously and independently from our work, it has also been shown that the Grow-cut algorithm is equivalent to the Belman–Ford algorithm, which calculates the shortest paths on a weighted graph. However, there, the motivation and emphasis was on fast hardware implementation of the CA algorithms, due both increasing availability of low-cost graphical hardware (GPUs), and CA algorithm's suitability to run on parallel processors. Shortest path idea was utilized in other works such as, where the Eikonal equation was solved with two different boundary conditions constructed from foreground and background seeds. Image-dependent speed functions were inserted into the right hand side of the Eikonal equation, whose solutions led to two distance functions: shortest paths of each pixel from the foreground seeds and the background seeds. For each pixel, the smaller distance to the foreground seeds produced the resulting segmentation.

The grow cut method, first find the maximum intensity variation which means that from this intensity to 0 we are sure that this is not the ROI. Second we cut the histogram from MAX to 0. Then, find the threshold from MAX to the highest intensity which separates the uncertainty area from the ROI. This is simply done using the well-known Otsu thresholding method. This is a parameter free thresholding technique which maximizes the inter-class variance. It is interesting to observe that the Otsu method is more accurate in cutting into two classes than a k-means for example, because the k-means just measures distances between data and classes' centroids but Otsu also take care to get compact clusters using the inter-class variance.

6. Morphological Process

A shape (in blue) and its morphological dilation (in green) and erosion (in yellow) by a diamond-shape structuring element Mathematical morphology (MM) is a theory and technique for the analysis and processing of geometrical structures, based on set theory, lattice theory, topology, and random functions. MM is most commonly applied to digital images, but it can be employed as well on graphs, surface meshes, solids, and many other spatial structures. Topological and geometrical continuous-space concepts such as size, shape, convexity, connectivity, and geodesic distance, can be characterized by MM on both continuous and discrete spaces. MM is also the foundation of morphological image processing, which consists of a set of operators that transform images according to the above characterizations.

7. Binary Morphology

In binary morphology, an image is viewed as a subset of an Euclidean space \mathbb{R}^d or the integer grid \mathbb{Z}^d , for some dimension d . Example application: Assume we have received a fax of a dark photocopy. Everything looks like it was written with a pen that is bleeding. Erosion process will allow thicker lines to get skinny and detect the hole inside the letter "o".

8. Grayscale Morphology

In grayscale morphology, images are functions mapping an Euclidean space or grid E into $\mathbb{R} \cup \{\infty, -\infty\}$, where \mathbb{R} is the set of real's, ∞ is an element larger than any real number, and $-\infty$ is an element smaller than any real number. Grayscale structuring elements are also functions of the same format, called "structuring functions".

9. Conclusion

A Segmentation algorithm for the problem of tumor delineation which exhibit varying tissue characteristics, as the change in enhancing part of the tumor after radiation therapy becomes important. The segmentation to partition the tumor tissues further into enhancing parts. Seed based segmentation is performed in the image for detecting the tumor region and then highlighting the region with help of level set method pre-processing. More importantly, the supervised segmentation method requires considerable amount of training and testing data which comparatively complicates the process. Whereas, this study can be applied to the minimal amount of data with reliable results. As future work, we will be trying to improve classification of Tumor using Radial basis function which is the type of ANN. The performance of the ANN classifier was evaluated in terms of training performance and classification accuracies. Artificial Neural Network gives fast and accurate classification than other neural networks and it is a promising tool for classification of the tumors.

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