A New Affinity Propagation Clustering with Active Contours for Automatic Segmentation of GBM tumors in MR Images

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Abstract: In this work a histogram based Affinity Propagation clustering method with level sets is used to segment GBM tumors. Glioma segmentation in MRI is an important task for early tumor diagnosis and surgical planning. There are many methods exist for brain tumor segmentation, still research is active in this field and scope for improvement. MRI images shows complex characteristics and identifying different tumor tissues is really a difficult task, (distinguishing hige-grade gliomas(HGG) and normal brain tissues), In fact, it is difficult to extract the tumor from the surrounding healthy parenchyma tissue without any risk of neurological functional sequelae. In this paper we proposed a hybrid method based on Histogram based Affinity Propagation clustering and level sets for glioma segmentation. We applied the proposed method on BRATS data set. The proposed method compared with K-means, FCM, FFCM and HSOFCM. The proposed method produces promising results for segmentation of GBM tumors effectively. **I**n the future work we plan to test the algorithm with dynamic contrast enhancement (DCE) and dynamic susceptibility contrast (DSC) MRI for finding gliomas.

Keywords: Low-Grade glioma, Glioblastoma Multiform(GBM),*MRI segmentation, level set; Affinity propagation clustering;*

1.Introduction:

MRI is the best imaging technique for examination of brain, it is widely used in the diagnosis of brain diseases [1], follow-up of patient [2], evaluation of therapy [3] and human brain mapping [4]. MRI has number of advantages over other methods, in particular it is non-invasive and highly sensitive to the contrast acquisition. Hence, it shows a good spatial resolution and an very good performance when visualizing different tissues of human body. In many practical cases, MRI is associated to conventional imaging of gliomas, Gliomas are the most common type of primary brain tumor of the central nervous system. They come mainly from glial cells in the brain. According to the World Health Organization (WHO), there are two types of gliomas. The first type concerns what it is called low-grade gliomas (grade I and grade II), such as astrocytomas or oligodendrogliomas. These tumors account 50% of gliomas and the medium age of patients affected is arround 40th year. They are characterized by irregular contour, shapes and a continuous growth before the malignant transformation occurs. The life expectancy of people diagnosed with this type of glioma is of several years, and intensive treatment is being administered in order to prevent malignant progression. The second category of gliomas concerns the high grade gliomas (grade III and grade IV). The most common malignant of this type of gliomas is called the glioblastoma (GBM). In this case, the median life expectancy of patients is less than 12 months. Despite the considerable progress in research on gliomas and the availability of technical and material resources established for the management of patients with gliomas, the diagnosis of these tumors remains insufficient. Precisely, the main difficulty consists in the operation and interpretation of these images by neurosurgeons. In fact, the segmentation of gliomas on MRI images is one of the most crucial procedures in the surgical and treatment planning. Currently, this process is performed manually in clinical practice. In addition to being time

consuming, manual gliomas delineation is unreliable and depends on the individual operator.

Recent reviews on brain tumor segmentation are on both supervised and unsupervised methods and other methods are soft computing and combination of different methods. Supervised approach applied for multiparametric MR datasets to segment health and pathological tissues[5,6]. In this paper we proposed histogram based Affinity Propagation clustering with level sets for glioma segmentation.

The rest of the paper is organized as follows, section 2 describes materials and methods in this the basic AP clustering, Level set method and the proposed methods are discussed. Section 3 presents Results and discussion and section 4 concludes the paper.

2. Materials and Methods:

2.1 Affinity Propagation clustering

Affinity propagation(AP) was first proposed by Frey and Dueck[7-8] for partitioning datasets into clusters, based on the similarities between data points. AP is useful because it is not sensitive to initialization, and produces clusters at a very low error rate. Basically, AP partitions the data based on the maximization of the sum of similarities between data points such that each partition is associated with its exemplar (namely its most prototypical data point). Unlike other exemplar based clustering methods such and k-means and fuzzy c-means(FCM), performance of AP does not rely on a "good" initial cluster/group. AP can use arbitrarily complex affinity functions since it does not need to search or integrate over a parameter space. Due to the flexibility of the AP method regarding.

AP initially assumes all data points (i.e., voxels) as exemplars and refines them down iteratively by passing two "messages" between all points: responsibility and availability. Messages are scalar values such that each point sends a message to all other points, indicating to what degree each of the other points is suitable to be its exemplar. The first message is called responsibility, indicated by r (i, k), and is how responsible point k is to be the exemplar of point i. In availability, denoted by a(i,k), each point sends a message to all other points and indicates to what degree the point itself is available for serving as an exemplar. These messages are sent iteratively until the messages do not change. The responsibility and availability were formulated as:

$$r(i,\ k) \leftarrow s\ (i,\ k)\ - \max_{k'\{k'\neq k\}}\{a(i,k') + s(i,k')\} \quad (1)$$

$$a(i,k) \leftarrow \min\ \{0, r(k,k) + \sum_{r'\{r'(i,k)\}} max\{0, r(i',k)\}\} \quad (2)$$

where s(i,k)is the similarity between point i and point k, and k is all other points except for i and k. Point k is not responsible to be the exemplar for point i if there is another point that describes i better than k; hence, the maximum value for responsibility is reached. The sum of availabilities and responsibilities at any iteration provides the current exemplars and classifications. Initially, all points are considered to be possible exemplars, which guarantees globally optimal solutions.

AP uses max-product belief propagation to obtain good exemplars through maximizing the objective function $argmax_k[a(i,k) + r(i,k)]$.When k=i, the responsibility (k, k),is set to the preference. The preference of a data point is set between 0 and 1, where 0 always prevents this point from being an exemplar and 1 always makes this point an exemplar. If the preference is anywhere between 0 and 1 , AP will not necessarily make that point an exemplar, but AP will use this prior information to cluster the data. The exemplar is the center point of each group and all other points in the group are connected by it. The preference of all the data was arbitrarily set between 0 and 1. It made no difference on the clustering result because all points were equally likely to be exemplars initially. In our implementation, we also allowed the AP to be semi-supervised by allowing the user to change the preference of a data point.

2.2 LEVEL SETS

Level set methods utilize dynamic variational boundaries for image segmentation. The parameters are set on trial and error basis.

Level set method embeds them into a time dependent PDE function $\emptyset(t,x,y)$. It is then possible to approximate the evaluation of active counters implicitly by tracking the zero level set $\Gamma(t)$.

$$\begin{cases} \emptyset(t,x,y) < 0 & \text{(x,y) is inside } \Gamma(t) \\ \emptyset(t,x,y) = 0 & \text{(x,y) is at } \Gamma(t) \\ \emptyset(t,x,y) > 0 & \text{(x,y) is outside } \Gamma(t) \end{cases}$$

The implicit interface Γ may be comprised of a single or a series of zero isocontours.

2.3 The Proposed histogram based AP clustering with level sets:

Algorithm AP will produce an N*N similarity matrix when the number of data is N. Consider a image if there are a total of 65536 pixels and each pixel is seen as a data point, then number of data point N will be 65536. The size of the similarity matrix need to be constructed is 65536*65536 bytes, and this scale is comparatively too large to process. To overcome this problem, we use the gray histogram to obtain the first k gray values which occur more frequently in the image as the clustering data. The value of k depends on the numbers of gray species w in the gray image. When w is greater than the threshold value m, we find that it will get good results when k is taken to w/2 as input number. In general, the value of m is 100 because most gray images usually have 256 kinds of gray value. In the following experiments, we take m = 100, which is based on the image size in experiments. In this way, we will reduce N data of the original image to k data for AP clustering. This method greatly reduces the space complexity, shortens the computational time, and improves the efficiency of the algorithm.

The steps of the proposed algorithm Histogram based AP are as follows:
Step 1: Find the gray histogram of the image. Count the number of gray value between 0 and 255 and the amount of nonzero gray value's category w; set the threshold value of m.
Step 2: If w>m, let k=m/2, if w<m, let k=w. Extract the first k most frequently appeared grey values, then input them to the AP algorithm.
Step 3: The original gray value of each pixel would be replaced by the center value of the cluster to which the original gray value belongs to.
Step 4: Apply the level sets method to obtain the accurate tumor part from MRI image.

3. RESULTS AND ANALYSIS

In this section, The performance of the proposed method is compared with K-means[9], conventional FCM[10], FFCM[11],HSOFCM[12]. We present the experimental results on The Brain Tumor Image Segmentation (BRATS) Benchmark dataset [13] is used. In this experiment , The BRATS dataset is publicly available through the annual Medical Image Computing and Computer Assisted Intervention (MICCAI) Society brain tumor segmentation challenge. The dataset consists of 30 fully anonymized multi-contrast MR scans of glioma patients along with expert annotations, i.e., ground truth manual segmentations. We use 22 images of the FLAIR MRI (axial plane) modality. Fig.1(a) is the FLAIR image,Fig.1(b) is T1C. The experiments were performed on a 2.99 GHz Intel Core 2 Duo processor, Windows XP with 3.21 GB RAM, using Matlab R2012a.

Segmentation results on BRATS data set are shown in Fig.2. The algorithms K-Means (Fig.1(c)), FCM(Fig.1(d)), FFCM Fig.1(d), HSOFCM(Fig.1(e) Proposed method (Fib.1(f)), Fig.1(g)Proposed method with active contours. From these results it is obvious that K-Means, FCM,FFCM,HSOFCM results are not upto the mark. Visually, the proposed method achieves the better result.

A.Quantitative results:

Performance of different image segmentation algorithm can be compared with following parameters:

True Positive (TP): Both proposed segmentation Algorithm and Ground Truth(GT) are positive
True Negative (TN): Both proposed segmentation algorithm and Ground Truth(GT) are negative

False Positive (FP): Proposed segmentation algorithm result is positive and Ground Truth(GT) are negative.
False Negative (FN): Proposed segmentation algorithm result is negative and Ground Truth(GT) is positive.
Dice: 2(TP+TN)/(P+N +P'+N')

PPV: TP/(TP+FP)

Sensitivity = TP / (TP+FN)

Where P to the real positives of the ground truth, N to the real negatives of the ground truth, P' to the estimated positives of the proposed segmentation, N' to the estimated negatives of the proposed segmentation. Quantitative results from table 1, gives better results than the existing methods.

4. Conclusion

This paper presented a hybrid method for segmentation of giomas, initially obtain few histogram bins which are more frequently occurred in the image as the cluster data, these pixel are the input for the AP clustering. Which improves the computational time and efficiency of the AP clustering algorithm. In the next step the resultant image is applied with active contours in order to extract the tumor part. We get the promising result when tested on BRATS data set. When we compared the proposed method with the existing methods we get promising results. However, in the future work we plan to test the algorithm with dynamic contrast enhancement (DCE) and dynamic susceptibility contrast (DSC) MRI for finding gliomas.

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Fig. 1 The FLAIR and T1C of brain image and results of different segmentation algorithms

Fig.1(a) FLAIR Image	Fig.1(b) T1C	Fig.1(C) K-Means	Fig.1(d) FCM

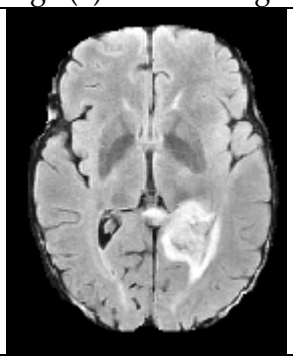
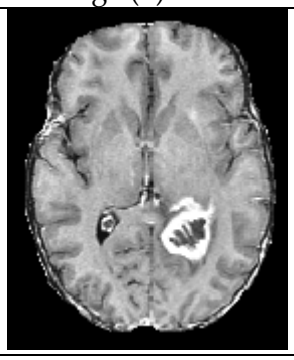
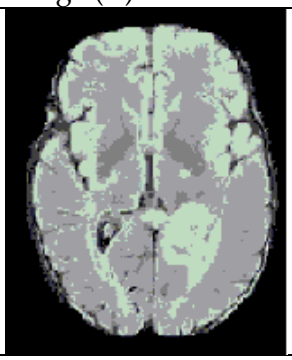

		

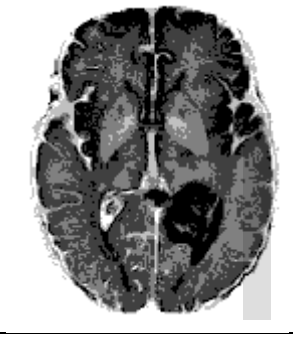
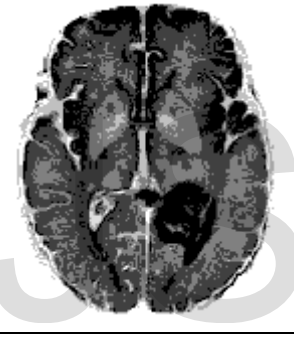
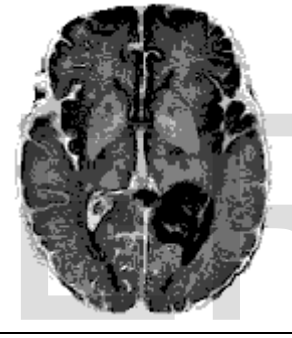
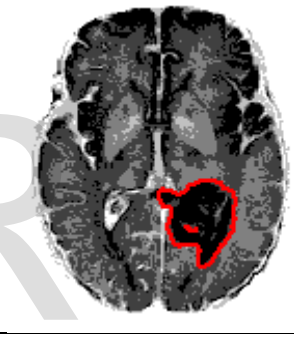
Fig.1(d) FFCM	Fig.1(e)HSOFCM	Fig.1(f)proposed method	Fig.1(g)Proposed method with active contours
			

Table 1. Summary of average results obtained by the different unsupervised algorithms

Algorithm	Dice			PPV			Sensitivity		
	complete	core	enhancing	complete	core	enhancing	complete	core	enhancing
K-Means	0.72	0.48	0.53	0.71	0.44	0.65	0.71	0.55	0.49
FCM	0.73	0.51	0.42	0.65	0.46	0.38	0.73	0.58	0.41
FFCM	0.76	0.49	0.56	0.66	0.51	0.64	0.76	0.62	0.52
Proposed method	**0.78**	**0.57**	**0.58**	**0.67**	**0.54**	**0.66**	**0.79**	**0.68**	**0.58**