Brain Tumor Segmentation Based on Non Negative Matrix Factorization and Fuzzy Clustering

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Abstract: The problem of computational brain tumor segmentation has attracted researchers over a decade because of its high clinical relevance and challenging nature. Automatic and accurate detection of brain tumor is one of the major areas of research in medical image processing which helps radiologists for precise treatment planning. Magnetic Resonance Imaging (MRI) is one of the widely used imaging modality for visualizing and assessing the brain anatomy and its functions in non-invasive manner. In this paper a novel approach for brain tumor segmentation based on Non-Negative Matrix Factorization(NMF) and Fuzzy clustering is proposed. Proposed algorithm is tested on BRATS 2012 training database of High Grade and Low Grade Glioma tumors with clinical and synthetic data of 80 patients. Various evaluation parameters like Dice index, Jaccard index, Sensitivity, Specificity are evaluated. Comparison of experimental results with other state of the art brain tumor segmentation methods demonstrate that proposed method outperforms existing segmentation techniques.

1 INTRODUCTION

Gliomas are the most frequent primary brain tumors in adults and account for 70% of adult malignant primary brain tumors with average survival time of one year. Glioma arises from glial cells and infiltrates the surrounding tissues such as white matter fiber tracts with very rapid growth [Menze et al., 2015]. Axial slice of T1 weighted, T2 weighted and Fluid-attenuated inversion recovery(FLAIR) magnetic resonance images are shown with Glioblastoma tumor in fig. 1. On the right side, different heterogeneous regions of the brain tumor i.e. edema, active and necrotic regions are shown. Accurate segmentation of brain tumor tissues from Brain MRI images is of profound importance in many clinical applications such as surgical planning and image-guided interventions.

Brain tumor segmentation is challenging task because of its non-rigid and complex shape, variation in size and position from patient to patient which make classical segmentation techniques, such as thresholding, edge detection, region growing, classification and clustering ineffective at accurate delineation of complex boundaries between tumor and healthy tissues. Brain tumor segmentation methods are broadly classified into four categories as: Threshold based, Region based, Pixel classification based and Model based techniques with pros and cons over each other [Gordillo et al., 2013]. Bauer et al. [S. Bauer and Reyes, 2012] proposed brain tumor segmentation approach based on integrated hierarchical classification and regularization in an energy minimization scheme. Geremia et al. [E. Geremia and Ayache, 2012] pre-

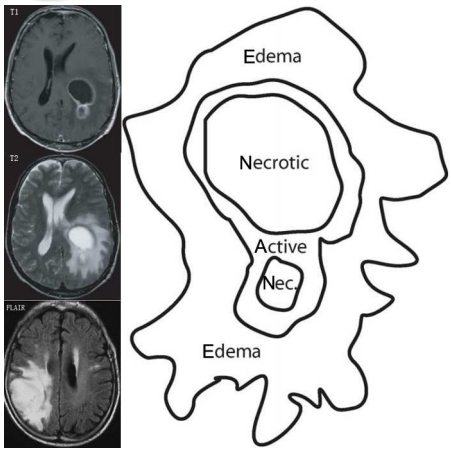

Figure 1: Left: Axial slice of MRI with T1, T2, FLAIR modalities and Right: intra-tumor tissues parts. [Corso et al., 2008].

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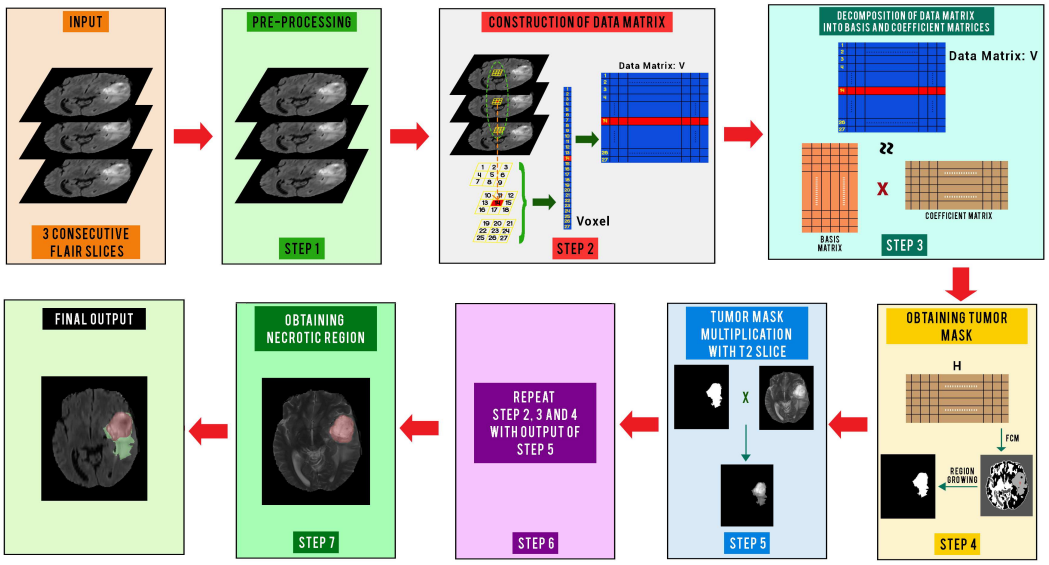


Figure 2: Proposed block diagram for Brain Tumor segmentation from MRI images.

sented automatic segmentation of gliomas in 3D MR images with random decision forest framework which gives a voxel-wise probabilistic classification. Many approaches to brain tumor segmentation have been implemented over decades but there is no winning theory.

Non-negative Matrix Factorization (NMF) is dimensionality reduction tool used in machine learning with wide range of applications in data mining. Non-negative Matrix Factorization (NMF) can cluster complex data with extracting features. These features can learn characteristics of data classes. This significance of NMF is of great use in image segmentation. In NMF segmentation features are extracted in a new space obtained by decomposing input data into basis matrix W and coefficient matrix H. Vectors of coefficient matrix H represent the degree of association of each data point to the basis feature [Lee and Seung, 2000]. There are very few approaches for medical image segmentation using NMF. Xie et al. [Xie et al., 2011] proposed a method for segmentation which extracts the basis tensor images from the diffusion tensor images DTI data.

This DTI data is factorised using NMF and then segmented. Sandler et al. [Sandler and Lindenbaum, 2011] proposed a segmentation approach where image is divided into several regions and histogram of each region is factorized using NMF. Hosseini [Hosseini-asl et al., 2014] proposed lung segmentation in CT images based on NMF with visual appearance modelling. Lung voxels were separated from chest voxels based on extracted model and k-means clustering. Dera et al. [Dera, 2015] proposed segmentation algorithm for brain MRI using level set and NMF. Number of distinct regions in image and and their local distribution is evaluated which is incorporated into energy function of Level set method. Though some researchers have proposed NMF for segmentation, applying NMF in MRI images is still challenging.

2 PROPOSED METHOD

In this paper a novel framework is proposed for Brain tumor segmentation. The block diagram for the proposed framework is shown in fig. 2 comprising seven steps. In first step MRI volume of FLAIR images is pre-processed with anisotropic filter. Data matrix(V) is generated in second step while decomposition of data matrix(V) into basis matrix(W) and coefficient matrix(H) is achieved in next step. The fourth step is used to cluster the coefficient matrix(H) with fuzzy C-means clustering which segments whole tumor in FLAIR slice. Step 5, step 6 and step 7 gives Necrotic tumor segmentation in T2 slices. The above steps are discussed below in detail.

2.1 Preprocessing on MRI Volume

Pre-processing operations like de-noising, skull stripping and intensity normalization have direct impact on brain tumor segmentation. FLAIR and T2 MRI volume is pre-processed with anisotropic diffusion filte-

ring for de-noising. Bias field normalization is carried out with ITK N3 from [Tustison and Gee, 2010].

2.2 Construction of Data Matrix V

The idea behind the construction of data matrix is to incorporate the contextual information present in inter-slices of MRI image volume for better segmentation. Every pixel in the slice to be segmented is represented by 27 pixels. These 27 pixels comprised of 9 pixels from the slice to be segmented, 9 pixels from the previous slice and 9 pixels from the next slice i.e. $(3 \times 3 \times 3)$ window as shown in step 2 of fig. 2. Thus, for every pixel a voxel of 27 elements is obtained. All voxels are concatenated to form data matrix(V).

2.3 Decomposition of Data Matrix (V)

As each pixel is represented by 27 pixels, size of the data matrix (D) is increased significantly and we need dimensionality reduction to overcome this problem. To decompose multi-dimensional matrix, Non-negative Tensor Decomposition(NTD) was proposed [Cichocki et al., 2009]. However, in this method large matrices are computed using iterative steps of multi-dimensional matrix product and division which is computationally complex. Hence, NMF is preferred over NTD to overcome this problem. NMF computes a lower rank approximation with non-subtractive combinations of non-negative basis vectors. Consider data matrix $V \in \mathbb{R}^{m \times n}$ and desired rank is $p \ll min(m,n)$. The data matrix V can be decomposed into basis matrix $W \in \mathbb{R}^{m \times p}$ and coefficient matrix $H \in \mathbb{R}^{p \times n}$ as shown in eq. 1. The coefficient matrix can also be termed as feature matrix.

$$V \approx WH \tag{1}$$

where, W and H are non-negative. W is basis matrix and H is coefficient matrix which can be obtained by reformulating the optimization problem in eq 2.

$$\min_{W,H} F(W,H) \equiv \| V - WH \|_F, \quad s.t. \ W,H \geqslant 0, \tag{2}$$

To optimize eq 2. several algorithms have been developed like Multiplicative Alternate Least Squares (ALS), Projected Gradient Descent (PGD) [Berry et al., 2007]. In our approach Alternate Non-negative Least Square Algorithm based on active set (ANLS-AS) is used [Kim and Park, 2008]. Cost function minimization (Convergence) is with less iterations and faster in ANLS-AS compare to other optimizing methods which is desirable. In ANLS eq. 3 is iterated till the convergence criteria is satisfied. While iterating in eq. 3 H is fixed whereas in eq. 4, W is fixed.

$$\min_{W \geq 0} \| H^T W^T - V^T \|_F^2 \tag{3}$$

$$\min_{H \geq 0} \| WH - V \|_F^2 \tag{4}$$

Generalised cost function for ANLS-AS algorithm is given in eq. 5

$$\min_{G \geq 0} \| BG - Y \|_F^2 \tag{5}$$

where, $B \in \mathbb{R}^{p \times q}$ and $Y \in \mathbb{R}^{p \times l}$ and we need to optimize G. Eq. 5 can be decomposed into l independent NLS equations with mono right hand side as given in eq. 6

$$\min_{G \geq 0} \| BG - Y \|_F^2 \rightarrow \min_{g_1 \geq 0} \| Bg_1 - y_1 \|_2^2, \ ... \\ ... \min_{g_l \geq 0} \| Bg_l - y_l \|_2^2 \tag{6}$$

where, $G = [g1, ..., g_l] \in \mathbb{R}^{q \times l}$ and $Y = [y1, ..., y_l] \in \mathbb{R}^{p \times l}$

Eq. 3 and eq. 4 are solved alternatively at each iteration and converted to the form of eq. 5. After the convergence criteria is fulfilled, each column of W represents basis vector and each column of H represents coefficient vector which is shown in step 2 of fig. 2.

2.4 Segmentation with FCM

In this step coefficient matrix H is segmented with fuzzy c-means clustering algorithm to cluster voxels. With region growing algorithm, whole tumor is segmented in FLAIR image and whole tumor mask is created. After this step whole tumor is segmented i.e. Edema and Necrotic part together.

2.5 Segmentation of Necrotic Tumor

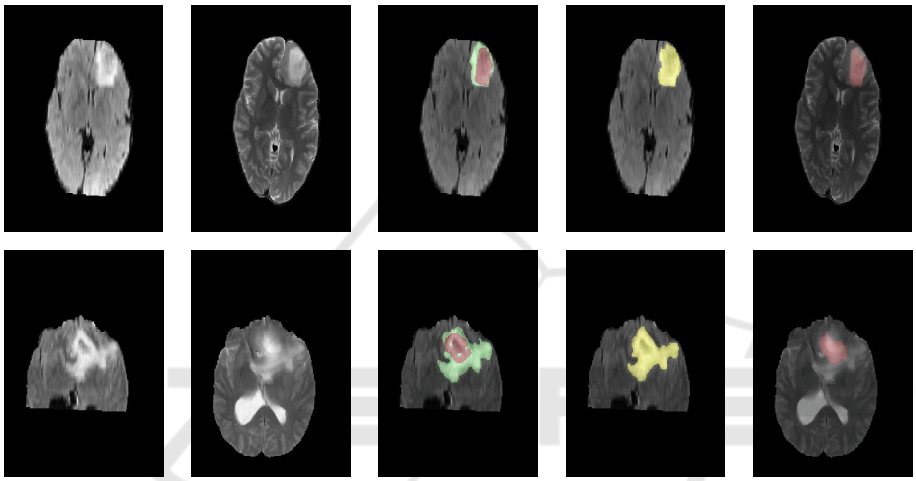
Tumor mask which was obtained by region growing segmentation in FLAIR slice is multiplied with corresponding T2 slice. It is observed that necrotic cells differs from Edema in T2 slice. Step two, three and four are repeated with the output of step five. Again with region growing algorithm necrotic part is segmented in $T2$ slice. In final step, segmentation output of necrotic tumor is overlayed on segmentation of whole tumor.

3 RESULTS AND DISCUSSION

In order to evaluate the accuracy of the proposed segmentation approach, we assess its performance on the

Table 1: Comparison between proposed method and other approaches in terms of dice similarity coefficient. Note that the results of our segmentation algorithm are obtained $(3 \times 3 \times 3)$ window.

Dataset	High Grade Real		Low Grade Real		Average	
	Edema	Tumor	Edema	Tumor	Edema	Tumor
[Zikic et al., 2012]	0.70	0.71	0.44	62		
[S. Bauer and Reyes, 2012]	0.61	0.62	0.35	0.49	0.59	0.73
[E. Geremia and Ayache, 2012]	0.56	0.68	0.29	0.52	–	–
[Hamamci and Unal, 2012]	0.56	0.73	0.38	0.71	–	–
[Menze et al., 2012]	0.69	0.70	0.49	0.23	–	–
[T. Riklin Raviv and Menze, 2012]	0.60	0.58	0.35	0.32	–	–
Proposed Method	**0.77**	**0.72**	**0.80**	0.**76**	–	–



(a) FLAIR slice (b) T2 slice (c) Ground Truth (d) Whole Tumor Segmentation (e) Necrotic Tumor Segmentation

Figure 3: Segmentation results of Low Grade Glioma Tumor (Real).

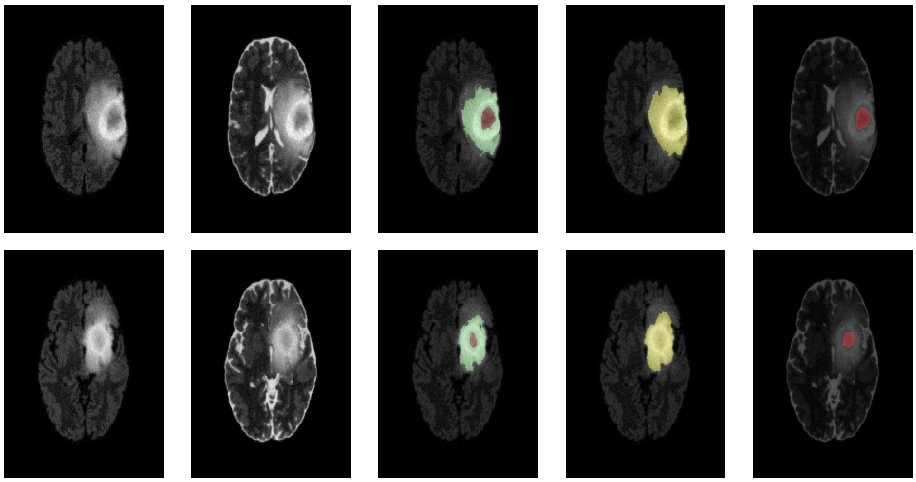
BRATS 2012 challenge dataset. BRATS 2012 training dataset consists of fully annotated 20 High Grade Glioma (Real), 10 Low Grade Glioma(Real), 25 High Grade Glioma (Synthetic) and 25 Low Grade Glioma (Synthetic) patients [Menze et al., 2015]. Real data images are obtained from various hospitals and synthetic images are generated using TumorSim software with ground-truth. MRI volume in the 2012 dataset contains skull-stripped multimodal MR image volume of 80 patients. For each patient, T1, T2, T1c, FLAIR MR images are available with ground truth marked by clinicians as edema, necrotic and whole tumor.

All volumes are skull stripped and linearly co-registered using affine registration and interpolated to 1mm isotropic resolution. We have segmented the volume into Whole tumor, edema and necrotic/core classes with proposed algorithm. Let, T_0 and T_1 be the normal tissue and tumor tissue marked in the ground truth. Similarly, P_0 and P_1 be the predicted normal tissue and tumor tissue segmented with the algorithms. Various performance parameters like Dice coefficient, Jaccard coefficient, Sensitivity, Specificity are evaluated for comparison. Dice and Jaccard coefficients are widely used as evaluation tool to find segmentation accuracy between segmented image and ground truth and given in eq. 7 and eq. 8

$$Dice = \frac{|P_1 \wedge T_1|}{(|P_1| + |T_1|)/2} \quad Jaccard = \frac{|P_1 \wedge T_1|}{(|P_1| \cup |T_1|)} \quad (7)$$

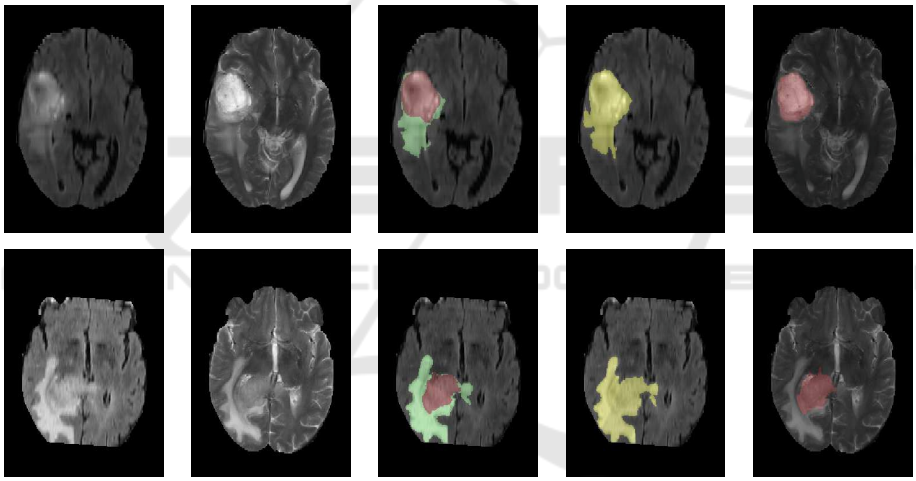
$$Sensitivity = \frac{|P_1 \wedge T_1|}{|T_1|} \quad Specificity = \frac{|P_0 \wedge T_0|}{|T_0|} \quad (8)$$

Segmentation results with the proposed algorithm are shown in fig. 5, fig. 3, and fig. 4 for High Grade Real, Low Grade Real and synthetic tumors respectively. Each row represents (from left to right) FLAIR slice, T2 slice, Ground Truth, Whole tumor segmentation in FLAIR slice, Necrotic tumor segmentation in



(a) FLAIR slice (b) T2 slice (c) Ground Truth (d) Whole Tumor Segmentation (e) Necrotic Tumor Segmentation

Figure 4: Segmentation results of Synthetic High Grade Glioma Tumor (1st row) and Synthetic Low Grade Glioma Tumor(2nd row).



(a) FLAIR slice (b) T2 slice (c) Ground Truth (d) Whole Tumor Segmentation (e) Necrotic Tumor Segmentation

Figure 5: Segmentation results of High Grade Glioma Tumor (Real).

T2 slice. The proposed method achieves mean Dice Similarity Coefficient as 0.77 for tumor and 0.81 for edema for $(3 \times 3 \times 3)$ window. The detailed experimentation results with dice similarity coefficient, sensitivity, specificity and Hausdorff distance are listed in Table 1.

Comparison with the existing segmentation techniques is shown in Table 1 which demonstrate that our method performs better in terms of dice similarity coefficient. Proposed algorithm is further evaluated on different window sizes $(5 \times 5 \times 3)$, $(7 \times 7 \times 3)$ and $(9 \times 9 \times 3)$. It is found that $(3 \times 3 \times 3)$ window outperforms over other sizes. Also, for the larger window sizes the dimension of the voxel increases which in turn increases computation complexity for factorization of data matrix (V).

4 CONCLUSION

A new method for brain tumor segmentation has been proposed based on Non Negative matrix factorization(NMF) and fuzzy c-means clustering. Segmentation accuracy in terms of dice similarity coefficient is

improved by incorporating pixel information present in previous slice and next slice in MRI volume data. The performance of our method is evaluated on 80 patients of BRATS 2012 training dataset and compared with other existing segmentation techniques. The results demonstrate that our method outperforms the other brain tumor segmentation algorithm. The performance of the proposed algorithm is also compared by varying window sizes i.e. voxel with different dimensions and it can be concluded that best results are obtained for $(3 \times 3 \times 3)$ window. In future, segmentation accuracy can be improved by delineating more accurate boundary using T1c MRI volume data which differentiates tumor boundary with non tumor tissue.

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