



GLIOBLASTOMA BRAIN TUMOR MODELING APPROACH

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Abstract— Brain is the master and commanding organ of human body. Human brain is affected by many dangerous diseases. Brain tumor or neoplasm is the abnormal growth of tissues in the brain and surrounding regions. MRI is one of the method used for brain tumor diagnosis. Glioblastomas are highly aggressive and malignant brain tumors. Due to the tumor's diffuse growth, the resection is a difficulty undertaking. To determine the resection extent, the tumor volume on pre-operative and post-operative magnetic resonance (MR) images should be calculated. Most of the research work focuses upon reaction diffusion model. Estimating the parameters of the reaction-diffusion model is difficult because of the lack of identifiability of the parameters, the uncertainty in the tumor segmentations, and the model approximation, which cannot perfectly capture the complex dynamics of the tumor evolution. Our approach aims at analyzing the uncertainty in the patient specific parameters of a tumor growth model, by sampling from the posterior probability of the parameters knowing the magnetic resonance images of a given patient. The estimation of the posterior probability is based on: i) a highly parallelized implementation of the reaction-diffusion equation using the Lattice Boltzmann Method (LBM), and ii) a high acceptance rate Monte Carlo technique called Gaussian Process Hamiltonian Monte Carlo (GPHMC).

Key words—tumor growth, GPHMC, LBM, Histogram of Oriented Gradients ,CSF, Linear Binary Pattern , Glioblastoma, First-order statistical features.

1. INTRODUCTION

Gliomas, the most common primary brain tumors, are thought to arise from the supporting glial cells of the brain or their precursors (1). Because they generally grow and invade extensively before the patient notes any symptoms, gliomas are almost impossible to cure.

Glioblastomas are the most malignant and most common gliomas in adults, accounting for about 50% of all gliomas. Glioblastomas are distinguished by necrosis, which may be massive centrally or more irregular between vascular supplies, and peripheral cells that diffusely invade the surrounding tissue. The aggressive behavior of these tumors is reflected in their 100% fatality rate within approximately one year even after extensive surgery, radiotherapy, and chemotherapy. Despite continual advances in imaging technology, glioma cells invade far beyond the abnormality shown on clinical imaging (e.g. CT, MRI, or PET) and even beyond gross and microscopic observations at autopsy. The extent is certainly beyond that guiding present-day radiotherapy of gliomas, which targets therapy to only an arbitrary 2 cm beyond the imaged bulk mass of the tumor. Clearly, it is the invasion into the normal-appearing surrounding tissue that is responsible for the tumor recurrence even in those tumors that are radio-sensitive.

The proposed method consist of multiple phases. First phase consist of texture feature extraction from Brain MR images. After feature extraction, these features independently are used for segmentation stage, which localizes the tumor area. The tumor region obtained using sliding window method. If the window is classified to have tumor, the central pixel of the window will be labeled as tumor. The MRI segmented brain images are identify whether the tumor is glioblastoma or non glioblastoma . In proposed technique, is successfully segmenting brain tumor tissues with high accuracy and low computational complexity. The advantage of this method is robust, accurate and efficient .It provides high accuracy and low computational complexity.Noises are completely removed in MRI .It is numerical stable in computation of the bias field.

1.1 RELATED WORKS

In this section, a review of different techniques and parameter estimation is made so that the tumor is identified and accuracy is measured.



David Corwin, Clay Holdsworth, Russell C. Rockne, Andrew D. Trister, Maciej M. Mrugala, Jason K. Rockhill, Robert D. Stewart, Mark Phillips, Kristin R. Swanson presented a paper entitled “Toward Patient-Specific, Biologically Optimized Radiation Therapy Plans for the Treatment of Glioblastoma” this provides knowledge about method of generating patient-specific, biologically-guided radiotherapy dose plans and compare them to the standard-of-care protocol. To integrated a patient-specific biomathematical model of glioma proliferation, invasion and radiotherapy with a multiobjective evolutionary algorithm for intensity-modulated radiation therapy optimization to construct individualized, biologically-guided plans for glioblastoma patients [3].

Erin Stretton, Ezequiel Geremia, Bjoern Menze, Herve Delingette, Nicholas Ayache presented a paper entitled “Importance of patient DTI’s to accurately model glioma growth using the reaction diffusion equation” this explores about the Tumor growth models based on the FisherKolmogorov reactiondiffusion equation (FK) have shown convincing results in reproducing and predicting the invasion patterns of gliomas brain tumors. Diffusion tensor images (DTIs) were suggested to model the anisotropic diffusion of tumor cells in the brain white matter. However, clinical patient-DTIs are expensive and often acquired with low resolution, which compromises the accuracy of the tumor growth models[6].

Zacharaki EI, Wang S, Chawla S, Yoo DS, Wolf R, Melhem ER, presented a paper entitled “Classification of brain tumor type and grade using MRI texture and shape in a machine learning scheme” this provides ideas about including ROI definition, feature extraction, feature selection and classification. The extracted features include tumor shape and intensity characteristics as well as rotation invariant texture features. Feature subset selection is performed using Support Vector Machines with recursive feature elimination. The binary SVM classification accuracy, sensitivity, and specificity, assessed by leave-one-out cross-validation, were respectively 85%, 87%, and 79% for discrimination of metastases from gliomas, and 88%, 85%, and 96% for discrimination of high grade (grade III and IV) from low grade (grade II) neoplasms. Multi-class classification was also performed via a one-versus-all voting scheme[15]

M.L[^]e, H.Delingette, Tracy Batchelor, Jan Unkelbach, Nicholas Ayache presented a paper entitled “Bayesian Personalization of Brain Tumor Growth Model” this describes about parameter estimation and bayesian

personalization method. estimates the posterior probability of the parameters, and allows the analysis of the parameters correlations and uncertainty. Moreover, this method provides a way to compute the evidence of a model, which is a mathematically sound way of assessing the validity of different model hypotheses.[10]

Rohini Paul Joseph presented a paper entitled “Brain Tumor MRI Image Segmentation and Detection in Image Processing” this introduces about Segmentation of brain MRI image using K-means clustering algorithm followed by morphological filtering which avoids the misclustered regions after segmentation of the brain MRI image for detection of tumor location. Image segmentation methods can be classified as thresholding, region based, supervised and unsupervised classification techniques. Various approaches have been carried out in the field of brain tumor detection have developed a brain tumor segmentation method and validated segmentation on two dimensional MRI data. this method based upon K-means clustering [13]

The paper is organized as follows, Section 2 shows the transformation of an image into its set of features is known as feature extraction. the extraction done by using different texture-based feature extraction techniques: GLCM, HOG, and LBP methods. Section 3 discusses about the results and performance analysis and finally section 4 concludes the project.

2. PROPOSED SCHEME

The main theme of this thesis is to identify the glioblastoma tumor and measure the accuracies. To identify the glioblastoma tumor by using two methods such as Lattice Boltzmann Method (LBM), Gaussian Process Hamiltonian Monte Carlo (GPHMC). The patient specific parameters of a tumor growth model, by sampling from the posterior probability of the parameters knowing the magnetic resonance images of a given patient. the accuracies can be measured by some important factors.

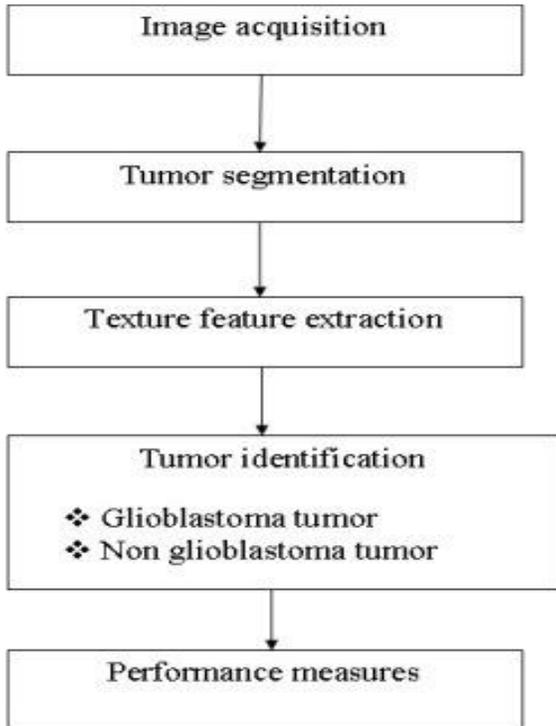


Figure 2.1 Flow diagram

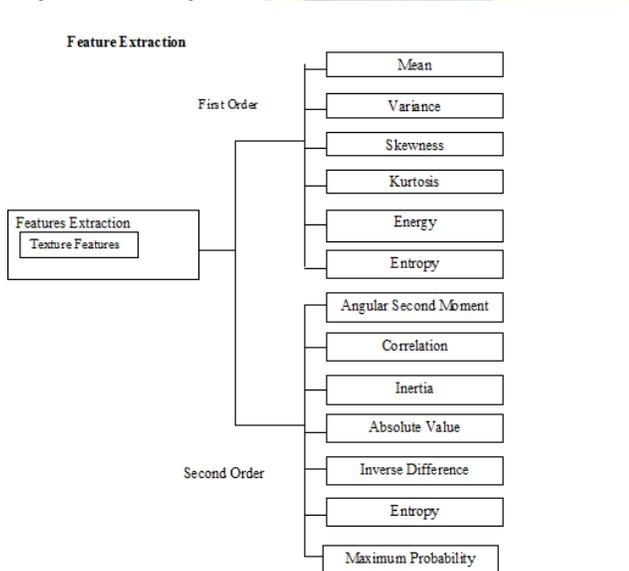


Figure 2.2 Texture Feature Extraction

Figure 1 and 2 portrays the work flow and texture feature extraction respectively. The proposed system methodology is described as follows

2.1 METHODOLOGY

The parameter estimation is very difficult in brain tumor identification. The proposed system helps to estimate the parameters and measure the accuracies by different texture-based feature extraction techniques: GLCM, HOG, and LBP methods.

i) HOG Feature

Histogram of Oriented Gradients is the expansion of HOG features. The HOG feature is a texture descriptor describing the distribution of image gradients in different orientations. HOG Features are texture features extracted from the images. The images are divided into smaller regions. Histogram values were calculated for that divided regions and the gradient information such as angle and magnitude are obtained from the histogram values. Using HOG 80 features were extracted.

ii) LBP Feature

Linear Binary Pattern is the expansion of LBP feature. The LBP operator sweeps a window over the image and gives labels to central pixel of the window by thresholding its neighborhood with the central value and specifying binary numbers for its neighbors. Then the LBP calculates the sum of the binary numbers multiplied by powers of two increasing clockwise counter clockwise. The histogram of these 256 different labels is used as a texture descriptor. Considered neighborhood can be in different sizes. Any radius and any number of pixels in the neighborhood can be used.

First-order statistical features

Histogram of the image gives summary of the statistical information about the image. So first order statistical information of the image can be obtained using histogram of the image. Probability density of occurrence of the intensity levels can be obtained by dividing the value of intensity level histogram with total number of pixels in the image.

$$P(i)=h(i)/NM, i=0,1,..G-1 \quad (1)$$

Where N is number of the resolution cells in the horizontal spatial domain and M is the number of resolution cells in the vertical spatial domain. G is the total gray level of an image. For quantitatively describing the first order statistical features of the image, useful features of the image can be obtained from the histogram. Mean is the average value of the intensity of the image. Variance tells the intensity variation around the mean. Skewness is the measure which tells the symmetry of the histogram around the mean. Kurtosis is the flatness of the



histogram. Uniformity of the histogram is represented by the entropy. Mean, median, average contrast, energy and entropy, skewness and kurtosis are useful first-order statistical features. Mean is the average value of the intensity of the image. Variance indicates the intensity variations around the mean. Skewness quantifies the asymmetry of the histogram around the mean. Kurtosis is the flatness of the histogram. Entropy reveals the randomness of intensity values. Formulae for these features are listed as follows:

Mean:

$$\mu = \sum_{i=0}^{G-1} i P(i) \quad (2)$$

Average Contrast :

$$\sigma^2 = \sum_{i=0}^{G-1} (i - \mu)^2 P(i) \quad (3)$$

Skewness:

$$\mu_3 = \sigma^{-3} \sum_{i=0}^{G-1} (i - \mu)^3 P(i) \quad (4)$$

Kurtosis:

$$\mu_4 = \sigma^{-4} \sum_{i=0}^{G-1} (i - \mu)^4 P(i) \quad (5)$$

Energy :

$$E = \sum_{i=0}^{G-1} P(i) \cdot P(i) \quad (6)$$

Entropy:

$$H = - \sum_{i=0}^{G-1} P(i) \log_2 P(i) \quad (7)$$

GLCM:

Histogram based features are local in nature. These features does not consider spatial information into consideration. So for this purpose gray-level spatial co-occurrence matrix $h_d(i,j)$ based features are defined which are known as second order histogram based features. These features are based on the joint probability distribution of pairs of pixels. Distance d and angle θ within a given neighborhood are used for calculation of joint probability distribution between pixels. Normally $d=1,2$ and $\theta=0^\circ, 45^\circ, 90^\circ, 135^\circ$ are used for calculation. Co-occurrence matrix calculation is illustrated in Fig. 3 for $d=1$. Texture features can be described using this co-occurrence matrix. Following equations define these features:

Correlation:

$$\sum_{i=0}^{G-1} \sum_{j=0}^{G-1} \frac{ij C_{ij}}{\sigma_i \sigma_j} \quad (8)$$

Angular second moment(energy):

$$\sum_{i=0}^{G-1} \sum_{j=0}^{G-1} [p(i,j) \cdot p(i,j)] \quad (9)$$

Absolute Value :

$$\sum_{i=0}^{G-1} \sum_{j=0}^{G-1} |i - j| p(i,j) \quad (10)$$

Entropy:

$$H = - \sum_{i=0}^{G-1} p(i) \log_2 [P(i)] \quad (11)$$

Maximum Proability:

$$\max_{i,j} p(i,j) \quad (12)$$

Finally ,features values are extracted from MRimages. then images are fed into tumor segmentation stage.

Tumor Segmentation

The detection of a tumor image (slice), which includes tumor tissue, the slice is fed into the segmentation stage, which localizes the tumor area. Segmentation tumor area is obtained using texture based feature extraction such as Gabor –wavelet feature and statistical feature. The tumor region obtained using sliding window method. If the window is classified to have tumor, the central pixel of the window will be labeled as tumor.

Lattice Boltzmann Method

A typical approach to implement the reaction-diffusion equation is to discretize the equation using the Crank-Nicolson scheme [36]. This requires the inversion of a large sparse matrix $n * n$ where n is the number of voxels in the image, using a preconditioned gradient method like the biconjugate gradient stabilized method. For 3D MRIs with $n \sim 10^6$, this approach is computationally expensive. In this paper, we use the more recent explicit method called the Lattice Boltzmann Method (LBM). LBM has been successfully applied to implement the reaction-diffusion equation in the fields of cardiac electrophysiology modeling [37], [26], and liver tumor radiofrequency-ablation [38]. The idea is to model the reaction-diffusion equation as a set of fictitious particles which collide and stream on the cartesian grid. The healthy tissues can be divided as GM(Grey matter), WM(White matter), CSF(Cerebro spinal fluid).

White Matter: Wm is component of the central nervous system. Wm of the brain is composed of nerve fiber and myelin. In the brain and superficial spinal cord consist mostly glial cells and myelinated axons. That transmit signal from one region of the cerebrum to another. Myelin is essential part of the white matter, when myelin sheath is



damaged or disappear the conduction of impulses nerve slow down or fails completely. The color of white matter is Pinkish White.

Grey Matter: Pinkish grey color in the living brain.

Cerebral spinal fluid : It protecting the brain and spine from injury. The fluid is normally clear. It has same consistency as water. The test is also used to measure pressure in the spinal fluid.

Gaussian Process Hamiltonian Monte Carlo (GPHMC)

In the HMC, computing the Hamiltonian dynamics - requires a significant amount of model evaluations. To circumvent this difficulty, Epot is approximated with a Gaussian process [42]. During the initialization phase, the forward model is evaluated on a coarse grid to initialize the Gaussian process. During the exploration phase, the forward model is evaluated at locations of low Epot and high uncertainty on the Gaussian process interpolation (details can be found in [42]). HMC is then run using the Gaussian process interpolation of Epot to compute the Hamiltonian dynamics. Given that the Gaussian process well captures Epot, the GPHMC benefits from the high acceptance rate of the HMC, with far less model evaluations.

2.2 Overview of the proposed system

Initially MRI of a brain is taken as a input image. Then the image is converted into the combined feature vector, the noises are completely removed. Then the tumor clustered is analyzed and this show the segmented image. By using LBM, GPHMC the tumor spreaded area is identified. The features of an image is extracted. Based upon this identify whether the tumor is glioblasoma or non glioblastoma. This system provides the high accuracy compared to an existing system. In this system, mean, skewness, energy, entropy are important parameters. LBM helps to identify the tumor spreaded area in MRI of a brain. GPHMC helps to evaluate the accuracies of a tumor in the MRI of a brain.

2.3 Performance Evaluation

The performance of the process is measured by measuring the accuracy of the process. Performance of each classifier is measure in terms of confusion matrix, sensitivity, specificity and accuracy.

Sensitivity is a measure which determines the probability of the results that are true positive such that person has the tumor.

Specificity is a measure which determines the probability of the results that are true negative such that person does not have the tumor.

Accuracy is a measure which determines the probability that how much results are accurately classified.

$$\begin{aligned} \text{ACCURACY} &= (\text{TP} + \text{TN}) / (\text{FP} + \text{TN}) + (\text{TP} + \text{FN}) \\ \text{SENSITIVITY} &= \text{TP} / (\text{TP} + \text{FN}) \\ \text{SPECIFICITY} &= \text{TN} / (\text{FP} + \text{TN}) \end{aligned}$$

3. RESULTS AND DISCUSSION

The proposed system achieves high accuracy, low computational complexity and reduce the noises when compared to existing system. The proposed system was implemented in a matlab environment. The results of the system are given below. Figure 3.1 shows the Input MRImage used in MATLAB.



Figure 3. 1 MRI input

By the combined feature vector, the noises are completely removed. Figure 3.2 shows the texture feature vector.

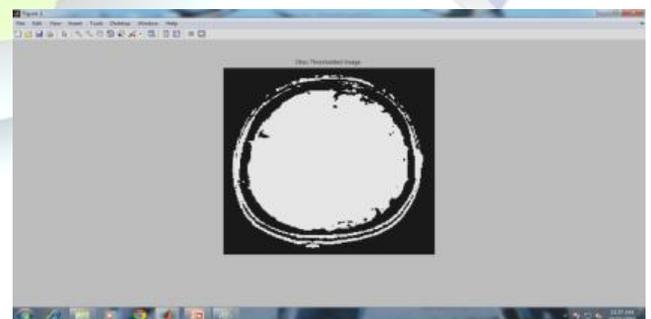


Figure 3.2 Combined Texture Feature Vector

After the combined texture feature extracted, the segmented area is identified correctly. Figure 3.3 shows the segmented tumor.

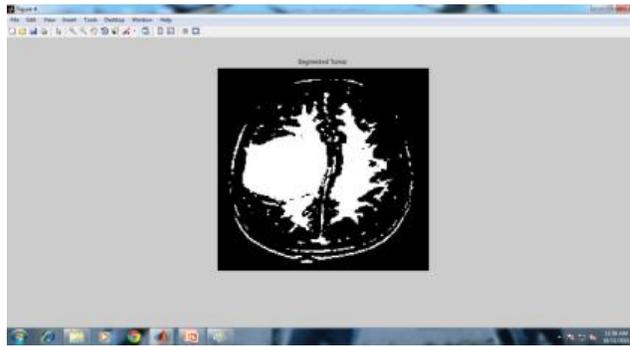


Figure 3.3 segmented tumor

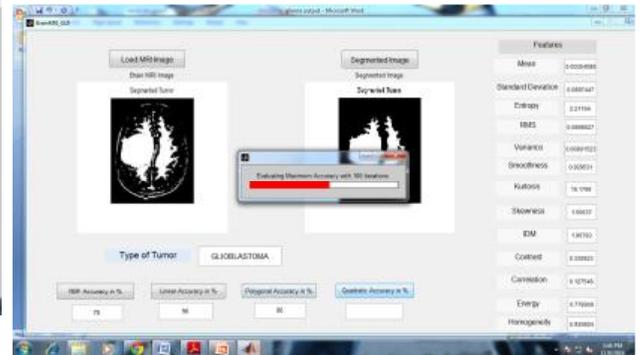


Figure 3.6 Evaluate accuracies of a MRI

The segmented tumor image must be saved as JPEG format. Load the segmented brain MR image and to display the particular segmented region.

Figure 3.6 evaluates the tumor accuracies in a MRI of a brain. After the feature extraction from MRI, the accuracies of a tumor in a brain is measured. Based upon the features and accuracies of a MRI of brain, identify whether the tumor is Glioblastoma or Non Glioblastoma tumor.



Figure 3.4 Pick an MRI

Figure 3.4 shows pick an MRI of a brain in a matlab environment. Import the saved jpeg image from the folder. Then the tumor can be identified. After the tumor identification measure the accuracies of a tumor spreaded area.



Figure 3.7 Non glioblastoma tumor

Figure 3.7 shows the non glioblastoma tumor. Based upon the feature extraction and the accuracies of a MRI of brain shows that the tumor is Non glioblastoma tumor.

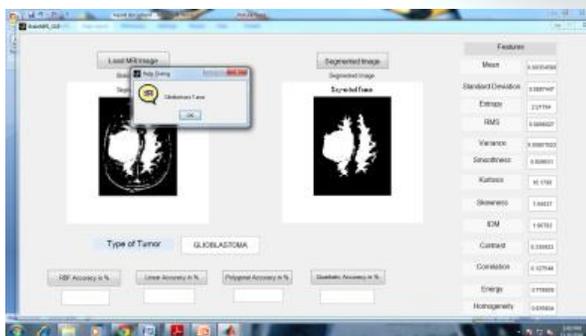


Figure 3.5 Glioblastoma tumor

This Figure 3.5 shows the glioblastoma tumor. In this the segmented tumor is imported and then measure the features of a MRI of brain. After feature extraction, Glioblastoma tumor is identified.

4. CONCLUSION

In this work, we presented an efficient implementation for the brain tumor growth based on the Lattice Boltzmann Method. We further presented estimation methods of the model's parameters of different levels of complexity. The proposed method is to identify tumor tissues accurately and identify the tumor tissues. The classification of the tumor tissue such as glioblastoma tumor and non glioblastoma tumor. The texture feature extraction is extract the values and segmented the brain images. The segmented brain MR image obtained the tumor area correctly. The system provides high accuracy and low computational complexity. In the future, we intend to apply the Bayesian personalization in order to explicitly take into account the



uncertainty in the expert's segmentation. More specifically, the segmentations used during each model evaluation could be sampled in the space of plausible segmentations [48]. We also believe that this work could be used for automatic personalized therapy planning. Some work has already been done on relating tumor growth models to radiation response models to better define radiation therapy plans [49], [50], [6]. Such a method could provide personalized therapy plans taking into account the uncertainty in the model's parameters.

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