

Quantitative MR Image Analysis for Brain Tumor

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Abstract. This paper presents an integrated quantitative MR image analysis framework to include all necessary steps such as MRI inhomogeneity correction, feature extraction, multiclass feature selection and multimodality abnormal brain tissue segmentation respectively. We first obtain mathematical algorithm to compute a novel Generalized multifractional Brownian motion (GmBm) texture feature. We then demonstrate efficacy of multiple multiresolution texture features including regular fractal dimension (FD) texture, and stochastic texture such as multifractional Brownian motion (mBm) and GmBm features for robust tumor and other abnormal tissue segmentation in brain MRI. We evaluate these texture and associated intensity features to effectively delineate multiple abnormal tissues within and around the tumor core, and stroke lesions using large scale public and private datasets.

1 Introduction

Accurate brain tumor segmentation is important for diagnosis, therapy, grading, and survival prediction. Because the current clinical practice of manual segmentation of tumors is time-consuming and tedious, automated or semi-automated method is required. However, the task of tumor and abnormal tissue segmenting is very challenging because of tissue heterogeneity, difference in shapes, sizes, types, and varying issue structures such as edema, necrosis, enhancing and non-enhancing abnormal tissues [1].

Abnormal brain tissues are known to have texture and intensity variations in MRI and, hence, the computer processing of these tissues needs features that are effective in capturing these variations. For example, the Gray-Level Co-Occurrence Matrix (GLCM) texture features have been used in [2, 3]. In [4] the authors use a combination of initial tissue probability and spatially non-local features such as the intensity difference, and the intensity between different MR image modality for segmentation. However, more effective features that target the complex and varying textures of brain tissues is still required.

This work discusses the effectiveness of using the stochastic multiresolution texture features along with random forest clustering in brain tumor segmentation and prediction. Medical images are known to have a degree of randomness associated with its spatial intensity distribution. This randomness allows the use of fractal texture modeling in order to measure the surface roughness in MR images. In addition, the uneven

growth and appearance of tumor in MRI further justifies the effectiveness of texture as a feature for abnormal brain tissue segmentation.

The method illustrated in this work combines features extraction and classification as illustrated in Fig. 1. We extract different spatially varying texture features such as piecewise triangular prism surface area (PTPSA), multifractional Brownian motion (mBm) and generalized multifractional Brownian motion (GmBm) along with other intensity features and then use these features for random forest (RF) classification of multiple abnormal tissues in brain MR imaging.

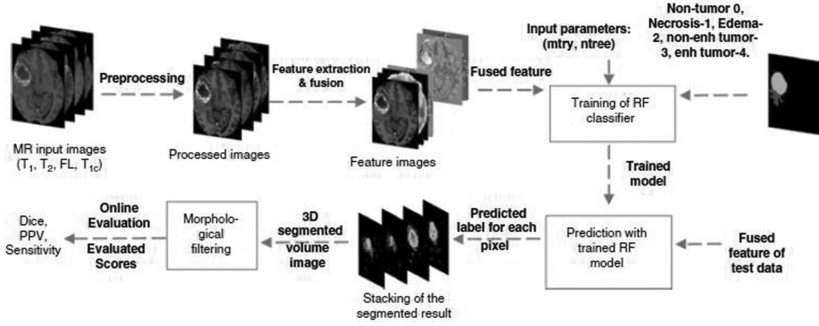


Fig. 1. General flow diagram for multiclass abnormal brain tissue segmentation [5]

2 Background Review

This work utilizes both static and spatially varying stochastic multiresolution texture features. The texture feature is estimated using Fractal Dimension (FD) using Eq. (1):

$$FD = E + 1 - H, \quad (1)$$

where E is the Euclidean dimension and H is Holder exponent. The value of Holder exponent gives an indication about the roughness of an object. For example, high values indicate a less roughness object. A detailed illustration and mathematical derivation can be found in [5]. Below we discuss different methods for FD-based texture feature extraction.

2.1 Piecewise-Triangular-Prism-Surface-Area (PTPSA)

PTPSA method is defined as the exponent of the number of self-similar objects, N , with magnification factor, $1/r$, into which a figure can be broken. In this method, an image first divided into $n \times n$, and each sub image into boxes of size $r \times r$. Then, the surface areas of the four triangles (as illustrated in Fig. 2) are calculated that are formed by the five intensity levels (p_1 , p_2 , p_3 , p_4 , and p_c). Then the FD is estimated by taking the slope of the log-log of the surface areas of the four triangles and the magnification factor ($1/r$). A detailed explanation of PTPSA is found in [6].

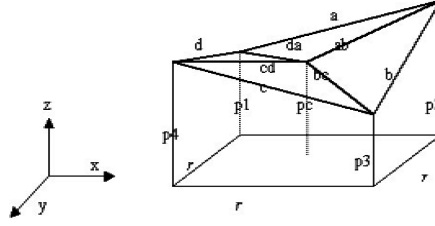


Fig. 2. Illustration of fractal PTPSA feature extraction for a sub-image [6]

2.2 Multi-fractal Brownian Motion (mBm)

Multi-fractal Brownian motion is a non-stationary Brownian motion with Holder exponent $h(t)$ and was first introduced in [7] where Holder exponent varies with time. The Brownian motion is a real random function with independent Gaussian increment with zero mean. In [5] the authors estimate $h(t)$ for mBm process using the variance method as follows,

$$2h(t) = \log \left(\frac{1}{N} \sum_{t_i=0}^{N-1} |W_x(t_i, a)|^2 \right) / \log(a), \quad (2)$$

where $W_x(t, a)$ is the wavelet transform of the mBm process $X(t)$ and a is the scaling factor.

3 Methodology

This section first obtains novel modeling of GmBm texture feature for abnormal brain tissue analysis in MRI. We then discuss the methods for brain tumor and stroke lesion analysis using texture and intensity features in MRI.

3.1 Generalized Multifractional Brownian Motion (GmBm)

In [8], the authors propose 1D generalized multifractional Brownian motion (GmBm) process in order to resolve the irregularity in the Holder exponent that mBm process may not resolve. This makes GmBm an excellent process to model a very complex data path such as a textured image. Also, GmBm may be treated as an extension of mBm process since CmBm is a locally asymptotically self-similar process with index (Holder exponent), $H(t)$.

To identify for the Holder exponent $H(t)$ for a GmBm model, a generalized quadratic variation meod is proposed [9]. The Generalized Quadratic Variation $V_N(t)$ of a discretized path $\{X(p/N); p \in \{0, \dots, N-2\}^d\}$, where $N \geq 2$ of a GmBm process $\{X(t); t \in [0, 1]^d\}$ is defined as,

$$V_N(t) = \sum_{p \in \tilde{v}_N(t)} \left(X\left(\frac{p+2}{N^\delta}, \frac{p+2}{N^\delta}\right) - 2X\left(\frac{p+1}{N^\delta}, \frac{p+1}{N^\delta}\right) + X\left(\frac{p}{N^\delta}, \frac{p}{N^\delta}\right) \right)^2; \quad (3)$$

where d is the dimension of the process $X(t)$, δ and γ are tuned and chosen such that $\delta - \gamma > 1/2d$ and $\gamma > \delta$, and the neighborhood $\tilde{v}_N(t)$ of the point t is given as,

$$\tilde{v}_N(t) = \tilde{v}_N^1(t_1) \times \dots \times \tilde{v}_N^d(t_d). \quad (4)$$

Here for all $i = 1, \dots, d$, we have,

$$\tilde{v}_N^i(t_i) = \left\{ p_i \in \mathbb{N}; 0 \leq p_i \leq N-2 : \left| t_i - \frac{p_i}{N^\delta} \right| \leq N^{-\gamma} \right\}. \quad (5)$$

Therefore, the Holder Exponent is given as,

$$H(t) = \lim_{N \rightarrow \infty} \frac{1}{2\delta} \left(d(1 - \gamma) - \frac{\log V_N(t)}{\log N} \right). \quad (6)$$

Figure 3 shows the proposed computational algorithm for computing the Holder Exponent $H(t)$ in MR images.

Algorithm

/ Initialization */*

Initialize δ and γ such that the two conditions $\delta - \gamma > 1/2d$ and $\gamma > \delta$ are satisfied

/ Assignment */*

For each block of image of size $N \times N$

For every point t in every dimension d

1. Determine the neighborhood $\tilde{v}_N(t)$ and its parameters $\tilde{v}_N^i(t_i)$ of each point t as indicated in “(4,5)”
2. Compute the variation $V_N(t)$ of the neighborhood $\tilde{v}_N(t)$ of point t using “(3)”
3. Compute $H(t)$ using “(6)”
4. Compute $FD = d + 1 - H(t)$

End

End

Fig. 3. Proposed computational algorithm for $H(t)$ in GmBm process

By choosing the right parameters, and applying the algorithm in Fig. 3 to a textured image such as MR brain tumor images, we obtain a novel feature that is useful in extracting tumors more precisely.

3.2 Brain Tumor Segmentation

We develop method [10, 11] for multiclass (edema, necrosis, enhance tumor, and non-enhance tumor) brain tumor segmentation in multimodality MRI (T1, T1C, T2, and FLAIR). Preprocessing step is needed before feature extraction for MR image. The preprocessing steps involve registration, resampling, re-slicing, skull stripping, histogram matching, and intensity inhomogeneity correction [12]. The intensity inhomogeneity correction method involves two main steps: 10 point histogram matching and intensity normalization with the mean value of the cerebrospinal fluid (CSF).

The stochastic multiresolution texture (mBm, PTPSA, and GmBm), regular texture (texton) [13] and intensity features are extracted from each preprocessed MRI modality. The selection of texture features captures both global and local characteristics of different tissues. Intensity features that represents normalized intensity of the four MRI modalities, and normalized intensity difference between the four MRI modalities are also considered. We then fuse all features to obtain a 3D feature matrix and then use the feature matrix for Random Forest (RF) Classification. The RF classifier is trained on a set of training dataset with known tissue (class) label to build the RF training model. RF is fast and efficient in handling multiclass classification problem [14]. Then we use this model to predict the class for test dataset. Figure 1 shows the complete pipeline for the brain tumor segmentation method.

3.3 Ischemic Stroke Lesion Segmentation

We also extend the brain tumor segmentation method discussed above into ischemic stroke lesion segmentation [15]. The lesion segmentation involves addition of a new feature; the structure tensor based local gradient. The method also includes addition of feature ranking and selection steps to the brain tumor segmentation method.

The structure tensor based local gradient [16] uses the local gradient information of an image in order to determine the structure tensor at each pixel of the image. These tensor values may indicate a uniform region, a corner or an edge. Feature selection using minimal-redundancy-maximal-relevance [17] criterion (mRMR) is applied in order to search features that have the largest dependency on the target class and the minimal redundancy.

4 Experimental Results

Figure 4 show an example of segmented tumor using the brain tumor segmentation method as illustrated in Fig. 1. In this example, 2 textures features (PTPSA, and mBm) are used along with other intensity features in the segmentation.

We evaluate our abnormal tissue segmentation method by performing a study using BRATS-2013 [18] and BRATS-2014 [19] datasets. The first study uses 213 cases from BRS-2014 and 20 cases from BRATS-2013, respectively. We train RF classifier using BRATS-2013 cases and test using BRATS-2014 cases. The average scores varies from 63%–76% using Dice overlap metric for tumor core and complete tumor, respectively. This result shows that our segmentation method is very promising, and offer

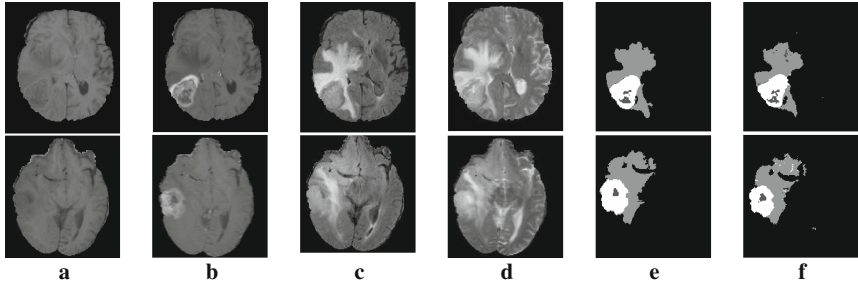


Fig. 4. Segmented tissues with corresponding input and ground-truth images. Input: a T1, b T1contrast, c Flair d T2, e ground-truth, f Segmented image. Labels in the ground-truth: 1 - necrosis, 2 - edema, 3 - nonenhance tumor, 4 - enhancing tumor, 0 - everything else

comparable performance when compared with state-of-the-art works proposed in BRATS challenges [18].

In the second study, we perform tumor segmentation using three texture features (PTPSA, mBm, and GmBm) along with other intensity features. In this study, we use cases from NIH's TCGA-GBM collection [20, 21] for training and testing. We use 10 patients for training and 33 patients for testing. The average classification scores varies from 63%–59% using Dice overlap metric for tumor core and complete tumor,

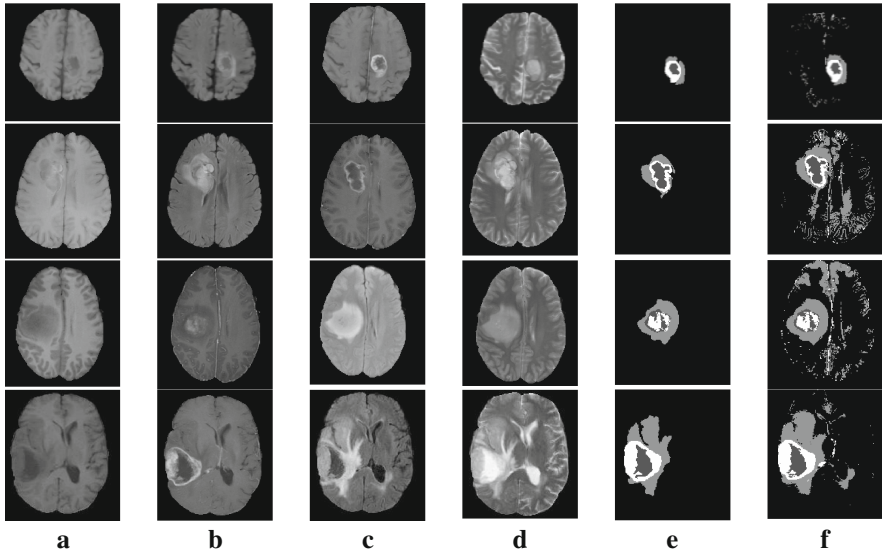


Fig. 5. Segmented tissues with corresponding input and ground-truth images. Input: a T1, b T1contrast, c Flair d T2, e ground-truth, f Segmented image. Labels in the ground-truth: 1 - necrosis, 2 - edema, 4 - enhancing tumor, 0 - everything else

Table 1. Dice overlap of using different types of multiresolution texture features in Brain Tumor Segmentation in Fig. 1

Method	Testing dataset (# of cases)	Training dataset (# of cases)	Tumor core dice	Complete tumor dice
Brain tumor segmentation (using mBm and PTPSA)	BRATS 2014 (213)	BRATS 2013 (20)	63%	67%
Brain tumor segmentation (using mBm, PTPSA, and GmBm)	TCGA-GBM collection (33)	TCGA-GBM collection (10)	63%	59%

respectively. Note that the dice overlap metric is evaluated before doing any post-processing in this study. Figure 5 shows examples of the results when using these three types of texture features. Table 1 shows the dice overlap for both the first and the second study.

In the third study, we evaluate ischemic stroke lesion segmentation method using 28 patients from ISLES-2015 SISS training dataset [22]. Across cross-validation shows an average dice overlap of 59%. In addition, our performance using the ISLES-2015 SISS testing datasets is very promising when compared to others state-of-art works in the ISLES 2015 challenge with a dice overlap of 43% [22]. Table 2 shows the average dice overlap for training and testing in the ISLES 2015 challenge.

Table 2. Average dice overlap for ISLES 2015 challenge

Method	Dataset (no. of cases)	Average dice
Lesion segmentation	ISLES-2015 SISS training dataset (28)	59%
Lesion segmentation	ISLES-2015 SISS training dataset (33)	43%

5 Conclusion

We discuss a novel stochastic multiresolution texture feature model for robust brain tumor and abnormal lesion segmentation. Different types of static and dynamic fractal texture features and intensity features are extracted. These features are fused using a RF classifier. In order to evaluate the effectiveness of our fractal features, we test our method on multiple large-scale publicly available clinical dataset known as BRATS and ISLES. We use both low grade glioma (LGG) and high grade glioma (HGG) patient data to show the efficacy of our method. The results show that our brain tumor segmentation performance is comparable with state-of-the-art works. Using BRATS 2013 and 2014 for training and testing, we achieved an encouraging results of an average dice overlap of 63% and 76% for tumor core and complete tumor, respectively. Adding another fractal feature (GmBm) to the brain tumor segmentation, results in dice overlap of 63% and 59% on the average for tumor core and complete tumor, respectively. Extending the brain tumor segmentation method into ischemic stroke lesion segmentation involves adding new feature and additional step for feature selection. The result of our ischemic stroke lesion segmentation with an average of dice overlap of

43% is reassuring, especially when compared to others state-of-art works. In future work, we plan to explore more predictive and specific texture features that characterize tumor microenvironment in the brain. In addition, we would like to study inherently 3D features that may characterize the variation of the whole 3D patient volumes.

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