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Image Segmentation for Early Stage Brain Tumor Detection using Mathematical Morphological Reconstruction

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Abstract

This study proposes a computer aided detection approach to diagnose brain tumor in its early stage using Mathematical Morphological Reconstruction (MMR). Image is pre-processed to remove noise and artefacts and then segmented to find regions of interest with probable tumor. A large number of textural and statistical features are extracted from the segmented image to classify whether the brain tumor in the image is benign or malignant. Experimental results show that the segmented images have a high accuracy while substantially reducing the computation time. The study shows that the proposed solution can be used to diagnose brain tumor in patients with a high success rate.

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Keyword: Brain Cancer, Accuracy, Processing Time, Segmentation

1. Introduction

Computer aided detection (CAD) of brain tumor is a preferred tool for non-invasively diagnosing brain tumor [1]. The brain images are obtained using Magnetic Resonance Imaging (MRI), which are prone to noise and artefacts such as labels and intensity variations during acquisition [2]. In addition, there are many structures in the brain image such as cerebrospinal fluid, grey matter, and white matter and skull tissues apart from the tumor [3]. A generic CAD brain tumor detection process follows the following steps: pre-processing the image to remove noise

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and artefacts, segmenting the pre-processed image to identify possible tumor regions, extracting useful features from the tumor regions and classifying whether or not tumor is present [4]. Different segmentation techniques have used to diagnose the brain cancer that are watershed segmentation [5, 6, 7], mathematical morphology [8], Fuzzy C-means and neural networks [1]. Despite certain advantages, the most common problem with prevalent techniques is their inability to predict brain tumor with high accuracy. The purpose of this study is to address the aforementioned limitations in existing methods– to improve the accuracy of brain tumor detection using image processing tools and to reduce the computation time of the steps involved so that a brain MRI image can be identified as malignant or benign in the least computation time possible.

2. Literature Review

Initially, the brain MRI image is pre-processed to remove noise, labels, compensate for intensity variations and strip skull tissues [2]. The pre-processed image is then segmented into regions of interest (ROI) – regions with probable tumor. Following this, different kinds of features are extracted from the segmented image. The number of features extracted is large which increases processing time and storage needs during the following stage. Hence, only the most useful features are retained [7]. The features are then sent to the classification process to determine whether or not they contain tumor. This process is repeated for a large number of brain MRI images in a data set. The performance of classification over all these images is then evaluated for accuracy and processing time [9].

Image acquired using MRI is affected by noise and artefacts that need to be removed before the image is processed to determine whether or not it has tumor. The preferred tool to filter noise in MRI brain images is the median filter, in which the value of a pixel is substituted by the median of the intensity values in its immediate neighbourhood [10]. Compared to other filters, this filter preserves edges in an image while at the same time it does not smoothen or blur the image.

Segmentation is the process of partitioning the image into mutually exclusive regions, with each region being spatially contiguous and containing pixels that are homogenous based on pre-defined criteria or [11]. In a brain MRI image, brain tumor tissues such as solid or active tumor, edema and necrosis need to be separated from normal brain tissues such as grey matter, white matter and cerebrospinal fluid [4]. Unsupervised segmentation techniques such as Fuzzy C Means (FCM) and Active Contour Model are adopted because image sets with ground truths are not [12]. Owing to its sensitivity, spatial FCM algorithm [10] is used. Among all the other segmentation methods available, the one that is the most efficient in extracting tumor regions more accurately in the least possible processing time is the mathematical morphological method. [13].

Features need to be extracted from the image to know whether or not there is a tumor in the image. The number of features identified is generally big which makes the classification process expensive in terms of processing time and memory [1]. Hence, the number of features are generally reduced using a feature reduction process [5]. Previous studies have extracted features using the Discrete wavelet transform (DWT), which has the advantage of being independent of image segmentation and availing information in both frequency and time scales [1]. Other studies use Gabor wavelet features, which are however limited to capture only the local structures of the MRI image such as frequency, localization and orientation [6]. Likewise, a number of authors have suggested using first order statistical features, grey level co-occurrence matrix features and grey level run length matrix features [6][7]. For the purpose of reducing the number of features, most of the authors have suggested to use the Principal Component Analysis (PCA), in which input features are transformed to interrelated variables while maintaining the variations among the input features [4], [6].

Classification is the process of classifying whether or not the input image has tumor by using the features extracted. A growing trend has been to use the neural network for classification purpose [1]. In another study, combinations of BPNN and Support Vector Machine (SVM) with kernel function have been used to obtain an accuracy of 85.4% [12]. However, this is a very low rate to be used under clinical conditions. In general, neural networks take a long training time and have parameters that need to be individually tuned. The limitations of neural networks can be overcome by using Support Vector Machine (SVM), the use of which does not need parameters to be tuned. In addition, the solutions obtained using SVMs are unique and global [6] [7].

After classifying a number of brain MRI images to be benign or malignant in a data set, the classification results have to be evaluated. The most common tool for evaluation is the accuracy with which the tumor is diagnosed. Accuracy is defined as follows [1]:

$$\text{Accuracy} = ((\text{TP} + \text{TN}) / (\text{TP} + \text{TN} + \text{FN})) * 100\% \quad (1)$$

TP: If the prediction is true (tumor) and the ground truth is true (tumor) as well, then the image has brain tumor.

FP: If the prediction is true (tumor) but the ground truth is false (healthy), then the image does not have tumor.

FN: If the prediction is false (healthy) and the ground truth is true (tumor), then the image is false negative.

TN: If the prediction is false (healthy) and the ground truth is false (healthy), then the image is false positive.

A high accuracy means that the MRI images have been classified correctly and hence, the CAD algorithm is good.

The computation time, which is the sum of the time required for image processing, segmentation, features extraction, features reduction, classification and evaluation, is another evaluation criterion [10]. The computation or processing time should be as less as possible without affecting the accuracy of classification.

Among the existing solutions, the proposed method by Dandil that uses median filter for pre-processing, sFCM for segmentation, first order statistical and textural features for feature extraction, Principal Component Analysis for feature reduction and SVM with non-linear kernel is considered the current best solution [10]. It will henceforth be abbreviated as MSFPS in this paper. The median filter used in de-noising images provides the advantage of preservation of edges and limited blurring. Likewise, first order statistical features and grey level co-occurrence matrix textural features are known to have defined features that can be computed with small computational cost. Furthermore, the number of features extracted can be reduced by transforming them into variables that preserve the inter-feature variance using Principal Component Analysis. Finally, owing to tuning by a non-linear GRB kernel and the possibility of providing a unique and global solution, Support Vector Machine is the most efficient and accurate classifier. The only stage of failure of the MSFPS solution is the segmentation process. Spatial FCM, used in the MSFPS solution to segment pre-processed image into regions of interest, is a very sensitive process that takes into account spatial pixel information in the MRI image. However, this method does not always produce a standard segmentation result as it is dependent on the random nature of initial membership values provided when the method is launched. In addition, this method only considers image intensity and hence, produces unsatisfactory segmentation accuracy in noisy images [1]. Lastly, since this method is iterative in nature, it takes a long computational time [1].

3. Proposed Model

A new solution to detect brain tumor in its early stage is proposed. The stages involved in this solution and the corresponding tool for each stage is given below:

- a. Image pre-processing using median filter
- b. Segmentation of the pre-processed image using mathematical morphological operations
- c. Feature extraction and reduction (extraction of first statistical features and textural features)
- d. Features reduction using principal component analysis
- e. Classification using Support Vector Machines with GRB kernel
- f. Evaluation of the classification

The proposed solution substitutes the segmentation approach, while employing the same techniques for the other stages. The proposed solution will henceforth be abbreviated MMFPS. As has already been established, each of the techniques used in the other stages have many advantages over competing techniques. It is only the sFCM algorithm used in the segmentation stage in the MSFPS solution that has limitations which need to be overcome.

The proposed method, mathematical morphology based segmentation, overcomes all the shortcomings of the sFCM algorithm. It always produces the same segmentation result as it is independent of any initial membership values. The segmentation accuracy is high as the effect of image intensity is minimized. Finally, since simple, fast and standard morphological operations are used, the proposed segmentation algorithm takes much less computational time [8].

A detailed block diagram of the MMFPS solution is shown in figure 1. The block diagram depicts the enhanced stage and the limitations it has overcome in green.

3.1 Strength of the Proposed Segmentation Method

The accuracy of segmentation can be realized from a high peak signal to noise ratio (PSNR). PSNR is calculated as follows:

$$\text{PSNR} = 10 \log_{10} (R^2 / \text{MSE}) \quad (2)$$

Here, for an 8-bit unsigned integer data type, $R = 255$. MSE stands for the mean square error. For an original image, and a reconstructed image, the MSE is calculated as follows:

$$\text{MSE} = \left[\frac{1}{MN} \right] \sum_{x=0}^{M-1} \sum_{y=0}^{N-1} [F(x, y) - \hat{F}(x, y)]^2 \quad (3)$$

An input image with a high segmentation accuracy has a high PSNR in the extracted regions of interest. The PSNR can be increased by decreasing the MSE, which in turn can be reduced by lowering the difference between the input image and the reconstructed image. Hence, in order to get a high accuracy, the reconstructed image (with regions of interest) should preserve the structures present in the input image.

Compared to the segmentation method sFCM used in the MSFPS solution, the proposed segmentation method of mathematical morphological operations better preserves the structures in the segmented image. As a result, this leads to better accuracy. In terms of computation time, the proposed mathematical morphological operation involves only a few steps, each of which only takes a few seconds, and is as a whole, faster than the iterative approach used in sFCM.

3.2 Proposed Algorithm

The brain MRI image is first pre-processed using median filter to remove noise, artefacts and labels. Skull tissues might be stripped by a skull stripping method. Following this, the image is subjected to segmentation. This proposed segmentation approach involves the following steps:

- A normalised global threshold is found and the brain MRI image is converted from grayscale to binary.
- The resultant image is opened by reconstruction. This process involves identifying an appropriate structuring element, determining the size of the structuring element and using the structuring element to obtain an eroded image.
- The resultant image is then morphologically closed. In this process, an appropriate structuring element is identified, its size is fine-tuned and a closed image is obtained.
- Finally, the reconstructed and morphologically closed images are multiplied to obtain a segmented image.
- The algorithm for the segmentation process is shown below and the proposed solution is given in figure 1.

Algorithm: Mathematical morphology for segmentation

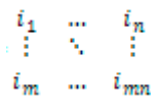
Input: Pre-processed MRI brain image,

Output: Segmented image, $I_{m \times n}$

BEGIN

Step 1: Read $I_{m \times n}$ and capture the grey values in a matrix form

$I_{m \times n} =$



Step 2: Convert grayscale image $I_{m \times n}$ into binary image $B_{m \times n}$ using a normalised global threshold level between 0 and 1.

For

For $i = 1$ to n with intervals of 0.1

Get binary image

Obtain $B_{m \times n}$ with the optimal

Step 4: Perform opening by reconstruction

Obtain an eroded image $E_{m \times n}$ by fine tuning the radius of disk structuring element (SE) for erosion.

For

For $i = 1$ to n with intervals of 1

Get eroded image

Obtain $E_{m \times n}$ with the optimal

Perform dilation to obtain a dilated image $D_{m \times n}$ from

and

Step 5: Perform morphological closing

Obtain a closed image $C_{m \times n}$ by fine tuning the length of a square structuring element (SE) for closing.

For

For $i = 1$ to n with intervals of 1

Get closed image

Obtain $C_{m \times n}$ with optimal

Step 6: Multiply $C_{m \times n}$ and $E_{m \times n}$ to obtain $I_{m \times n}$.

END

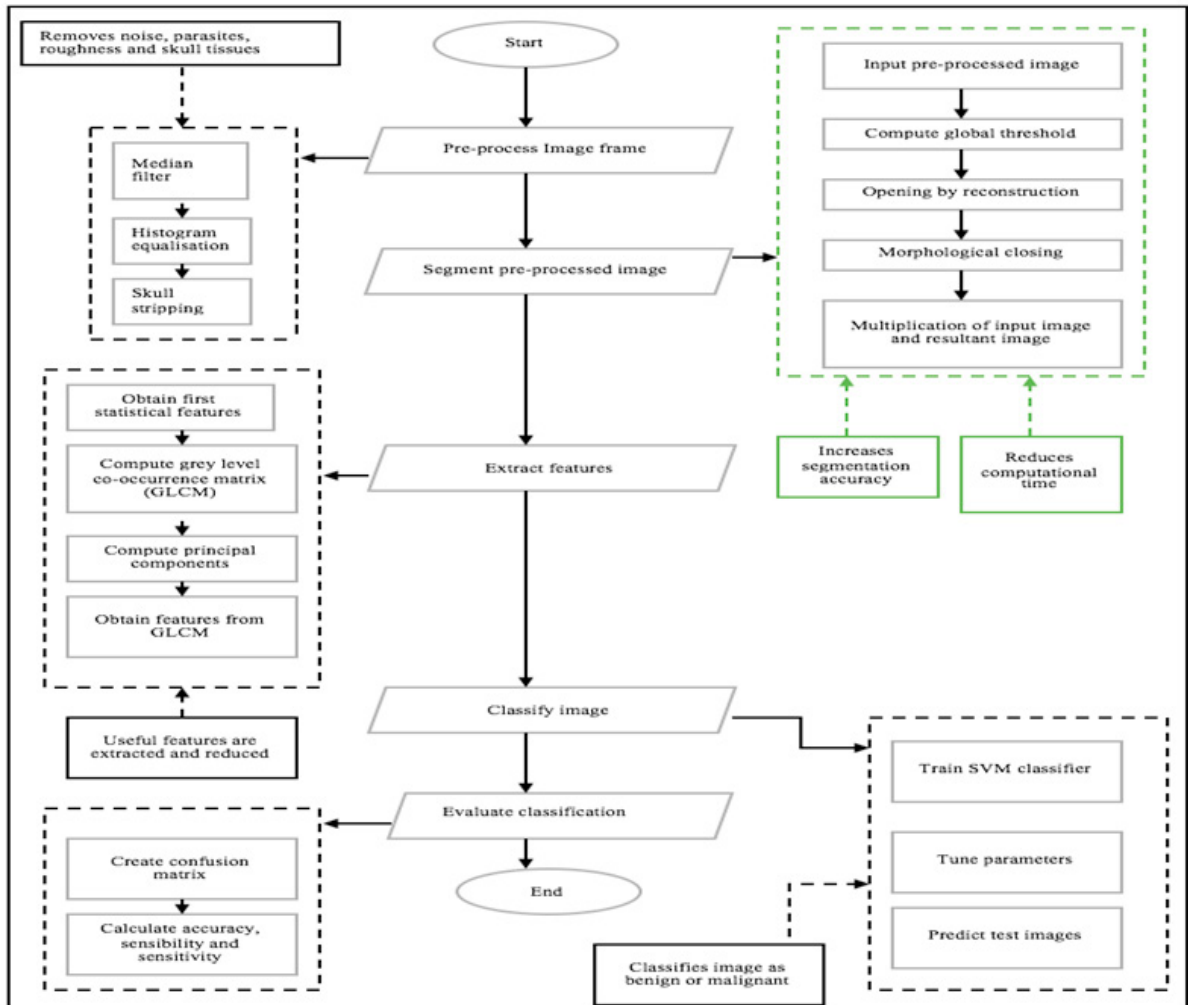






































Fig. 1. Proposed Solution






















4. Implementation

The proposed segmentation method is implemented in a set of 19 brain images affected by four different types of tumor - Glioma, Metastatic_Adenocarcinoma, Meningioma and Sarcoma. The size of tumor can be big, small or large. After pre-processing the image using median filter, the proposed segmentation algorithm is applied on the image. A result of segmentation for Glioma images is displayed in Table 1. The implementation is done in MATLAB 2016a.

The current best model has no satisfactory result of accuracy and does not classify degree of cancer of detected nodules. Therefore new system is proposed. The proposed system is used to detect the cancerous nodule from the lung CT scan image using watershed segmentation for detection and SVM for classification of nodule as Malignant or benign. Proposed model detects the cancer with 92% accuracy which is higher than current model and classifier has accuracy of 86.6%. Overall, we can see improvement in the proposed system in comparison to current best model. However, this proposed does not classify into different stages as stage I, II, III, IV of cancer. Therefore, as future scope improvement in this can be done by implementing classification in different stages. Also, further accuracy can be increased by proper pre-processing and eliminations of false objects.

Table 1. Segmentation Results of Proposed and Current Solution

Segmentation results							
		Proposed Solution			Current Solution		
Tumor size	Input Image	Segmented Image	PSNR[dB]	Computation time [s]	Segmented Image	PSNR[dB]	Computation time [s]
Group 1 – Glioma							
Small			27.26	0.07		26.06	0.7
Small			26.24	0.06		25.95	0.7
Medium			26.94	0.05		26.75	0.7
Medium			27.89	0.06		27.76	0.8
Large			27.89	0.05		27.73	0.8
Large			27.86	0.06		27.41	0.8
Group 2 - Metastatic_Adenocarcinoma							
Medium			24.95	0.05		24.75	0.7
Medium			24.75	0.06		24.04	0.7
Group 3 - Meningioma							
Medium			26.65	0.06		26.01	0.7
Medium			26.55	0.06		26.03	0.7
Large			26.64	0.05		25.9	0.6
Large			26.43	0.07		26.08	0.7
Group 4 - Sarcoma							

Small			25.95	0.06		24.52	0.7
Small			26.89	0.07		25.28	0.8
Small			26.67	0.07		25.32	0.8
Small			26.93	0.07		25.53	0.8
Small			27.90	0.06		26.49	0.8
Small			27.99	0.06		26.58	0.7
Small			25.93	0.07		24.83	0.6

Group 1 is a collection of Glioma images. It can be observed that the PSNR of the segmented image using the proposed segmentation method is superior to that the one in the MSFPS solution. However, as the mass of tumor increases, the difference in PSNR values reduces as well. This can be attributed to the fact that regions of heavy tumor cannot easily be differentiated by the proposed method.

It can further be observed that the computation time of the proposed method is roughly about ten times better than the MSFPS solution. This can be attributed to the iterative nature of the MSFPS solution, which makes the computation expensive. In contrast, the proposed method only has a few morphological steps which are non-iterative and quick to compute. The same pattern can be found in brain tumor images of other types as well.

The average PSNR value for each of the four brain tumor types, arrived using proposed method and current best method. It is clear that the average PSNR value of the proposed method beats that of the MSFPS solution. For Glioma, the difference in PSNR between proposed and current systems is less than that of other diseases. This can be attributed to the presence of tumors with large masses in Glioma images. Hence, the MMFPS solution is not as effective in differentiating tumor with large mass as it is with smaller mass.

The average computation time of the four types of brain tumor, using the proposed MMFPS and current best MSFPS solution. It is clear that in all the cases, the proposed method beats the MSFPS solution by a factor of 10. This is owing to the few, simple computation steps (reading image, converting to binary, eroding, dilating and multiplying) involved in the proposed method when compared to the iterative manner of the MSFPS solution.

6. Conclusion

The purpose of the research was to propose a new method to diagnose brain tumor in its early stage using brain MRI images. Among the available solutions, a solution that implemented a median filter for pre-processing, spatial Fuzzy C-Means for segmentation, first statistical features and textural features for feature extraction, Principal Component Analysis for feature reduction and Support Vector Machine with non-linear kernel for classification was found to be the most effective. Owing to the limitations in the segmentation method such as poor accuracy and high computational cost, an alternative method for segmentation, which addressed these two limitations was proposed. The proposed segmentation method which utilized mathematical morphology for segmenting the pre-processed image produced superior accuracy in the segmented images and a ten-fold decrease in the computation time.

One limitation is that the proposed solution has not been tested up to the evaluation stage, to compare with current best solution. Since the other methods after segmentation are the same for the remaining stages (feature extraction, feature reduction and classification), it can be expected that the proposed method will give a superior classification accuracy. However, this still needs to be implemented. This is one direction that the research should be continued with. Another major limitation is that the proposed solution has not been tested in a large data set with an abundance of variations. Since the sample size on which the proposed solution has been implemented is small, the positive result obtained could have been skewed. Hence, this is another direction in which future research should be carried out – testing if the proposed solution works on MRI images acquired using different types of machines in different parts of the world with different types of brain structures.

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