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

B. Devkota[a], Abeer Alsadoon[a], P.W.C. Prasad[*a], A. K. Singh[b], A. Elchouemi[c]

[a]School of Computing and Mathematics, Charles Sturt University, Sydney, Australia
[b]Department of Computer Applications, National Institute of Technology, Haryana, India
[c]Walden University, USA

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

*Corresponding author
E-mail address: CWithana@studygroup.com

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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].