

An Efficient Segmentation and Classification of MRI Brain Images to Identify the Damage Area

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Abstract

Both computational intelligence and pattern recognition include brain damage segmentation and classification as essential components. In this procedure, an effective algorithm was used to segment the damaged area and extract the data from the images using characteristics like GLCM. Based fuzzy C-means clustering technique (M-FCM) is suggested for clustering during the segmentation process. In order to categorise the severity of the brain input, a procedure to identify brain lesions is used in the medical area, along with a way to classify its characteristics using KNN. The major goals of this method are to locate the malignant area on an MRI of the brain and to categorise the severity of that brain in order to increase process efficiency.

Keywords: GLCM, KNN, malignant, efficiency, clustering

1. Introduction

A tumour is an unchecked cell proliferation in any area of the body. There are several forms of tumours, each with unique traits and therapies. Brain cancers are currently divided into two categories: Unlike the former, which begin inside the brain and have a tendency to remain there, the latter develop as a cancer elsewhere inside the body before spreading to the brain. One of the key steps in planning of surgery and treatment is brain tumour segmentation. An active field of study has been utilising MRI to segment brain tumours. Brain tumours can occur anywhere in the brain and come in a variety of sizes and forms. The automated segmentation of tumours is quite difficult because of the fluctuating intensity of tumours in brain magnetic resonance imaging (MRI). Tumor segmentation on magnetic resonance imaging has been proposed using a variety of intensity-based approaches. One of the most used features for picture categorization and retrieval is texture. The best textural characteristics of a brain tumour are retrieved from the MRI images of the brain using the FCM and JAYA algorithm technique. After classifying the tumour and non-tumor tissues using these techniques, the tumour is segmented. When compared to segmentation techniques based on current practises, this technology segments brain tumours more effectively and yields more accurate results. The abnormal development of tissues is a tumour. A brain tumour is collection of unneeded cells that is accumulating in the central canal of the brain. Tools and techniques for analysing tumours and their behaviour are becoming increasingly commonplace nowadays. Undoubtedly, the last century's efforts have resulted in significant advancements. But we've also come to understand that improvements in diagnostic tools are necessary to maximise survival benefits. Though a cure for brain tumours has not yet been found, significant progress has been made in this direction. A growing number of scientists have incorporated metrics in clinical studies, and each new development gives hope to the healthcare professional and, more crucially, the individuals with this diagnosis. Particularly in brain imaging, where MRI's soft tissue contrast and non-invasiveness are obvious benefits, magnetic resonance imaging, or MRI, has grown to be a frequently utilised technique for high-quality medical imaging.

Monitoring the size of a brain tumour as it reacts to therapy is a significant application of MRI data. Consequently, a helpful tool would be an automated and trustworthy way for segmenting tumours. A computerised depiction of tissue properties that may be acquired in any tissue plane is provided by MRI. The easiest way to explain the pictures created by an MRI scanner is as slices across the brain. The ability to produce images that traverse the brain in horizontal as well as vertical planes is an additional benefit of MRI. This makes the MRI-scan pictures a perfect source for locating, categorising, and detecting the right brain areas that are affected. The majority of existing conventional diagnosis methods rely on human judgement when evaluating the results of an MRI scan; undoubtedly, this raises the risk of incorrectly detecting and identifying a brain tumour. However, using digital image processing guarantees the early and accurate diagnosis of the tumour. The segmentation procedure is one of the best ways to extract data from intricate medical pictures, and it is widely used in the medical industry. Picture segmentation's fundamental goal is to separate an image into spatially

contiguous, mutually exclusive, exhausted portions, every one of which includes pixels that are homogenous with respect to predetermined criterion. Most instances lack an identified cause. Genetic syndromes such the Epstein-Barr virus, neurofibromatosis, exposure to the chemical vinyl chloride, and ionising radiation are some conditions that may occasionally exist.

The most effective method for identifying brain tumours and tracking their progress after therapy is magnetic resonance imaging (MRI). To tackle the complexity, time and objectiveness restrictions, many MRI modalities of each patient are obtained. Computer-based image analysis algorithms are then used to process these images. This thesis presents two key unique methods for automatically assessing tumor-bearing brain images: To offer quantitative volumetric information, multi-modal tissue categorization with integrated regularisation may distinguish between normal and diseased brain tissues, encompassing their sub-compartments. The technique has been tested on several clinical and artificial pictures with positive outcomes. The algorithm's quick run-time makes it simple to include into the clinical work flow. A modest dataset from a multi-center clinical study was used to test the feasibility of a suggested extension for integrated segmentation of longitudinal patient studies. The findings were encouraging. It has been demonstrated that segmenting the healthy brain regions surrounding the tumour using atlas-based segmentation with integrated tumor-growth modelling is an effective method. A solution to deal with the missing tumour from the atlas during registration is provided by tumor-growth modelling. Two alternative tumor-growth models have been contrasted for this purpose.

A more complex multi-scale tumour development model demonstrated superior ability to give a more genuine and relevant prior for atlas-based segmentation, even if a simpler tumour growth model had advantages in computing performance. A comprehensive framework for assessing tumor-bearing brain pictures has been created by combining both methods and employing all of the imaging data that is often accessible in clinics. This segmentation approach paves the path for improved brain tumour radiation and neurosurgery diagnosis, planning, and monitoring.

2. Literature Survey

In this article, we offer a technique for analysing PAP smear images based on segmentation using histograms and structuring elements as well as a size and shape analysis of the cell nuclei. As was previously indicated, human observation is not always accurate, and according to Marroquin, 61.5% of accessible pathological tests that are manually screened are still unclassified. This study proposes a method for analysing PAP smear pictures of the cervical area based on an examination of the distribution and size and shape of the cell nuclei. An effective and simple approach to find any abnormalities in cervical cells is the PAP smear test. However, analysing a lot of PAP smear photos by hand is a laborious operation and human inspection is not always gratifying. This study's objectives include automating the screening procedure and providing detailed statistical information that will be useful in identifying anomalies in the cervical area. It is possible to programme MATLAB to discriminate between normal and suspect cervical cells by examining the distribution of cell nuclei and taking into consideration aspects of form and size [1].

This study was started in order to make a contribution to the field by identifying and maximising the presence of cancer cells in lungs. When cancer patients are treated when it is still treatable, there are not only more treatment choices accessible, but also higher survival rates. One of the most common and major causes of mortality globally is lung cancer. It has the lowest survival rate following diagnosis and is the second most chronic condition in both men and women. Therefore, it is essential to forecast and diagnose lung cancer at an early stage. The different methods for detecting lung cancer nodules were compared in this study along three dimensions, encompassing imaging modalities, image processing methods, and genomics analysis. In order to identify lung nodule cancer using medical imaging, many existing image processing approaches have been compared. Additionally, genetics is a major factor in the emergence of lung cancer. A summary of the genetics structure with prospective genes for lung cancer diagnosis and risk assessment was also provided [2].

As the increase in automatic breast cancer diagnosis utilising image processing, we are going to provide a wonderful approach to identify breast cancer stem cells for an image in this work. A crucial diagnostic imaging method to identify brain cancer earlier is Magnetic Resonance Imaging. Among the most deadly illnesses that affect people frequently is brain cancer. If the cancer is discovered in its early stages, the prospects of survival can be boosted. Radiologists rely heavily on MRI brain images to access patients for diagnosis and therapy.

Radiologists must spend a lot of time and effort studying medical images, also their accuracy varies according to their level of expertise. This study discusses the merits and limitations of the many existing approaches of segmenting brain images through automated algorithms that are precise and require little user input. This review article offers advice on how to combine two or more procedures to reach an accurate outcome [3].

In this study, the threshold operation, watershed segmentation, and morphological operation are used to identify cancer cells. The cancer cell will be found when the picture has been analysed using morphological methods. One of the most complex and developing areas of study nowadays is medical image processing. Magnetic Resonance Imaging processing is among the components of this area. Multispectral MRI has become a viable replacement to ultrasound (US) imaging in recent years for accurate identification of liver, breast, prostate, and other organ cancers. Physicians believe that the most effective imaging technique for identifying cancer existing in multiple organs is magnetic resonance imaging (MRI). As a result, MR imaging analysis is necessary for accurate illness diagnosis. This suggested approach includes some noise reduction, segmentation, and morphological functions, which are thought to be the fundamental elements of image processing. Using the MATLAB programme, cancer cells are found and extracted from MRI prostate images [4].

The goal of this job is to identify any cancer cells that may be present in a bodily component. The procedure involves taking a digital image of the afflicted region and processing it to provide morphologic patterns that distinguish between normal and cancer cells. Early diagnosis of cancer illness is a challenging issue since it can be lethal if it is not discovered in the early stages. The current medical treatments that are utilised to identify cancer in body parts are laborious and need additional laboratory work. The goal of this job is to identify any cancer cells that may be present in a bodily component. The procedure involves taking a digital photograph of the afflicted region and processing it to create a morphological pattern that distinguishes between normal and cancerous cells. The method is distinct from ocular inspection and the biopsy procedure. Image processing enables the high-resolution representation of cellular structure. Purpose of this work is to use image processing techniques to take advantage of the variations in cellular organisation between malignant and normal tissue, enabling automated, quick, and accurate diagnosis [5].

3. Proposed System

In the current system, a unique approach for interactive multi-label segmentation of N-dimensional pictures is described. A Cellular Automaton automatically segments the remaining portions of the image given a small sample of user-labeled pixels. The procedure is iterative; while the automaton labels the picture, the user may see the progress of the segmentation and direct the algorithm with human input in areas where the segmentation is challenging to calculate. There is no further human effort needed in the sections where segmentation is consistently computed automatically. Results of separating stock photographs from medical images are shown. This technique could only be used to enhance tumours with distinct enhancing edges. The fact that graph-based approaches are difficult to adapt to multi-label tasks is one of its few limitations. Additionally, they are not particularly adaptable. The cost function coefficients and graph weighting are the only variables that may be changed. This technique could only be used to enhance tumours with distinct enhancing edges. These are a few of the approach's drawbacks. The system put out a brand-new, semi-automatic segmentation technique based on collective and individual statistical data to separate brain lesions in magnetic resonance (MR) pictures. The morphologically based FCM is used to evaluate the likelihood that each pixel is in the foreground (tumour) or background. These probabilities are built into a feature extraction algorithm based on GLCM, which then extracts the features from the picture. Realizing that the fully or partially automated segmentation and classification techniques are actually techniques for segmenting regions is simple. The following is a list of the suggested approach's benefits:

- The zones with the identical characteristics that we describe may be appropriately separated using this approach.
- This technique may deliver the original photos with crisp edges and effective segmentation outcomes.

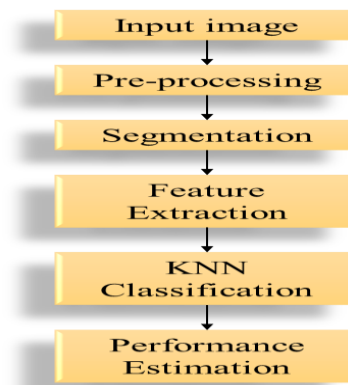


Fig 1: Block Diagram

Various phases that are involved during implementation of proposed approach are described under following section:

1. Input image

With the `imread` command, an image is read into the workspace. The example reads a picture, which is one of the sample images supplied with the toolbox, and puts it in an array referred to as `I`. The graphic file format is Tagged Image File Format, according to what the `imread` deduces from the file (TIFF). Use the `imshow` function to display the picture. The Image Viewer software also lets you see images. The `imtool` function launches the Image Viewer application, which offers a unified setting for viewing pictures and carrying out certain standard image-processing operations. The Image Viewer app gives users access to a number of additional tools for browsing and studying photos in addition to all the image display features of `imshow`.

2. Pre-Processing

Resizing a digital image is referred to as picture scaling in digital imaging. The expansion of digital material is known in video technology as upscaling or resolution improvement. Vector graphic picture may be resized without compromising quality of image by utilising geometric transformations on the graphic primitives that form the image. Scaling raster graphics pictures requires making a new picture with more or less pixels. When the number of pixels is reduced (scaling down), there is typically a noticeable quality reduction.

3. Segmentation

Fuzzy c-means (FCM) is the most efficient fuzzy clustering method. Despite being a widely used clustering method, fuzzy C Means fails to produce huge spherical clusters. FCM can only successfully cluster "spherical" clusters since it only uses squared norm for classifying similarity between data points. But various clustering algorithm may be generated from FCM for grouping more general dataset. The major goal of this KFCM is to correctly transform the input data in higher-dimensional feature space, which will enhance likelihood that the patterns there can be separated linearly. After that, the feature space will be used to execute FCM. Another benefit of the KFCM is that it estimates the number of clusters in the dataset.

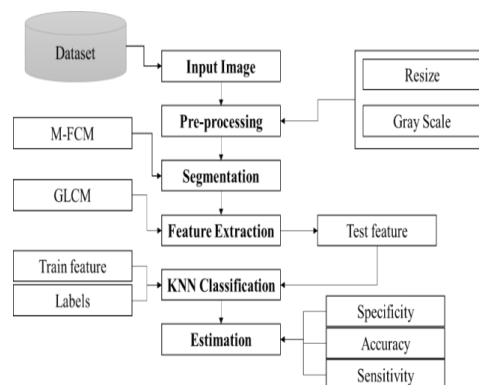


Fig 2: Flow Diagram

4. Feature Extraction

The GLCM is a tabulation of how frequently certain fusions of grey levels co-occur in a picture or portion of picture given an image with each having intensity. Calculations of texture features employ the information in the GLCM to provide a measurement of the intensity variation at the target pixel. Image analysis methods include the Gray Level Co-occurrence Matrix (GLCM) and related texture feature computations. The GLCM is a tabulation of the frequency with which various combinations of grey levels co-occur in a picture or portion of picture given an image made of pixels each with an intensity (a distinct grey level). Calculations of texture features employ the information in the GLCM to provide a measurement of the intensity variation at the target pixel.

5. Classification

In machine learning, convolutional neural networks (CNNs) are a type of deep, feed-forward artificial neural networks that are widely used to examine visual input. CNNs employ a modified multilayer perceptron that requires minimal preprocessing. Since the connecting arrangement between neurons mirrors how the animal visual brain is set up, convolutional networks were motivated by biological processes. Individual cortical neurons only react to stimuli in the restricted region of the visual field known as the receptive field. To complete the entire visual field, the receptive regions of several neurons partly overlap each other. This suggests that the network learns the filters, which were manually created for conventional procedures. This lack of reliance on past knowledge and manual labour while designing features is a significant benefit.

6. Performance Measures

Statistical measurements of effectiveness of a binary classification test, usually referred to as a classification function in statistics, include sensitivity and specificity: Sensitivity is the percentage of genuine positives that are accurately classified as such (also known as true positive rate, the recall, or likelihood of detection in some industries) (e.g., the proportion of unwell patients who are diagnosed with their ailment appropriately). Specificity measures the percentage of real negatives that are accurately classified as such (also known as true negative rate) (e.g., the proportion of healthy persons who are appropriately diagnosed as not having the illness among people).

4. Results

The major goals of this method are to locate the malignant area on an MRI of the brain and to categorise the severity of that brain in order to increase process efficiency. In this procedure, an effective algorithm was used to segment the damaged area and extract the data from the picture using characteristics like GLCM. Based fuzzy C-means clustering technique (M-FCM) is suggested for clustering during the segmentation process. The approach used here in the medical profession to identify brain lesions and classify their characteristics using KNN then aids in determining the severity of the brain input. The following screenshots illustrate the sensitivity, accuracy and specificity outcomes of suggested technique.

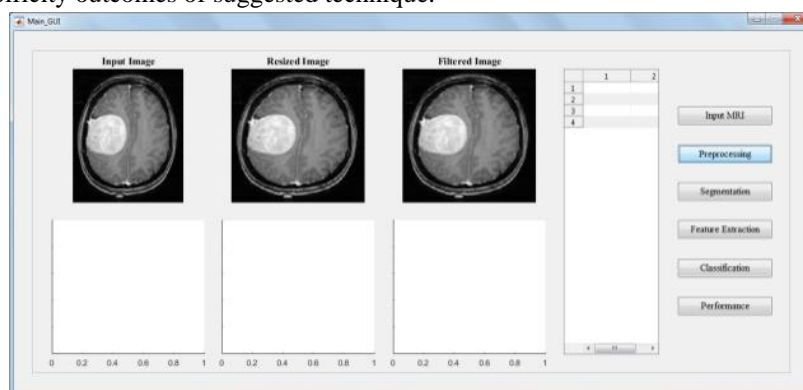


Fig 3: Pre-Processing

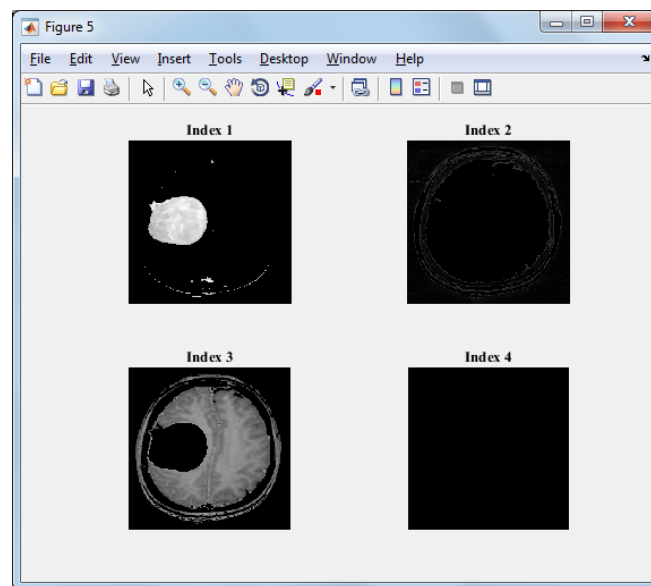


Fig 4: Indexing

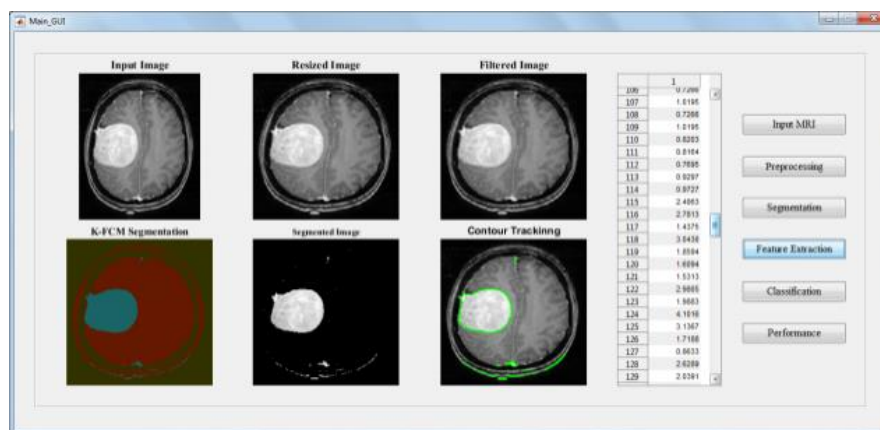


Fig 5: Feature Extraction

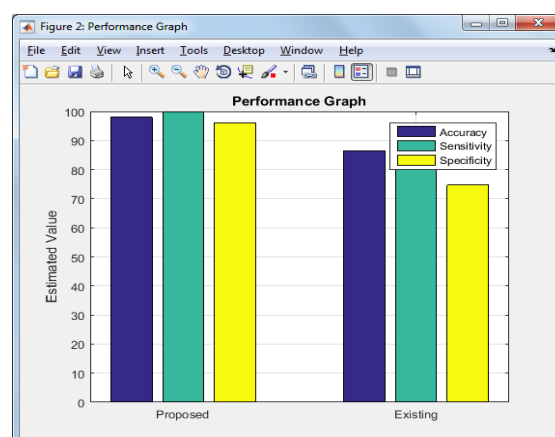


Fig 6: Performance Analysis

5. Conclusion

It has always required time to analyse medical images, and handling them is challenging in and of itself. We looked at KNN, AE, and wavelet transformation from a number of perspectives after the results of this study. in comparison to current classifiers like KNN, AE, and others, the proposed M-FCM classifier demonstrated great results when it comes to performance parameters like specificity, accuracy, sensitivity and other. The

outcomes demonstrate that the suggested DWA-DNN method performs better in terms of accuracy and statistical measure than other non-deep learning strategies. It would be much more intriguing to look into the potential of mixing the DNN with several different versions of the auto encoder in order to assess the influence or efficiency in same brain MRI dataset.

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