

e-ISSN:2582-7219



INTERNATIONAL JOURNAL OF MULTIDISCIPLINARY RESEARCH IN SCIENCE, ENGINEERING AND TECHNOLOGY

Volume 5, Issue 6, June 2022



INTERNATIONAL
STANDARD
SERIAL
NUMBER
INDIA

Impact Factor: 7.54



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Brain Tumor Detection and Classification of MRI Brain Image using Neural Network

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ABSTRACT: The project presents the MRI brain diagnosis support system for structure segmentation and its analysis using K-means clustering technique integrated with Fuzzy Cmeans algorithm. The method is proposed to segment normal tissues such as White Matter, Gray Matter, Cerebrospinal Fluid and abnormal tissue like tumour part from MR images automatically. These MR brain images are often corrupted with Intensity Inhomogeneity artefacts cause unwanted intensity variation due to non- uniformity in RF coils and noise due to thermal vibrations of electrons and ions and movement of objects during acquisition which may affect the performance of image processing techniques used for brain image analysis. Due to this type of artefacts and noises, sometimes one type of normal tissue in MRI may be misclassified as other type of normal tissue and it leads to error during diagnosis. The proposed method consists of pre-processing using Gaussian filter to remove noise and Kmeans clustering technique integrated with Fuzzy C-means algorithm segments normal tissues by considering spatial information because neighbouring pixels are highly correlated and also construct initial membership matrix randomly. The system also uses to segment the tumour cells along with this morphological filtering will be used to remove background noises for smoothening of region. The project results will be presented as segmented tissues and classification using neural network classifier.

KEYWORDS: Fuzzy C-means algorithm, MRI, Neural Network Classifier

I. INTRODUCTION

In many recent object recognition systems, feature extraction stages are generally composed of a filter bank, a non-linear transformation, and some sort of feature pooling layer. Most systems use only one stage of feature extraction in which the filters are hardwired, or two stages where the filters in one or both stages are learned in supervised or unsupervised mode. This paper addresses three questions: 1. How does the non-linearity's that follow the filter banks influence the recognition accuracy? 2. does learning the filter banks in an unsupervised or supervised manner improve the performance over random filters or hardwired filters? 3. Is there any advantage to using an architecture with two stages of feature extraction, rather than one? We show that using non-linearity's that include rectification and local contrast normalization is the single most important ingredient for good accuracy on object recognition benchmarks. We show that two stages of feature extraction yield better accuracy than one. Most surprisingly, we show that a two-stage system with random filters can yield almost 63% recognition rate on Caltech-101, provided that the proper non-linearity's and pooling layers are used. Finally, we show that with supervised refinement, the system achieves state-of-the-art performance on NORB dataset (5.6%) and unsupervised pre-training followed by supervised refinement produces good accuracy on Caltech-101 (> 65%), and the lowest known error rate on the undistorted, unprocessed MNIST dataset (0.53%).

II. LITERATURE SURVEY

Haibo Wang et al discussed the concept of breast cancer (BCa) grading plays an important role in predicting disease aggressiveness and patient outcome. A key component of BCa grade is mitotic count, which involves quantifying the number of cells in the process of dividing (i.e. undergoing mitosis) at a specific point in time. Currently mitosis counting is done manually by a pathologist looking at multiple high power fields on a glass slide under a microscope, an extremely laborious and time consuming process. The development of computerized systems for automated



detection of mitotic nuclei, while highly desirable, is confounded by the highly variable shape and appearance of mitoses. Existing methods use either handcrafted features that capture certain morphological, statistical or textural attributes of mitoses or features learned with Convolutional neural networks (CNN). While handcrafted features are inspired by the domain and the particular application, the data-driven CNN models tend to be domain agnostic and attempt to learn additional feature bases that cannot be represented through any of the handcrafted features. On the other hand, CNN is computationally more complex and needs a large number of labeled training instances.

Kevin Jarrett et al proposed the recent object recognition systems, feature extraction stages are generally composed of a filter bank, a non-linear transformation, and some sort of feature pooling layer. Most systems use only one stage of feature extraction in which the filters are hard-wired, or two stages where the filters in one or both stages are learned in supervised or unsupervised mode. This paper addresses three questions: 1. How does the non-linearities that follow the filter banks influence the recognition accuracy? 2. does learning the filter banks in an unsupervised or supervised manner improve the performance over random filters or hardwired filters? 3. Is there any advantage to using an architecture with two stages of feature extraction, rather than one? We show that using non-linearities that include rectification and local contrast normalization is the single most important ingredient for good accuracy on object recognition benchmarks. We show that two stages of feature extraction yield better accuracy than one. Most surprisingly, we show that a two-stage system with random filters can yield almost 63% recognition rate on Caltech-101, provided that the proper non-linearities and pooling layers are used. Finally, we show that with supervised refinement, the system achieves state-of-the-art performance on NORB dataset (5.6%) and unsupervised pre-training followed by supervised refinement produces good accuracy on Caltech-101 (> 65%), and the lowest known error rate on the undistorted, unprocessed MNIST dataset (0.53%).

Xavier Glorot Yoshua Bengio described several algorithms have been shown to successfully train them, with experimental results showing the superiority of deeper vs less deep architectures. All these experimental results were obtained with new initialization or training mechanisms. Our objective here is to understand better why standard gradient descent from random initialization is doing so poorly with deep neural networks, to better understand these recent relative successes and help design better algorithms in the future. We first observe the influence of the non-linear activations functions. We find that the logistic sigmoid activation is unsuited for deep networks with random initialization because of its mean value, which can drive especially the top hidden layer into saturation. Surprisingly, we find that saturated units can move out of saturation by themselves, albeit slowly, and explaining the plateaus sometimes seen when training neural networks. We find that a new non-linearity that saturates less can often be beneficial.

Mohak Shah et al proposed the topic of Tissue intensity standardization. Tissue intensity standardization is an important preprocessing step in the study and analysis of Magnetic Resonance Images (MRI) of human brain. Sources of variations in the intensity ranges across different MRI volumes, even after intensity inhomogeneity correction, can result from heterogeneity of data due to difference in scanners, presence of Multiple Sclerosis (MS) lesions and the stage of disease progression in the brain. As a result, intensity normalization plays a significant role in standardizing the tissue intensity ranges across MRI volumes on which most automatic image analysis methods base their distributional assumptions. The method of Nyul et. al. [3] has become a widely used standard for intensity normalization. However, an extensive validation of this approach on multi-site multi-scanner data in the presence of MS has yet not been performed. We aim to undertake this validation in this work and show the effectiveness of this procedure on standardizing tissue intensities in the MRI volumes.

III. EXISTING SYSTEM

Earlier systems will detect the tumor but the drawback in the existing system is that the stages in the tumor identification is somewhat tedious process, without the level and stage of the tumor further proceeding to the treatment will not be desired.

IV. PROPOSED SYSTEM

The Project proposes to spot the tumor from MRI scanned medical images using multi clustering model and morphological process. The segmentation refers to the process of partitioning a digital image into multiple segments. The brain MRI is taken and its noises are removed using filters and then applied spatial Fuzzy C means Clustering algorithm for the segmentation of MRI brain images. The morphological process will be used to smooth the tumor



region from the noisy background. The segmented primary and secondary regions are compressed with hybrid techniques for telemedicine application.

ADVANTAGES

Using this system we can identify the different stages in the brain tumor, based on the stage of the tumor such as normal, moderate and severe, further treatment can be proceeded based on the results.

SYSTEM IMPLEMENTATION

LIST OF MODULES:

- Preprocessing
- Glcm features extraction
- Cnn classifier

Preprocessing:

Image Pre-processing is a common name for operations with images at the lowest level of abstraction. Its input and output are intensity images. The aim of pre-processing is an improvement of the image data that suppresses unwanted distortions or enhances some image features important for further processing.

Image restoration is the operation of taking a corrupted/ noisy image and estimating the clean original image. Corruption may come in many forms such as motion blur, noise, and camera misfocus. Image restoration is different from image enhancement in that the latter is designed to emphasize features of the image that make the image more pleasing to the observer, but not necessarily to produce realistic data from a scientific point of view. Image enhancement techniques (like contrast stretching or de-blurring by a nearest neighbor procedure) provided by "Imaging packages" use no a priori model of the process that created the image. With image enhancement noise can be effectively be removed by sacrificing some resolution, but this is not acceptable in many applications. In a Fluorescence Microscope resolution in the z-direction is bad as it is. More advanced image processing techniques must be applied to recover the object. De-Convolution is an example of image restoration method. It is capable of: Increasing resolution, especially in the axial direction removing noise increasing contrast.

GLCM Features

To create a GLCM, use the graycomatrix function. The graycomatrix function creates a gray-level co-occurrence matrix (GLCM) by calculating how often a pixel with the intensity (gray-level) value i occurs in a specific spatial relationship to a pixel with the value j . By default, the spatial relationship is defined as the pixel of interest and the pixel to its immediate right (horizontally adjacent), but you can specify other spatial relationships between the two pixels. Each element (i,j) in the resultant GLCM is simply the sum of the number of times that the pixel with value i occurred in the specified spatial relationship to a pixel with value j in the input image. Because the processing required to calculate a GLCM for the full dynamic range of an image is prohibitive, graycomatrix scales the input image. By default, graycomatrix uses scaling to reduce the number of intensity values in gray scale image from 256 to eight. The number of gray levels determines the size of the GLCM. To control the number of gray levels in the GLCM and the scaling of intensity values, using the Num Levels and the Gray Limits parameters of the graycomatrix function. See the graycomatrix reference page for more information.

The gray-level co-occurrence matrix can reveal certain properties about the spatial distribution of the gray levels in the texture image. For example, if most of the entries in the GLCM are concentrated along the diagonal, the texture is coarse with respect to the specified offset. To illustrate, the following figure shows how graycomatrix calculates the first three values in a GLCM. In the output GLCM, element (1,1) contains the value 1 because there is only one instance in the input image where two horizontally adjacent pixels have the values 1 and 1, respectively.

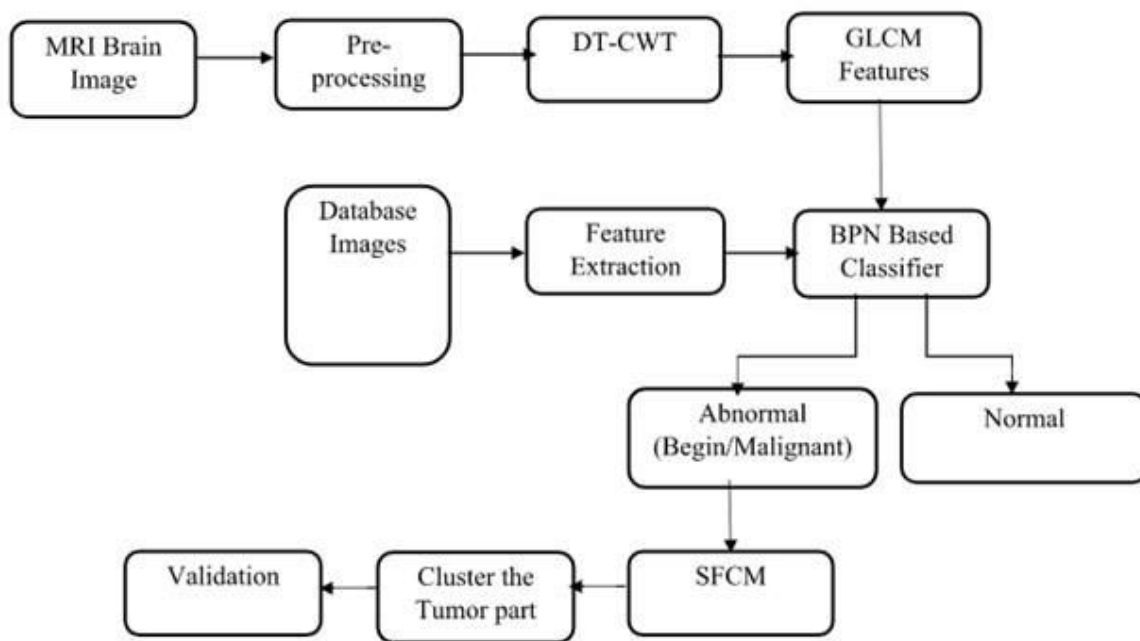
CNN Classifier:



Convolutional Neural Network (CNN) is a type of deep neural network primarily used in image classification and computer vision applications.

A simple neural network has an input layer, a hidden layer, and an output layer. A deep neural network can have two or more hidden layers. A convolutional neural network has convolution layers followed by a fully connected neural network.

ARCHITECTURE DIAGRAM



V. CONCLUSION

Thus the defects in the MRI images is identified with the help of image processing, in that the deep learning concept called neural network is used to identify the tumour in the image. In test image the features are extracted to classify the image. The same features will be extracted in the data set image, by these set of features we can classify the input image is normal or abnormal. Based on the training the convolutional neural network, the detection is achieved.

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