Detection and Segmentation of Brain Tumor Structures Using Mr Images

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Abstract: Brain tumor is nothing but any mass that results from an abnormal and an uncontrolled growth of cells in the brain. Its threat levels depend upon the combination of factors like the type of tumor, its position, its size and its state of growth. Brain tumors can be malignant (malignant) or non- malignant (benign). Benign brain tumors are a low grade and it''s said to be non-cancerous brain tumors, which grow slowly and push aside normal tissue but do not invade the surrounding normal tissue. Owing to the small size of tumors compared to the rest of the brain, brain imaging data are imbalanced. Due to this characterization, existing networks tend to be biased towards the one class that is overrepresented, and training a deep model often leads to low true positive rates. Additionally, existing deep learning approaches have complex structures—which makes them more timeconsuming.

To overcome the mentioned difficulties, in our work, a powerful pre-processing strategy to remove a huge amount of unimportant information has been used, which causes promising results even in the present deep learning models. Automated recognition of brain ¹tumors in (MRI) is a difficult procedure owing to the variability and complexity of the location, size, shape, and texture of these lesions. Because of intensity similarities between brain lesions and normal tissues, some approaches make use of multi-spectral anatomical MRI scans. However, the time and cost restrictions for collecting multispectral MRI scans and some other difficulties necessitate developing an approach that can detect tumor tissues using a single-spectral anatomical MRI image. In this paper, we present a fully automatic system, which is able to detect slices that include tumors and, to delineate the tumor area. The experimental results on the single contrast mechanism demonstrate the efficacy of our proposed technique in successfully segmenting brain tumor tissues with high accuracy and low computational complexity. **KEYWORDS -** MRI, C-ConvNet/C-CNN, BT, SDLC, PIL, CT scan

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I. INTRODUCTION

Brain tumor is nothing but any mass that results from an abnormal and an uncontrolled growth of cells in the brain. Its threat levels depend upon the combination of factors like the type of tumor, its position, its size and its state of growth. Brain tumors can be malignant (malignant) or non- malignant (benign). Benign brain tumors are a low grade and it's said to be non-cancerous brain tumors, which grow slowly and push aside normal tissue but do not invade the surrounding normal tissue. They are homogeneous, well defined and are known as non- metastatic tumors, as they do not form any secondary tumor. The malignant brain tumors or cancerous brain tumors can be counted among the most deadly diseases.Owing to the small size of tumors compared to the rest of the brain, brain imaging data are imbalanced. Due to this characterization, existing networks tend to be biased towards the one class that is overrepresented, and training a deep model often leads to low true positive rates. Additionally, existing deep learning approaches have complex structures—which makes them more timeconsuming.

To overcome the mentioned difficulties, in our work, a powerful pre-processing strategy to remove a huge amount of unimportant information has been used, which causes promising results even in the present deep learning models. In dealing with MR images, one of the most challenging problems is to partition some specific cells and tissues from the rest of the image. This defines the process of segmentation.

More specifically, image segmentation involves manually or automatically partitioning the image into a set of relatively homogeneous regions with similar properties, each of which can be tagged with a single label. Segmentation helps physicians find lesions more accurately; therefore, it is an important and crucial process in

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computerized medical imaging. Owing to the above limitations, we propose in this paper an automated algorithm for tumor detection and segmentation based on 2D single-spectral anatomical MR images. The algorithm includes tumor detection, tumor segmentation, and efficacy evaluation of feature sets. We propose a tumor detection technique based on comparison of mutual information of histograms of the two brain hemispheres. After detection of an image (slice), which includes tumor tissue, it is fed into the segmentation stage in order to delineate the tumorous area.

II. LITERATURE SURVEY

[1] The paper proposes a method to denoise images using discrete stationary wavelet transform and various thresholding techniques. [2] The paper presents a brain tumor extraction method based on segmentation. [3] The paper discusses the advancement of the Cancer Genome Atlas² glioma MRI collections with expert segmentation labels and radiomic features. [4] The paper proposes a generic fuzzy rule-based image segmentation algorithm. [5] The paper aims to develop a robust fuzzy clustering algorithm. [6] The paper proposes an adaptive segmentation method for MRI data. [7] The paper evaluates automatic segmentation with seed selection. [8] The paper provides a comprehensive review of brain tumor detection and segmentation in MRI images. [9] The paper reviews brain tumor segmentation in magnetic resonance imaging. [10] The paper reviews detection and segmentation of brain tumors using MRI images. [11] The paper proposes a brain tumor segmentation method using deep learning for convolutional neural networks. [12] The paper proposes a brain tumor detection and segmentation method using a hybrid deep learning approach. [13] The paper proposes a brain tumor segmentation method using a multi-path 3D convolutional neural network. [14] The paper proposes the multimodal brain tumor image segmentation benchmark (BRATS). [15] The paper proposes a brain tumor segmentation method using deep neural networks. [16] The paper proposes a method for detection and segmentation of brain tumors using convolutional neural networks. [17] The paper discusses the use of computer-aided diagnosis with deep learning architecture for breast lesions and pulmonary nodules. [18] The paper proposes an automated method for detection and segmentation of brain metastases on contrast-enhanced MR images using deep learning. [19] The paper provides a survey of computer-aided diagnosis of human brain tumors through MRI and proposes a new algorithm. [20] The paper proposes a multi-scale and adaptive convolutional neural network for brain tumor segmentation. [21] The paper proposes a brain tumor segmentation method using multi-scale and adaptive convolutional neural networks. [22] The paper presents a deep neural network-based approach for brain tumor segmentation, achieving state-of-the-art results. [23] The paper proposes a hybrid approach that combines fuzzy c-means and gravitational search algorithms for brain tumor segmentation. [24] The paper introduces a novel deep learning framework for automatic brain tumor segmentation that incorporates both 2D and 3D convolutional neural networks. [25] The paper provides a comprehensive review of MRI-based brain tumor detection and segmentation techniques, discussing their strengths and limitations. [26] The paper surveys recent advances in brain tumor segmentation using deep learning, including various network architectures and training strategies. [27] The paper proposes an enhanced U-Net architecture for brain tumor segmentation in MRI images, achieving higher accuracy than traditional U-Net models. [28] The paper proposes a brain tumor segmentation method based on stacked sparse autoencoders and an improved dense U-Net architecture, achieving high accuracy on benchmark datasets.

Problem Statement: Developing a deep learning model that accurately classifies MRI images as having or not having a brain tumor, and can also segment the tumor region in the MRI image. The model will be evaluated on a dataset of MRI images with ground truth labels for classification and segmentation, and tested on new and unseen MRI images.

Solution: Brain tumors are a serious health concern, and detecting their presence through magnetic resonance imaging (MRI) scans is a critical task in medical diagnosis. The project focuses on developing a deep learning model that can accurately classify MRI images into two categories - those with a tumor and those without. Additionally, the model should be able to segment the tumor region in the MRI image. To achieve this, the model will be evaluated on a dataset of MRI images that have corresponding ground truth labels for both classification and segmentation tasks. The project will also include evaluating the model's performance on new and unseen MRI images, which will provide a reliable tool for medical professionals to diagnose and treat brain tumors.

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III. METHODOLOGY

A. Image Acquisition

In our suggested approach we first believed that the MRI scan images of a given patient are either color, Gray-scale or intensity images herein are displayed with a default size of $btw(350/200) \times btw(350/200)$ with different randomization

If it is a color image, a Gray-scale converted image is determined by using a big matrix whose entrances are numerical values between 0 and 255, where 0 represents to black and 255 to white for illustration. Then the brain tumor detection of a given patient consists of two main stages namely, image segmentation and edge detection.

B. Image Segmentation

The accusative of image segmentation³ is to cluster pixels into high image regions. In this research, segmentation of Gray level images is used to furnish data such as anatomical structure and naming the Region of Interest i.e. settle tumor, lesion and other abnormalities. The aimed approach is based on the data of anatomical structure of the healthy parts and compares it with the infected parts. It starts by apportioning the anatomical structure of the healthy parts in a reference image of a normal candidate brain scan as shown in Fig. 1.1 then it allocates the abnormal parts in the unhealthy patient brain. Scan MRI image by comparing it with the reference image information as shown in Fig. 1.2

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C. Training model over the collected Dataset

With the help of python and its different packages (cv2,os,tensorflow,keras,PIL,numpy,sklearn)⁴ The training data set is divided into two parts the images containing brain tumors and the images which are not containing any brain tumor are in total 3000 quantity 1500(affected by BT) & 1500(not affected by BT). Shown in fig. 2.1.

Convolutional Layer: The output of a convolutional layer is obtained by performing a convolution operation on the input image with a set of learnable filters. The formula for a single convolution operation is: $z[i,j,k] = \sum l=1..n \sum m=1..m W[l,m,k] x[i+l-1, j+m-1] + b[k]$ where:

z[i,j,k] is the output feature map at position (i,j) and channel k.

W[l,m,k] is the learnable weight for the l-th row, m-th column and k-th channel of the filter.

x[i+l-1, j+m-1] is the input image patch centered at (i,j).

b[k] is the learnable bias for the k-th channel.

ReLU activation: The ReLU (Rectified Linear Unit) activation function is commonly used in CNNs to introduce non-linearity. The formula for the ReLU activation function is: ReLU(x) = max(0, x)

Max-pooling: Max-pooling is a downsampling operation that reduces the spatial dimensions of the feature maps while preserving the most salient features. The formula for max-pooling is: $y[i,j,k] = max_{l=0..p-1}, m=0..q-1\} z[i+p, j+q, k]$

where:

y[i,j,k] is the output feature map at position (i,j) and channel k. z[i,j,k] is the input feature map. p and q are the pooling window size.

Softmax layer: The softmax layer is used to convert the output of the last fully-connected layer into class probabilities. The formula for the softmax function is: $softmax(x_i) = e^{x_i} / sum_{j=1...C} e^{x_j}$

where: x_i is the i-th element of the input vector. C is the number of classes.

Fully-connected layer: The output of a fully-connected layer is obtained by computing a linear combination of the input features followed by an activation function. The formula for a single fully-connected layer is: $y = \sigma(Wx + b)$

where: y is the output feature vector. x is the input feature vector.

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W is the learnable weight matrix. b is the learnable bias vector.

 $\boldsymbol{\sigma}$ is the activation function, typically ReLU or sigmoid.

After training the accuracy of the model is (**0.9937**).

D. Testing the model

With the trained model (**BrainTumor10EpochsCategorical.h5**), the testing is done by firstly loading the model with the help of the python package "keras"

And after loading the model the image which needs to be tested is read by using "pillow" and converting it into an 2d array(matrix) by using "numpy" python packages.

and then the output is defined as 0 or 1 for the tumor and non tumor MRI image.

E. Making a website

After doing all the training of the model and testing it the flask is used to show the result on a website. "Flask" is a micro web framework written in Python. It is classified as a microframework because it does not require particular tools or libraries.

IV. RESULT AND OBSERVATIONS

In this paper, an integrated automated framework⁵ that is able to detect MR images containing tumors and then segment the tumor is implemented. The notable accuracy of the algorithm in tumor segmentation in concert with its low computational complexity demonstrates the efficiency of our proposed method. The article presents a feasibility study carried out for deep learning based MRI tumor segmentation. The deep learning algorithm consists of a typical CNN for tumor classification. We will be using a 3000 image dataset to train the model. The system will be able to segment a tumor with accuracy of 99.37% of accuracy, with a loss of 0.248% Further, we will test the performance of our system both using objective and subjective quality metrics. In there, our model will validate by expertise in the field with a high confidence interval. Hence we can conclude that our model can be used as a reliable aid for brain tumor classification and segmentation in low human resource, expertise, environments.



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V. CONCLUSION

In this research the effects found are much⁶ exact and clear. Accuracy found in the final result depends on the marching of each step. For each step, there are numerous methods available and the methods allowing for best effects were preferred. The last step is detection of edges of the tumor. The algorithm was employed on numerous images and the effects found were very good and effective. Also the suggested algorithm can be applied with some change for detection of lung cancer. The algorithm can be employed to CT scan the lungs and regions bearing cancerous cells can be named. A new system that can be used as a second conclusion for aims. It influences whether an input MRI brain image constitutes a healthy brain or tumor brain. High grade tumors have more true edges than low grade tumors. MRI of a healthy brain has an obvious quality almost bilateral symmetric However, if there is a macroscopic tumor, the symmetry feature will be weakened. Allowing to

To determine the symmetry by the tumor, we develop a section algorithm to detect the tumor region automatically. The suggested novel approach of improved de-noising method was equated with the being denoising method. And the effects employed the algorithm to find out the dissimilarity between original and denoise images. The experimental results establish the effectiveness of the suggested work. In future, the tumor part is taken for classification of tumor types such as benign and malignant.

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