DETECTION OF CANCER CELLS IN BRAIN TUMOR

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Abstract*— Brain disorders are primarily brought on by abnormal brain cell growth, which can harm the structure of the brain and eventually result in malignant brain cancer. Major obstacles exist when using a Computer-Aided Diagnosis (CAD) system to make an early diagnosis that will allow for decisive treatment, particularly when it comes to accurately identifying various diseases in magnetic resonance imaging (MRI) images. In this paper, a novel Deep Convolutional Neural Network (DCNN) architecture for efficient diagnosis of glioma, meningioma, and pituitary tumors is proposed along with a three-step preprocessing method to improve the quality of MRI images. For quick training with a higher learning rate and simple initialization of the layer weights, the architecture uses batch normalization.With few convolutional, max-pooling layers and training iterations, the suggested architecture is a computationally light model. The proposed architecture is demonstrated against the other models that are discussed in this paper.

Keywords—Brain tumors, deep convolutional neural network, image processing, MRI images.

I. INTRODUCTION

The majority of human behaviors, including memory, speech, thought, and leg and arm movements are controlled by the brain, making it the most crucial organ in the body [1]. Additionally, brain cells are the primary cause of brain cancer and other brain diseases [2, and abnormal growth directly harms brain anatomy]. According to the World Health Organization (WHO)[3], 9.6 million people will die from cancer worldwide in 2018, with brain cancer having the highest mortality rate. MRI images offer better contrast and greater spatial clarity[4]. In order to detect abnormalities in MRI images, the technique of detecting abnormalities in the brain is crucial. Since 2012, deep convolutional neural networks (DCNNs) have been widely used by scientists who have successfully used them to categorize images[6]. Recently, DCNN has also successfully classified medical photos [7][11]. First, a three-step pre-treatment approach is recommended.The pre-processing method enhances the MRI images' quality and widens their histogram, increasing their contrast. BRISQUE (Brisque, Blind Reference Image Spatial Quality Evaluator), which is used during pre-processing, evaluates the final image's quality.

Diagnostic model using DCNNs to separate meningiomas, pituitary or glioblastomas from normal MRI images. Use stack normalization, speed up model training, increase learning speed, and simplify layer weight initialization. The proposed architecture will be compared to established systems and more modern systems in an analytically rigorous comparison of meningioma, glioblastoma and pituitary tumor detection approaches such as CNN-SVM.

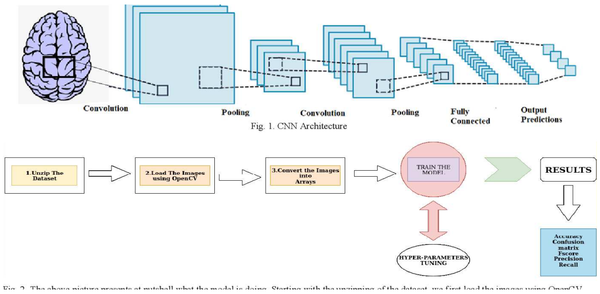

Figure 1 : CNN Layers

II. LITERATURE REVIEW

Machine learning (ML) and deep learning (DL) algorithms, especially those derived from MRI, have recently been used to identify and evaluate brain tumors using a variety of imaging modalities. The most recent research and pertinent research on the subject of the article are presented in this section. A system that combines deep learning (DL) methods with Discrete Wavelet Transform (DWT) functionality was presented by Mohsen, Heba, et al. [8].The brain tumor was segmented using a fuzzy c-means approach, and DWT was used to extract features from each lesion found. Prior to being sent to the Deep Neural Networks (DNNs), the features were sent to the PCA to reduce their size.With two sets of features—contrast with homogeneity and contrast with correlation—the Gl-Pt data set offered the highest precision, 82.27%.

Results from their testing of their methods on four different data sets (Mg-Gl, Mg-Pt, Gl-Pt, and Mg-Gl-Pt) were positive.To automatically identify and score brain tumors, Seetha, J. and S.S. Raja [12] proposed a thorough CNN-based method.

The algorithm uses fuzzy C means to segment the brain (FCM).These improvements have been applied to Bag of Words (BoW), GLCM, and other feature extraction methods.These feature vectors are then supplied to a classifier. Choosing the best feature vector to feed a classifier, like an artificial neural network (ANN), is the technique's main step[10] .The results show that only 4 out of a total of 29 features were selected by the genetic algorithm and that using only those features, it was able to achieve a 98 accuracy rate. Khawaldeh, Saed, et developed a technique using a modified version of AlexNet CNN for non-invasively classifying glioma brain tumors.

III. METHODOLOGIES

A. THE PRE-PROCESSING APPROACH PROPOSED

The secret to correctly identifying the problem of detecting brain tumors using magnetic resonance imaging is to find that pattern customization. Magnetic resonance imaging classification models face a number of problems that can cause learning errors and poor classification accuracy scores. As a result, we present a three-step preprocessing approach corresponding pattern [13] . Magnetic resonance imaging classification models face a number of problems that can lead to poor learning errors and classification accuracy scores. As a result, we present a three-step preprocessing approach.

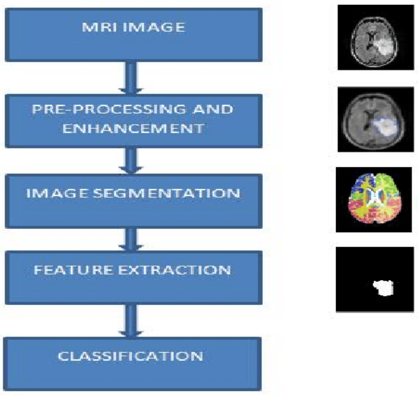

Figure 2 : Preprocessing steps

1) EXCLUSION OF COMPLEX ARTICLES

The specific brain element was made apparent by removing 100 pixels from each side of the image to reveal any conflicting elements, such as text and the dark areas to the right and left of the image.

2) MRI IMAGE ANALYSIS

The non-local averaging algorithm (NLM) deals effectively with noisy MRI images [12]. Because of the noise in these photographs, unwanted patterns are learned that reduce the accuracy of the classification. In comparison to the Gaussian [13] and Median [14] algorithms, the NLM perspective significantly increases the quality of MRI images, according to the Blind Reference less Image Spatial Evaluator (BRISQUE) [14].

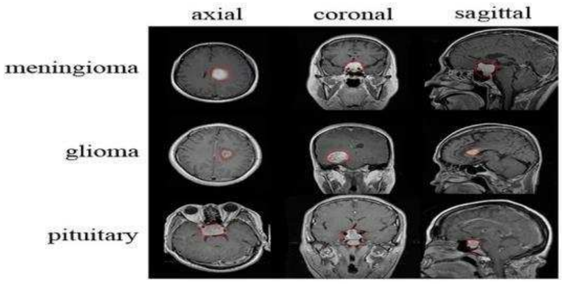

Figure 3 : Depiction of different types of tumors at different levels using standardized magnetic resonance imaging (MRI).

3) HISTOGRAM ALIGNMENT

In MRI, histogram equalization improves contrast significantly[15] . It also makes it easier to see fine details by reducing contrast when necessary. This process is done by dividing the most common intensity levels. It also eliminates interference caused by the most common MRI brain patterns.

B. DATASET

The data sets used for testing and research were derived from the Navoneel Brain Tumor Dataset and the Sartaj Brain MRI Imaging Dataset. Two different MRI scan types are included in the dataset. images that have been T1 and T2 weighted. Short echo time (TE) and repetition time (RT) limitations of 14 and 500 milliseconds, respectively, are used to generate T1-weighted images.

When creating T2-weighted images, the TE and RT limits are raised by 90 and 4000 milliseconds, respectively. The data set was split into three files with subfolders for the classes GLIOMA, MENINGIOMA, NO-TUMOR, and PITUITARY (training, testing, and validation). 3,394 MRIs were performed in total, with the most common diagnoses being GLIOMA (934), MENINGIOMA (945), NO TUMOR (606) and the pituitary feels better (909).

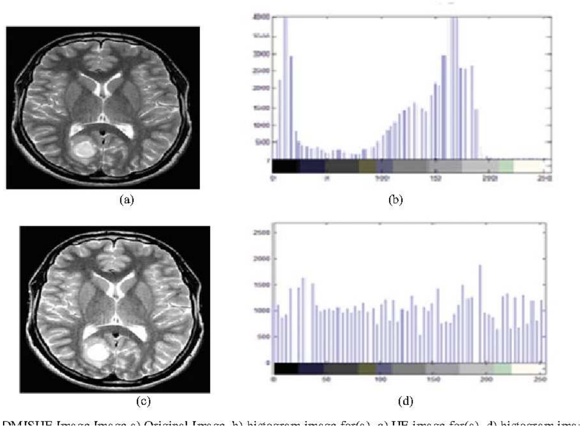

Figure 4 : Improved MRI brain image

C. PROCESSING STRATEGY

We can conclude that our model is problem-based because we used a completely new learning method. An image data generator was used to generate numerous MRI images for the training procedure]. The models were only collected for the desired features because the data generated during the build phase came from the same domain as the dataset used. The training technique has 60 epochs, 16 stack sizes and 385-step epochs. With a batch size of 16, 16 samples are fed into the trained model at a time, eventually providing training data for a single epoch.

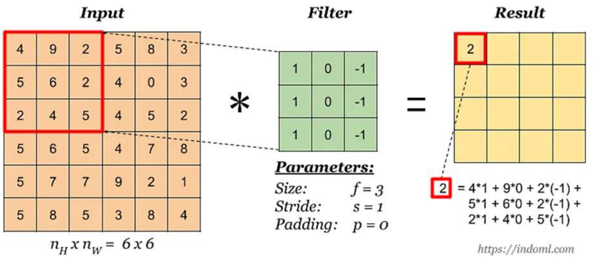

Figure 5 : Kernel or filter of 3x3 matrix and an equal size of sub matrix is obtained.

D.THE APPROPRIATE MODEL

This study describes a DCNN (Deep Convolutional Neural Network) model. Reduced clustering , slow learning speed and insufficient learning accuracy due to batch normalization operations are some of the initiatives taken by the proposed model. The proposed model consists of a convolution component and a classification component. The convolution part consists of 5 batch normalization levels, 10 convolution levels and 4 maximum pooling levels. The classifier component consists of 2, discarded layers and 3 dense layers.

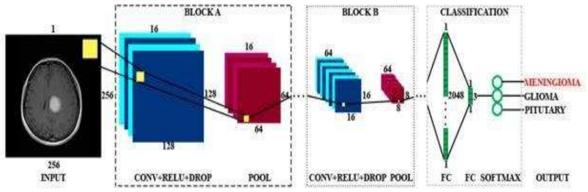

Figure 6 : The input layer of a convolutional neural network (CNN) is depicted crudely in this image.

IV. CONCLUSION

To quickly achieve high classification accuracy in the diagnosis of gliomas, meningiomas, and pituitary diseases, deep convolutional neural networks are advised. First, a brain tumor dataset that can be used for quick testing and training. Second, ambiguous areas are removed from MRI images, noise is reduced, and contrast is enhanced using a three-stage pre-processing technique.

This scheme had a beneficial and significant effect on all models tested. Finally, as part of the training mode, we teach our model the desired models right from the start. Finally, we used our model to easily and accurately analyze pixels based on their properties. We tested the proposed model on 396 MRI images from the dataset.

Meningioma detection was 98.26 accurate, neuroblastoma detection was 99 accurate, pituitary was 95.95 accurate, and normal image detection was 97.14 accurate for the proposed model. The suggested framework can be used as an automated computational tool in real-world applications to find abnormalities in the brain in MRI data.

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