

Comprehensive CNN Model for Brain Tumour Identification and Classification using MRI Images

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Abstract: Brain tumours are critical malignancies that develop as a result of aberrant cell division. Typically, tumour classification involves a biopsy, which is conducted after the final brain operation. Technological advances have facilitated the utilization of medical imaging by physicians to diagnose a wide range of symptoms within the domain of medicine. In this project, we propose the Comprehensive CNN method for the detection and classification of brain tumours. For experimentation, we used the SARTAJ, Br35H, and Figshare datasets. This proposed model outperforms in terms of accuracy, recall, F1 score, and precision as compared to other traditional methods. This research contributes to the ongoing efforts to enhance the capabilities of medical imaging and paves the way for more accurate and efficient brain tumor analysis.

Keywords - Comprehensive model, convolutional neural network, brain tumour MRI.

I. INTRODUCTION

The brain is a vital organ for decision making, protected by a hard skull. A brain tumour is the growth of abnormal cells that form a mass present in the brain. Any growth in or around the brain can cause serious health problems [1]. The vast majority of tumours are not cancerous, that is, benign, and a small number of tumours result in the formation of cancerous cells [2]. Primary brain tumours comprise pituitary, meningiomas, and glioma tumors. Glioma is a tumour that starts in the supporting tissues, while meningiomas start in the membranes around the spinal cord and brain.

The Pituitary gland, located in the central region of the brain, is a tiny gland. When there is an abnormal development in the vicinity of the Pituitary gland, it is referred to as a Pituitary tumor [3]. Brain tumors can grow in diverse positions of the brain which can vary in size and shape. Because tumours vary in type, they require different treatments. Misdiagnosis can be fatal. Brain tumour biopsies are more complex than biopsies of other body parts because they require surgery. Therefore, there is a need for noninvasive methods for accurately diagnosing brain tumours [4].

II. RELATED WORK

In [5], the authors proposed a Convolutional Neural Network (CNN) to extract the features from the Magnetic Resonance Imaging (MRI) images. Following that, the Kernel Extreme Learning machine classifies the given images using the features that were extracted. This study used a data set

made up of T1-weighted contrast-enhanced computed tomography (CT) scans of four types of brain tumours, including pituitary, meningiomas, glioma tumours, and No-tumour, to assess efficiency. Furthermore, to validate the kernel extreme (KE) - CNN model, its performance was compared with other commonly used classifiers such as radial base function and support vector machine(SVM). The KE-CNN model shows promising outcomes for the prediction and cataloging of brain tumors.

An analysis of MRI images was performed in [6] to identify tumour-containing regions and designate them as containing glioma, meningioma, or pituitary tumours. The deep learning (DL) approach is a robust and comparable methodology used for the purpose of image classification. Therefore, we can call a DL technique faster Region-based CNNs has been used and implemented via the TensorFlow library. For the classifier's training and testing, 233 patients' 3,061 CT scans (706 Meningiomas, 1425 Gliomas, and 930 Pituitary tumors) from a publicly accessible dataset were used. The faster Region-based CNN method produces accuracy ratings of 92%, its highest than the comparable work used on the same dataset.

In [7], the CNN was proposed by employing a genetic algorithm (GA), as opposed to the current models of choosing a DL architecture. Typically, it is achieved through the implementation of predefined standard frameworks or through experimentation. The bagging technique, which is an ensemble algorithm, was applied to the best method that was evolved by the GA to reduce the variance of prediction error. To briefly summarize the findings, it was possible to classify three different grades of glioma with 90.9% and 94.2% accuracy with two experiments respectively. These experiment results indicate that the cataloging of brain tumors using MRI images is effective. The adaptability also makes it easy to use in practice, assisting doctors in making early diagnoses of brain tumours.

In [8] The author's proposal suggests the use of pre-trained CNNs for the classification and diagnosis. Considering an ensemble of nontumour MRI images, three distinct categories of tumours were classified. The DL networks used are ResNet50, Efficient NetB1, EfficientNet87, and Efficient NetV281, among many other. EfficientNet's scalable design has yielded promising outcomes. The training accuracy reached 87.67% and the validation accuracy reached 89.55%, respectively.

In [9] the brain tumour was classified as either glioma, meningioma or pituitary tumor. The data set utilised in this study comprised 3064 brain MRI images, which were obtained from patients diagnosed with brain tumours. CNN was used by the authors, which is a popular deep learning architecture. The CNN classification tool developed is a reliable tool with an overall efficiency of 98.18% sensitivity and the accuracy of cropped tumours is 98.93%. The accuracy rate is 97.40% and the sensitivity is 98.52% for uncropped tumours, while the accuracy rate is 97.62% for segmented tumour images.

In [10], the authors concentrated on the implementation of four consecutive CNN approaches to categorise brain tumors in MRI images. The first step the author took was preprocessing the data, and the second step she used CNN to automatically classify the preprocessed images. A dataset consisting of 3,000 MRI images. Magnetic resonance images were classified into two categories, one for tumour and one for normal-was used for the experiments. The author's accuracy of 98.27% is superior to that of other models currently in use.

An effective multilevel segmentation method is created in this work by fusing the best thresholding and watershed segmentation techniques[11]. Then morphological process is employed to isolate the tumor. The Kernel SVM is then used for the classification of the resulting data, which is supported by experimental evaluation, after the CNN is applied for feature extraction. Experimental findings demonstrate that the suggested approach successfully identifies and accurately categorises the tumor as cancerous or noncancerous.

III. PROPOSED MODEL

The most frequently used algorithm to perform the analysis of any kind of health-related issues is deep learning. In DL generally, CNN is the most commonly used algorithm to perform any kind of animal image cortex to extract the clearly visible and hidden features in the given image and form a grid pattern which is exactly suitable for this paper, and it is as shown in Fig. 1. This proposed methodology for brain tumour detection and classification is shown in Fig. 1 which is used to classify the brain tumour into its types (pituitary, meningiomas, glioma, and notumors).

A. Dataset

In this paper, we combined three publicly accessible datasets from Kaggle are taken and they are: the Figshare dataset, the SARTAJ dataset, and the Br35H dataset [12]. This dataset includes 7023 different types of grayscale and JPG-formatted human brain MRI images. The dataset contains images of four different types of brain tumors: pituitary, meningiomas, glioma and notumors. However, to give each model an adequate input size and enhance the number of samples to be employed to train the model, data augmentation and resizing were used on the dataset during the preprocessing stage. Notumor samples have been gathered from the Br35H dataset. The SARTAJ dataset's glioma image class were incorrectly classified, so they were removed from the input data. Thus, the data set from FigShare is utilized. The samples of all classes of the data are shown in Fig.2.

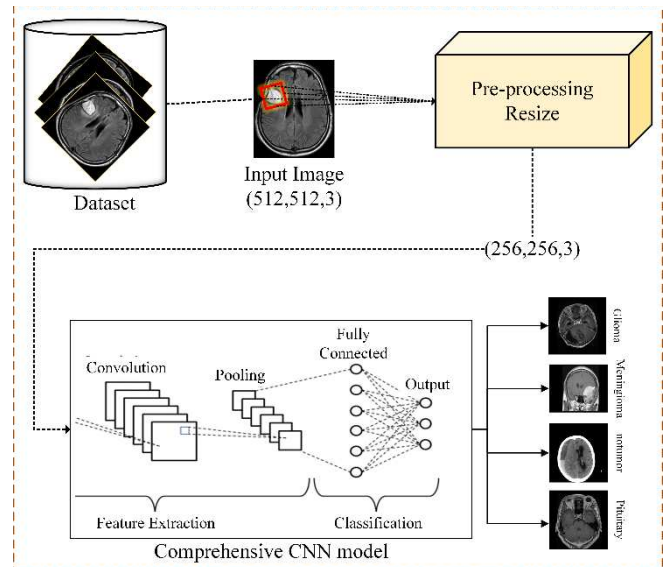


Fig. 1. Proposed system architecture

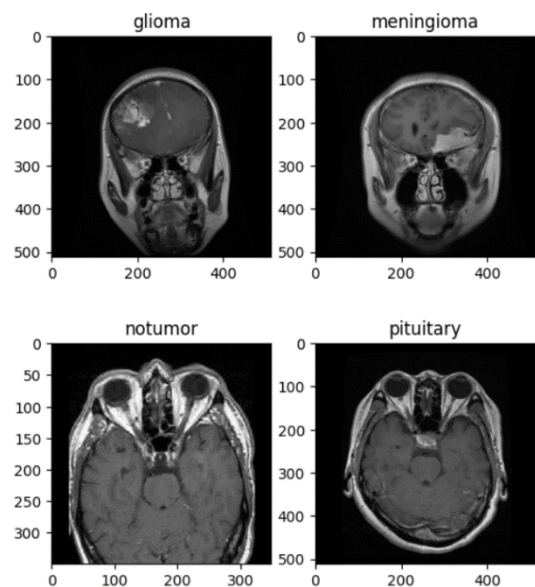


Fig. 2. Samples images from the ISIC dataset.

B. Preprocessing

The pre-processing block resizes the raw data that are provided as input and produces the resized image that is appropriate for use in machine learning models. Given input data is of size 512*512*3 which is resized to 256*256*3 in this process to get a balanced dataset which we will apply to the CNN model as shown in Fig.3.

C. Comprehensive CNN Model

The proposed comprehensive CNN contains multiple layers convolution layer, flatten layer, fully connected layer and is shown in Fig.4. The detailed descriptions of the layers are as follows:

Convolution Layer:

This is the very first layer of the Comprehensive CNN model which performs a convolution operation where the network of this layer can be called CNN. In this layer, the features of the input samples are extracted. Convolution is a linear operation which can be done by multiplication of a set of weights with the input. This technique was dedicated to a

two-dimensional input array of the extracted data from images. The multiplication is done between the data of input array of 2D array of weights known as a kernel or filter. Here, the size of filter should be less than the input data. Multiplication performed between a filter size and input data and generate a single digit value. And then the filter or kernel can be applied to the input array any number of times, and it produces a 2D array of output value called feature map.

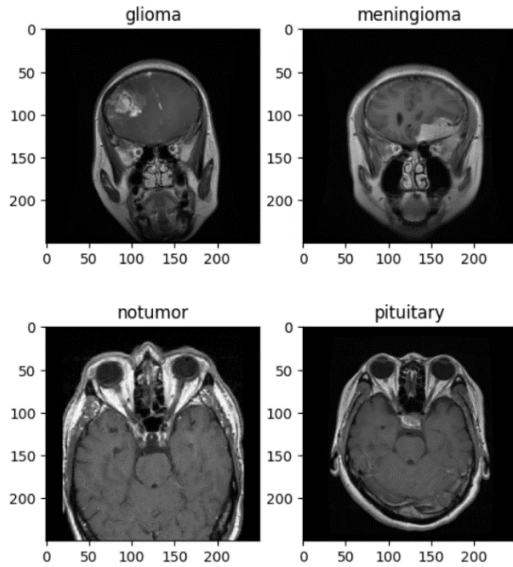


Fig. 3. Images after preprocessing

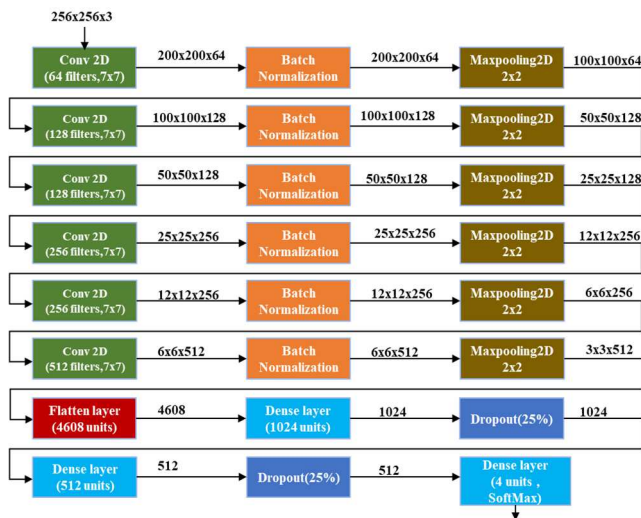


Fig. 4. The architecture of comprehensive CNN model

$$\text{Formula: } \frac{(\text{weight} - \text{Filter size} + 2\text{padding})}{\text{stride} + 1} \quad (1)$$

As shown in Fig 4, this paper includes six consecutive convolutional layers, each configured with a 7x7 filter size and 'ReLU' activation. Between each convolutional layer, batch normalization is applied to stabilize training and improve convergence. Additionally, max-pooling layers of pool size 2x2 follow each convolutional layer, progressively downsizing the spatial dimensions of feature maps. This sequential arrangement of convolutional layers, max-pooling,

and batch normalisation operations allows the model to efficiently extract hierarchical features from input images, making it well-suited for intricate image analysis tasks, particularly in research areas like medical imaging or object recognition, where precise feature extraction is pivotal for accurate classification and detection.

Flatten Layer:

The process which converts all the 2D arrays into vectors is known as Flattening. The Flatten layer is utilized to transform the data into a 1D array and input it into the subsequent layer.

Fully connected Layer:

As shown Fig 4, there are three fully connected layers used in this paper with 1024, 512 and 4 units. The first two dense layers with 1024 and 512 units, using the 'relu' activation function to capture intricate data patterns. To improve model robustness and mitigate overfitting, two dropout layers with a 0.25 dropout rate are employed. The final layer, with four neurons and 'softmax' activation, produces class predictions by converting raw output scores into class probabilities. This design balances complexity and performance, facilitating accurate image classification, particularly in applications such as medical imaging and object recognition where robustness and precision are crucial.

IV. EXPERIMENTATION RESULTS AND DISCUSSION

The experimentation is performed on Kaggle using a laptop with specifications Intel Core i5 10300H CPU, a dedicated GPU featuring NVIDIA GeForce GTX 1650, 64bit OS, and 8GB RAM. The libraries tensorflow, os, cv2, matplotlib.pyplot, seaborn are used in the proposed model. A brain tumor dataset with 20% testing and training data was used and shown in Fig. 5.

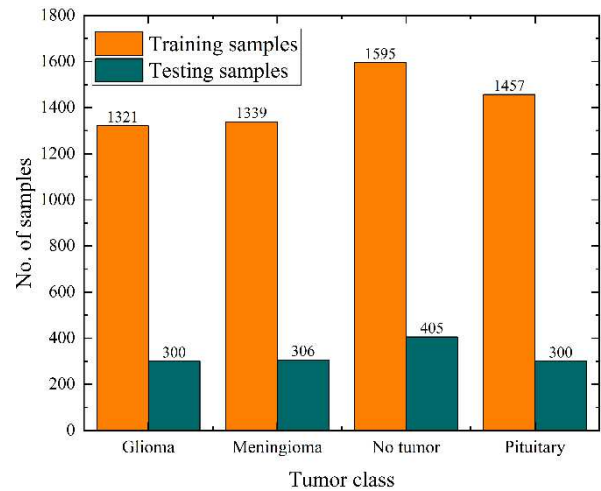


Fig. 5. Dataset samples in each class

The dataset employed for train and test a Comprehensive CNN model is MRI brain tumor dataset. There are 1321 training images and 300 testing images in Glioma, meningiomas have 1339 training images and 306 testing images, pituitary tumors have 1457 testing images, and 300 training images and no-tumors have 1595 training images and 405 testing images. Stochastic Gradient Descent (SGD) optimiser is used to compile the model, using a categorical

cross entropy as the loss function, learning rate of 0.001 and categorical accuracy as the evaluation metric and the hyper parameters are shown in Table I.

TABLE I. HYPERPARAMETER SETTING.

Parameter	Training value	Testing Value
Epochs	100	100
Batch size	32	32
Learning rate	10^{-3}	10^{-3}

Figure 6 and Fig 7 represent Model Accuracy and Model Loss respectively. This model was trained for 100 epochs, but if the validation loss fails to improve, the training process is terminated using an approach known as early stopping. In Fig. 6, the x-axis indicates epochs, and the y-axis indicates precision. For the proposed model the training accuracy is 99.96% and the testing accuracy is 98.93%. In Fig. 7, loss is shown on y-axis and epochs are shown on the x-axis. The loss of the testing data is 0.045.

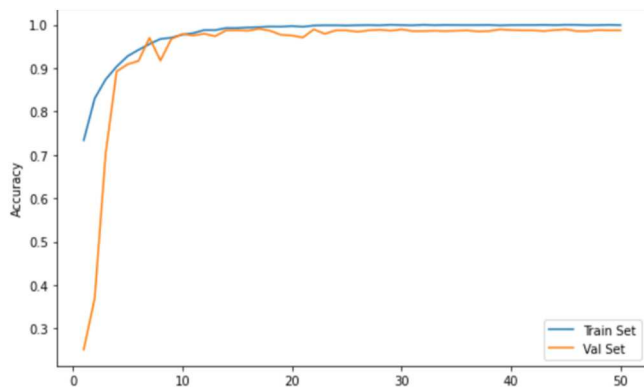


Fig. 6. Accuracy plots of the proposed model

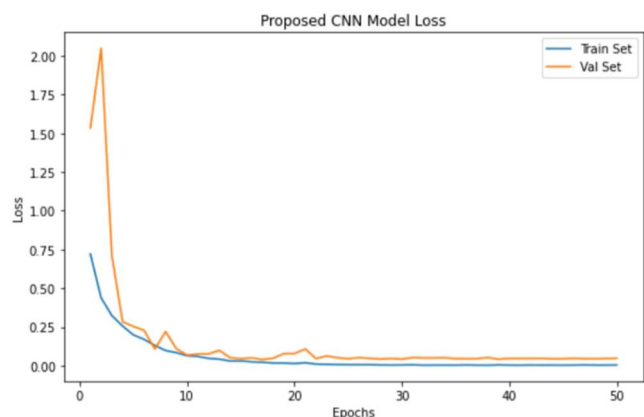


Fig. 7. Loss plots of the proposed model

The four main components of a confusion matrix are True Positives (TS), which represent the accurate prediction of positive occurrences; True Negatives (TN), which denote the right prediction of negative instances; False Positives (FP), which indicate the erroneous prediction of positive instances; and False Negatives (FN), which signify the inaccurate prediction of negative instances. The proposed model confusion matrix is illustrated in Fig 8.

True Label	Glioma	289	9	0	2
	Meningioma	1	300	3	2
	notumor	0	0	405	0
	Pituitary	0	1	0	299
		Predicted Label			
		Glioma	Meningioma	notumor	Pituitary

Fig. 8. Proposed model Confusion Matrix

By analyzing these components, the overall performance metrics precision, recall, accuracy and F1-score are computed as illustrated in Table II, which are crucial for assessing the effectiveness of a classification model. The individual performance metrics for each brain tumour class are shown in Table III. A comparison study is conducted to validate the effectiveness of the suggested model by comparing it with other state-of-the-art methodologies. Table IV presents a comparative analysis of the proposed model and competing methodologies.

TABLE II. PROPOSED SYSTEM PERFORMANCE METRICS

Metric	Formulae	Value
Recall	$\frac{\sum TP}{\sum (TP + FN)}$	0.9850
Precision	$\frac{\sum TP}{\sum (TP + FP)}$	0.9111
Accuracy	$\frac{\sum (TP + TN)}{\sum (TP + FP + FN + TN)}$	0.9061
F1 Score	$\frac{2TP}{2TP + FP + FN}$	0.9136

TABLE III. PERFORMANCE METRICS OF TUMOR CLASS.

Type of tumor	Support	Recall	Precision	F1score
Pituitary	300	1.00	0.99	0.99
Meningioma	306	0.98	0.97	0.97
Glioma	300	0.96	1.00	0.98
Notumor	405	1.00	0.99	1.00

TABLE IV. COMPARATIVE ANALYSIS OF PROPOSED MODEL WITH TRADITIONAL MODELS.

Reference	Model	Accu racy	Recall	F1-score	Precis ion
Proposed model	Comprehensive CNN model	98.93	98.5	98.5	98.75
S Ullah [13]	Gabor+ResNet50+SVM	95.73	-	95.72	95.90
MA Gómez-Guzmán [14]	InceptionV3	97.12	-	-	-
T Rahman [15]	PDCNN	97.60	-	97.00	97.00

The combination of Gabor filter, ResNet50 and the SVM deep learning model yielded an accuracy of 95.73%, an F1 score of 95.72% and a precision of 95.90% in the

experimental investigation carried out by S Ullah [13] using the figshare, SARTAJ, and Br35H data sets. MA Gómez-Guzmán [14] provided an InceptionV3 model was trained and tested that resulted an accuracy of 97.12% and evaluated using the figshare, SARTAJ and Br35H data sets. T Rahman [15] used the PDCNN model with data enrichment using the figshare dataset which obtained an accuracy of 97.60%, F1-score of 97.00% and precision of 97.00%. Table IV shows the comparison with other approaches that were performed using same the dataset and their respective accuracy, recall, F1 score, and precision are shown. By observing Table IV, we can conclude that the proposed model is much better than the existing model in comparison to accuracy, recall, F1-score and precision.

V. CONCLUSION

In this paper, the detection and classification of brain tumours using comprehensive CNN was proposed. The goal of this work is to create a model that can accurately determine brain tumours from MRI images. The CNN machine learning algorithm is the basis for this model, which uses 5712 datasets for training and 1311 datasets for testing brain MRI images. The model assists in predicting by resizing and cropping the image without erasing any information that will be utilised in the prediction process, the model helps with prediction. The accuracy, recall, F1-score, and precision of the proposed model are 98.93%, 98.5%, 98.5% and 98.75% respectively. The loss of the proposed model is 0.045 which progressively drops as the number of epochs rises. The proposed models outperform in terms of accuracy in contrast with the traditional models. Further, to improve the overall accuracy of this model, additional datasets will be added in the future.

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