

Cancerous brain tumor detection using hybrid deep learning framework

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ABSTRACT

Computational models based on deep learning (DL) algorithms have multiple processing layers representing data at multiple levels of abstraction. Deep learning has exploded in popularity in recent years, particularly in medical image processing, medical image analysis, and bioinformatics. As a result, deep learning has effectively modified and strengthened the means of identification, prediction, and diagnosis in several healthcare fields, including pathology, brain tumours, lung cancer, the abdomen, cardiac, and retina. In general, brain tumours are among the most common and aggressive malignant tumour diseases, with a limited life span if diagnosed at a higher grade. After identifying the tumour, brain tumour grading is a crucial step in evaluating a successful treatment strategy. This research aims to propose a cancerous brain tumor detection and classification using deep learning. In this paper, numerous soft computing techniques and a deep learning model to summarise the pathophysiology of brain cancer, imaging modalities for brain cancer, and automated computer-assisted methods for brain cancer characterization is used. In the sense of machine learning and the deep learning model, paper has highlighted the association between brain cancer and other brain disorders such as epilepsy, stroke, Alzheimer's, Parkinson's, and Wilson's disease, leukoaraiosis, and other neurological disorders.

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1. INTRODUCTION

Brain tumours develop as a result of irregular cell growth, including uncontrolled development in the brain. When such cells not identified early and reliably, they may result in death. Some brain tumours are more prominent than others, such as sarcoma, glioma, and thyroid tumours. The most common tumour method in the epithelial cells that include the brain and spinal cord is meningiomas. The majority of meningiomas tumours are benign. Gliomas are a group of tumours inside the brain's substance and often mix in brain tissue. When the tumour size is comparatively high, gliomas tumours result in a very short life span. Pituitary tumours are irregular brain cell development. Pituitary tumours are benign tumours that arise in the anterior pituitary of the brain. Some pituitary tumors result in the abnormal and dangerous increase in the hormones that regulate important functions of the body. These tumors can appear anywhere from the brain

because of their intrinsic nature. Also, they do not have a uniform shape. They have different sizes, shapes, and contrasts. Magnetic resonance imaging (MRI) is a diagnostic imaging technique commonly used in clinical practise for the management and therapy of brain tumours. Three distinct directions are used to take MR pictures. Sagittal, axial, and coronal views are the three types of views. Mechanisms for brain tumour segmentation are an essential part of tumour detection. Since image analysis is the moment and prone to human discrepancies, using machine learning to obtain a brain tumour pattern is advantageous. Diagnostics, growth estimation, and diagnosis of brain tumours benefit from automatic segmentation of medical images. Early detection of a tumour in the brain means a quicker response to care, helping people live longer. Manual processes for locating and classifying brain tumours in vast medical image databases used in routine clinical activities significantly cost effort and time. It is beneficial and worthwhile to provide accurate control, position, and classification process.

2. LITERATURE SURVEY

2.1. Existing methodologies

Based on dual-energy computed tomography (DECT) knowledge, deep learning (DL) and multi-atlas (MA) approaches have been used to differentiate normal tissue from tumour tissues referring to as organs-at-risk (oARs). While evaluated with single-energy computed tomography (CT), the dual-energy CT (DECT) dataset has higher-resolution images. In terms of identification and quantification, DL methods outscored single-energy CT for DECT segmentation [1]. For image recognition, classification, and optimization, other techniques and variations of pre-trained networks have been proposed [2]. Numerous medical image databases have been used to examine different approaches, including MRI images depicting brain tumours and tumours from various parts of the human body. This system has very effective to detect brain tumour in the initial stages, and it has good results on a large heterogeneous image dataset.

Cheng *et al.* [3], the first to show the feature vectors, has been utilized for augmented tumour detection, including objects of interest, image dilatation, or partition to classify the tumour forms. The system first extracted features using the strength histogram, grey level co-occurrence matrix (GLCM), and bag-of-words (BoW) models. This system also discusses more techniques that used the same index. They go through various kinds of networks, including pre-trained networks, capsules net networks, other convolutional infrastructure components, and variations of neural networks for extracting features and classifiers for the output result. The topic also includes methods that use various database changes and also the original database.

This system utilized the training with default Adam optimization algorithms, including the mini-batch size of data chunks; it is around 16. The data has also been shuffling in each iteration during the execution. One epoch correlates to the early phase, which determines when the network training phase will end. It was tuned to complete the learning algorithm after the first period, whenever the loss begins to increase. The learning period rate has been set to 0.0004, and the regularisation factor was set to 0.004. A Glorot efficient and productive, also recognized as a Xavier initializer, was used to set the weight of the convolution operation [4]. As per literature survey performed during this research work, Tripathi and Bag [5] have the best result in the literature using segmented image parts as inputs, with 94.64% accuracy. They use features extracted from the segmented brain from the image as input to the classifiers. They used a 5-fold cross-validation method to evaluate their method.

For the diagnosis and treatment of a brain tumour, various image-processing techniques and methods have been used. The infected brain tissue region is extracted from MRIs using segmentation, which is a fundamental step in image processing techniques [6]. The task of segmenting the tumour region is critical for cancer diagnosis, treatment, and treatment outcomes assessment. For tumour segmentation, a variety of semi-automatic and automatic methods and techniques are used [7]. T1-weighted (T1) and T1-weighted contrast-enhanced (T1c) MRI techniques, as well as T2-weighted and T2-weighted fluid attenuated inversion recovery (FLAIR) techniques, are used for brain tumour segmentation.

For efficient segmentation of the brain tumour region, random forest (RF) and binary decision tree (BBD) use multi-spectral MR images. By reducing the effect of relative intensities and increasing the features information at each voxel of the MR image, random forest and bagged decision tree (RF-BDT) preprocesses the image dataset [8]. D. presented semi-automatic images segmentation (SAMBAS). Gering for tumour segmentation, a long axis of the 3D segmented image is drawn using multi-plane reformat (MPR). When MPR performs 3D segmentation, the 2D segmentation is updated in real-time. On the MPR plane, all additional short axes, long axes, and other editing operations are drawn. SAMBAS uses probability distribution in MPR segmentation and speeds up the 3D segmentation process [9]. The brain tumour is automatically segmented from multi-model MRIs using a deeply supervised neural network based on holistically-nested edge detection (HED). The HED method can detect binary edges in images for

classification, but it can also be used to segment multi-class tumours. The HED method divides the brain tumours into three categories: whole, core, and enhancing tumours [10].

The positron emission tomography (PET) imaging tool is used to evaluate brain tumours and distinguish tumour progression from reactive changes. The fluoroethyl-L-tyrosine (FET-PET) method, which combines Fluoro Ethhlyl Tyrosine and PET, adds valuable information to MRIs for better decision-making. In the FET-PET method, the term "attenuation correction" describes how the tumour is accepted. CT-AC metrics are more effectively generated using the Deep-UTE and Resolute methods. Using CT-AC, the Deep-UTE method produces more robust clinical metrics and a longer overall patient survival time. Due to better noise handling capability and fewer runtime properties, the Deep-UTE method's attenuation correction in PET/MRIs is reliable for brain tumour evaluation [11].

The main goal of brain surgery is to perform more precise tumour resectioning while preserving the patient's normal brain cells. To support reliable real-time tumour resection, the development of label-free and non-contact methods and frameworks is required. Hyperspectral imaging is non-ionizing, non-contact, and label-free. The deep-learning framework preprocesses the hyperspectral images in vivo brain tissues. The framework creates a thematic map of the brain's parenchymal area and the location of the tumour, which aids the surgeon in performing a successful and precise tumour resection [12].

Al-Smadi *et al.* [13] proposed detecting COVID-19 using X-ray images. This study is split into two sections: a binary classification problem to see whether or not a person is infected with COVID-19, and a multi-task classification problem to differentiate between normal, COVID-19, and pneumonia cases. This method has achieved a detection accuracy of 100% for imbalanced data. Masad *et al.* [14] proposed a hybrid deep learning approach for pneumonia utilising chest X-ray pictures. The three kinds of classifiers, support vector machine (SVM), K-nearest neighbor (KNN) and RF, were used with the classic convolutional neural network (CNN) classification method (Softmax) to diagnose pneumonia from chest X-ray pictures. The hybrid systems were equivalent to the traditional CNN model with Softmax, except for the RF hybrid system, which performed worse than the others in accuracy, precision, and specificity. The KNN hybrid system, on the other hand, had the fastest consumption time, followed by the SVM, Softmax, and finally, the RF system. Watermarking colour photos using virtual concealing and El-Gamal ciphering, according to Ayooob *et al.* [15]. A novel way of using an red, green, and blue (RGB) mark to protect colour photographs against unauthorised trafficking has been suggested. When the owner asserts the rights to such photos, the approach relies on obtaining logo data from particular places in the host to construct a logo. Because the pixels in these places match the logo data, they were picked. To maintain anonymity, the positions of matched pixels are recorded in a database that goes through two steps of treatment.

Deep learning has revolutionised the design of medical imaging systems, and researchers have embraced novel methodologies in recent years. A new era of cooperation between machine learning scientists and radiologists has begun [16]. However, all of the above-described research intended to partition brain tumour regions without having to identify these areas as belonging to various brain tumour categories. Our study's goal was to create a novel Deep Learning model for tumour segmentation and classification. Mohsen *et al.* [17] suggested a deep learning classifier paired with a discrete wavelet transform and PCA to categorise a dataset containing three distinct brain cancers. Four other related deep learning research utilise the same dataset as we do, which is vital to compare and support the performance findings of the proposed model provided here. Abiwinanda *et al.* [18] A CNN model was employed for classification in Pashaei *et al.* [19], whereas the characteristics retrieved by CNN were inputs to a kernel extreme learning machine (KELM) technique. The KELM approach uses layers of hidden nodes to learn. Sultan *et al.* [20] presented a 16-layer CNN. They suggested a hybrid strategy that uses CNNs and genetic algorithm (GA) criteria to optimise network design.

3. PROPOSED SYSTEM DESIGN

The CNN consists of input layer, convolution layer, rectified linear unit (ReLu) layer, pooling layer and fully connected layer. In the convolution layer the given image is separated into various small regions. It gives the output in matrix form. Relu layer is used activation function and it is responsible for transforming the summed weighted input from the node into activation of the node. Pooling layer is optional. Pooling layer is mostly used in down sampling. Fully connected layer is used to generate the class score or label score value based on probability between 0 and 1. In dropout layer, randomly selected neurons are ignored during training. Flatten layer feed the output in fully connected layer and it gives the data in list form. Activation is used the sigmoid function to predict the probability as an output and it exists between the range of 0 and 1. The block diagram of brain tumor detection based on CNN is shown in Figure 1.

3.1. Research contribution

This research carried out on brain tumor classification using deep learning, and CNN is a classification algorithm utilized for classification. The hybrid feature extracted, such as luminance, chrominance, histograms-based features, binary features, sobel features, autoencoder, alfa features, beta features, gamma features, and epsilon, in the convolutional layer and feed to the pooling layer. In dense layer, classification has done as an image is normal or abnormal.

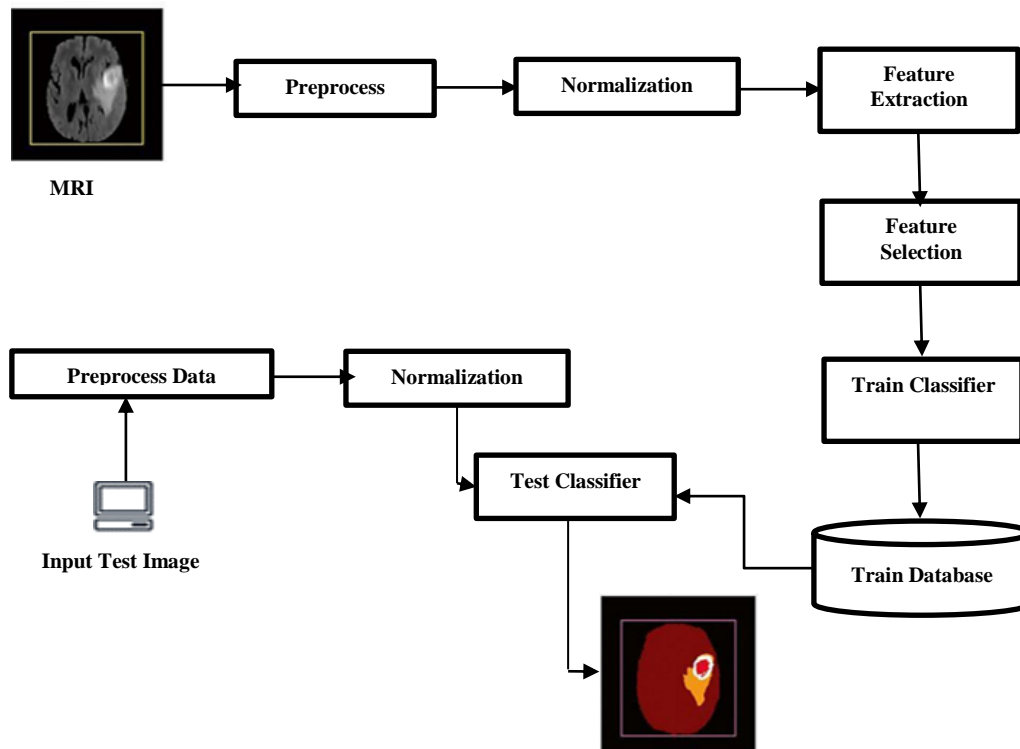


Figure 1. Architecture of proposed system

3.2. Execution process

This brain tumour detection and classification approach has been dividing into two phases, such as module training and testing. Before module training, various pre-processing, normalization, feature extraction and feature selection steps will be performed. Finally testing phase will demonstrates result of system including accuracy and precision.

3.2.1. Pre-processing

In the MR image there are several irrelevant noises. To remove noise, the eminence of the medical images is expanded by pre-processing methods. This technique's main goal is to increase the constant noise ratio, adjust the visual aspect of the MR image, remove noise and unwanted parts in the context, smooth the internal components, and keep the edge [21].

3.2.2. Skull stripping

Skull stripping is a valuable biomedical image processing method because it allows us to examine brain tumours from MR images. Increased brain picture tissues, such as fat, skin, and skull, can be removed using this method. Complete skull stripping using object contour, skull shedding based on differentiation and morphological action, and skull stripped based on histogram analysis, or a confidence score is just a few of the popular skull stripping methods [22].

3.2.3. Morphological operation

To remove boundary regions from brain images, the wavelet transform is used. Since this procedure only reorders the relative positions of pixel values and not their numerical values, it is only appropriate for binary images. Morphology's basic operations are dilation and erosion. Dilation applies pixels to the object's boundary area, while erosion eliminates the objects boundary regions pixels.

3.3. Feature extraction

The process of extracting higher-level knowledge about an object, such as structure, texture, colour, and comparison, is known as feature extraction. The visual processing time schedules and the machine learning system both use texture analysis. Finding and analysing textures can help with diagnosis at various stages of tumour detection. It's being used to enhance a diagnostic method's precision by choosing statistical features such as mean, contrast, energy, entropy, standard deviation, and skewness. The image segmentation is a method to distribute an image object into minor parts to examine and distinguish the significant evidence of a image. It creates several no of pixels in the image and given label to share particular feature information. Image segmentation has following three techniques Threshold segmentation; region based segmentation, K-means techniques [23].

3.3.1. Convolutional layer

A CNN's base layer is a convolutional layer. The convolution process operates on a tiny local region of the information using a convolutional kernel of a specific dimension. A convolutional kernel is a weighted sum that can be learned. The convolutional layer's information is fed via an objective function, and then binaries feature map is produced. The feature map may be used as the input for the convolution layers that follows. As a result, after stacking multiple convolutional layers layer by layer, more complex characteristics may be retrieved. Furthermore, the cells in each feature map contribute the strength of a convolutional kernel in an activation function, ensuring that the dimensionality in the structure does not substantially grow even as the quantity of convolutional layers expands, lowering the model's memory footprint. As a result, this model may aid in the formation of a more complex network structure.

3.4. Feature selection

3.4.1. Pooling layer

After such a convolution operation, a combining layer is usually used. The greatest, intermediate, and randomised pooling layers are examples of general pooling layers. The highest and averaged pooling algorithms identify the greatest and averaged values of neighbouring neurons, correspondingly, whereas the randomised pooling algorithm chooses values from neurons based on likelihood. Other types of convolution layer, such as overlaying pooling and geometric pyramid pooling, are frequently superior to the conventional pooling layers. Max pooling, independent of which kind is employed, seeks to collect features but is unconcerned with their exact positions, ensuring that the connectivity can learn important features even if the input layer shifts a little amount. Furthermore, a wavelet transform does not change the amount of feature maps in the preceding layer, but it lowers their spatial complexity and retains the critical data in the feature vector, decreasing supervised learning computation even more. The feature has been extracted such as binary features, Sobel features, autoencoder features, histogram features and some gray-level co-occurrence matrix (GLCM) base features [10].

3.5. Segmentation

3.5.1. Threshold Segmentation

Segmentation means distributing a digital image toward no. of fragments that included no set pixels and super pixel collection. With the segmentation's help, it could be simple and easy to represent an image, and it will enhance a more comprehensive, significant method of investigation. Grouping of an object and edges in images such as edges, paths could be improving within image segmentation. Throughout image segmentation, every pixel has a label, and an unusual pixel consists of the same label serving a specific visual characteristic. Each pixel in the region is similar concerning some characteristic and contains colour, intensity or texture. Threshold methodology is the easiest process of image segmentation. This technique is utilised to transform a grayscale image into a binary image. The main benefit of this approach is selecting the threshold value to be used [24].

3.5.2. Region based

This method is based on continuity. This method spilt the complete image into substitute region depends on defined strategy like all pixel in specific region must have similar kind of pixels. This technique basically depends on collective patterns in the intensity value with in a constellation of neighbour pixels [25].

3.5.3. Classification algorithms

This method has no. of image processing techniques for image segmentation. Supervised is the simplest way to classify data. It is very useful for large image but has a poor contrast [24]. The classification method first trained data using supervised learning model with labelled dataset and validate the test dataset accordingly [26], [27]. During the module it extracts various features of training data and generates feature

vectors of those selected features. Once training has done similar feature extraction have been applied on testing dataset and classify test data accordingly.

4. ALGORITHM DESIGN

Input: Test Dataset with multiple instances testDB[], Train dataset instances for cancer care dataset and diabetic dataset as trainDB[], Threshold T. Output: HashMap <Disease_Name, Weight> contains entire dataset weight which is higher than threshold.

Step 1: Extract all test data instances as in (1). Here A[i] is the respective attribute after the data preprocessing.

$$testF(x) = \sum_{x=1}^n \left(\frac{Normalize[A[i], \dots, A[n]]}{\Sigma testDB} \right) \quad (1)$$

Step 2: Split the testF(x) using equation (2). Here m is number of attributes has selected from test instances likewise.

$$FeatureSetx[] = \sum_{x=1}^m (t) \leftarrow testF(x) \quad (2)$$

Here each (t) is the term which illustrates the attribute value extracted from test dataset and stored into FeatureSetx.

Step 3: Read Train instances as in (3). Here A[i] is the respective attribute after the data preprocessing.

$$trainF(y) = \sum_{y=1}^n \left(\frac{Normalize[A[i], \dots, A[n]]}{\Sigma trainDB} \right) \quad (3)$$

Step 4: Split the testF(x) using equation (4). Here m is number of attributes has selected from test instances likewise.

$$FeatureSety[] = \sum_{x=1}^m (t) \leftarrow tainF(x) \quad (4)$$

Here each (t) is the term which illustrates the attribute value extracted from train dataset and stored into FeatureSety.

Step 5: Now, evaluate each test feature vector with training model or training rules as in (5).

$$CorrectInstances + 1 = if (FeatureSetx || == || \geq || \leq \sum_{i=1}^n FeatureSety[y]) \quad (5)$$

Step 6: Calculate the current weight for each instances using (6).

$$weight = \frac{CorrectInstances}{Featuresety.length} * 100 \quad (6)$$

Step 7: Evaluate the current weight with desired threshold (7).

$$if(weight \geq Th) then Hashmap.add (trainF.class, weight) \quad (7)$$

Step 8: Go to (1) and continue till testF(x) == null.

Step 9: Return Hashmap calculated in (7).

5. RESULTS AND DISCUSSION

Intel i7 CPU 2.7 GHz has used with 16 GB Random Access Memory for execution. The RESENT (32,50, 101 and 152) version has used for experimental investigation of proposed systems including 5G network. The major factors has considered as detection accuracy for real time synthetic dataset of MRI images, The numerous deep learning frameworks have been evaluated on both dataset, and the accuracy of system is demonstrated in Table 1. Table 1 describes a brain tumor classification for MRI images for all deep models using TensorFlow for different data samples.

5.1. Performance evaluation

Performance of classification algorithm can be evaluated by performance metrics. Performance metrics involves terms like TP, FP, TN, FN, Confusion Matrix, Precision, Recall, Accuracy, F1Score, ROC AUC, AP and can be visualized using ROC curve and precision-recall curve.

Table 1. Data processing time with various deep models

Data samples	CNN	RCNN	FCNN	PNN	CBTD
100	92.30	96.30	97.4	94.10	97.20
200	93.10	96.50	95.6	94.30	96.30
500	92.50	95.10	94.8	94.25	98.40
1000	91.00	96.20	96.2	94.40	97.50

Performance metrics terms are briefed here:

- a. True Positive (TP): These are the cases when actual class of the observation is True and predicted class is also True.
- b. FP: These are the cases when actual class of the observation is False and predicted class is also True.
- c. TN: These are the cases when actual class of the observation is False and predicted class is also False.
- d. FN: These are the cases when actual class of the observation is True and predicted class is also False.
- e. Confusion Matrix: It is easiest metrics for finding accuracy and correctness of the model. It can be used with classification problem with two or more classes. Confusion Matrix is not a performance measure but all performance metrics are based on it and number inside it.
- f. Accuracy: It is the ratio of correctly predicted positive observations to the total observations given in (8).

$$Accuracy = \frac{TN+TP}{TN+TP+FN+FP} \tag{8}$$

- g. Precision: It is ratio of correctly predicted positive observations to the total predicted positive observations. It can be defined as the probability that given a positive test result, the sample is positive calculated using (9).

$$Precision = \frac{TP}{TP+FP} \tag{9}$$

- h. Recall: also called as sensitivity or True Positive Rate (TPR), is ratio of correctly predicted positive observations to all observations in actual class. It is probability of, given a positive example, a positive test result. It is calculated using (10).

$$Recall = \frac{TP}{TP+FN} \tag{10}$$

5.2. Performance Metrics of deep learning algorithms with proposed algorithm

Table 2 gives details of performance measures used for comparing output of proposed research with existing algorithms. This shows that proposed research is giving approximately similar results to FCNN. The Figure 2 also describes a visual interpretation of Table 1 that provides how time should be increased when data load has enlarged.

Table 2. CBTD comparison with existing algorithms

Performance Metrics	CNN	RCNN	FCNN	PNN	CBTD
Accuracy	88.80	91.10	90.30	90.60	94.20
Precision	89.00	91.15	91.00	91.20	94.30
Recall	89.30	91.20	90.25	91.00	94.15

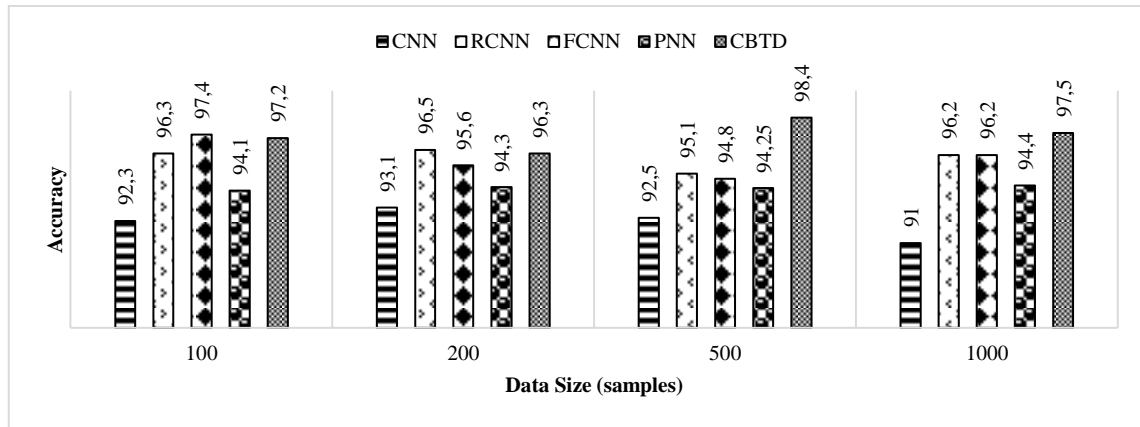


Figure 2. Detection of brain cancer using various deep learning algorithms

The Figure 3 demonstrates a default time reduction by proposed methodology after using all deep modelling with TensorFlow. Based on that experiment it can be concluded that residual neural network (ResNet) can reduce around 30% time than default execution time. Though multiple models and multiple deep learning algorithms are compared to understand performance of the proposed research work, it is necessary to understand hyper parameters used during experimentation work.

- Learning rate – To start with learning rate of 0.01 is selected which is then updated to 0.1 to increase accuracy.
- Batch size – During preprocessing and training, samples are increased gradually. Initially 100 samples were used which is increased upto 1000 samples in batch of +100, +300 and +500.
- Number of Epochs: Experimentation is performed in 10-fold and 15-fold cross validation with 7 and 8 epochs respectively.

The Figure 4 to Figure 6 illustrated on module training time required for different deep learning frameworks by using cafes. The ResNet provides slightly effective than other deep learning frameworks. It provides around 20% effective results than others. The compressive efficiency evaluation has been done on mobile computing file systems that is initially consider as input of system. The Figure 7 to Figure 9 describes the data testing time required for five different deep learning frameworks by using TensorFlow. Here also the ResNet provides slightly effective than other deep learning frameworks. It provides almost 16.5% effective results than other deep learning frameworks.

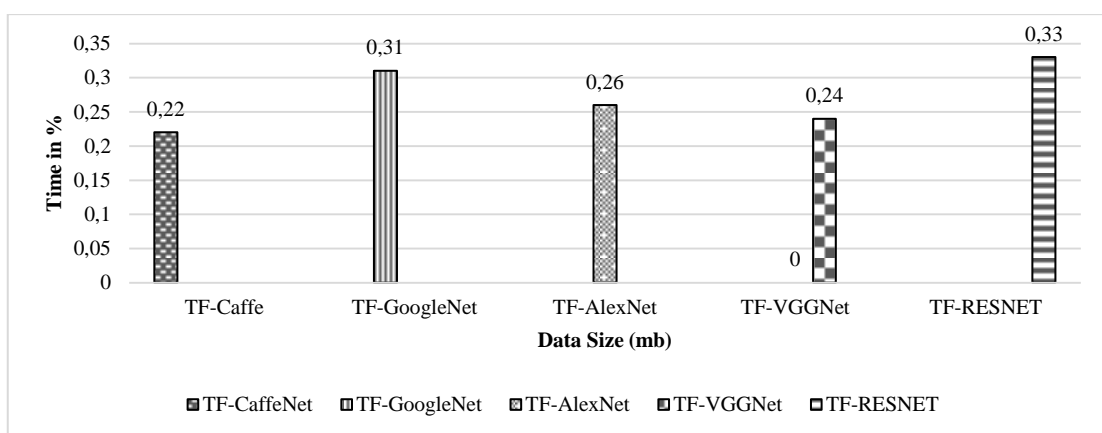


Figure 3. Default time reduction by Tensorflow by using different deep learning models

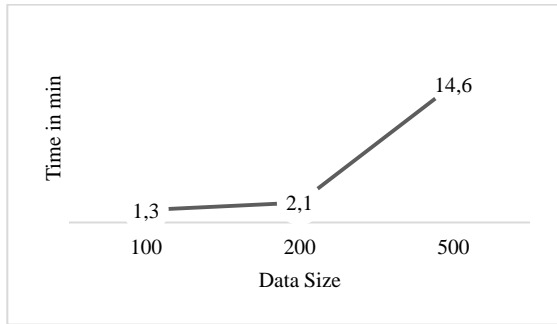


Figure 4. Data training caffe with CaffeNet

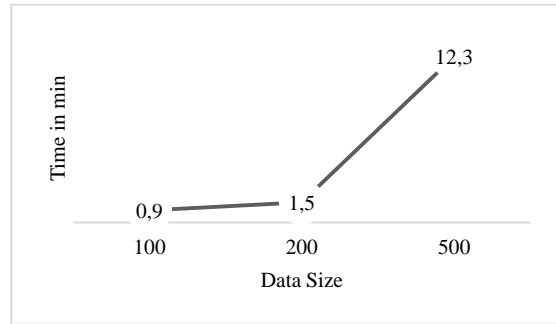


Figure 5. Data training caffe with GoogleNet

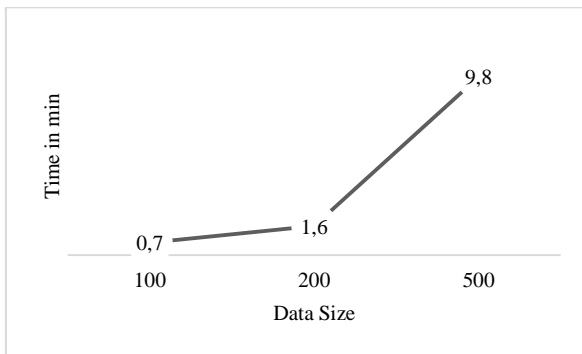


Figure 6. Data training caffe with ResNet

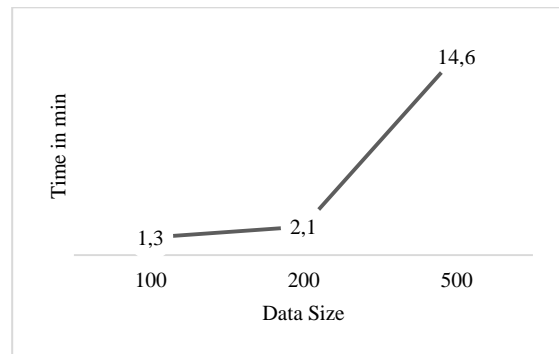


Figure 7. Data downloading tensorflow with CaffeNet

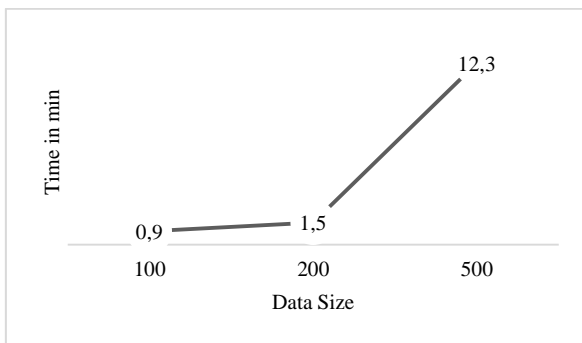


Figure 8. Data downloading tensorflow with GoogleNet

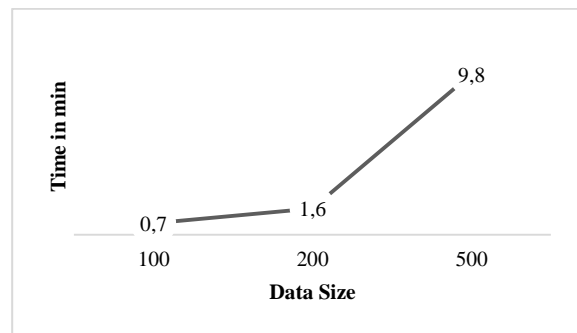


Figure 9. Data downloading tensorflow with ResNet




6. CONCLUSION

This research proposed a new Classification algorithm for brain tumour detection. The input MRI image database with three tumour types has been used to classify the images. Since proposed research has used the entire image as an input, the pre-process, normalization and segmentation has done. Proposed built neural network is easier to use than pre-trained networks, and the system can work on standard modern computers. Since the algorithm needs far fewer resources for both training and implementation, this is feasible. Proposed research has used performance and subject-wise 10-fold, 15-fold cross-validation to validate the network on both the initial and augmented image databases. In clinical diagnostics, generalization capacity refers to making predictions about subjects for which no data is available.




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