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## Efficient and low complex architecture for detection and classification of Brain Tumor using RCNN with Two Channel CNN

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### ABSTRACT

The Brain Tumor is one of the most serious scenarios associated with the brain where a cluster of abnormal cells grows in an uncontrolled fashion. The field of image processing has experienced remarkable growth in the area of biomedical applications with the invention of different techniques in deep learning. Brain tumor classification and detection is a subject of prime importance where Convolutional Neural Networks (CNN) find application. But the main drawback of the existing technology is that it is complex with a huge number of parameters contributing to high execution time and high system specifications for implementation. In this paper, a novel architecture for Brain tumor classification and tumor type object detection using the RCNN technique is proposed which has been analyzed using two publicly available datasets from Figshare (Cheng et al., 2017) and Kaggle (2020). Here we aim to decrease the execution time of a conventional RCNN architecture with the use of a low complex framework and propose a system for brain tumor analysis. We first use a Two Channel CNN, a low complex architecture to classify between Glioma and healthy tumor MRI samples which was successfully done with an accuracy of 98.21 percentage. Later this same architecture is used as the feature extractor of an RCNN to detect the tumor regions of the Glioma MRI sample that has been classified from the previous stage and the tumor region is bounded using bounding boxes. Also, this method has been extended to other two types of tumors Meningioma and Pituitary tumor. The methodology was able to achieve very low execution time as compared with the other existing architectures with an average confidence level of 98.83 percentage.

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### 1. Introduction

Cancer is the most common life-threatening disease nowadays, and among the various types of cancer, the most aggressive form is brain cancer or brain tumor. (Ali et al., 2020). Despite many technical advancements in the medical diagnosis and treatment, the survival rates are very low (Ghaffari et al., 2020). Brain is the most complex organ which plays a remarkable role in our day to day activities (Biju et al., 2017) and the uncontrolled irregular growth of tissues within the brain is known as a brain tumor, which is a very severe disease. It can be least the aggressive type called the benign or the life-threatening type called the malignant tumor

and if left untreated it can be fatal to the human life. It can be diagnosed using scanning techniques like Magnetic resonance imaging (MRI), Positron emission tomography (PET), Computed axial tomography (CT) among which MRI is popular due to its high resolution imaging property (Ali et al., 2020). For our research we are mainly concentrating on the three commonly found types of brain tumors specifically, Glioma, Meningioma and Pituitary Tumor. Gliomas are most common type of tumors with highest mortality rate (Pereira et al., 2016) which can be either higher grade or lower grade commonly found in the supporting tissue cells, called astrocytes and also in the cerebral hemispheres. Meningioma is usually a benign tumor that is slow growing in nature and is found at the outer coverings of the brain just under the skull. The type of tumor we are dealing with next is Pituitary Tumor. The gland located at the base portion of the brain is known as the pituitary gland and the tumor associated with this gland is called as the pituitary tumor. Meningioma and pituitary tumors are easy to detect because of their location of occurrence but Gliomas are hard to analyze (Somasundaram, 2019). However, our proposed method shows noticing improvement in the detection of Glioma tumor.

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Brain tumor detection and segmentation deals with separating the tumor portions from the normal tissues like Grey matter, White Matter and Cerebrospinal Fluid (Wadhwa et al., 2019). It can be done manually or automatically with the aid of a software. However human decisions are not always accurate and are time consuming which leads to computer analysis of tumor samples (Gawande and Mendre, 2018). Image processing plays a huge technical role in the above process. Object detection finds the location of a specific object in the image and bounds them using a bounding box. Whereas segmentation provides the exact outline of the image by assigning class labels to each pixel of the object. Traditional techniques for image detection and segmenting include thresholding method, edge-based method, region-based method, clustering method, watershed method etc. (Kaur and Kaur, 2014). However the recent studies show that Machine Learning which is a subset of artificial intelligence enables us to identify regions of interest in data in the most effective manner than the above mentioned traditional algorithms (Myszczyńska et al., n.d.). Deep learning which is a subset of machine learning has the ability to analyze multiple levels of data representation for the prediction and detection task (Wainberg et al., 2018). Deep neural networks like Convolutional neural networks (CNN) work efficiently on images producing remarkable results (Ker et al., 2017) which includes image classification, object detection, and segmentation (J. Liu et al., 2018). This research is concentrated mainly on classification and object detection.

Various researches have been taking place in the area of brain tumor classification, detection, segmentation and several good reviews are available which highlights the current scenario. In one of the review papers methods like K-means clustering, Statistical Region Merging, Bayesian Fuzzy Clustering approach etc. are discussed as the few new trends in machine learning for classification and detection which are said to perform better than traditional methods (Lather and Singh, 2020). The authors in (Ali et al., 2020) processes the tumor images and classifies them using Residual networks with skip connections to improve the performance which also helped to reduce the complexity and overfitting. Even though there are skip connections Resnet is again complex in nature and takes a huge time to execute. U-Net (Ronneberger et al., 2015) which is a specific network for biomedical image segmentation has separate sections for convolution and deconvolution for segmenting an image. Despite its high performance it requires 62M FLOPS and around 370 megabytes of storage which leads to the fact that it cannot be deployed on hand held devices with low computational complexity and also has a total number of training parameters of about 31.1 million (Gadosey et al., 2020). Javaria Amin et al. have put forward a novel idea of using CNN with batch normalization to detect Glioma and stroke lesion which has been successfully executed in different databases (Amin et al., 2020). In (Çinar and Yildirim, 2020), a convolutional hybrid neural network, in which the last five layers of the Residual networks are replaced by a hybrid model of ten layers and is used for tumor detection from MRI images. Multi modal Brain tumor classification which is a very important area that classifies between different modes of MRI samples using machine learning has been analyzed in (Khan et al., 2020). The textural features are extracted from a brain tumor image by using a local binary mode algorithm and a convolutional neural network in (A. Yang et al., 2019). Qiao Ke et al proposes Adaptive independent subspace analysis that helps to reduce the problem of large and high complex MRI (Ke et al., 2019). Enhanced convolutional network with loss optimization is done to segment tumor images to reduce overfitting in (Thaha et al., 2019). Multimodal information fusion and convolutional neural networks can be combined to detect the presence of tumor from MRI images (Li et al., 2019). The authors in (Yang et al., 2018) does Glioma grading on MRI database using the traditional deep

learning architectures with the help of transfer learning. Authors in (Selvapandian and Manivannan, 2018) proposes Glioma detection and segmentation using fusion based adaptive neuro fuzzy inference system and was tested on both low grade and high grade Glioma tumors. Genetic algorithm also finds its application in brain tumor grading and classification (Anaraki et al., 2018).

Region based convolutional neural networks (RCNN) is an object detection scheme using CNN which is applied in several image processing areas. RCNN is widely used for object detection applications, like foreign object detection on power transmission lines (Liu et al., 2019), detection of plant pests (Dalai, n.d.), biomedical applications etc. The authors in (Dalai, n.d.) proposes an automatic method to detect pests on plants using RCNN which showed a good improvement in detection accuracy. A stream path based RCNN framework in which the features are extracted from the CNN are passed through the Region proposal networks for ocean eddy detection (object detection), which shows an improved performance as compared with faster RCNN (Bai et al., 2019). The region proposal network in Faster RCNN has been modified in (Jinzhao et al., 2018) to detect vehicle types. Another variation of faster RCNN uses a deep residual network for feature extraction and K means clustering to cluster the bounding boxes (Zhang et al., 2020) which shows higher recognition accuracy and a high detection speed than the conventional Faster RCNN. A Face detection approach using Faster RCNN is used in (Sun et al., 2018), which added techniques like feature concatenation, multi scale training etc. to improve performance but with an increased computational complexity. Saliency guided faster RCNN method to generate the region proposals can improve the efficiency of object detection (Sharma and Mir, 2019). In (Ezhilarasi and Varalakshmi, 2019) benign and malignant tumors are detected where Alexnet is considered as the base network for feature extraction and these features are processed by the region proposal network for producing the region of interests. In (Kaldera et al., 2019), faster RCNN is used to detect Glioma and Meningioma from MRI slices with an average confidence of 94.6 percent. Three types of tumors are detected in (Murali and Meena, 2019) using faster RCNN where the CNN structure is made up of kernels of size  $3 \times 3$  only. Few of the important works in the literature about classification and detection of brain tumors has been incorporated in Table 1.

In this paper we propose a novel method for brain tumor detection using Two Channel CNN (Kesav and Jibukumar, 2021) which has been used in our earlier work for the classification of Meningioma and Pituitary tumors. The proposed low complexity method effectively reduces the number of parameters to be trained and the execution time for classification with a comparable accuracy. As compared with our earlier work (Kesav and Jibukumar, 2021), in this paper in addition to classifying the images into tumor types it also detects the region where the tumor is found. We have also included the third type of tumor Glioma in our classification and detection. At first, we use a classification mechanism to classify between Glioma and other healthy images using Two channel CNN. Then all these Glioma images are passed to the RCNN based detection system where the tumor parts from MRI images are detected and bounded using bounding boxes. The CNN used as a feature extraction layer of RCNN is replaced by the Two Channel CNN. The entire analysis and comparison are carried out initially on Glioma database and later it is also tested and verified for Meningioma and Pituitary Tumor. This method has been compared to other existing architectures combined with RCNN and with Fast and Faster RCNN. From the experiments we concluded that our proposed model has the least execution time with better efficiency. So, a complexity reduced CNN architecture with RCNN can reduce the total time and this model efficiently detects the three different tumor types which is elaborated in the result section. The section 2

**Table 1**  
Summarized related works on classification and detection of brain tumor.

Authors	Methodology	Classification	Detection/ Segmentation
Ali et al., 2020	Residual networks and skip connections	✓	
Ronneberger et al., 2015	U-Net		✓
Javaria Amin et al., 2020	CNN with batch normalisation	✓	✓
Çinar and Yildirim, 2020	Convolutional hybrid neural network	✓	
Khan et al., 2020	Deep learning with DCT and extreme learning mechanism	✓	
A. Yang et al., 2019	Local Binary Mode algorithm and CNN	✓	
Thaha et al., 2019	Enhanced convolutional network with loss optimization		✓
Li et al., 2019	Multimodal information fusion and CNN		✓
Ke et al., 2019	Adaptive independent subspace analysis	✓	
Y. Yang et al., 2018	Deep learning with transfer learning mechanism	✓	✓
Selvapandian and Manivannan, 2018	Fusion based adaptive neuro fuzzy inference system	✓	✓
Ezhilarasi and Varalakshmi, 2019	Alexnet with Region proposal networks		✓
Kaldera et al., 2019	Faster RCNN		✓
Murali and Meena, 2019	Faster RCNN with only $3 \times 3$ filters		✓

contains the methodology and materials used, section 3 deals with the results and section 4 concludes the work.

## 2. Methodology and materials

### 2.1. Region based convolutional neural network (RCNN)

Convolutional neural networks (CNN) have brought about remarkable changes in the area of image processing where any classification or segmenting tasks can be easily carried out precisely which is very important in biomedical applications. Also, CNN requires comparatively much less pre-processing than other conventional algorithms for diagnosis of MRI slices. CNN is a class of deep neural network which gets its inspiration from the cortex of our eyes where small group of cells are receptive to specific kind of visual field parameters such as vertical and horizontal features. A CNN basically consists of convolutional layer, pooling layer, ReLU layer and fully connected layer. However, compared with common artificial neural network all the nodes from the previous layer are not connected to the next layer.

Convolutional layer is responsible for extracting the features such as edges, lines etc. from the image given. It extracts the features using convolution operation with a sliding window matrix called a filter or kernel. Specifically, the filter performs a pixel wise multiplication operation with a subset of input image pixels and summation of the pixel wise multiplication results are performed. Then the filter slides along the entire image to carry out the similar operation. Now the result of each convolution operation is concatenated into a matrix which is called as a feature map in CNN terminology. There will be several convolutional layers depending upon

the complex nature of the application. It seems like the initial layers capture the basic information as edges and gradients etc. and the layers towards the end captures the detailed features of the image from the results of initial layers. We can add a valid padding if we have to increase the feature map size than the input image dimension. Mathematically the above-mentioned operation can be shown as is Eq. (1). Suppose we have an image input  $I$  of pixel size  $m \times n$ , a convolutional square kernel  $F$  of size  $l \times l$  and the output feature map  $S$  of size  $i \times j$ , the convolution operation can be defined as:

$$S[i,j] = (I * F)[i,j] = \sum_p \sum_q F(p,q) \times I [i-p,j-q] \quad (1)$$

Following the convolutional layer a pooling layer that is used to reduce the dimension of the output feature map. The feature map ( $S$ ) which is like an image is divided into several non-overlapping subsets and from each subset the relevant parameter is obtained. There are two types of pooling based on the parameter selected namely Max pooling and Average pooling. In Max pooling the maximum value from the subset is selected and in average pooling the average value of the subset is selected. We have selected Max Pooling as it was found to give better results in our research. The main purpose of the pooling layer is to reduce the overall computational complexity. Next is the activation layer which adds essential non linearity to the architecture which is needed in any neural network. Without the addition of non-linearity, the system will be linear in nature which will lead to failure in analyzing complex applications. There are several activation functions like Sigmoid, tanh, ReLU etc. Generally ReLU function,  $\max(0, \text{input})$  is used for CNN as it avoids vanishing gradient problem during the learning process. Final layers are fully connected layers which represents a basic artificial neural network where all the nodes from previous layer are connected to the next layer. The output feature matrix of the final convolution layer is flattened to form a one hot vector which is then given to the above fully connected layers. This layer learns a nonlinear function from the features and generates the classification results. Now CNN combined with region proposal layers can be used for higher level tasks like object detection and segmentation. This group of networks is known as Region based CNN (RCNN).

RCNN is a very famous object detection mechanism using CNN which efficiently classifies image regions and generates the detected bounding boxes containing the region of interest (Girshick et al., 2016). It basically consists of two additional modules, region proposal layer and detection layer along with CNN. The first module, region proposal layer produces the region proposals out of the input image which is then processed by the CNN. The third module, which is the fully connected final layer of CNN implements a Support Vector Machine (SVM) classifier which will detect the presence or absence of a specified object and also generates the bounding box around the object. The detailed steps are given in Fig. 1.

Region proposal layer: The region proposal layer divides the image into several sub blocks called candidate regions or proposed regions which are then fed to the CNN that will be compared with the ground truth bounding boxes. Out of the several region proposal algorithms RCNN typically uses, selective search algorithm (Smeulders, 2013) to produce candidate regions which is simple in nature and has got high recall. It creates an initial sub segmentation using a specified method (Felzenszwalb and Huttenlocher, n. d.) and later similar such small regions are combined into larger regions. Those proposed regions are passed on to the next layer.

Feature extraction layer: Before giving the proposed regions to the input of the CNN they are converted to a fixed size. From each proposed region constant length feature vectors are computed from the extracted features using CNN. The CNN used can be any

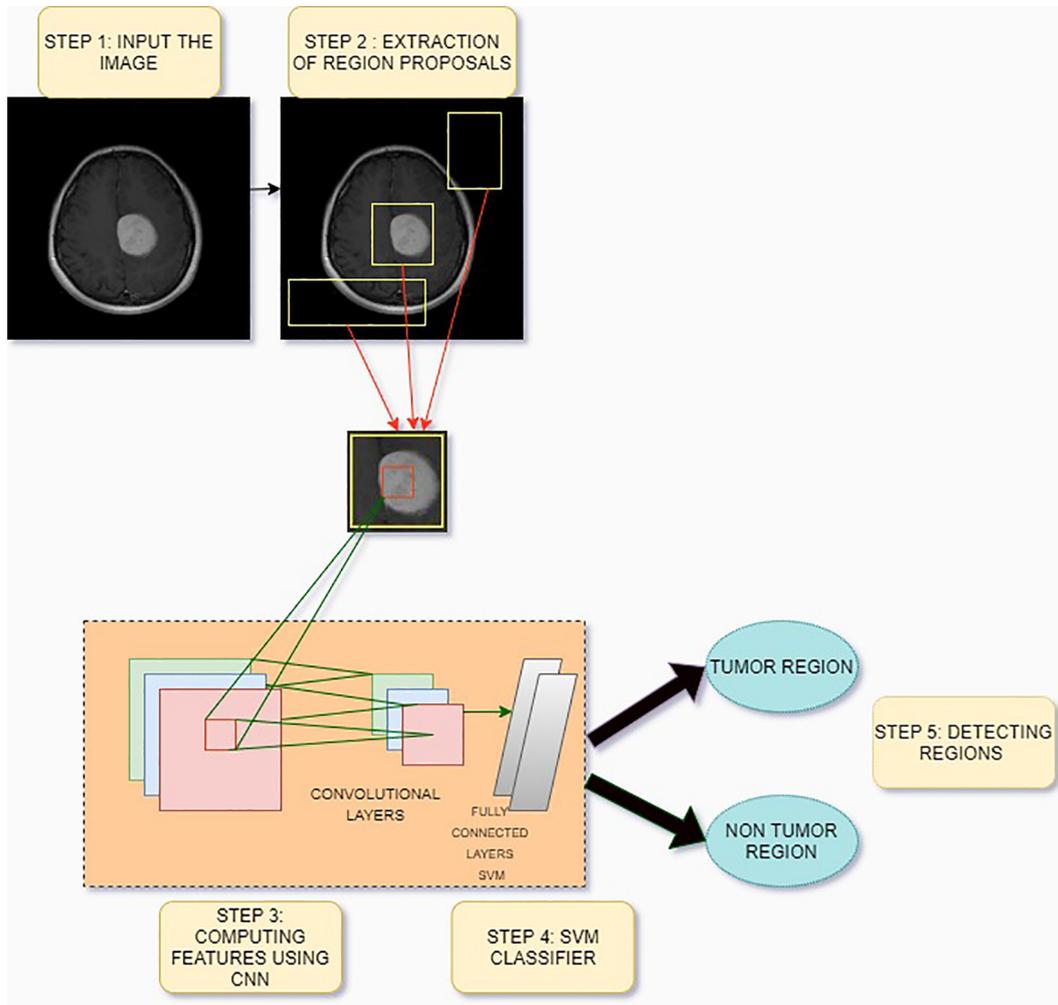


Fig. 1. Basic Block Diagram Of RCNN.

of the famous architectures like Alexnet (Krizhvesky et al., 2007), VGG16 (Tammina, 2019), VGG19 (Wen et al., 2019), Resnet (He et al., n.d.), Googlenet (Szegedy et al., 2015) etc.

**Detection Layer:** The feature vector from the final convolutional layer is passed onto the fully connected layer, a classifier, which is SVM in the case of RCNN. It detects the presence or absence of the required object and also provides a regression output of the bounding box coordinate values of the proposed region.

The problem with the above RCNN is that it is said to be slow in nature. It is because it will take huge amount of time to train the network as there are a huge number of region proposals that is being fed into the CNN. Also, selective search algorithm is generally considered to be consuming a lot of time. So, researchers have come up with another two architectures called fast and faster RCNN. Fast RCNN improves its speed by first getting features from the input image using a CNN and then finding region proposals out of them. Faster RCNN replaces the entire selective search algorithm with a new region proposal network. This network incorporates learning and helps to increase the speed. Fast and Faster RCNN methods usually take an entire image as it is without any resizing which adds additional complexity to the network. This is completely in contrast to RCNN which crops and resizes into region proposals initially and are fed to the CNN. Also, faster RCNN uses a region proposal network to determine region proposals which again contributes more parameters to be trained.

However, the use of a CNN with less complex architecture may increase the speed of the RCNN network while keeping the performance comparable to fast and faster RCNN. Based on the above intuition we propose an RCNN scheme where the feature extraction is replaced with a Two Channel CNN with reduced number of parameters (Kesav and Jibukumar, 2021). It is well known that as number of parameters increase the accuracy will start to saturate, leading to degradation of the performance with additional problems like exploding or vanishing gradients (Ali et al., 2020). Thus, low complex architectures with small convolutional kernels will help to improve the quality of feature extraction (X. Liu et al., 2019).

## 2.2. Proposed methodology

In our proposed methodology we first use Two Channel CNN (Kesav and Jibukumar, 2021) to classify the Glioma images from MRI samples and we send them to an object detection system using RCNN, where we replace the feature extraction layer of RCNN with Two Channel CNN which showed better performance in our initial studies. The block diagram of the proposed Two Channel CNN (Kesav and Jibukumar, 2021) which serves as the feature extraction layer of RCNN is shown in Fig. 2. As shown in Fig. 2 channel A consists of two convolutional layers and a pooling layer in between. First convolutional layer of the channel A is of filter

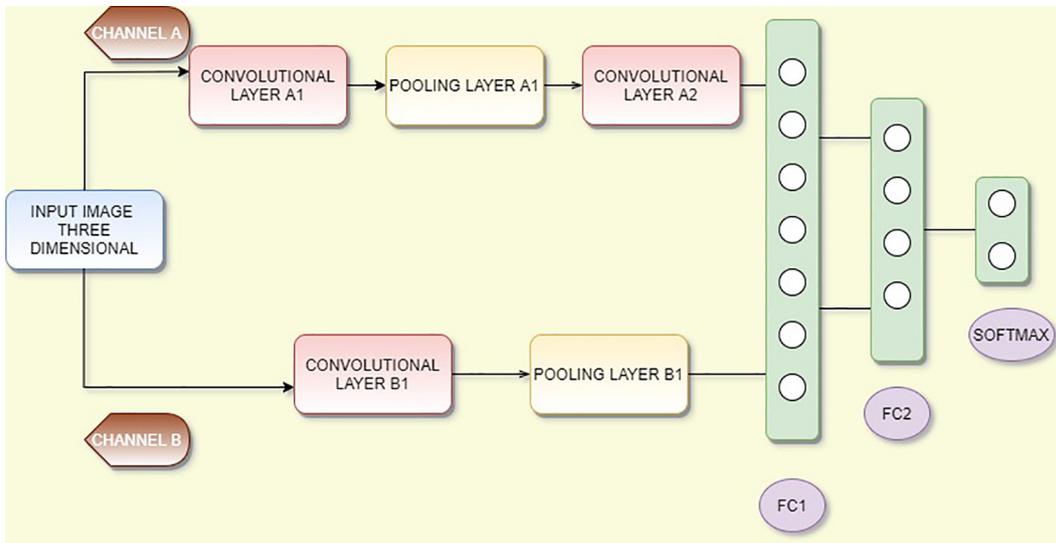


Fig. 2. Architecture Of Two channel CNN.

size  $3 \times 3$  followed by a pooling layer of dimension  $3 \times 3$ . The result of the first pooling layer is passed on to a second convolutional layer of filter size  $3 \times 3$ . However channel B is different from channel A. The channel B consists of a single convolutional layer followed by another pooling layer. This convolutional layer has filter size of  $13 \times 13$  and pooling layer dimensions are fixed at  $3 \times 3$ . All these dimensions were fixed based on the several analysis and experiments done in our earlier research (Kesav and Jibukumar, 2021). These two channels are then connected to a the fully connected layer followed by a softmax layer which could effectively classify different classes. The proposed Two Channel CNN was tested and proved to classify Meningioma and Pituitary tumors and was found to show better performance in terms of complexity and execution time previously. Here we are aiming to use this Two channel CNN to first classify between healthy and tumor MRI slices and then it is used as the feature extraction layer for tumor type detection using RCNN.

Fig. 3 shows the flow diagram of the proposed system that is used to detect the location of tumor. Firstly, the Glioma images

are separately classified from healthy tumor images using two channel CNN. These classified glioma images are then passed on to a region proposal layer. The region proposals or the candidate regions are extracted using the selective search algorithm. Later these regions are passed again to our architecture, Two Channel CNN for extracting the features. These features are converted into a one hot feature vector that is processed by SVM to detect the presence of a specific tumor and bounding them using bounding boxes so as to separate the specified part from other areas of the image.

### 2.3. Dataset and pre-processing

To evaluate the performance of the proposed architecture we use two freely available dataset. First dataset is from figshare which is a benchmark dataset for tumor diagnosis (Cheng et al., 2017) and second one is an open source dataset from Kaggle (Kaggle: Accessed date: June, 2020). The first database consists of 3064 T1 contrast enhanced image slices of a total of 233 patients.

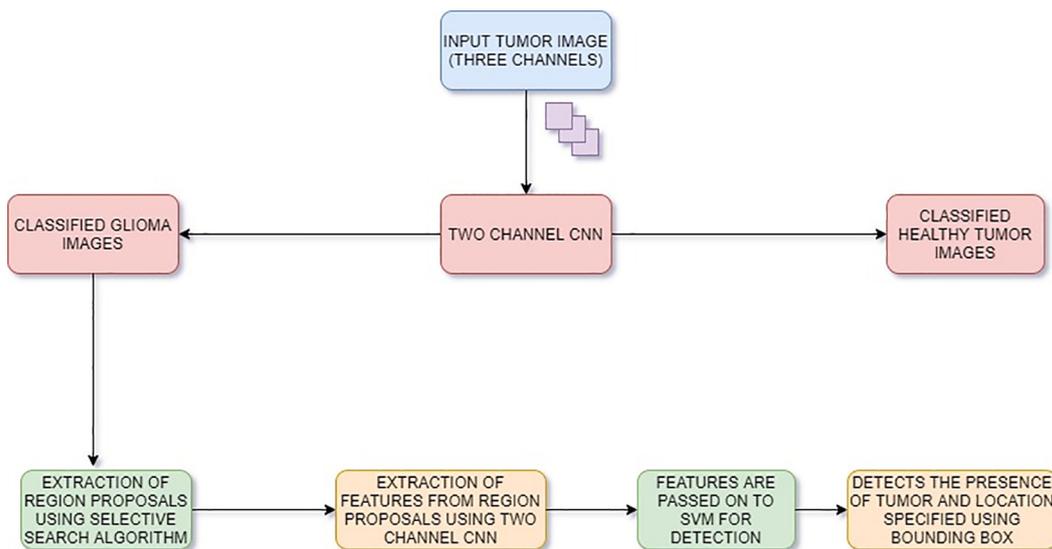


Fig. 3. Block diagram of the process for classifying and detecting tumor region using proposed method.

The MRI images contain all three types, Glioma, Meningioma and Pituitary tumor. The dataset was actually collected from two leading hospitals in China namely Nanfang Hospital and Tianjing Medical University. The images were acquired from patients during the period 2005 to 2010. The pie chart of the sample distribution in each tumor type case for first dataset is shown in Fig. 4.

There are 1426 MRI samples of 92 Glioma patients, 708 MRI samples of 82 Meningioma patients and 930 MRI samples of 62 Pituitary tumor patients. The MRI slices corresponding to all the three orientations axial, coronal and sagittal are available. From the total number of samples 80% is set aside for training and 20% for testing. The three types of tumor images are shown in Fig. 5. All these images are grey scale in nature and are of the dimension  $512 \times 512$  pixels. We need to resize them to  $227 \times 227$  pixels for our architecture. Later it was replicated three times to get three input channels.

We use a second dataset (Kaggle) as our first dataset could not provide healthy tumor images. The second dataset consists of 255 MRI images of T1 modality. It contains 98 MRI slices of healthy brain and 155 MRI slices of tumor condition. From this dataset we have only made use of the healthy images. All these images were of different dimensions and so we had to resize it according to our image specifications.

### 3. Results and discussion

The result section is divided into two sub divisions to highlight the classification and detection separately where first division deals with the classification between Glioma and healthy brain

samples and second division is the detection of the location of tumor type. The architecture specification and the parameters analyzed are different for both the cases. All the experiments are performed in MATLAB 2020. The system specification includes single CPU processing with 8 GB RAM and 2.6 GHz clock frequency.

#### 3.1. Classification of Glioma and healthy tumor images

In our previous work we tested and proved that the two channel CNN can classify Meningioma and Pituitary tumor images (Kesav and Jibukumar, 2021). Here we are extending the research on classification between Glioma and Healthy tumor images using the same two channel CNN. For the above classification about 30 percent of the total Glioma samples from the dataset 1 and all the healthy tumor images from the dataset 2 are used. Out of that 80% is used for training and 20% for testing in each category. The performance parameters that are used for the analysis are given below:

- Sensitivity(Recall) =  $\frac{TruePositive}{TruePositive + FalseNegative}$
- Specificity =  $\frac{TrueNegative}{TrueNegative + Falsepositive}$
- Precision =  $\frac{TruePositive}{TruePositive + Falsepositive}$
- Accuracy =  $\frac{TruePositive + TrueNegative}{TruePositive + Falsepositive + TrueNegative + FN}$
- F1score =  $\frac{2 * recall * precision}{recall + precision}$

The training parameters used for the training of the architecture is given in Table 2.

The optimal number of epochs have been chosen depending upon the validation error and training error. We chose to stop the iteration when the validation accuracy reached a high value

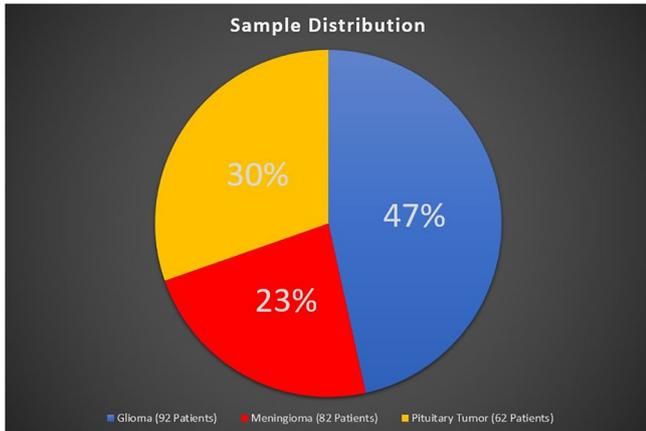


Fig. 4. Sample Distribution of Dataset 1.

Table 2  
Training Parameters for classification.

Parameters	Proposed Method
Initial learning rate	0.0003
Mini batch size	30
Iterations per epoch	35
Learning algorithm	ADAM
Maximum epochs	10
Data augmentation	Rotation applied
Validation frequency	20
Learning rate drop factor	0.9
Squared gradient decay factor	0.99

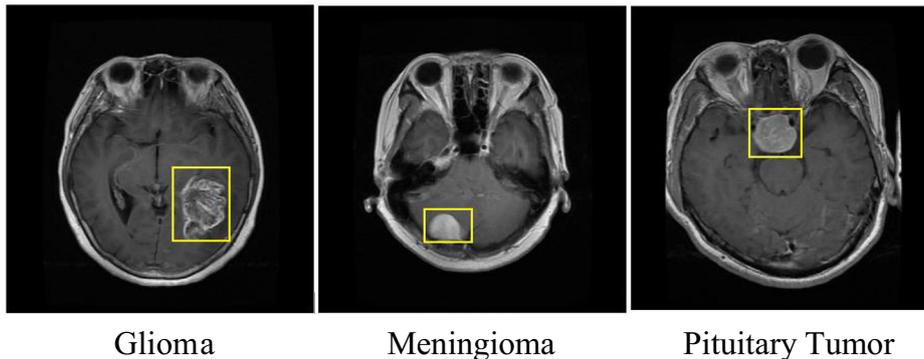


Fig. 5. MRI slices of Glioma (5a), Meningioma (5b) and Pituitary tumor (5c) MRI slices respectively.

**Table 3**  
Performance parameter results for analysis of classification.

Parameters	Value for proposed system
Accuracy	98.21%
Sensitivity	100%
Specificity	96.3%
Precision	96.7%
F1 score	0.9832
Execution time	64.592 s
No. of parameters	1,00,82,692
Area under the curve Glioma	0.9833
Area under the curve Healthy	0.9833

and the graph of validation error dropped to a very low value. The training is done for a total of 10 epochs and it is seen that the architecture could effectively classify Glioma images and healthy brain MRI samples with very small dataset. The validation and training accuracy starts from a lower value and reaches 100% at the final epoch. Similarly, the loss function curve starts at a higher value and ends with a value nearing to zero. All the parameters are calculated and tabulated in Table 3.

During the training process the most important problem to be addressed is that we should check whether our system works well on the test set even if it gives a good result using the training set. So, this problem of overfitting or underfitting can be tackled with the use of a validation set. At first, out of the total number of images used for training, 80% was set apart for actual training and 20% for validation. After each iteration the model is checked with this validation dataset and the training continues until the validation error drops to a value nearing to zero. But normal validation has several disadvantages like use of same data again and again, choice of the right validation set etc. For much more improved efficiency we also implemented cross validation scheme where the data is again split up into several subsets. We implemented 10-fold cross-validation scheme where one subset is used to validate the model that has been trained using the nine other subsets. The average cross-validation loss of 0.0581 was obtained after the completion of the process.

The parameters for observation are obtained from the confusion chart shown in Fig. 6 and are tabulated in Table 3. From Table 3 it is observed that Glioma and healthy brain samples are classified with an accuracy of 98.21%. The other parameters like specificity, sensitivity, precision etc. are also above 95% which shows a good performance. The F1 score is also nearly 1. The main parameters of attraction are execution time and no. of parameters. The execution time of our proposed method in this classification scenario is also low as 64.5s with a total number of only 1,00,82,692 parameters similar to our earlier research (Kesav and Jibukumar, 2021). This is due to the low complex nature of the architecture which enables it to perform well on system with less specifications. This can also help in reducing the total time consumption of the system so that the system can be used for real time processing efficiently. The receiver operator characteristics (ROC) is also plotted in Fig. 7 which has true positive rate on x axis and false positive rate on y axis. The area under the curve (AUC) of the ROC calculated for each case is above 0.9 which proves that the classifier shows an efficient performance. So, from this section we could conclude that the two channel CNN can effectively be used for classification between Glioma and Healthy tumor. The classified Glioma images are passed on to the next stage for detecting the tumor area.

### 3.2. Detecting the tumor type and specifying their location using RCNN

Now we are coming to the detection and locating the tumor part using RCNN with two channel CNN. Here we only make use of the dataset 1. Initially the analysis and comparisons are carried

out on Glioma MRI samples. Later the system is also tested on Meningioma and Pituitary tumor samples. The performance parameters that are used for analysis are Final accuracy, Final loss, Elapsed time, Bounding box values and Confidence score.

Final accuracy and loss correspond to the training progress of the RCNN. Accuracy measures how accurate is our prediction of the model when compared to the ground truth data. Loss evaluates how poorly the system behaves after each iteration of optimization. Ideally the accuracy should be high and the loss should be minimum at the end of the total number of epochs. Elapsed time which is the time taken for completion of the entire detection process is a crucial parameter which is used to evaluate the performance of different types of architectures. Bounding box values are the coordinates representing the dimensions of the box enclosing the required object. It mainly consists of four predictions namely x and y coordinates of the center portion, width of the box and height of the box. Finally, confidence is the parameter associated with the RCNN which plays a very important role in the design of an object detection network. It gives the probability that the detected region contains the required object. It is given by the formula:

$$C = P(\text{Object detected}) \times \text{IoU} \quad (2)$$

Where C is the confidence, P is the probability and IoU is the intersection over union between the predicted area and the ground truth given by:

$$\text{IoU} = \frac{\text{area under}(\text{BoundingBox} \cap \text{GroundTruthBox})}{\text{area under}(\text{BoundingBox} \cup \text{GroundTruthBox})} \quad (3)$$

The ground truth box is obtained by manual labelling of the images using the image labeler process. The training parameters for this specific system are given in Table 4.

#### 3.2.1. Comparison of proposed model with different architectures of RCNN

To evaluate the performance, we have compared the different existing architectures along with RCNN namely Alexnet, VGG16, VGG19, Googlenet and Resnet with our proposed model. As mentioned earlier the two channel CNN has already been tested successfully for brain tumor classification and now we are applying it as the base of the RCNN network for tumor detection. Now we are only concentrating and comparing with different architectures of RCNN later we also compare it with fast and faster RCNN in the coming sections.

From Table 5 it is very clear and evident that our proposed system is less complex than other systems and works better than all the other architectures compared. In terms of accuracy all architectures are able to produce 100% validation accuracy during training except for VGG19 and Resnet. The loss is also quite low except for the above-mentioned architectures. Now coming to the main parameter execution time, it is seen that our model is the fastest which only needs 277.17s to perform entire training and testing. It can perform speedy detection compared with other networks which is due to its low complex nature. It clearly outperforms every other architecture in tumor detection of glioma samples. All these parameter values are obtained and compared for the same database.

Fig. 8 gives the accuracy comparison for all the architectures with RCNN. All the architectures are trained for a total of 10 number of epochs. The accuracy shown here is specifically the validation accuracy during the training part. For all the architectures accuracy is low at the beginning of the training and towards the end of the training it gets to a value of 100%. It is completely evident from the comparison graph that the better performance is given by our proposed method with RCNN. It has got a better

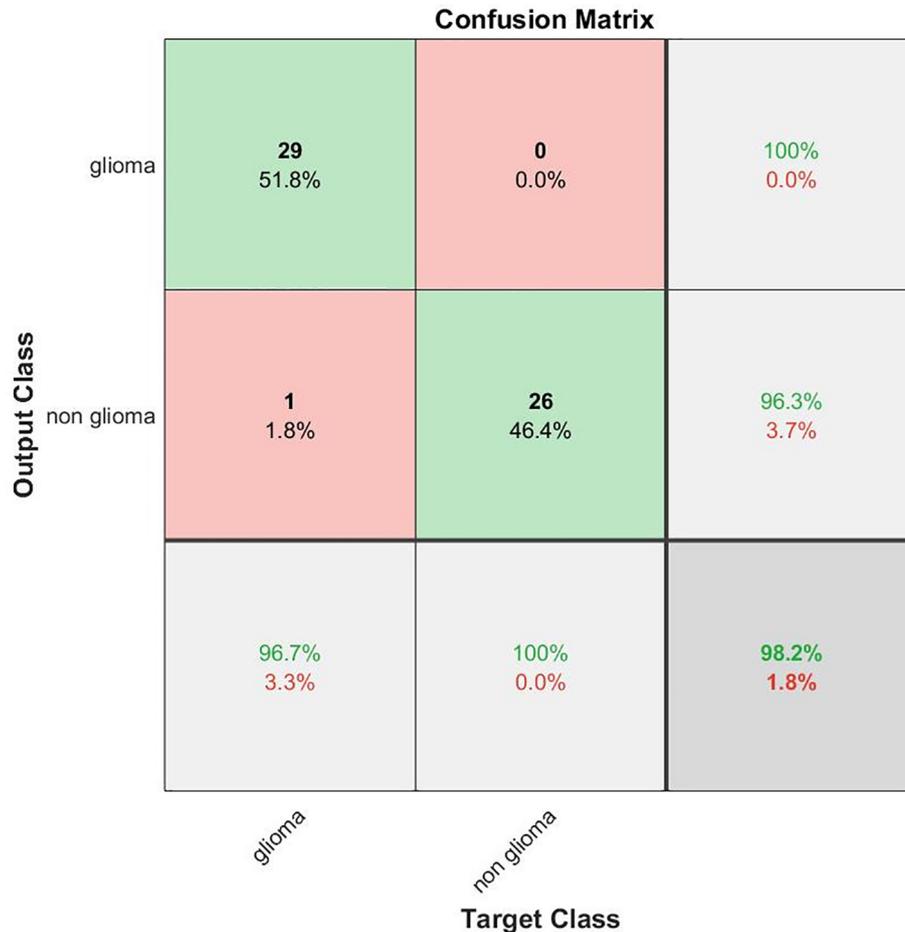


Fig. 6. Confusion Chart.

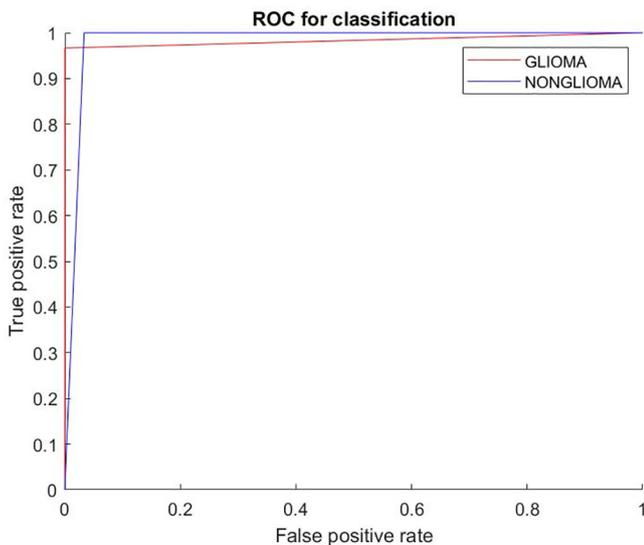


Fig. 7. Receiver Operator Characteristics.

**Table 4**

Training Parameters for detection using RCNN.

Parameters	Values
Mini Batch Size	32
Initial Learning Rate	0.001
Maximum number of epochs	10
Learning Algorithm	Stochastic Gradient Descent

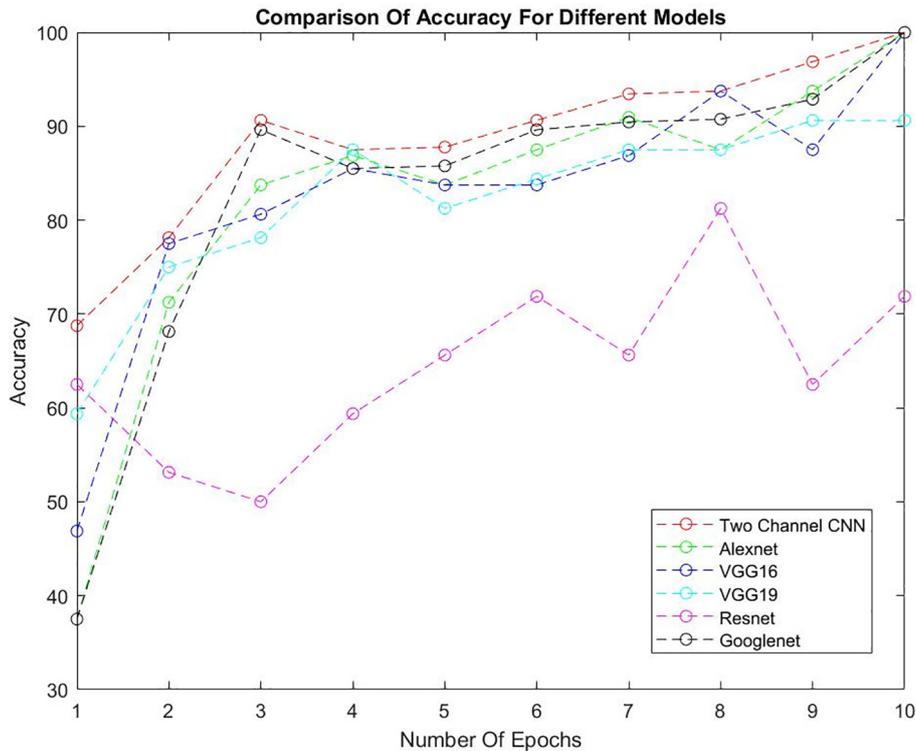
curve initially. But resnet has got a dip in the initial epochs. Later it reaches a high value but cannot reach 100% validation accuracy during training like our proposed model. We would like to also mention that the accuracy and loss mentioned are all during the training phase.

Now coming to Fig. 9 we can see that the loss rate for all the architectures has a high value at the starting of epoch one and converges to a value nearing to zero at the tenth epoch. Out of all the different architectures our proposed RCNN with two channel CNN has a better convergence rate. It converges to the minimum value among all the other architectures. A very high value for loss is found for Alexnet but it successfully converges towards the end. VGG16 also starts from a very high value and later it converges. Again, here the loss rate of google net has got a slight variation from the others. It peaks to a high value in between and then shows a sudden convergence which is not a steady pattern. The problem with resnet is that it fails to converge to a value near zero. This affects the total performance of the system. But our system shows a steady performance throughout the training session. So, from the accuracy and loss comparison plot we can conclude that

accuracy curve and convergence rate than other architectures. All the other architectures like Alexnet, VGG16, VGG19 and Googlenet shows similar performance curve like our proposed method. But the performance of Resnet is poor as compared to other architectures. For all the other architectures there is a peak in the accuracy

**Table 5**  
Comparison of performance parameters of different architectures of RCNN with proposed method.

Parameters	Alexnet	VGG16	VGG19	Resnet	Googlenet	Proposed method
Final Validation Accuracy	100%	100%	90.63%	71.88%	100%	100%
Final Loss	0.0371	0.0939	0.2059	0.5463	0.0196	0.0186
Elapsed Time	1209.994 s	19984.367 s	25543.174 s	8439.802 s	3209.704 s	277.17 s



**Fig. 8.** Comparison of accuracy for RCNN.

our proposed model has superior performance for detection of the location of Glioma tumors.

The output obtained using two channel CNN as base network of RCNN for locating Tumor from Glioma samples is shown in Table 6. Out of 50 samples tested three Glioma samples are randomly chosen and tabulated to showcase the results. The detected region is enclosed in a bounding box. The Table 6 also gives the bounding box values of the predicted area for each sample that specifies the four coordinate locations. It is seen from the table that the bounding box correctly encloses the region of the MRI affected by tumor. Every image is detected with an individual confidence score. The average confidence score of all the 50 samples tested is 98.83%. It shows that the detection scheme used is efficient enough to detect Glioma tumor and locate them.

The classification section using the Two Channel CNN takes an execution time of 64.5s. According to our previous work (Kesav and Jibukumar, 2021), it has been already proved that two channel CNN has got much less execution time than other architectures like Alexnet, VGG-16 etc. For detection section the execution time taken by our proposed RCNN in which the feature extraction layer CNN is replaced with Two channel CNN is 277.174s. So, combining both these processes it takes a total time of only 341.674s which is very much less than all the architectures that have been compared in Table 4, where it shows only the time taken for detection process (classification not included). Hence, in total there is only an addition of 64.5 s which still helps to claim our proposed idea that our system has least execution time.

**3.2.1.1. Comparison of RCNN using two channel CNN with fast and faster RCNN.** After establishing the performance of the proposed architecture with RCNN, we have compared its performance with fast and faster RCNN. We have mentioned the reason for reduced speed of RCNN and the evolution of fast and faster RCNN earlier. But this problem of reduced speed can be solved with the help of the Two Channel CNN, as it is a very less complex structure with only a total number of 1,00,82,692 trainable parameters. Here for the analysis and comparison we have considered two cases, Alexnet with Fast RCNN and Alexnet with Faster RCNN. Our conventional RCNN with two channel CNN as backbone is compared with the above mentioned two architectures and the results are tabulated. Again, this analysis is also carried out on Glioma samples, which has been classified from the classification stage. Here we use the same performance parameters as we have discussed earlier.

From Table 7 it is very much evident that the proposed method has got comparable performance with fast and faster RCNN. We could see that our system has the maximum validation accuracy of 100% along with faster RCNN with Alexnet. Also, we were able to complete training with very minimal loss. Our main aim was to reduce the total time taken by RCNN so that we don't have to go for fast or faster RCNN. The elapsed time for Fast RCNN with Alexnet is 272.572s and Faster RCNN with Alexnet is 232.235s. It is clear that faster RCNN works better than fast RCNN. But the fact here to be noted is that our proposed model also shows low execution time of 277.174s which is very much comparable to fast and

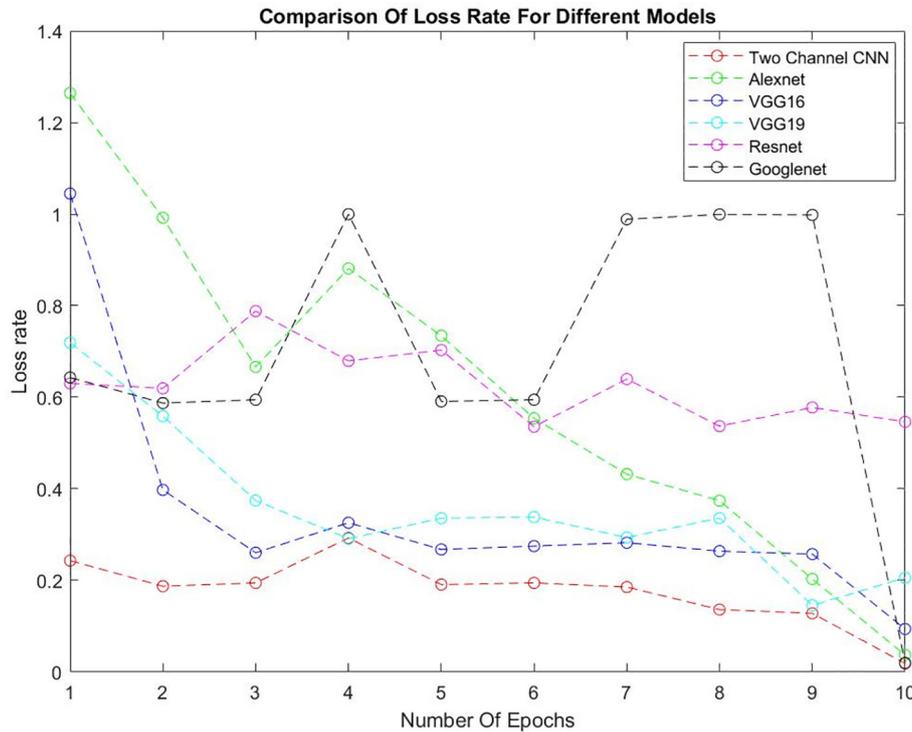


Fig. 9. Comparison of loss rate for RCNN.

faster RCNN with Alexnet. This concludes that our model was able to give speedy and accurate results comparable to Fast and Faster RCNN for Glioma samples. According to our knowledge it may be due to the fact that the other architectures combined with fast and faster RCNN needs more time for training due to huge number of parameters. Whereas two channel CNN has only very few parameters to be trained which increases the speed of the conventional RCNN technique. Our aim is to design a simple system that works well with very low system specifications without the help of any parallel processing capabilities which has been satisfied.

Fig. 10 gives the bar graph comparison of average confidence score of 50 test samples for all the different architectures we have compared till now which includes RCNN, Fast RCNN and faster RCNN. Confidence score of 100% means that the predicted area exactly overlaps with the ground truth. We could easily observe that out of all the architectures compared our model was able to achieve 98.83% average confidence score which is very near to the highest value obtained by faster RCNN which is 98.99%. Alexnet with Fast RCNN also has an average confidence score of 97.41%. It is seen that most of the architectures could obtain above 96% average confidence except Resnet with RCNN which could achieve only 85%. Fig. 11 gives the comparison chart of execution time for all the architectures mentioned above. VGG 19 with RCNN takes the maximum time of 25543.17s which is due to its high number of parameters to be trained. After that comes VGG16 with RCNN taking an execution time more than 10000s. Alexnet with RCNN takes less than 2000s. The least execution time is taken by Alexnet with Faster RCNN, Alexnet with Fast RCNN and our proposed model. Our model is superior to all the architectures with RCNN and it has comparable results with faster RCNN. Our concentration was to reduce the complex nature of the RCNN model and increase the speed of detecting the location of tumor. All these results prove that we could achieve this above-mentioned statement.

Table 8 represents the percentage reduction or decrease in execution time of RCNN with two channel CNN as compared to other architectures with RCNN. The percentage decrease is given as:

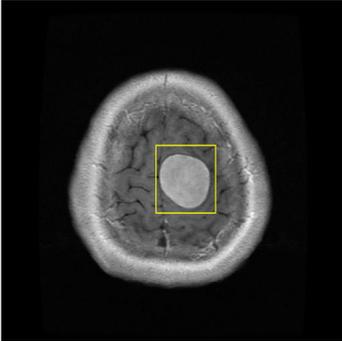
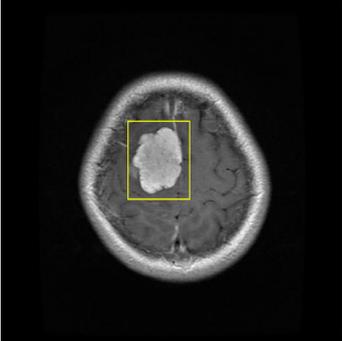
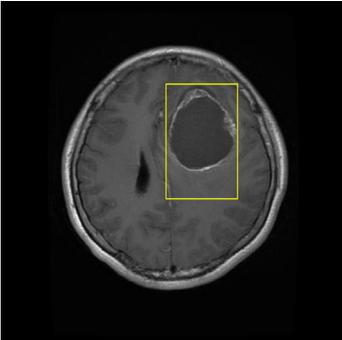
$$\text{PercentageDecrease} = \frac{\text{InitialValue} - \text{FinalValue}}{\text{Initialvalue}} \times 100\% \quad (4)$$

RCNN combined with different architectures are compared to RCNN with two channel CNN and the percentage decrease is calculated. According to the given values as we compare our model to RCNN with VGG16, RCNN with VGG19, RCNN with Resnet and RCNN with Googlenet, there is a percentage decrease greater than 80%. When comparing with RCNN with Alexnet we obtain a percentage decrease in the range of 70%.

The main aim of the research was to try to reduce the amount of overfitting caused. Over fitting is said to happen when the system performs well on the training data but it cannot correctly distinguish between the test data. There are several causes for over fitting like too much variance or noise in training data, smaller number of training samples and most importantly complexity of the model. One way of reducing over fitting is by using regularization and we have incorporated L2 regularization in the model. Another method is to incorporate cross validation mechanism and we have used a Ten-fold cross validation method to ensure proper validation. But our major concentration was to reduce complexity of the architecture by reducing the total number of parameters of the architecture. Our prescribed Two channel CNN has got a total of only 1,00,82,692 parameters which is very much less than the existing architectures (Kesav and Jibukumar, 2021). Again when it is combined with RCNN, the performance of RCNN has increased and it was able to put up a comparable performance with the very complex Fast and Faster RCNN. So the complex architectures of fast and faster RCNN can be replaced with RCNN using Two channel CNN. As a result, we were able to successfully reduce complexity, which in turn minimised overfitting by lowering the validation error.

3.2.1.2. Application on Meningioma and Pituitary tumor samples. In the previous sections we have concentrated on a particular type of brain tumor which was Glioma. It has been proved that RCNN with two channel CNN can effectively detect portions of Glioma

**Table 6**  
Detection results of Glioma images.

Glioma MRI samples	Bounding Box Values	Confidence of single sample	Output samples
Sample 1	[228 224 97 94]	1.0000	
Sample 2	[187 178 95 120]	0.9912	
Sample 3	[242 143 151 200]	0.9210	

**Table 7**  
Comparison of proposed model with fast and faster RCNN.

Parameters	Fast RCNN with Alexnet	Faster RCNN with Alexnet	Proposed model with RCNN
Final Validation Accuracy	99.02%	100%	100%
Final Loss	0.0485	0.0270	0.0186
Elapsed Time	272.572 s	232.235 s	277.174 s

tumor from MRI samples. Also, in our previous research we were able to classify between Meningioma and Pituitary tumors. Now we are extending our research to detection and locating other two types of brain tumors, Meningioma and Pituitary Tumor. As we know all these tumors differ in their location. We first labelled each of the tumors separately and built a ground truth label data which is fed into the same algorithm. Then we tried simulations on Meningioma and Pituitary Tumor samples and the results were tabulated. The performance parameters and training parameters used are all same as in the above sections.

Table 9 portrays two samples one from each category. The detection results are tabulated and it can be seen from the table that this proposed method could efficiently detect Meningioma

and Pituitary tumor from the given MRI samples. The bounding box values that correctly enclose the tumor portion is given in the table. It is also clear that both Meningioma and Pituitary tumor are detected from the given MRI samples with an average confidence score of 99.1% for meningioma and 97.6% for pituitary tumor. Hence it can be stated that our RCNN with Two Channel CNN can effectively work not just on Glioma samples but also on Meningioma and Pituitary tumor samples. So, this system can be considered as a brain tumor detection scheme for all three types of tumors providing speedy and accurate results.

### 3.3. Limitations of the proposed system

The proposed system could efficiently classify and detect all three different types of tumors Glioma, Meningioma and Pituitary tumor with very less execution time and comparable performance to leading architectures. However, the system's main drawback is that it is limited to object detection. The detection scheme just provides the location of the specific tumor using the bounding box. But for more precise diagnosis we need to implement the segmentation task. Segmentation task is capable of assigning class labels to each of the pixels in the detected portion containing the required object. So, it basically gives the exact outline of the object which

## Average Confidence comparison chart

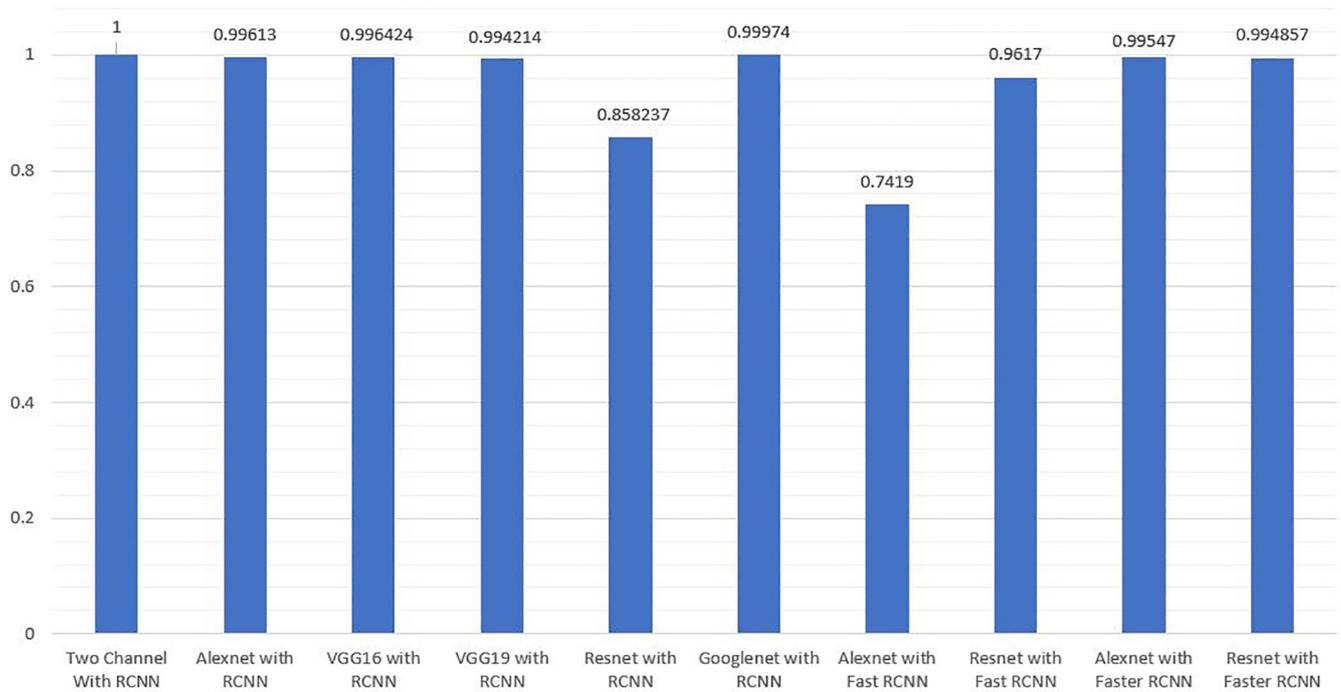


Fig. 10. Average Confidence Comparison.

## Execution Time Comparison

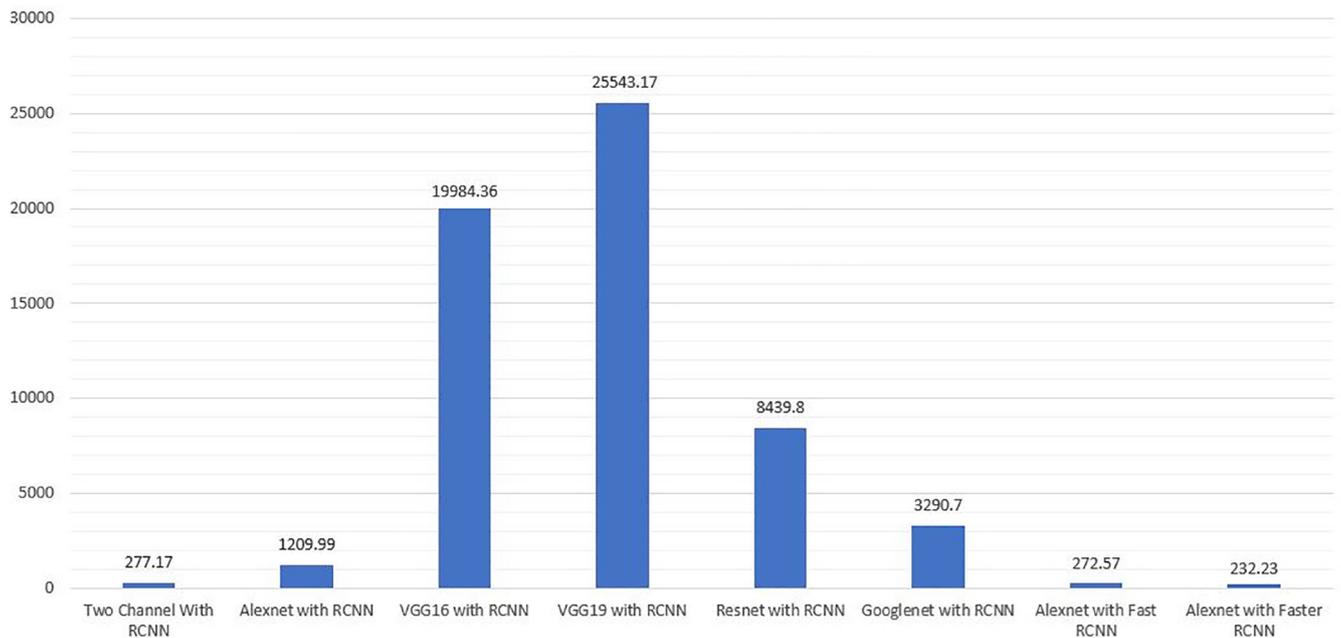


Fig. 11. Execution Time Comparison.

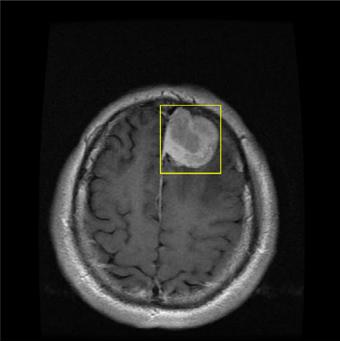
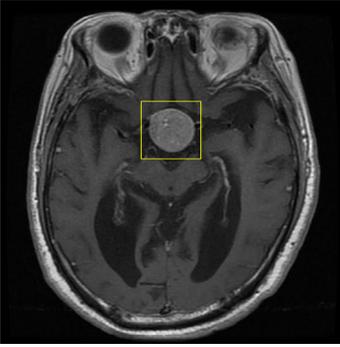
**Table 8**

Percentage reduction in execution time of RCNN with Two Channel CNN as compared to other architectures with RCNN.

Architecture	Percentage Decrease In Execution Time While Comparison
RCNN with Alexnet	70.96%
RCNN with VGG16	98.24%
RCNN with VGG19	98.62%
RCNN with Resnet	95.83%
RCNN with Googlenet	89.05%

**Table 9**

Detection results for Meningioma and Pituitary Tumor.

Tumor Type	Bounding Box Values	Confidence	Output image
Meningioma	[229 150 111 112]	0.9895	
Pituitary Tumor	[207 150 99 99]	0.9768	

is essential for treating the disease. This limitation will be tackled in the future extension of the proposed work.

#### 4. Conclusion

In this paper, we have proposed a method for classification and speedy object detection of Brain Tumor type MRI slices which detects and identifies the location of the tumor. Firstly, our proposed low complex Two Channel CNN architecture effectively classified Glioma and healthy tumor images with an accuracy of 98.21% along with a very low execution time of 64.5s, and these Glioma images are passed on to the object detection section. For the detection part, we have modified the famous RCNN technique to locate the required regions, where the CNN used for extracting features is again our Two-Channel CNN. The idea was to reduce the total number of parameters and computational time of the existing architectures used for detection so that it can be easily implemented in handheld devices with low computational facilities. We obtained good results for object detection using RCNN with an execution time of 277.174s and an average confidence score of 98.83%. The bounding box coordinates were also given which covers the required tumor region. The proposed method has been compared with various existing architec-

tures combined with RCNN and results show that it has been found to perform well than all of them. Again, a comparison is also carried out with Fast and Faster RCNN from which we got a conclusion that the results are comparable in terms of accuracy and execution time. So, our aim of reducing the total time taken for execution by the conventional RCNN has been achieved. The main advantage of this model is that it can work on systems with very few system specifications which will help in real time processing. Hence this proposed method can be efficiently used to classify and detect tumor types. The future work includes pixel wise segmentation of the tumor areas.

#### Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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