Available online at www.sciencedirect.com

ScienceDirect

Procedia Computer Science 218 (2023) 2468–2479

Procedia Computer Science

www.elsevier.com/locate/procedia

International Conference on Machine Learning and Data Engineering

Ensemble of Deep Learning Models for Brain Tumor Detection

Suraj Patil[1,2*], Dnyaneshwar Kirange[3]

.[1]*Research Scholar, SSBT's COE, Bambhori, KBC North Maharashtra University, Jalgaon, India*
[2]*Department of Computer Engineering, SVKMs MPSTME, Shirpur, India*
[3]*Department of Computer Engineering, SSBT's COE, Bambhori, KBC North Maharashtra University, Jalgaon, India*

Abstract

In the last two decades, improvement in artificial intelligence and medical imaging technology have made healthcare sector to achieve some remarkable achievements in diseases analysis and prediction. Due to advancement in medical imaging technology the brain images are taken in different modalities, that gives 3D view of different sections of brain for tumor diagnosis. The ability to extract relevant characteristics from magnetic resonance imaging (MRI) scans is a crucial step for brain tumor classifiers. As a result, several studies have proposed various strategies to extract relevant features from different modalities of MRI to predict the growth of abnormal tumor. Most of techniques used conventional techniques of image processing for feature extraction and machine learning for classification. More recently, the use deep learning algorithms in medical imaging has resulted in significant improvements in the classification and diagnosis of brain tumor. Since tumors are located at different regions of brain, the localizing the tumor and classifying it to particular category is challenging task. In this paper, we have solved this problem by designing deep ensemble model. In the proposed approach, first shallow convolutional neural network (SCNN) and VGG16 network were designed with T1C modality MRI image and subsequently loss and accuracy were examined. To improve the performance of model in terms accuracy and loss information, the extracted features from both the deep learning model were fused to improve the classification accuracy of three types of tumors. The obtained results from ensemble deep convolutional neural network model (EDCNN), proved that the fusion of deep learning model improves the accuracy of multiclass classification problem and also tries to address the problem of overfitting of model for imbalance dataset. The proposed model tries to give classification accuracy up to 97.77%. Furthermore, the proposed framework, achieves competitive results when compared with other state of art studies.

*Keywords:*MRI;Deep Learning;Ensemble;CNN;feature extraction

1877-0509 © 2023 The Authors. Published by Elsevier B.V.
This is an open access article under the CC BY-NC-ND license (https://creativecommons.org/licenses/by-nc-nd/4.0)
Peer-review under responsibility of the scientific committee of the International Conference on Machine Learning and Data Engineering
10.1016/j.procs.2023.01.222

1. Introduction

According to the (WHO)[1], cancer is the second leading cause of death globally. The severity and complexity of brain tumor can be minimized with precise automatic segmentation and classification technique that are deployed recently with deep learning approach. As per the radiologist the brain tumor can be broadly classified as benign and malignant. Benign tumor is non-cancerous and do not spread to other parts of body, whereas malignant tumor is cancerous and need surgical treatment. Early classification of brain tumour types can assist doctors and radiologists to decide line of treatment. Further depending upon the location of tumor and its severity brain tumor is classified into three different classes as gliomas, meningiomas, and pituitary tumor respectively[2,3]. Gliomas are tumor that arise from common brain stem cell and grow abnormally when these immature stem cell mutate. Meningiomas, on the other hand develop from the membranes that protect and surround the brain and central nervous system, whereas pituitary tumor is located in center of the head behind eyes[3]. The three types of tumors are distinctive in terms of severity, surrounding tumor tissue and location. So, it's important to examine distinctive features of three types of tumors for classification as malignant or benign. Meningiomas and pituitary tumours are usually benign, but most tumor of high-grade glioma are malignant. Because of these different characteristics of tumor, proper classification of brain tumor type is important in clinical diagnosis and effective assessment of tumor treatment.

Nomenclature

MRI	magnetic resonance imaging
SCNN	Shallow Convolutional Neural Network
EDCNN	Ensemble Deep Convolutional Neural Network
T1C	T1 with contrast image modality

Magnetic resonance imaging (MRI) is the most popular modality technique for tumor classification. However, it is prone to human error in manual segmentation and classification. To get exact location of tumor, the MRI images are taken in slice with different modalities. Early brain tumor identification is mostly dependent on the radiologist's experience. The manual segmentation and classification of tumor is time consuming process and takes 2-4 hours when executed by different radiologist. Therefore, it is critical and important to build an excellent diagnostics tool for tumor classification of brain MRI images in order to get exact diagnosis of brain tumor type and avoid future complexity of surgery [4].

Due to advancements in medical imaging technologies, particularly in artificial intelligence and deep learning, the analysis of brain tumor in terms of automatic segmentation and classification is becoming a popular and challenging problem. Moreover, during model training, the network becomes deep, some important information about the tumor gets lost [20]. A novel deep learning ensemble model is proposed to address the solution to this problem. The two-way path ensemble architecture consists of two models: i) Shallow Net CNN model (SCNN) and ii) the VGG16 model. The shallow CNN model and VGG16 are both designed in Kera's framework. The shallow CNN model aims to extract high-level information about tumors, as VGG16 gives deep features. The fusion of these two features is done using an ensemble deep CNN model (EDCNN). The extracted features from two models are fused to get optimal features for brain tumor classification. This approach not only preserves the spatial information of the tumor but also reduces information loss during training. So, the main motivation of this work is to learn the surrounding tissue of tumor that are more distinctive in tumor classification and to minimise the information loss during deep feature extraction with the help of an ensemble of deep learning models. These will assist the doctors and radiologist by providing them with a second option for doing the diagnosis tumor in the brain without opening too much of the body in a surgical operation.

The following is summary of paper contributions:

1. A shallow CNN model is designed to avoid brain tumor misclassification error, since MRI image can contain one or more distinctive tissue in real medical scenario. To overcome these challenge shallow features are used to get spatial properties of tumor classification that helps in localization of tumor.

2. A fusion of shallow and deep features is done to compensate for information loss during model training, since as the network gets deeper, some level of information gets lost.
3. Novel data frame approach with K-fold cross validation is used to handle imbalance dataset during ensemble of deep learning model.

The organization of the paper is as follows: The second section discusses the various deep learning and machine learning model for tumor classification. The third section discusses methodology used to designed shallow net CNN model (SCNN) and fused with VGG16 model to get ensemble deep convolutional neural network (EDCNN) model. The fourth section explains the experimental setup, dataset augmentation for model building. The fifth section discusses the result analysis and tuning of deep learning model. The final section highlights merits, limitation of current deep learning model and possible future research scope.

2. Related Work

In order to automate process of tumor detection, various machine and deep learning algorithms are proposed and become popular due to its promising solution and accuracy in diagnosis [12,21]. Sachdeva et al.[5] used a semi-automatic approach to determine the tumor contour, and then used the intensity profile, co-occurrence matrix, and Gabor functions to compute 71 features for tumor classification. The author [6] The multiscale deep learning approach was used in automatic segmentation and classification of three types of tumors with 97.3% accuracy[7]. The model could not be generalized, has author had done validation of model only on test dataset. The author Mohsen et al.[8] designed CNN model to classify four types of brain tumor images: non-tumor, glioblastoma, sarcoma, and metastasis with dataset of size 64 images. They achieved 96.97 percent accuracy using a deep neural network and extreme learning features (DNN). The author in[9] designed fused lightweight CNN model for diagnosis of Covid-19 using CT scan images. The proposed ensemble model combines the output of Squeeze Net (86.4%) and Shuffle Net (95.8%). The ensemble model outperformed the two-base model with accuracy of 97%. In [10] hybrid of 2D Gabor filtering and 2D DWT method used for feature extraction and classification was done using BPNN (Back Propagation Neural Network) model. The hybrid approach of feature extraction increases accuracy to 91.9%. Anaraki et al.,[11]proposed a hybrid strategy for improving network design that combines the usage of CNNs with genetic algorithm (GA) criteria to classify different grades of glioma tumor. Unlike traditional way of designing deep learning model with trial and error to minimize variance of prediction error, the architecture of CNN model was evolved using genetic algorithm. With this architecture author was able to get accuracy of 94.2% of classification of three types of tumors. The author in [12] , have designed deep learning model for chronic kidney diseases. The foremost important features were extracted using recursive feature elimination technique and deep learning classification outperform with other machine learning techniques with 100% accuracy.

3. Proposed Methodology

The proposed methodology uses an ensemble approach by fusion of shallow models and deep VGG16 models as seen in Figure.1. The first shallow CNN model (SCNN) is designed to extract shallow features from brain tumor MRI images. The first benefit of designing a shallow CNN model is to compensate for the loss of information incurred by a deep learning model when executed alone. The second benefit of shallow CNN model is that it reduces the complexity of the CNN model in terms of hyperparameters and computing cost. In order to improve the classification accuracy of brain tumor, the VGG16 model was designed using transfer learning to extract deep, fine-tuned features. The fusion of shallow model features with deep model fine-tuned features is done to compensate for information loss incurred during deep feature extraction and to retain spatial information about the tumor. In the proposed ensemble approach, the concatenation of the fully connected layers of both models is taken to have output-1 and output-2, respectively. The neurons of both the layers are fused into a single fully connected vector (FC-V3) and (FC-V2). The neurons coming from the fully connected layer are finally reduced to 1024 and fully connected to 3 neurons in the output layer. The output layer neurons depict the probabilities of output class meningioma, pituitary, and glioma tumours. Finally, by adjusting hyper parameter values and 50% dropout neurons, the classification is done with a sigmoid function on the output layer.

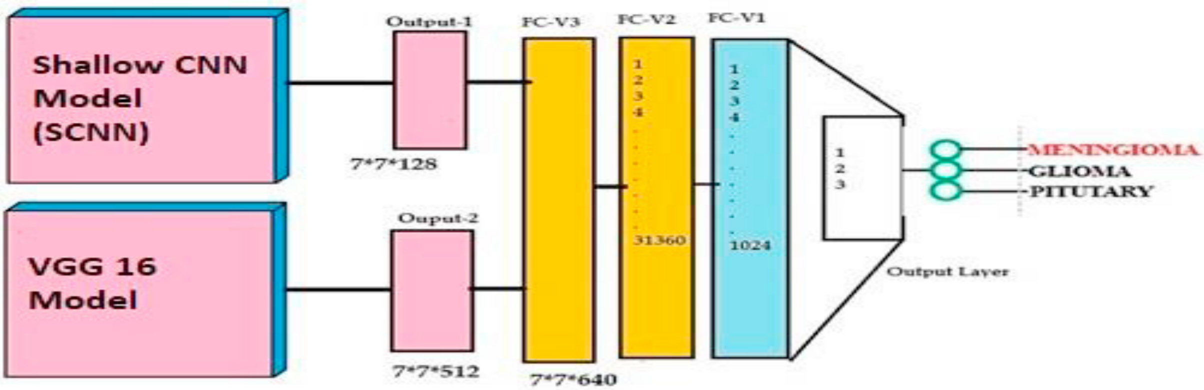

Figure.1. Proposed Pipeline of Deep Ensemble Convolutional Neural Network (EDCNN)

3.1. Shallow CNN Model (SCNN)

In Fig 2, a shallow convolutional neural network (SCNN) uses four convolution layers. The low-level features are extracted from the first and second convolutions. The high-level features are extracted from the third and fourth convolution layers. The low-level features give information such as pixel intensities of different white and black patches, edges, etc., whereas high-level features give information about different tissues based on tumor location. For the given proposed architecture, it is essential to understand how feature maps are generated for a given input image with a kernel of size k x k and the size of the convolution layer is given by equation (1): where Cf denotes the filter size of the kernel, P indicates the number of zero padding if required, and S refers to the number of strides in *l* convolutional layers.

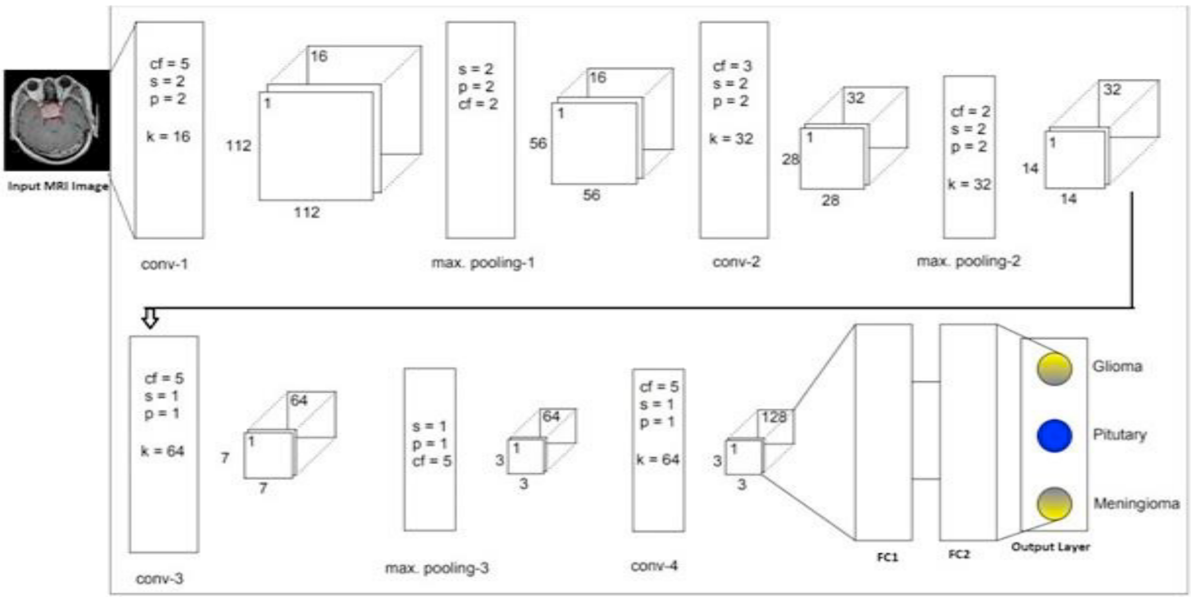

Figure.2. Pipeline of Shallow CNN Model (SCNN)

$$\left(ConvN_{wh}^{[l]}\right) = N_{wh}^{[l]} + \frac{2P^{[l]} - Cf^{[l-1]}+1}{S^{[l]}} \text{.................} \text{(Eq 1)}$$

The feature map generation mechanism of size *N X N* for above architecture is illustrated in following steps.

Step1: Input MRI image of Size 224 x 224.

Step2: $Conv_1$(convolution filter of size 5 x 5, Stride=Padding=2 and kernels of 32 feature map) are applied.

$$Covn1 = 2\frac{24 + 2 - 5}{2}+1=112$$

Therefore, in first convolutional layer, there will be 32 feature maps with 112 X112 X 32=401,408 neurons.

Step3: Applying Max Pooling operation

$$MaxPooling1 = \frac{112}{2} = 56$$

After applying Max Pooling with stride of *S=2*, the feature map reduces to size:56 X 56 X 32=100,352 neurons.

Step4: $Conv_1$(convolution filter of size 3 x 3, Stride=Padding=2 and kernels of 32 feature map) are applied.

$$Covn2 = \frac{56 + 2 - 5}{2}+1 =28$$

Therefore, in Second convolutional layer, there will be 32 feature maps with 28 X 28 X 32=25,008 neurons.

Step5: Applying Max Pooling operation

$$MaxPooling2 = \frac{28}{2} =14$$

Step6: $Conv_3$(convolution filter of size 5 x 5, Stride=Padding=2 and kernels of 64 feature map) are applied.

$$Covn3 = 14\frac{+ 2 - 5+}{2}1 =7$$

Therefore, in Third convolutional layer, there will be 64 feature maps with 7 X 7 X 64=3,136 neurons.

Step7: $Conv_4$(convolution filter of size 5 X 5, Stride=Padding=1 and kernels of 128 feature map) are applied.

Step8: Finally,1,152 neurons are flattened in single vector and are fully connected with another fully dense layer of 1024 neurons with 3 neurons in output layer to produce prediction of 3 types of tumors has shown in Fig.3.

3.2 Ensemble Deep Convolutional Neural Network(EDCNN)

The pictorial representation of proposed ensemble deep convolutional neural network (EDCNN) is designed by running tensor board on GPU as shown in Figure3. The proposed ensemble deep convolutional neural network generates hybrid feature, with shallow features of SCNN on right side and fine-tuned deep features of VGG16 model on left as shown in Figure3. The ensemble deep convolutional neural network uses VGG16 architecture with total trainable learning neurons 12,800 which are fuse with 6,272 neurons of SCNN as Fully connected layer (FC). The concatenated output of two models generates 640 feature maps as FCV3 (Fully Connected Vector-3) with 7 X 7 filters.

The additional flatten layer is created with 1024 neurons which are densely connected with 31,360 neurons coming from previous layer as FCV2(Fully Collected Vector-2). The batch is normalized and dropout of 0.5 percent is done to avoid overfitting problem. Finally, a dense layer of 1024 neurons with FCV1 (Fully Collected Vector-1) connected to output layer with 3 neurons for prediction of glioma, meningioma and pituitary tumor respectively.

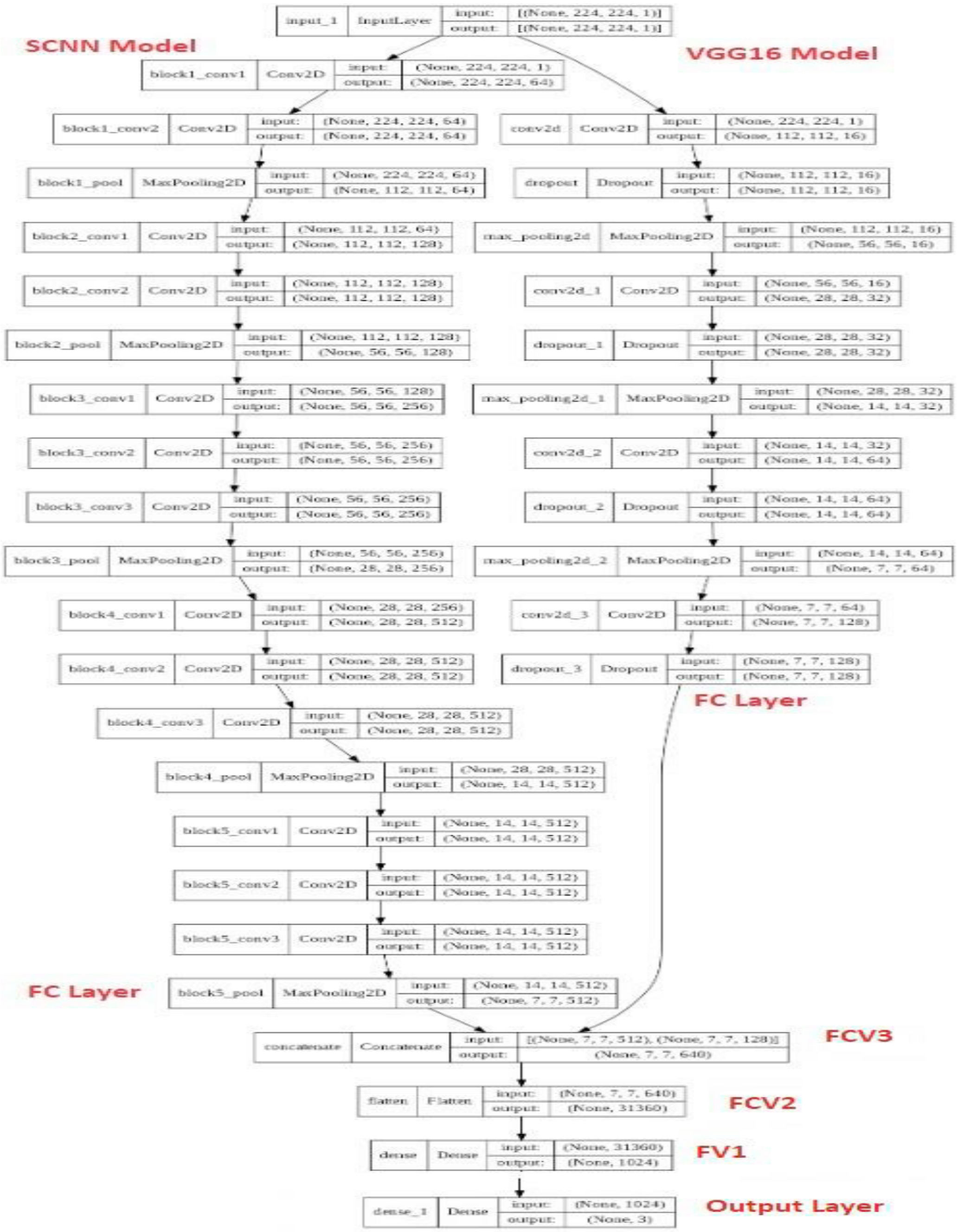

Figure.3. Proposed Ensemble Deep Convolutional Neural Network model (EDCNN)

4. Experimental Setup and Dataset Pre-processing

The proposed deep learning models is designed and trained on NVIDIA K80 GPU with 25 GB RAM. The model is tested and evaluated on brain MRI dataset [14]. The Adam optimizer is used to trained models with batch size of 30 and learning rate 0.0001. The experimental parameter setting is shown in Table1. The shallow CNN model and VGG16 model are trained separately using the parameter shown in Table1. The hybrid EDCNN model generated by merging fully connected layer of VGG16 and Shallow CNN is again trained with same parameter for next 30 epoch as shown in Figure5.

The dataset contains 3064 images of three types of brain tumor collected from 233 patients. There are 708 images of meningioma, 1426 images of glioma and 930 images of pituitary tumor. The dataset is highly imbalance with respect to three types of tumors, so data augmentation done with 90-degree rotation and flipping image vertically to increase size of dataset to 9000 images. The images are normalized to standard network size 224*224 pixel.

Table1. Parameters used with proposed ensemble brain tumor detection framework.

Hyperparameter	VGG16 Model	Shallow CNN Model
Optimizer	Adam	Adam
Batch Size	30	30
Epoch	20	50
Learning Rate	10^{-4}	10^{-4}
L2 Regularization	None	None
Momentum/Decay	Beta_1=0.9, beta_2=0.999, epsilon=1e^{-07}	Beta_1=0.9, beta_2=0.999, epsilon=1e^{-07}
Loss Function	Flatten Cross-Entropy	Flatten Cross-Entropy

5. Network Training

The accuracy of the custom shallow CNN model shows a lot of miss classification for meningioma tumor class due to dataset imbalance. Also, the loss and accuracy curves of the shallow CNN model show a lot of variations during model training, as seen in Figure 4. To overcome this problem, a data frame approach for training models with K-fold cross validation is used for the ensemble deep CNN model (EDCNN). The given approach creates a csv index file that contains information about the MRI image and brain tumor type. The index file is then used in 10-fold cross validation where each block of 10-fold contains images covering all three types of samples to minimize the variance during training. Algorithm1 shows the pseudo code used for the training model.

Algorithm1:
-Pseudo code for generating data frame and building Mixed Ensemble CNN weights.

Input: Input MRI Image(I)
Fully Connected vector v1 of SCNN and V2 of VGG16 Model
Output: ensemble model weights
Begin:
Step1: For each image in I performed two operations has:
i. Generate data frame index file with file name and tumor type information.

ii. Convert images into data frame with training and test set with .75 and .25 ratio and return data frame

Step2: Input the data frame with image shape (224,224,1)

Step3: Initialize the value of k=10 for cross validation.

Step4: Initialize Adam optimizer learning rate to 10^{-4} with cross entropy loss function.

Step5: Trained the model with .70 for training and .30 for validation ratio batch_size=30,epoch=50.

Step6: Merged weights of vector1 and vector v2 as FC Layer

Step7: Add dense layer and drop out .5%

Step8: Save Optimized Weights if no improvement in loss and return best accuracy ensemble model

End.

6. Result and Discussion

The ensemble deep convolutional neural network model (EDCNN) has been designed step by step by analysing the performance of the shallow (SCNN) and VGG16 model. The number of layers after merging two deep learning models is decided based on the cross-entropy loss function. The effect of three different models on the brain tumor dataset is shown in Table 2. The average training time taken by the custom shallow CNN model is low as compared to the VGG16 deep model and ensemble model. This is because the custom shallow CNN model was designed to extract high-level information specific to tumor localization, and hence it has high loss and low accuracy compared to other models. VGG16 model was designed to learn low-level information about tumor such as abnormal tissue and hence average training time increases. The ensemble deep learning model has taken the benefit of both of these models in terms of information loss and training time and got promising network training accuracy with minimum information loss and training time as shown in Table2.

Table 2. Effect of ensemble on model training

Model Type	Average Accuracy	Average Loss	Average Training Time in Seconds
Shallow CNN Model (SCNN)	77.96%	0.57	11s
VGG16 Model	95%	0.032	208s
Ensemble Deep Learning Model (EDCNN) [SCNN+VGG16]	96.49%	0.12	91s

After training model Figure4, shows loss and accuracy of custom shallow CNN model. The fluctuations that were seen in loss and accuracy during training of the shallow CNN model are minimized into the fine smooth curve by concatenation of last fully connected layer of shallow CNN model with VGG16 model as seen in Figure5. The fully connected layer of two models becomes input layer to proposed ensemble model. From experiment results, it is seen that the addition of a dense layer and a dropout layer reduces the amount of information loss during training of the EDCNN model with K-fold cross validation, as seen in Figure5. The confusion matrix in Figure 6. (A). shows the accuracy of the SCNN model, and Figure 6. (B). shows the accuracy of the EDCNN model on test data. As shown in Figure 6. (A), the SCNN model makes numerous misclassifications for meningioma tumors, resulting in a decrease in the model's overall accuracy by 30.66%. This misclassification is overcome in EDCNN model with an ensemble of

SCNN and VGG16 models as seen in Figure6. (B). resulting overall accuracy of 96.66%.

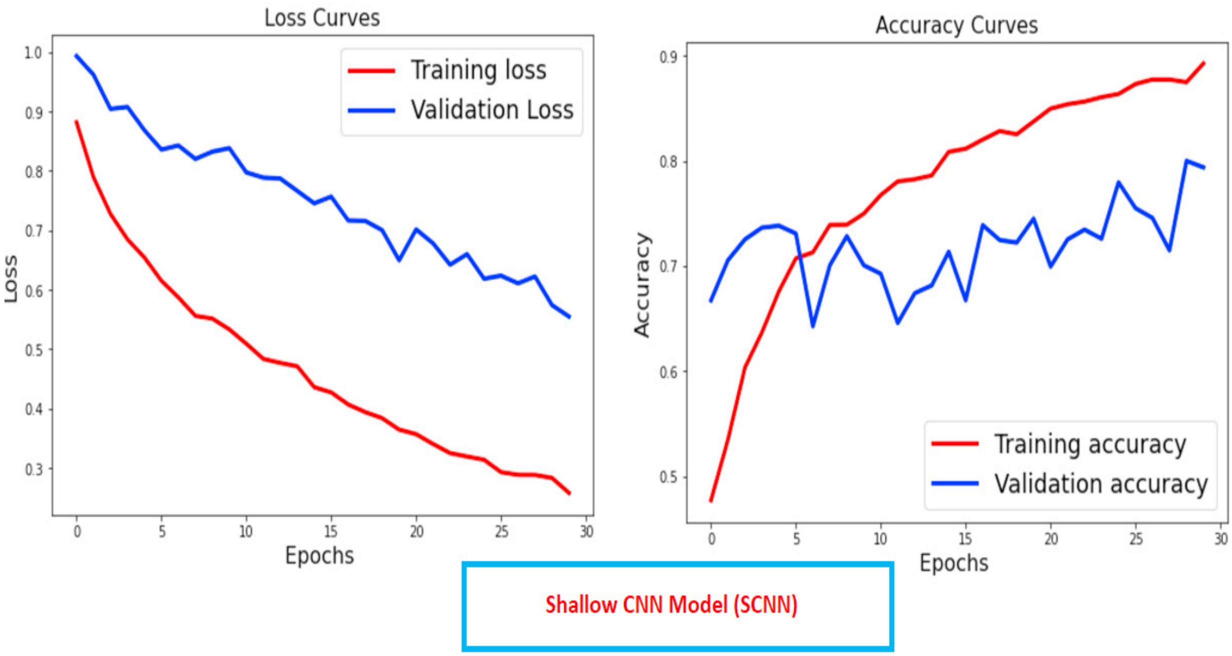

Figure.4. Loss and Accuracy Curves of custom Shallow CNN model (SCNN)

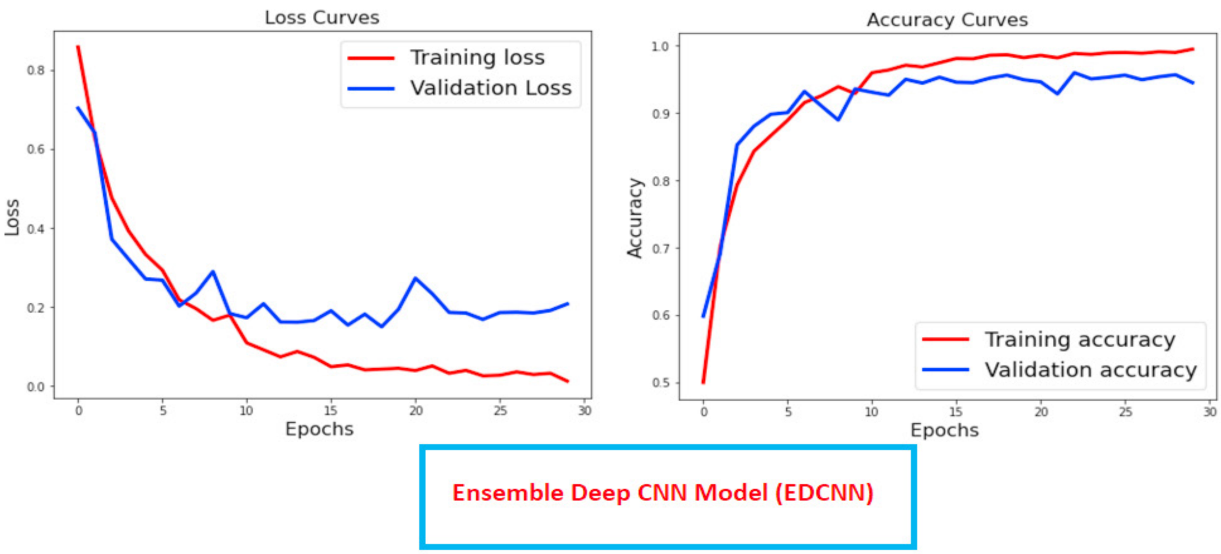

Figure.5. Loss and Accuracy Curves of Ensemble Deep CNN model (EDCNN)

		Predicted Label		
		Glioma	Meningioma	pituitary
	Glioma	99%	0%	0%
True Label	Meningioma	83%	12%	6%
	pituitary	13%	0%	87%

(A)

		Predicted Label		
		Glioma	Meningioma	pituitary
	Glioma	95%	4%	1%
True Label	Meningioma	3%	95%	2%
	pituitary	0%	0%	100%

(B)

Figure.6. (A) Confusion Matrix SCNN Model (B) Confusion Matrix EDCNN Model

Table 3. The comparison of the proposed model with other network architectures, trained on the same Fig share dataset[13] using K-fold cross-validation technique.

References	**K-Fold Cross Validation**	**Accuracy [%]**	**Average Precision [%]**	**Average Recall [%]**	**Average Sensitivity [%]**	**Average Specificity [%]**	**Average F1-Score [%]**
Phaye et al.**[15].**	8-fold; data division not stated.	95.03	X	X	X	X	X
Pashaei et al.**[16] .**	10-fold; 70% data in training set,30% in	93.68	94.60	91.43	X	X	93
Gumaei et al.**[17].**	10-fold; 70% data in training set,30% in	92.61	X	X	X	X	X
Swati et al. **[20].**	5-fold: 70% data in training set and 30% in	96.13	96.06	94.43	X	96.9	X
Proposed Model EDCNN	**10-fold; 70% data in training set,30% in**	**97.77**	**96.66**	**98.30**	**96.66**	**98.33**	**97.47**

To compare results of proposed model to those of earlier studies, we included papers that have used full MRI image instead of segmented parts of tumor, and tested deep CNN networks using the k-fold cross-validation approach.

Most of the papers designed CNN models and showed only accuracy as a performance parameter. In a real-time scenario, accuracy alone cannot be used to judge the model's performance. Our proposed model outperforms other state of the art methods proposed by different authors in terms of accuracy, precision, recall, sensitivity, specificity, and F1-score as shown in Tabel3. Furthermore, as shown in Table2, training an ensemble model with K-fold cross validation effectively handles imbalance datasets with minimal loss and training time.

7. Conclusions and Future Work

In this work, a novel new ensemble deep convolutional neural network (EDCNN) architecture for brain tumor classification is presented that take benefit of both shallow model and deep model. In the proposed method, the weights of two individually designed deep learning models are combined. With this approach, the proposed deep learning model outperforms other deep learning methods with a prediction accuracy of 97.77%. The model accuracy is also compared with other performance parameters like precision, recall, specificity and sensitivity. The finding in this work demonstrates that features extracted from shallow CNN helps in getting some high-level information about tumor, which helps in localization of tumor in brain. When these features are fused with deep features extracted from deep model like VGG16 to get hybrid features helps in increasing overall accuracy of tumor detection. From the experiment results, it is seen that the fusion of weights of deep learning models not only improves the accuracy of deep learning models but also minimizes information loss and reduces the computation time of training on very large datasets. In future more robust optimized shallow CNN model can be designed with optimal hyper parameter and use of meta heuristic algorithm for feature selection.

Acknowledgement

Suraj P Patil acknowledge to SSBT's College of Engineering and thankful for providing research center lab to carry out experiment as part of PhD research work.

References

[1] World Health Organization Cancer 2022:1–1.

[2] Viswa Priya V. An Efficient Segmentation Approach for Brain Tumor Detection in MRI. Indian Journal of Science and Technology 2016;9. https://doi.org/10.17485/ijst/2016/v9i19/90440.

[3] Patil S, Kirange D, Nemade V. Predictive modelling of brain tumor detection using deep learning. Journal of Critical Reviews. 2020;7.

[4] Chhabda S, Carney O, D'Arco F, Jacques TS, Mankad K. The 2016 World Health Organization Classification of tumours of the Central Nervous System: what the paediatric neuroradiologist needs to know. Quantitative Imaging in Medicine and Surgery 2016; 6:486–9. https://doi.org/10.21037/qims.2016.10.01.

[5] Kirimtat A, Krejcar O, Selamat A. Brain MRI Modality Understanding: A Guide for Image Processing and Segmentation, 2020, p. 705–15. https://doi.org/10.1007/978-3-030-45385-5_63.

[6] Sachdeva J, Kumar V, Gupta I, Khandelwal N, Ahuja CK. A package-SFERCB-"Segmentation, feature extraction, reduction and classification analysis by both SVM and ANN for brain tumors." Applied Soft Computing 2016; 47:151–67. https://doi.org/10.1016/j.asoc.2016.05.020.

[7] Díaz-Pernas FJ, Martínez-Zarzuela M, Antón-Rodríguez M, González-Ortega D. A Deep Learning Approach for Brain Tumor Classification and Segmentation Using a Multiscale Convolutional Neural Network. Healthcare 2021; 9:153. https://doi.org/10.3390/healthcare9020153.

[8] Mohsen H, El-Dahshan E-SA, El-Horbaty E-SM, Salem A-BM. Classification using deep learning neural networks for brain tumors. Future Computing and Informatics Journal 2018; 3:68–71. https://doi.org/10.1016/j.fcij.2017.12.001.

[9] Krishnaswamy Rangarajan A, Ramachandran HK. A fused lightweight CNN model for the diagnosis of COVID-19 using CT scan images. Automatika 2022; 63:171–84. https://doi.org/10.1080/00051144.2021.2014037.

[10] Ismael MR, Abdel-Qader I. Brain Tumor Classification via Statistical Features and Back-Propagation Neural Network. 2018 IEEE International Conference on Electro/Information Technology (EIT), IEEE; 2018, p.

0252–7. https://doi.org/10.1109/EIT.2018.8500308.

[11] Kabir Anaraki A, Ayati M, Kazemi F. Magnetic resonance imaging-based brain tumor grades classification and grading via convolutional neural networks and genetic algorithms. Biocybernetics and Biomedical Engineering 2019; 39:63–74. https://doi.org/10.1016/j.bbe.2018.10.004.

[12] Litjens G, Kooi T, Bejnordi BE, Setio AAA, Ciompi F, Ghafoorian M, et al. A survey on deep learning in medical image analysis. Medical Image Analysis 2017; 42:60–88. https://doi.org/10.1016/j.media.2017.07.005.

[13] Akkus Z, Galimzianova A, Hoogi A, Rubin DL, Erickson BJ. Deep Learning for Brain MRI Segmentation: State of the Art and Future Directions. Journal of Digital Imaging 2017; 30:449–59. https://doi.org/10.1007/s10278-017-9983-4.

[14] J. Cheng. Figshare Brain tumor dataset. Https://FigshareCom/Articles/Dataset/Brain_tumor_dataset/1512427/5 (Accessed April 14, 2022) 2021.

[15] Phaye SSR, Sikka A, Dhall A, Bathula D. Dense and Diverse Capsule Networks: Making the Capsules Learn Better 2018.

[16] Pashaei A, Sajedi H, Jazayeri N. Brain Tumor Classification via Convolutional Neural Network and Extreme Learning Machines. 2018 8th International Conference on Computer and Knowledge Engineering (ICCKE), IEEE; 2018, p. 314–9. https://doi.org/10.1109/ICCKE.2018.8566571.

[17] Gumaei A, Hassan MM, Hassan MR, Alelaiwi A, Fortino G. A Hybrid Feature Extraction Method with Regularized Extreme Learning Machine for Brain Tumor Classification. IEEE Access 2019; 7:36266–73. https://doi.org/10.1109/ACCESS.2019.2904145.

[18] Priyanka Rastogi, Vijendra Singh, Monika Yadav. Deep Learning and Big Data Technologies in Medical Image Analysis. 5th IEEE International Conference on Parallel, Distributed and Grid Computing (PDGC-2018), 20-22 Dec, 2018, Solan, India,978-1-5386-6026-3.

[19] Vijendra Singh, Vijayan K. Ansari, Rajkumar Rajasekaran. A Deep Neural Network for Early Detection and Prediction of Chronic Kidney Diseases. Artificial Intelligence in Healthcare, 5 Jan 2022, https://doi.org/10.3390/diagnostics12010116

[20] Swati ZNK, Zhao Q, Kabir M, Ali F, Ali Z, Ahmed S, et al. Brain tumor classification for MR images using transfer learning and fine-tuning. Computerized Medical Imaging and Graphics 2019; 75:34–46.

[21] Chaturvedi P, Jhamb A, Vanani M, Nemade V. Prediction and classification of lung cancer using machine learning techniques. InIOP Conference Series: Materials Science and Engineering 2021 Mar 1 (Vol. 1099, No. 1, p. 012059). IOP Publishing.