

Fusion of Convolutional Neural Networks and Random Forests for Brain Tumor Classification in MRI Scans

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Abstract:

This paper proposes a combined framework of CNN+RFC to brain tumor categorization/classification using MRI (Magnetic-Resonance Imaging) images, which combines both CNN (Convolution Neural Networks) and RFC (Random Forest Classification). Preprocessing, Feature bring-out, and Categorization are the three phases of the proposed framework. In the first step, we use the Gaussian Filter Method on the data set then we combine the original data set with processed data in parallel. The feature extraction of magnetic resonance imaging was performed automatically by CNN in the second step. We also called such a type of process in this paper as non-hand-crafted feature extraction. Several classification algorithms, including RFC (Random Forest Classifier), KNN (K-Nearest Neighbor Classifier), DT (Decision Tree Classifier), SVM (Support Vector Machine Classifier), and NB (Naïve Bayes Classifier), are used in the final step. The extracted features from the CNN model are then given to the classifier algorithms, which predict Glioma tumor, Pituitary tumor, Meningioma tumor, and no tumor as a result of the testing data set. Experiments are carried out on an open data set of images selected for classification from the Kaggle databases. This data set is very complex since it contains images of brain tumor with different angles and different depths. We don't alter this data set at all. We make a separate CSV file that contains testing images' name and their specification. Using this proposed approach, we were able to achieve 99.61% accuracy on the training data set, 92.16% on the validation data, and 71.2% on the CSV/testing data.

1. Introduction

The brain, which is made up of billions of cells, is the most compound organ in the human body. It is a gateway to intelligence, a meaning translator, a movement initiator, and a controller of action and speech. It is the origin of all the numbers that characterize our humanity. When certain brains cells grow abnormally, a brain tumor develops. A primary brain tumor are those that occur in the brain, whereas subordinate brain tumor are those that broaden to the brain from other areas of the body. The most common cancers that broaden to the brain are kidney, breast, lung and, bladder [1-17]. A primary brain tumor may be benign or cancerous, while subordinate tumor are often

cancerous. Both forms of brain tumor are life-threatening and can result in long-term impairment even after treatment [18,19]. It causes the brain's healthy cells to die and interferes with its normal functioning. The space inside the human skull is limited, as we know from brain anatomy, and is fill up by brain cells and Cerebrospinal Fluid [20-30]. The pressure inside the brain will rise if brain tissues are stretched out. This increase in pressure causes brain injury, seizure, edema, coma, stroke, or death [24].

The CBTRUS (Central-Brain Tumor Registry of the US) has reported that cancer of the Brain and Nervous System is the 10th leading cause of death in both males and females [25,26]. This year, primary cancerous brain and CNS tumor are

expected to kill 18600 adults (10500 males and 8100 females). In this report, they also explain the 5-year survival statistic policy. The 5-year survival statistic indicates how many people survive for at least 5 years after a tumor were discovered. People with brain cancer or CNS tumor have a 36% 5-year survival statistic [27]. The 10-year survival statistic is approximately 31%. When people get older, their chances of surviving decrease. People under the age of 15 have a 5-year survival statistic of more than 75%. The 5-year survival statistic to people aged 15 to 39 is more than 72 percent [28]. People aged 40 and up have a 5-year survival statistic of more than 21%.

Therapy of a brain tumor in its initial stages is a difficult due to the wide range of sizes, shapes, and locations that only is done by a qualified specialist neuroradiologist [29]. For the therapy of a brain tumor, both the category and the grade of the tumor must determine. In most cases, MRI is used to diagnose a brain tumor. When an MR imaging reveals a brain tumor, the most usual way to ascertain the category of tumor is to examine the result of a biopsy or operation on a sample of tissue. It uses to assess the tumor grade [31]. This grading indicates the likelihood of the tumor growing in size and spreading. Several examine have been conducted in the past to enhance the early detection and treatment of tumors. Computer technology has been extensively using in medical decision-making in a variety of medical fields. We must examine the character of the tumors and make decisions based on the results of the test subject's medical imaging studies. We use MR imaging in this study because it is Non-Invasive and has no established Biological risks [32]. MR imaging scans can produce images with a high level of information material. It has different variations such as T1, T2 Weighted, and FLAIR. These all variations of MRI are present in our training and testing data set that make the data set very complex. In T1-Weighted, TE and TR times are short, and in T2-Weighted, TE and TR times are long. FLAIR imaging is similar to T2 Weighted imaging. These imaging techniques can represent the scale, variance, and position of objects along an axis coordinate in an accurate manner [33].

We consider three kinds of brain tumors in our study: Glioma, Pituitary Tumor, and Meningioma Tumor. Primary tumors may be cancerous or benign. In adults, glioma tumors and meningiomas tumors are common. Glioma tumors develop from glial cells, which sustain the structure of your central nervous system and provide nutrition to it. Meningiomas tumors arise in the Meninges and, Pituitary Tumors are benign tumors that affect the Pituitary Gland [34].

In the medical community, brain tumor categorization is a critical role. Manual categorization of MR imaging is a difficult, expensive process that can lead to declassification; therefore, automated or semi-automatic classification techniques are required to distinguish between different tumor types. [35] Semi-automatic classification techniques, such as GLCM (Grey-Level Co-occurrence Matrix), PCA (Principal Component Analysis), 3D-Gaussian Filter, VOI of the image, and wavelet transformation (DWT), are used to bring out features from the given images data set and feed these extracted features to the classifier algorithms, while automatic classification techniques, on the other hand, features were extracted by the model itself it is also called as non-hand-crafted feature extraction such model as CNN. A CNN is a DNN (Deep Neural Network) class. It operates with the convolution kernels' shared-weight architecture, which slides along input features and provides function maps. This function map is used for more complex operations like image classification. The CNN learning network uses machine learning to optimize convolution kernels or filters. Pooling, flattening, and the number of input and output channels are all hyper parameters in CNN, in addition to kernels. Additionally, additional convolution hyper parameters such as padding, stride, and dilation are used to build a CNN model.

In this paper, we use a CNN-based automated model to solve a classification problem. This model is used to extract features without the need for human intervention. In the Methodology session, the architecture of such a model is briefly defined. We can use other classification algorithms including SVM, KNN, RFC, DT, and NB to categorize the class of the given MR imaging brain images once the CNN model extracts the features. CNN-RFC, CNN-KNN, CNN-SVM, CNN-DT, and CNN-NB models combine the benefits of both approaches. CNN has two advantages: sparse communication among neurons between layers and weight sharing between layers. This CNN-RFC model automatically selects the most relevant elements, saving you time and effort. As a result, this proposed model outperforms other models such as CNN+KNN, CNN, CNN+SVM, CNN+DT, and CNN+NB.

The arrangement of the paper is as follows: In section II we talk about the related work, section III talk about the proposed methodology (Data set Description, Methodology and Feature selection, Experimental Result and Discussion), section IV discusses the conclusion, and section V references used.

2. Related Work

This section discusses several automated or semiautomatic methods for the categorization of brain tumors that have been proposed over the years such as.

Kharat, & et al. [1] presents two DNN techniques for the organization of the MR imaging image of brain tumor. The three stages of this deep neural network technique are feature dissociation, dimensional depletion, and organization. Two classification algorithms are feed-forward ANN and second Back-Propagation NN. This network was created for image processing, differentiation, validation, extraction of features, object detection, and classification.

Zulpe, N., & Pawar, V. [2] proposed a brain tumor classification scheme based on automatic recognition. They used four separate types of brain tumors and extricated the GLCM based appearance features for each type, which they then applied to a two-layered Feed-forward NN, resulting in a 97.5 percent classification score.

Sachdeva, & et al. [3] proposed a model PCA-ANN to classify six classes namely glioblastoma multiforme, normal regions, childhood tumor medulloblastoma, secondary tumor-metastatic, meningioma, and astrocytoma. Two experiments are used first with the ANN only and the other with the PCA-ANN approach, and they found that classification accuracy has improved from 77% to 91%.

Suganthe, & et al. [4] for the identification of tumor cells, proposed an RNN (Recurrent Neural Network) architecture with a 90% accuracy. They use MRI images for model training.

Ari, A., & Hanbay, D. [5] proposed an automated tumor detection system, there are three steps to this process. In the first step, they introduce non-native means and native-smoothing methods to noise reduction. Local-Receptive Fields Based Extreme-Learning Machine (ELM-LRF) is used to correlate MR imaging images as a noncancerous tumor or cancerous tumor in the second step. In the last step, the tumors are partitioned. The ELM-LRF method produces a classification accuracy of 97.18 percent.

Arasi, & et al. [6] proposed a method for determining and classifying brain tumors. The GLCM function extraction method was used to isolate the tumor area for detection. For classification, a LOB (Lion Optimized Boosting) Algorithm with SVM model was used.

Gaikwad, & et al. [7] to brain tumor categorization, they use a PNN (Probabilistic Neural Network) method. Feature extraction is done by PCA and then classification by PNN. With the help of their system, they classified the brain tumor into three

categories they are Normal, Benign, and Malignant. They get an accuracy of 97.14% and 100% with spread values $=10^7$ and 10^6 .

Simonetti, & et al. [8] to brain tumor classification, features combined from MRSI and MRI data show the better result by MRSI data only. They also use water intensities in the data set to increase accuracy.

Billar, & et al. [9] use Na-MR imaging for PFS prediction, which is better than IDH mutation and improves the accuracy of brain tumor categorization.

Roy, & et al. [10] For brain tumor classification, they use the Adaptive Neuro-Fuzzy Inference System. And they compare the result with other classifiers namely, ANN with Backpropagation and KNN. They got an accuracy of 98.25%.

Sapra, & et al. [11] use a revised PNN (Probabilistic NN) model that is base on LVQ (Learning Vector Quantization) that gives an accuracy of 100%.

Madhusudhanareddy, P., & Prabha, I. S. [12] For tumor identification, they, utilizing histogram equalization, image correction, and threshold functions. They often use the BW label feature to determine the tumor's centroid and the Dilate operator to draw the tumor's boundaries. Finally, they deploy a feed-forward network with the backpropagation method.

Gauvain, & et al. [13] Diffusion coefficient can be used to predict tumor classification as well as characterizing Tumor Cellularity and Total Nuclear Region. These boundaries aren't accessible in regular MRI images, they reveal. As a result, diffusion-tensor imaging can help with diagnosis.

Rajesh Sharma, R., & Marikkannu, P. [14] proposed a 3D novel brain tumor categorization model that uses MR imaging images with both micro and macro scale features to distinguish between benign and malignant brain MRI. VOI of the image was bring out using 3D-volumetric (SCLGM) along with 3D-run length and co-occurrence matrix with the aid of a 3D-Gaussian filter.

Sarhan, A. M. [15] proposed a new CAD technique for MR imaging image categorization of brain tumors using the DWT's (Discrete Wavelet Transform) strong energy compactness property, this device bring out features from brain MR imaging images (DWT). This feature feed into CNN for classification which gives an accuracy of 99.3%.

Rathi, & et al. [18] Segmentation, feature extraction, and classification are the three modules that make up the proposed technique. MKPC (Multiple Kernels Probabilistic Clustering) is used to segment the data, and major features are selected

using LDA (Linear Discriminant Analysis) and fed into a FFBN (Feed-Forward Back Propagation Network). The precision of this technique is 0.88, 0.80, and 0.83.

Pathak, A. N., & Sunkaria, R. K. [20] proposed a hybrid of PCA-SVM that gives an accuracy of 100%. They use discrete wavelet transformation (DWT) using Haarwavele for feature extraction then feature reduction has been done using Principal Component Analysis (PCA) these selected features feed into SVM for classification of various types of brain tumor.

Srinivas, B., & Rao, G. S. [21] proposed a compound model (CNN+KNN) to brain tumor categorization using MRI images. CNN (convolution neural networks) extracts features and feeds them into KNN (K-Nearest Neighbor), which has a 96.25 percent accuracy.

3. Proposed Method

We implement this proposed work at Windows 10 with Intel Core i5 7th Gen and 8 GB of RAM configuration. We used the Google Colab server for

better computational power. In the Google Colab server, we have used the GPU as the run time, 12 GB of RAM, and 100 GB of Disc space for running the code efficiently. We have used some libraries such as TensorFlow version 2.x, Pandas, NumPy, Seaborn, Matplot library, Sklearn library, and Keras.

A. Data SetDescription

The data set which we have used in this study is from Kaggle with the name Brain Tumor Classification (MRI) that contains classify MRI images into four classes. This data set has a size of 87 MB that contains two dictionary names testing and training. Each dictionary has 4 classes name Glioma, Meningioma, Pituitary, and No Tumor. These classes represent the type of brain tumor. In testing dictionary with four classes contain 100, 115, 74 and 105 images respectively. Similarly, a training dictionary with four classes contains 826, 822, 827 and 395 images respectively. The CNN model's architecture is listed in CNN model framework and illustrated in Figure 1.

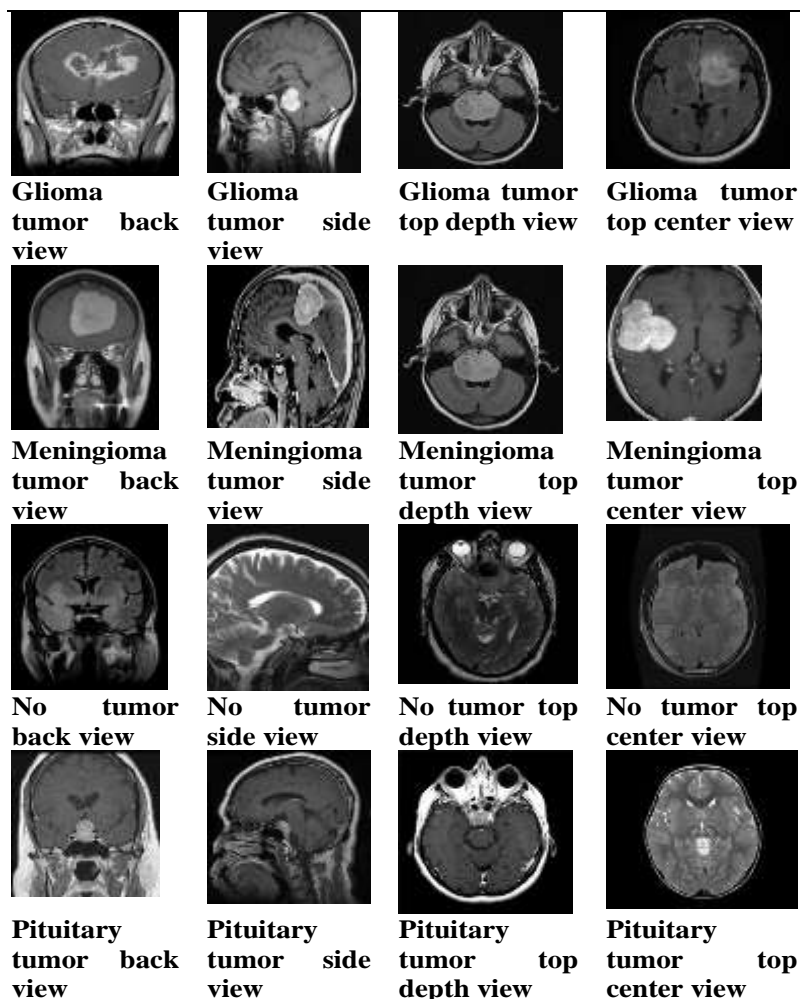


Figure 1. Training dataset and Testing dataset sample MRI images

These data set images are taken with different angles that is why the data set is very complex and prone to error. We convert each image to an array and store each image in the 2D array for pre-processing phase. The reason for doing this is to train my model with a data set that has an original image and preprocessed image concatenate parallel for an efficient outcome. This process depends on RAM. Due to limited resources i.e., 12 GB of RAM We have to decrease the magnitude of the data set.

So, we took 2870 images for the training data set and 80 images out of 394 images for the testing data set. We also create a CSV file for the testing data set that contains two columns, the initial column contains the name of the image, and the next column contains the type of the image (Disease).

B. Methodology and Feature Selection

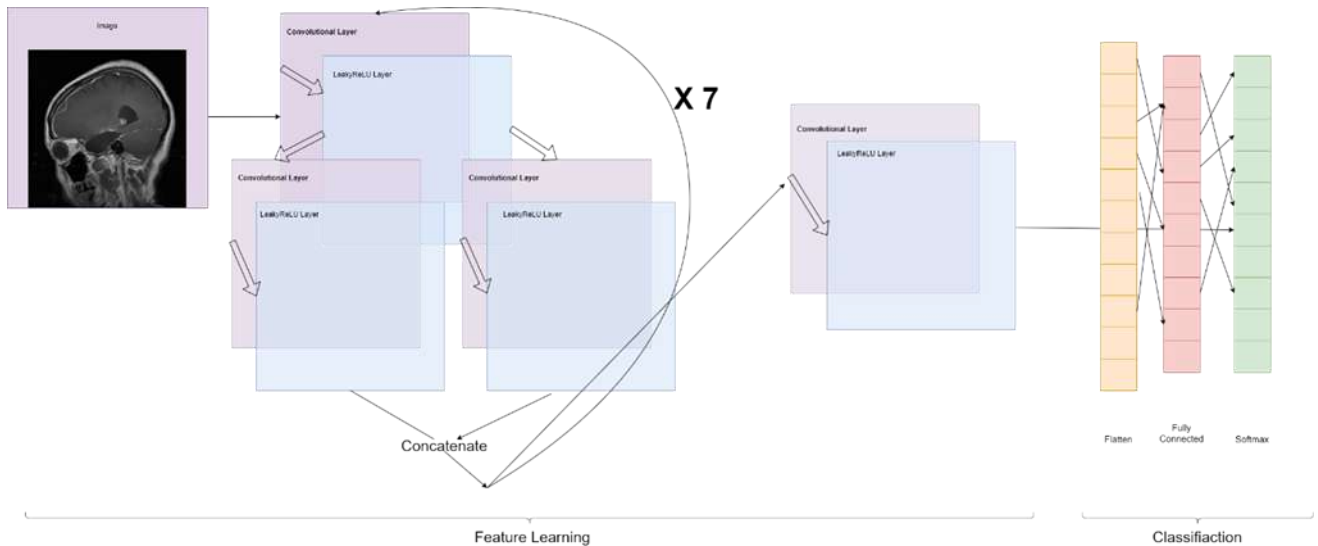


Figure 2. Shows the architecture of the hybrid model

The structure of the fusion CNN and RFC model, as well as the suggested model's approach and layers, are shown in Figure 2. First, since the data set is very complex it has two dictionaries for training and testing dictionary and each of them contains 4 different sub-dictionaries with the name Glioma, Meningioma, Pituitary, and No Tumor. Training dictionary contains 2870 images i.e., a mixture of four sub-dictionary, and testing dictionary contains 80 images i.e., a mixture of all four sub-dictionary. For the training dictionary, we open each sub-dictionary and take images, and put

them inside Pandas Dataframe and easy access. Second, some pre-processing is done before training the model, we convert each image into an array and combine processed images parallel to the original image to increase the efficiency and data set. That's why it depends on RAM size. We used the image sharpening method with the help of the Gaussian Filter Method. We can also use TM (Threshold Method), RBS (Region-Based Segmentation), CBS

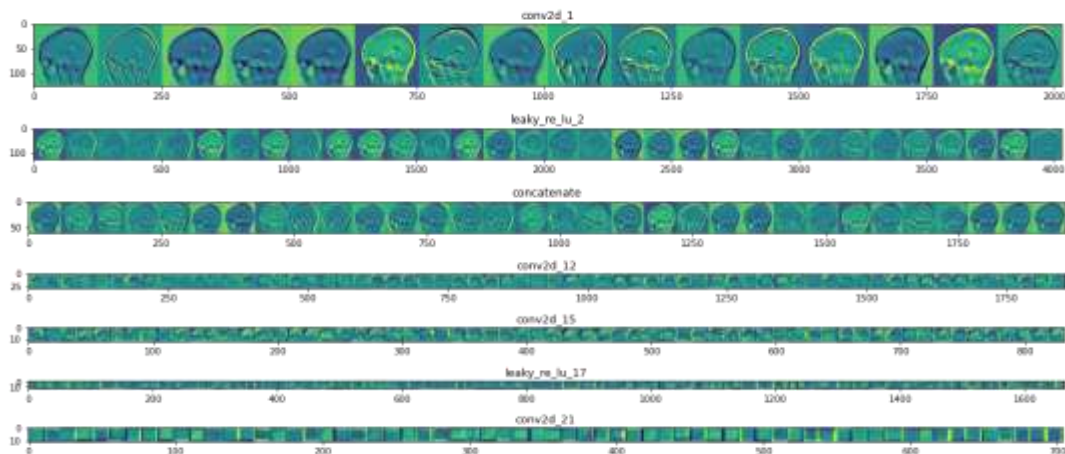


Figure 3. Shows few steps of Feature selection

(Clustering Based Segmentation Method), and WB (Watershed-Based Method) but we got the best result by using the simple Gaussian Filter Method. Then, with an 80-20 split, we split the data set into training and testing sets.

We used Functional API in this architecture that provides a flexible way of defining models. It allows defining multiple inputs or output models that share layers. It is necessary for building a hybrid model that can share features, input, and output layers to other models. Sequential Model and Model Sub-classing are not appropriate for this model design. The sequential model doesn't give flexibility for layer sharing and Model Sub-classing becomes complex and hard to implement and understand. This architecture includes 15 layers in which 7 are complex method definition for Convolution Layers, and the initial layer of this model is an input image of $256 \times 256 \times 3$ dimension with zero-center normalization.

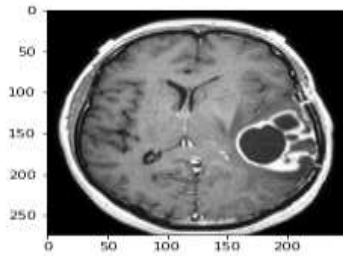


Figure 4. Sample image

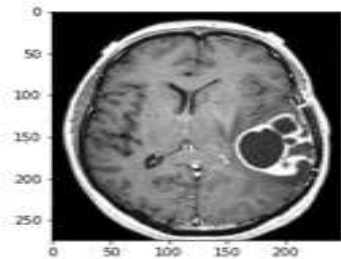


Figure 5. Sample image resize $256 \times 256 \times 3$



Figure 6. Processed image with resize $256 \times 256 \times 3$

Here Figure 3 shows the sample images of the feature extraction process of CNN with defined architecture. Figure 4 show sample image. Figure 5 show sample image resize $256 \times 256 \times 3$. Figure 6 show processed image with resize $256 \times 256 \times 3$. Figure 7 shows Training accuracy and Validation accuracy at 50 epochs. Figure 8 shows Training

loss and Validation loss at 50 epochs. In 3 out of 7 complex method definition layers, there are three convolution layers in which the first convolution layer has a

filter size of 16, kernel size of (1,1), and output of this layer is transferred to LeakyReLU with an alpha of 0.15, then the output of this layer is transfer to the next layer. Other two convolution layers with a filter size of 64 and kernel size of (1,1) that layer share with LeakyReLU with an alpha of 0.15 for both are combined and transfer the output to the next layer. And other 4 complex method definition layer, there are three convolution layers in which the first convolution layer has filter size of 16, kernel size of (5,5), strides of (2,2) and output of this layer is transferred to LeakyReLU with an alpha of 0.15, then the output of this layer is transfer to the next layer. The other two convolution layers with a filter size of 64 and feature detector size of (3,3) and (5,5) accordingly and padding with the same configuration as layer share with LeakyReLU with an alpha of 0.15 for both are combined and transfer the output to the next layer.

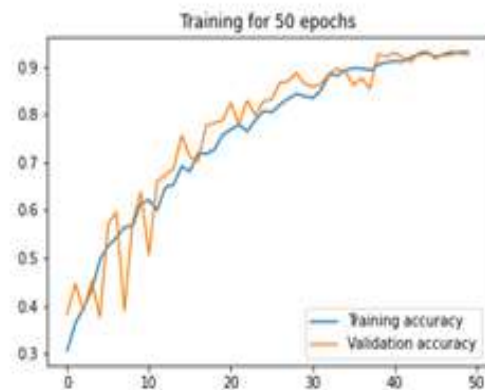


Figure 7. Training accuracy and Validation accuracy at 50 epochs

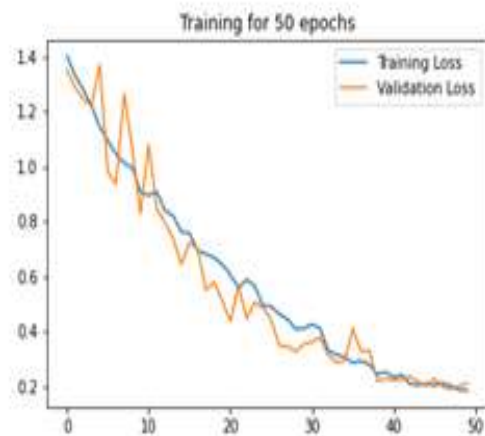


Figure 8. Training loss and Validation loss at 50 epochs

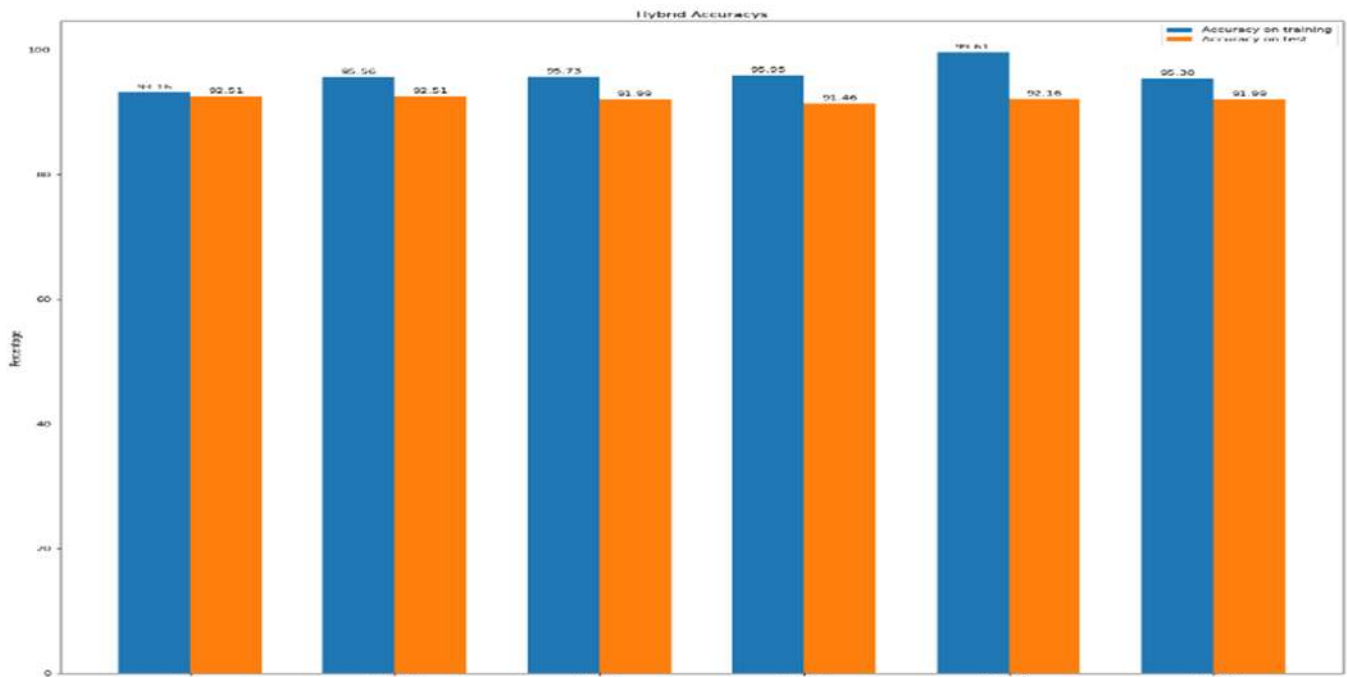


Figure 9. Shows the Overall accuracy of Training and Test validation for each hybrid

Layers other than the above layers are convolution layers with filters 64 and kernel size of (3,3). After layer sharing LeakyReLU with an alpha of 0.15 after this Flatten layer is used. After all, this layer is shared or transferred with a Fully connected layer i.e., Dense with 512 neurons attached with LeakyReLU and Dropout layer. And finally, the output of the final layer is introduced by Dense with neurons equivalent to the size of distinct types of disease in the data set and activation function i.e., softmax. This final layer has all the features of the training model which is used by all different

Classification algorithms. There are four groups in this classification problem: Glioma, Meningioma, Pituitary, and No Tumor. As a result, the final completely connected layer is changed to a four-class categorization task with specifications such as the BLRF (Bias-Learn Rate Factor) and WLR (Weight-Learn Rate Factor). Figure 9 shows the Overall accuracy of Training and Test validation for each hybrid. Figure 10 shows Truth classification by each hybrid on the Testing dataset.

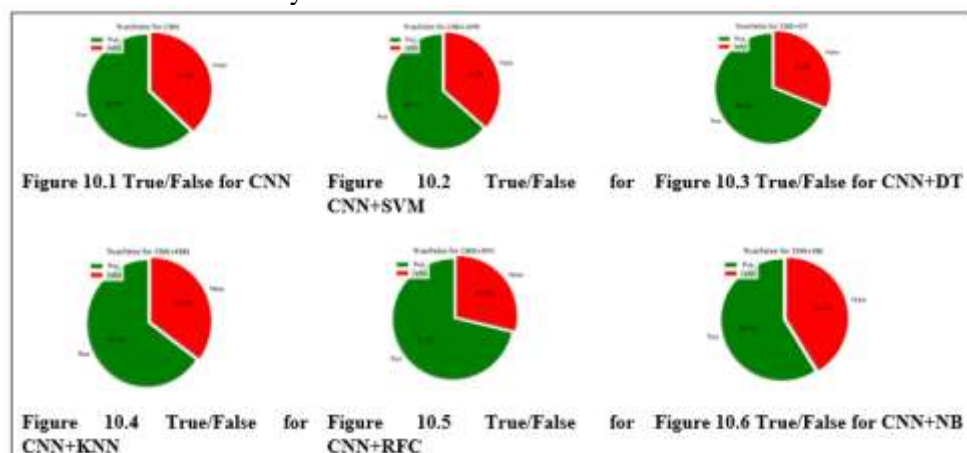


Figure 10. Shows Truth classification by each hybrid on the Testing dataset

The model is compiled using Adam optimizer with a 0.00025 learning rate and categorical-cross-entropy loss. With the help of learning rate reduction i.e., ReduceLROnPlateau that helps to reduce the learning rate whenever metric has stopped improving further. Data generation is also

taken i.e., ImageDataGenerator that helps to generate more data with rotation, zooming, width shifting, height shifting, the horizontal and vertical flip of images. Then the model is trained. Batch size and epochs are taken 32 and 50 respectively. The experiment is also done by taking 25,50,75 and

100 epochs but the best result we got at 50 epochs. After 50 epochs model become over fitting that reduces the overall result quality and accuracy.

3. Experimental Result and Discussion

The CNN model was trained on 2870 images of four different classes. An activation mechanism is used to bring out high-level features from a completely connected layer. CNN extracts non-handcrafted features from each image. Testing data set images are preprocessed, converted into an array, and store in a 2D array is prediction purposes. Feature extracted model then evaluate that gives an accuracy of 92.51%. After that, we predict our model on a testing data set and compare the result with a hand-created CSV file. This complete process is for CNN only.

For hybrid models such as CNN+RFC, we take our model first layer and last output layer with a name dense_1. Our model then predicted 80% of the training data set, and complete testing data set. After that, we implement each classification model separately such as SVM, KNN, RFC, DT, and NB. Each classifier algorithm is implemented and fits with our CNN feature-based model predicted output. That means RFC fit with an output of predict of 80% training data set, and complete testing data set. Then, the classifier predicts on the testing data set, and then we store the predicted output by each classifier in the CSV file as the 3rd column. Later we can compare the 2nd and 3rd columns of the CSV file and gives many correct and incorrect results. We repeat this process for every classifier algorithm. And finally, we compare the result of every algorithm and take the best hybrid. CNN is applied in different fields and reported in the literature [36-44].

4. Conclusions

In this paper, a compound of the CNN+RFC framework is considered for the MR imaging to brain tumor categorization issue, and the framework is trained using the Kaggle brain tumor data set. In this case, CNN extracts non-handcrafted features and uses them as a load to various Classifiers such as SVM, CNN, KNN, RFC, NB, and DT to predict the output class. Performance measures such as accuracy are used to assess the advantage and viability of the proposed combined CNN+RFC framework. Since the research data set includes MR imaging images of the brain from various angles, our framework prediction is more complicated. However, in such complex conditions, our framework produces some promising results.

The findings show that combining the frameworks yields several benefits. This combination of the CNN+RFC framework appears to be an optimistic framework for MR imaging to brain tumor categorization, based on the findings. To begin with, the framework automatically brings out the important features, that saved time and effort compared to other conventional classifiers, which took longer to bring out the allowable hand-crafted features. Second, this proposed combined CNN+RFC framework combined the benefits of CNN and RFC, two of the most efficient and influential image identification and categorization classifiers. Ultimately, during the decision-making process, the combined framework's complexity is slightly increased. The proposed CNN+RFC framework outperformed all other frameworks, including CNN, CNN+SVM, CNN+DT, CNN+KNN, and CNN+NB, with an accuracy of 99.61 percent.

Author Statements:

- **Ethical approval:** The conducted research is not related to either human or animal use.
- **Conflict of 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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- **Data availability statement:** The data that support the findings of this study are available on request from the corresponding author. The data are not publicly available due to privacy or ethical restrictions.

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