Deep Learning CNN Model-based Anomaly Detection in 3D Brain MRI Images using Feature Distribution Similarity

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***Abstract*—Towards detecting an anomaly in brain images, different approaches are discussed in the literature. Features like white mass values and shape features have identified the presence of brain tumors. Various deep learning models like the neural network has been adapted to the problem tumor detection and suffers to meet maximum accuracy in detecting brain tumor. An Adaptive Feature Centric Distribution Similarity Based Anomaly Detection Model with Convolution Neural Network (AFCD-CNN) is sketched towards disease prediction problem to handle the problem. The model considers black-and-white mass features with the distribution of features. First, the method applies the Multi-Hop Neighbor Analysis (MHNA) algorithm in normalizing the brain image. Further, the process uses the Adaptive Mass Determined Segmentation (AMDS) algorithm, which groups the pixels of MRI according to the white and black mass values. The method extracts the ROI with the segmented image and convolves the features with CNN at the training phase. The CNN is designed to convolve the features into one dimension. The output layer neurons are designed to estimate different Feature Distribution Similarity (FDS) values against various features to compute the Anomaly Class Weight (ACW). According to the ACW value, anomaly detection is performed with higher accuracy up to 97% where the time complexity is reduced up to 32 seconds.**

Keywords*—Deep learning; brian tumor; disease prediction; anomaly detection; CNN; FDS; ACW

I. Introduction

The entry of modern diseases challenges human society. There are several diseases identified every year which have a significant impact on human life. Some of the diseases produce temporary illnesses, and some of them introduce permanent damage to the human. More than that, some diseases are claiming the lives of humans. The brain tumor is among them, producing permanent illness and is identified as a more challenging one. Whatever the disease, diagnosing the disease at the earliest would support the person in increasing survival. Analyzing the disease at the earliest would help the medical practitioner effectively treat the person.

Brain tumor analysis has been identified as a complicated task in the medical sector where such a disease would claim a person's life. Various detection models are available, and MRI images become the source of finding the disease, which must be passed through several stages to extract the features. For example, the classification system would use texture, mass values, shape, and binary features in classifying the brain image. Also, several methods include Support Vector Machine (SVM), Decision Tree, Ensemble learning, Genetic algorithms, and Neural networks. The methods differ regarding features being considered and the similar way being used.

Deep learning is the modern development of machine learning models which helps automated decisive support systems in handling huge volume of data towards solid support. Convolution neural network has been identified as more effective than the other deep learning models. The CNN has been designed with layers like the convolution layer, which involves convolving the ROI features into a single dimension. Such dimensionality reduction and feature retention support handling massive volumes of MRI images to support the process of image classification. The brain image classification is done according to the texture features and other features obtained from the ROI. The accuracy can be significantly improved by having a massive volume of samples.

An Adaptive Feature Centric Distribution Similarity Based Anomaly Detection Model is detailed to improve the performance, focusing on including multiple brain image features and their distribution metrics in finding the image class. A Multi-Hop Neighbor Analysis (MHNA) algorithm is discussed to normalize the brain image. Also, Adaptive Mass Determined Segmentation (AMDS) algorithm is adapted toward segmenting the regions of the brain image. Similarly, a convolution neural network with two convolution and pooling layers is designed.

The article is structured to present the introduction of brain tumor detection and anomaly detection in detail with disease prediction at Section I. Section II, discusses the complete related work and methods available in literature in detail. Section III discusses the complete working of the proposed anomaly detection and disease prediction system. Section IV details the experimental results and presents a detailed discussion. Finally, conclusion about the entire work is presented in Section V while future area of research is presented in Section VI.

II. Related Works

The problem of brain image classification has been discussed in various articles, and a subset of methods is discussed in this section.

A CNN-based model is presented in [1], which preprocess the brain images and extracts the features to train CNN. The method uses a T1 weighted image, enhancing the contrast of MRI images to support the classification. Further, a Deep CNN model is sketched in [2] to predict the status of gliomas. The method generates various mutations of the features and based on that, the classification is performed. A modified version of DCNN is discussed in [3], which focuses on adjusting the feature weights at various layers by removing the fully connected layers. A metastases segmentation model with CNN is presented in [4] to support brain image classification. The model segments the images to obtain the metastases and trains the CNN for efficient classification.

In [5], a transfer learning model named GoogleNet is presented for classifying various classes of tumors. The model extracts the features using a pre-trained CNN model and performs classification using algorithms like SVM, KNN, and softmax. A detailed analysis of various CNN models is sketched in [6], which considers the models like S-CNN (CNN trained from scratch). The method uses two brain image data sets to analyze the performance of various approaches.

An ADAM optimizer model is sketched in [7] for brain image classification, which uses different pre-trained models like Xception, NasNet Large, DenseNet121, and InceptionResNetV2 to extract the features. The features extracted are used to train the CNN model with an ADAM optimizer to perform classification. A cumulative variance-based feature selection approach is presented in [8] to classify various grades of malignant brain tumors. The method extracts the features, selects optimal features using CVM (Cumulative Variance Method), and classifies using KNN, NN, and multiclass SVM.

To support automatic diagnosing and help the medical practitioner, an integrated model is presented in [9], which extracts the features using CNN from MRI images. Extracted features are classified using LSTM (Long Short Term Memory) model. A novel classification model is presented in [10], which uses multi-view DNN to perform segmentation, and segmented features are fused with the dynamic fusion method. Segmented results are used to analyze the performance of segmentation.

A transfer learning-based deep learning model is presented in [11], which classifies the tumor according to the features extracted and compares it with the performance of others. An efficient brain tumor segmentation model is presented in [12], which uses the correlation among the features. The correlation model transformed the features and was used to perform classification. A deep convolution neural network-based model is presented in [12], which fine-tunes the layers to perform classification with higher accuracy. A Gaussian convolution neural network-based model is sketched in [13] for brain image classification. The model is designed to classify pituitary, glioma, and meningioma tumors.

A time-distributed CNN LSTM (TD-CNN-LSTM) scheme is discussed in [14], which extracts the features from time-dependent images using CNN. The classification is performed using LSTM. A DCNN model with Feature SVMnamed ((DCNN-F-SVM) is sketched in [15], which trains features and fuses the network to perform classification with SVM. A dilated 3D CNN model is illustrated in [16], which uses feature maps as the key to classification. A U-Net-based CNN model is discussed in [17], which uses U-Net for segmentation and performs classification with the 3D-CNN model. In [18], the author presents a detailed review and identifies the several challenges in classifying brain images into various classes. A forgery detection model is sketched in [19], which uses a propagation-based scheme in organizing the fingerprint image. A PCA-based classification model is sketched in [20], which classifies the finger quickly. A face recognition model is sketched in [21], which considers contour features in classification.

The methods analyzed in this section are subject to producing poor accuracy in classifying the brain images against different classes considered.

III. Adaptive Feature-Centric Distribution Similarity-Based Anomaly Detection with CNN Model (AFCD-CNN)

The proposed model (see Fig. 1) reads the brain image MRI data set and considers black-and-white mass features with the distribution of elements. The Multi-Hop Neighbor Analysis (MHNA) algorithm is initially applied to normalize the brain image and remove the noise from the image. Further, the method uses Adaptive Mass Determined Segmentation (AMDS) algorithm to group similar pixels of brain images to support feature extraction. Once the segmentation is done, the process extracts the ROI and the features passed through CNN to train the network. The CNN design convolves the elements into one dimension. The output layer neurons are subject to measuring Feature Distribution Similarity (FDS) values against various features to compute the Anomaly Class Weight (ACW). According to the ACW value, the classification is done.

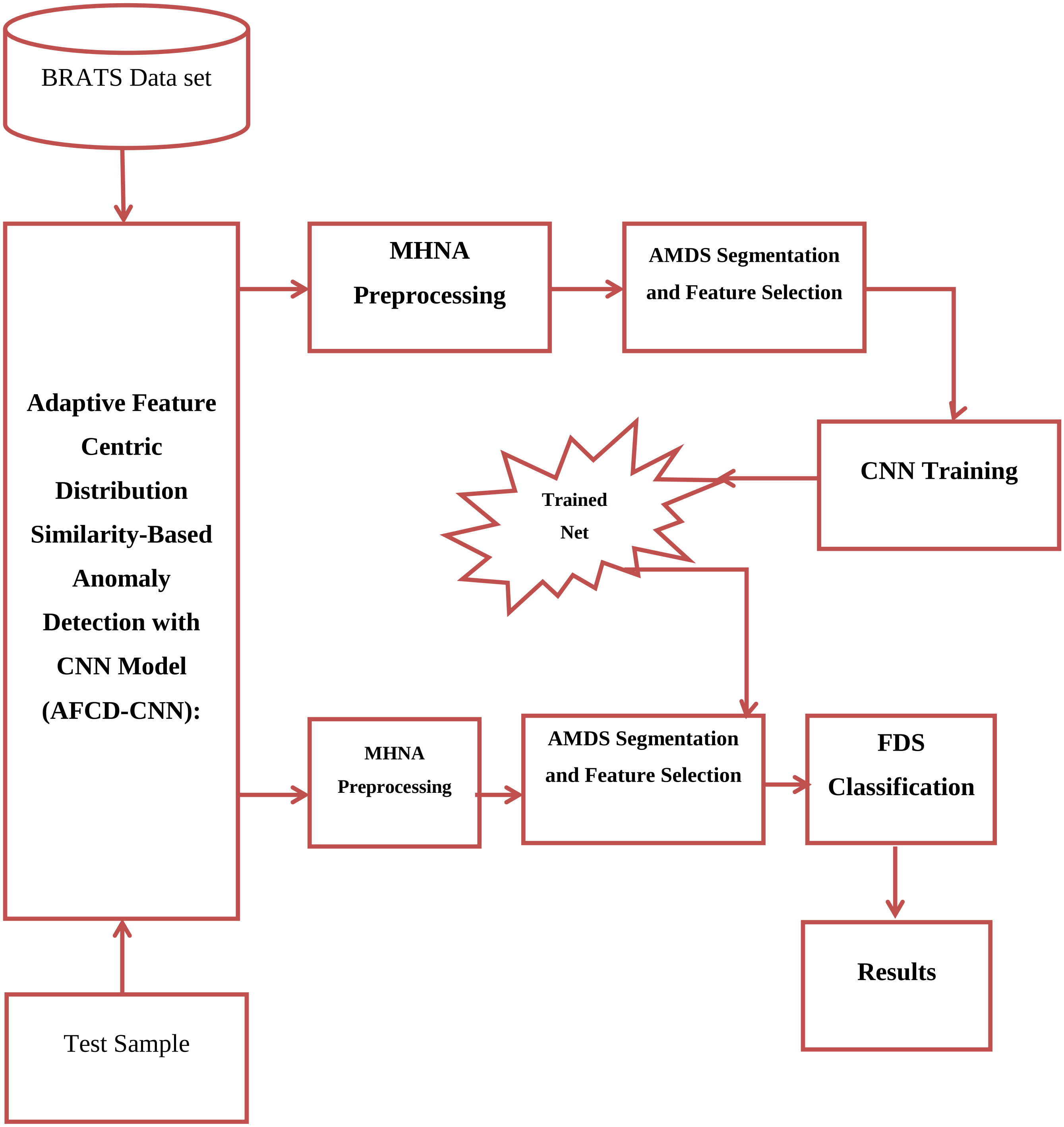


Fig. 1. Architecture of proposed AFCD-CNN anomaly detection model.

The proposed brain tumor detection model reads the brat's image data set and applies MHNA preprocessing and AMDS segmentation to extract the features. Extracted are trained to a convolution neural network with two convolution layers and pooling layers to compute weight measures for anomaly detection.

A. MHNA Preprocessing

The brain image considered has been read towards improving the quality of the image. To perform normalization, the method initializes a window size x, which covers K hops for any pixel. The window is further divided into four regions, and the standard deviation value is measured at each region. Second, a region with the least standard deviation of pixels is identified and selected. Selected region pixels are used in estimating the mean standard value (MSV), and based on that, and the method adjusts the pixel value to normalize the pixel. This will be iterated for the k number of iterations, which denotes the hops. Such normalized image has been used to perform segmentation.

TABLE I. SAMPLE WINDOW

112	135	132	124	75
128	148	72	32	87
136	147	**58**	67	77
121	139	42	51	69
119	122	136	145	55

TABLE II. WINDOW WITH ONE NEIGHBOR

148	72	32
147	**58**	67
139	42	51

TABLE III. WINDOW WITH 2 NEIGHBORS

112	135	132	124	75
128	148	72	32	87
136	147	**58**	67	77
121	139	42	51	69
119	122	136	145	55

The example window considered for the problem is given in Table I and a sub section from the Table I with single neighbor is shown in Table II and a window with two neighbors is shown in Table III. According to Table I considered, the proposed MHNA preprocessing algorithm computes the standard deviation value with four different region pixels as follows:

Standard deviation {112,135,132,128,148,72,136,147,58 } among the region one values are computed. Similarly, the same has been measured for other region pixel values according to the center pixel marked. Now according to the standard deviation value, a single region with the least value is selected. For the selected region, the mean standard value is measured, and based on that, the method computes the new value for the concerned pixel.

Algorithm:

Given: Brain Image Bmg
Obtain: Normalized Image Nmg.
Start
    Read Bmg.
    Initialize window size w.
    Initialize neighbor k.
    For each pixel
        W= Construct K hop window.
        Crop image feature as Cm = Crop (Bmg,w,k)
        For each region R
            Compute standard deviation Rstd $= \sum_{i=1}^{size(Rs)} Std(R)$
        End
        Region R = $\max_{i=1}^{size(Rs)} (Rs(i).Rstd)$
        Compute Mean standard Ms = $\frac{\sum_{i=1}^{Size(R)} Dist(p,R(i))}{size(R-1)}$
        Nmg(p) = p+($\frac{3}{8} \times Ms$)
    End
Stop

The MHNA preprocessing algorithm computes any pixel's mean standard value according to the selected region. Based on the value measured, the method normalizes the pixels to perform normalization. The normalized image has been used to perform segmentation and classification.

B. Adaptive Mass Determined Segmentation

The brain image obtained from preprocessing has been used for segmentation. The adaptive mass-determined segmentation algorithm uses two different mass values in grouping the tumor's pixels and other brain cells. To perform this, the method traverses through the entire image and finds the set of black mass values and white mass values. The method computes the boundary between the sets using these white and black mass values. Based on the identified boundary, the method groups the pixels under two classes to produce the segmented image.

Algorithm:

Given: Brain Image Pimg
Obtained: Segmented Image Simg
Start
    Read Pimg.
    Initialize black mass set Bms, white mass set Wms.
    For each pixel p
        If p.value<100 then
            If p.value ! $\in Bms$, then
                Bms = Bms$\cup\, p.value$
            End
        Else
            If p.value ! $\in wms$ then
                wms = wms$\cup\, p.value$
            End
        End
    End
    Identify boundary set Bs = $\sum_{i=(size(Wms)-5)}^{size(wms)} Bs \cup wms(size(wms)-i)$
    For each pixel p
        If p.value$\in Bs$ then
            Simg(p) = 256
        Else
            Simg(p) = 0
        End
    End
Stop

The segmentation algorithm finds the black-and-white mass values in the image. According to the different sets identified, the method detects the most optimal sets for grouping the pixels under two classes and produces a segmentation image.

C. CNN Training

The method reads the Brats image data set and applies MHNA preprocessing on each of them. The method applies an adaptive mass determination segmentation algorithm with the preprocessed image. The result of segmentation is used to extract the tumor's texture and computes black-and-white mass distribution values. All these features extracted are used to train the neural network. The CNN has been designed with an input layer to take the features and have two different convolution layers where the features are convolved into single-dimensional features. The max pooling layers help to shape the features and pad the features. Finally, the network is designed with a fully connected layer to support classification.

The texture obtained from the image has been split into four regions. According to the areas identified, the method would compute the gray mean value, which produces the following result.

TABLE IV. FEATURE OBTAINED FROM THE TEXTURE

R1	R2	R3	R4
167	185	175	169

Table IV shows the features obtained from the texture extracted from the brain image. Similarly, the method extracts the white and black mass distribution values to form the feature vector as follows:

TABLE V. EXAMPLE FEATURE VECTOR

R1	R2	R3	R4	WMD	BMD
167	185	175	169	76	45

Table V shows the example feature vector produced by the proposed model. The value of WMD is measured as follows:

$$\text{Wmd} = \frac{\sum_{i=1}^{size(T)} T(i) > 180}{size(T)}$$

Similarly, the value of BMD is measured as follows:

$$\text{Bmd} = \frac{\sum_{i=1}^{size(T)} T(i) < 100}{size(T)}$$

Accordingly, generated feature vector has been used to train the CNN. At the first convolution, the method computes the gray mean values at each region to produce four values, whereas in the second convolution; the method computes the average among the four values to produce a single value, reducing the feature vector size to three. Such feature vector has been used to compute the similarity measure at the test phase.

D. FDS Classification

The proposed model classifies the brain image according to the feature distributional similarity measured against image features. The method applies MHNA preprocessing, eradicating the image noise to perform this. Further, AMDS segmentation is applied to group the pixels of various features. From the segmented image, ROI has been extracted and estimates white and black mass distribution values. Such features extracted are passed through the CNN trained, where the features are convolved in two-stage and apply max pooling. The convolved features are obtained at the output layer, and the method computes the FDS values towards various features like texture, white mass, and black mass values. Using these values, the method computes the similarity value to compute anomaly class weight (ACW). According to the ACW value, the method performs classification.

Algorithm:
Given: Brain Image Bmg, CNN Tcn Obtain: Class C Start Read Bmg, Tcn. Pmg = MHNA-Preprocessing (Bmg) Smg = AMDS-Segmentation (Pmg) Wmd = compute White mass distribution. Bmd = Compute Black Mass distribution. Texture T = Extract tumor feature. Feature vector fv = {T, Wmd, Bmd }. Pass through CNN. Convolve Fv at stage 1. Perform max pooling. Perform stage 2 convolution. Perform max pooling. For each class a Compute Texture Distribution similarity TDS. $\text{TDS} = \frac{\sum_{i=1}^{size(C)} Dist(C(i).T.value, T.value)}{size(C)}$ Compute white mass distribution similarity Wds. $\text{WDs} = \frac{\sum_{i=1}^{size(C)} Dist(C(i).wmd, T.wmd)}{size(C)}$ Compute black mass distribution similarity Bds. $\text{BDs} = \frac{\sum_{i=1}^{size(C)} Dist(C(i).bmd, T.bmd)}{size(C)}$ **Compute** ACW = $\frac{Wds}{Bds} \times Tds$ End Class C = choose the class with maximum ACW. Stop

The proposed approach performs classification by computing ACW value for the sample towards various classes of brain tumors. Finally, a single class is selected according to ACW.

IV. Results and Discussion

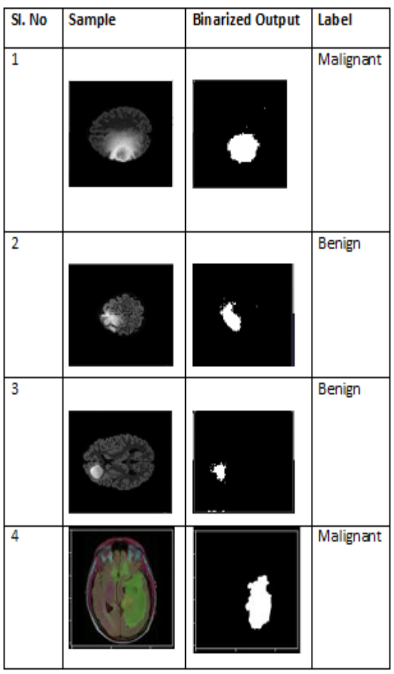
The proposed AFDS-CNN-based anomaly detection on brain images is enforced, and the performance of the model is measured against various classes with different constraints. The results achieved in each test case are discussed in this part. The method uses the Brats data set for performance evaluation.

TABLE VI. EVALUATION DETAILS

Factor	Value
Data Source	Brats 2019
Total Images	3000
No of Image Class	3
Platform	Python

Table VI denotes the constraints used in evaluating the performance of the models where the data set has three tumor classes, and the performance is measured on various factors.

TABLE VII. RESULTS OF CLASSIFICATION



Sl. No	Sample	Binarized Output	Label
1			Malignant
2			Benign
3			Benign
4			Malignant

The classification result produced for different brain images is plotted in Table VII, which has been used in measuring the accuracy of the method toward classification.

TABLE VIII. ANALYSIS OF CLASSIFICATION ACCURACY

Classification Accuracy in % vs. No of Samples			
	1000 samples	2000 samples	3000 samples
ADAM	74	78	82
TD-CNN-LSTM	77	81	86
3D-CNN	80	84	89
AFDS-CNN	85	91	97

The performance of methods in classification accuracy is analyzed in Table VIII, where the AFDS-CNN approach achieved higher classification accuracy in all the test cases.

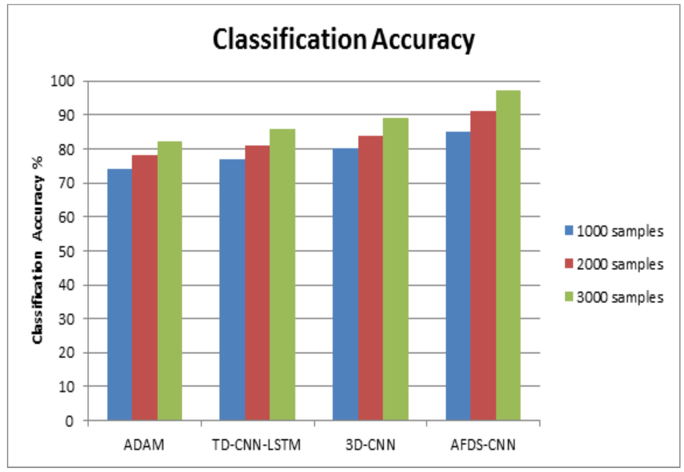


Fig. 2. Performance on classification accuracy.

The classification accuracy produced by different schemes is compared in Fig. 2, where AFDS-CNN achieved higher accuracy in all cases.

TABLE IX. ANALYSIS OF FALSE CLASSIFICATION RATIO

False Ratio in Classification % vs. No of Samples			
	1000 samples	2000 samples	3000 samples
ADAM	26	22	18
TD-CNN-LSTM	23	19	14
3D-CNN	20	16	11
AFDS-CNN	15	9	3

The false ratio introduced in brain image classification is measured and plotted in Table IX. The AFDS-CNN model achieves less false classification ratio compared to others.

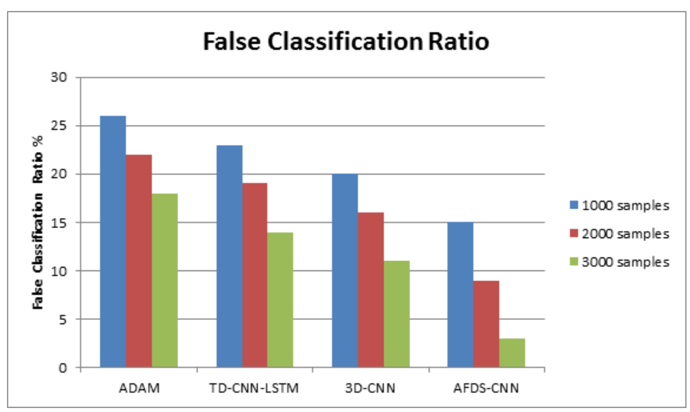


Fig. 3. Performance on false classification ratio.

The ratio of false classification is measured for different approaches according to the number of samples in the data set in Fig. 3. In each class, and the proposed AFDS-CNN has produced less false ratio than others.

TABLE X. ANALYSIS OF TIME COMPLEXITY

Time Complexity in Classification Seconds vs. No of Samples			
	1000	2000	3000
ADAM	54	61	86
TD-CNN-LSTM	43	52	77
3D-CNN	39	46	71
AFDS-CNN	21	27	32

The time complexity in classifying the images is measured and plotted in Table X. The RBP-CNN model produces little time complexity.

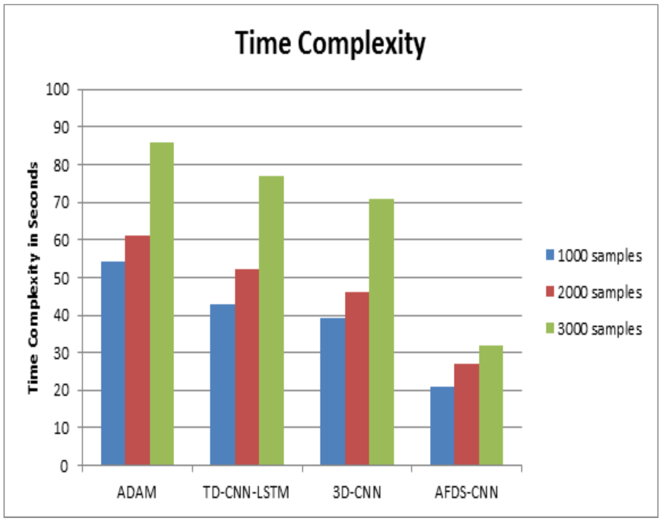


Fig. 4. Time complexity.

The time complexity in classifying the images is measured according to the total time taken for classifying the given image and plotted in Fig. 4. The RBP-CNN model produces negligible time complexity.

V. CONCLUSION

This paper presented a novel adaptive feature distribution similarity-based brain image classification with a convolution neural network (AFDS-CNN). The model applies MHNA preprocessing algorithm to the brain images to normalize the image features. Further, the method applies an adaptive mass discrimination segmentation algorithm to segment the images. With the segmented images, the method extracts texture, white mass distribution, and black mass distribution values. Extracted features are convolved with the CNN designed with different convolution and max pooling layers. At the test phase, the features extracted are used to compute texture distribution similarity (TDS), White mass Distribution Similarity (WDS), and Black mass distribution similarity (BDS) to compute the value of Anomaly class weight (ACW). Based on the value of ACW, the method performs classification and produces an accuracy of up to 98.6% with a reduced complexity of 21 seconds

VI. FUTURE WORK

The problem of brain tumor detection and disease prediction can be further improved by adapting time variant directional and distribution growth of tumor cells in classifying the brain image.

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CONFLICTS OF INTEREST

The authors declare they have no conflicts of interest to report regarding the present study.

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