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The Effective Quantitative Analysis for Brain Tumor Diagnosis Using an Efficient Deep Learning Algorithm

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Abstract— In the medical field, imaging analysis is the hottest topic. It has attracted many researchers to accurately analyses the disease severity and predict the outcome. However, if the trained images are more complex, the noise pruning results have decreased, which has tended to gain less prediction exactness score. So, a novel Chimp-based Boosting Multilayer Perceptron (CbBMP) prediction framework has been built in this present study. Moreover, the objective of this study is brain tumor prediction and severity analysis from the MRI brain images. The boosting function is employed to earn the most acceptable error pruning outcome. Henceforth, the feature analysis and the tumor prediction process were executed accurately with the help chimp solution function. The planned framework is tested in the MATLAB environment, and the prediction improvement score is analyzed by performing a comparative analysis. A novel CbBMP model has recorded the finest tumor forecasting rate.

Keywords-component; formatting; style; styling; insert (key words).

I. INTRODUCTION

In a human biological system, the brain tumor is considered a harmful disease category [1]. Hence, the early tumor diagnosis framework is a major concern in recovering human lives with proper treatment procedures [2]. Several medical analysis tools exist for these diagnosis systems [3]. However, those tools are high in cost also that is not suitable for predicting all tumor types [4]. Considering these drawbacks, intelligent models have been introduced for the disease prediction problem, which functioned as a neural model [5]. The neural framework process without the optimum layer is defined as machine learning (ML) [6]. Also, the neural models processed with optimal layers for the tuned prediction outcome are termed deep learning (DL) networks [7]. However, the neural models have needed more periods to train the system [8]. Furthermore, the imaging analysis was introduced to the medical framework for the finest visualization results [9]. Some imaging schemes have required more image features to train the system that has maximized the complexity score of the imagining system [10]. Different sequential models have been executed in the imaging system to find the present statistical

features in the trained image [11]. Using those sequential models, the possible features were extracted that are imported to the classification function for further processing [12]. The existing numerical models like kernel model, belief deep networks system, regression, and logical system were widely utilized for analyzing the image features [13]. But those approaches required the additional combination approaches for training and classification [14].

Hence, those combined approaches might increase the computational complexity [15]. Considering these demerits, the neural system has been applied in imaging [16]. The imaging

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system has functioned in different process steps: filtering, feature analysis, disease region tracing, and prediction [17]. After the disease detection function classification process has been implemented to specify the disease types [18]. Moreover, different components in the imaging system have maximized the resource cost and computational complexity [19]. So, the recent research works have implemented the neural system and optimized neural system for detecting the disease-affected region with maximum exactness score. Few contemporary approaches are recurrent neural model, convolutional network, boosting model, ensemble learning, and spatial network [20]. However, those techniques are not suitable for detecting all kinds of tumor in an early stage. Those models have detected the specific tumor based on the trained features by the ground truth resources. So, the current study has planned to design optimized deep networks for detecting the disease prediction from the imported MRI brain images. Here, the boosting function is adopted for a better error pruning outcome.

Hence, this boosting function is processed in the hidden layer of the proposed optimized deep networks. Besides, feature analysis and tumor detection are executed with the help of chimp fitness. The main motive of this present study is to design optimized boosting deep networks for forecasting the brain tumor from the brain MRI image. Also, the primary novel in this work is incorporating the boosting and optimization function in the deep networks. Here, the optimization function is given to the classification phase for predicting the tumor with a good exactness score. Moreover, the critical contribution steps of the designed prediction system are described as follows,

- Initially, the brain MRI images have been gathered and considered as the input of the designed model
- Then a novel CbBMP was built with sufficient boosting and prediction features
- Henceforth, pre-processing has been performed to neglect the noise features from the trained data
- Consequently, a feature analysis process has been executed to identify and extract the meaning of features
- Finally, the tumor region has been tracked and detected by matching the testing image features with the trained, healthy brain image features
- Subsequently, the parameters were measured based on time, error rate, prediction accuracy, F-value, recall, and precision.

This research discussion has been arranged in the way of recently associated brain tumor prediction work is reviewed in section.2. Conventional brain tumor prediction system with the problem is described in the 3rd section. The solution to the discussed problem is exposed in the 4th section, and the outcome of the discussed solution is expressed in the 5th section. The 6th section concluded the research discussion with improvement rate and future direction.

II. RELATED WORKS

Some of the recent works related to brain tumor segmentation are described as follows, In medical technology, tumor area fragmentation from the Magnetic Resonance Imaging (MRI) image is very difficult. Therefore, R. Pitchai*et al.*[21] presented a novel hybrid approach by combining the attributes of the fuzzy algorithm and artificial neural system. This model was validated with the BRATS dataset, and the results are estimated. This approach provides the most satisfactory results in classifying abnormal images. Moreover, the fuzzy logic provides tumor regions separately. However, the computation time is high in this approach.

The fragmentation of the tumor region from the MRI image is the primary concern in the medical diagnostic system. It is observed that the multimodal MRI images provide more information about tumor fragmentation. Hence, Tongxue Zhou *et al.* [22] developed an algorithm with multimodal features for tumor segmentation. The robustness of the approach was verified with a correlation matrix. The presented work was validated with BRATS 2019 dataset. However, the implementation is more complex.

The fragmentation of the tumor region from the MRI image manually is a time-consuming and complex task. Thus, Gökay Karayegena and Mehmet Feyzi Aksahin [20] presented an automatic brain tumor segmentation method based on the convolution neural system. This approach was verified with the BRATS dataset, and the outcomes are estimated. This involves 3-dimensional imaging of the brain to extract the tumor region with its height and breadth. However, the segmentation results are accurate.

Nowadays, tumor segmentation is one of the biggest challenges in the medical diagnostic approach. Several image processing approaches are developed to accurately segment the tumor images from the MRI image. Among these techniques, deep learning approaches yield highly accurate tumor segmentation. But, the complexity is high in deep learning-based approaches. So, Siyu [23] proposed a tumor fragmentation process based on a field programmable gate array. This method was easy to implement, and the time consumed by this approach was low. But, the implementation cost is high in this approach.

In tumor diagnosis, the multimodal MRI image provides highly accurate tumor fragmentation. However, the missing modalities are one of the concerns in multimodal-MRI. Therefore, Tongxue [24] Zhou *et al.* [5 5] developed a segmentation technique for missing modalities. This approach consists of three classes: improved attribute generator, fragmentation

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phase, and correlation block. This method was evaluated with the BRATS dataset, and the outcomes were determined. But, this approach failed to fragment the tumor region separately.

III. SYSTEM MODEL WITH PROBLEM DESCRIPTION

The imaging system has been widely utilized in medical applications to visualize the disease features with more possible clarity. However, few demerits in the imaging framework have degraded the prediction system [25]. Hence, the usual imaging system with the described problem is defined in fig.1.

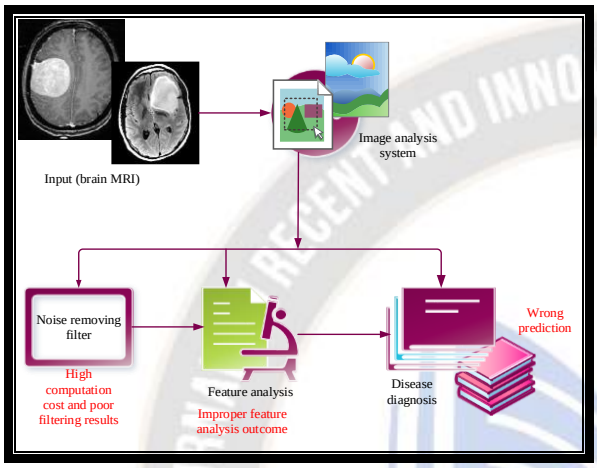

Fig.1 conventional tumor prediction system with problems

Usually, the conventional filter is utilized for filtering the noise features in the trained data. Those filters have required additional features to predict and neglect the noise data. Moreover, it has increased the computation and resource costs. Also, if the images are too complex, it will filter the noisy features only up to the possible level. So, the proper, refined data has not been gained,which has resulted in poor feature analysis outcomes. At last, the wrong prediction outcome has been gained; these issues have motivated this current study to build an optimized deep neural system for detecting brain tumor types.

IV. PROPOSED CBBMP FOR BRAIN TUMOR PREDICTION

A novel Chimp-based Boosting Multilayer Perceptron (CbBMP) has been designed as a disease prediction model in this current research solution. The database that was taken to validate the success score of the built model is brain MRI images. Hence, different kinds of brain MRI images as been gathered and imported into the system. Consequently, a novel proposed framework has been built to analyze the image features and forecast the disease-affected region. Primarily, the filtering function was processed to eliminate noisy features, then the refined data was imported to the classification phase for the feature analysis, and then the disease diagnosis function was performed. The proposed design is explained in fig.2.

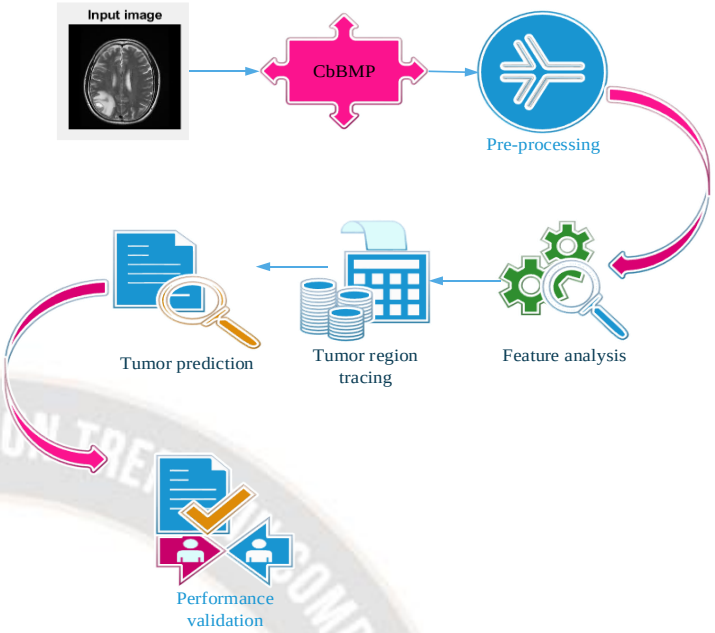

Fig.2 proposed methodology: CbBMP

Finally, a novel CbBMP effectiveness was measured by calculating the performance parameters based on F-score, sensitivity, exactness score, error rate, and precision. Subsequently, the prediction improvement score over existing prediction frameworks is analyzed by processing the comparative analysis.

4.1 Proposed of the developed CbBMP

The designed CbBMP has five phases: data importing function, error pruning, feature analysis, disease prediction, and severity analysis. Hence, this layer diagram is detailed in fig.3.Also, this proposed algorithm is functioned based on the principle of Boosting algorithm [26], chimp fitness [27], and multilayer perceptron [28]. Here, the data importing process is executed in the input phase of the novel CbBMP. Moreover, outcome boosting parameters were utilized in the hidden phase for the finest error elimination. Henceforth, the refined data is imported to the classification phase, in that feature analysis, disease forecasting, and severity analysis have been performed. Besides, the chimp fitness function is executed in the optimal layer, providing the finest tuned results from the classification phase.

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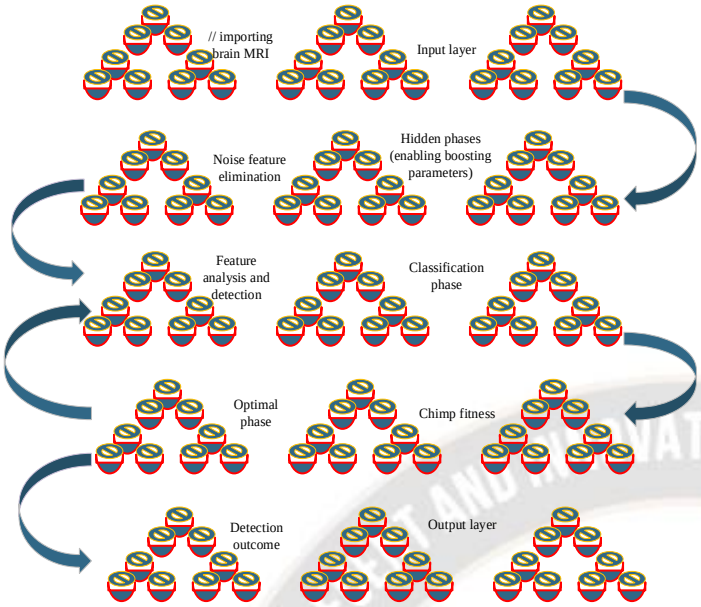

Fig.3 CbBMP layer

Furthermore, the data importing process is described in Eqn. (1). Here, the MRI brain tumor data is considered as B_t, and the n number of the data training process is determined as $1,2,3,4,....n$. Also, the training process parameter is exposed $F(B_t)$.

$$F(B_t) = B_t\{1,2,3,4,.....n\} \quad \textbf{(1)}$$

After importing the data, it is entered into the hidden phase for filtering the present noise features from the trained sets.

4.1.1 Pre-processing

The significant parameter in the ML and image analysis framework is eliminating the unwanted noisy features that have helped to minimize the over-fitting rate and computational cost. Considering these advanced measures for the pre-processing process, the boosting framework has been utilized to remove the redundant and noisy features like sharpness and blur.

$$K(B_t) = A(B_t(u,r)) \quad (2)$$

The raw database contains both normal and noisy features detailed in Eqn. (2). Here K is the pre-processing variable, image feature analysis parameter is described as A, noise feature is denoted as r, and the normal image features are determined as u.

$$K(B_t) = B_t[A(u-r)] \quad (3)$$

Also, the function of the filtering is exposed by Eqn. (3), here, the analyzed noise features were eliminated which is equated as $u-r$. By performing these functions, the refined data has been gained then the attained refined data is utilized for the further process.

4.1.2 Feature Analysis

In this step, the meaningful features were extracted separately; the trained brain images have more additional features. Henceforth, the required significant features were extracted in the features analysis process. The extracted features from the feature analysis process are given as the input to the disease prediction process. Hence, the feature extraction process has been performed by Eqn. (4)

$$C = |s(B_t) - Y(B_t)| \quad (4)$$

Here, feature analysis parameters are determined as C, s denoting the meaningful features and Y describes the meaningless features parameter. By performing this feature analysis function, meaningful features have been gained.

4.1.3 Tumor prediction

Here, the abnormal feature was identified with the help of the chimp solution by matching a normal healthy MRI brain image with an abnormal brain image. Then the different features from the healthy brain MRI were detected. Also, the designed novel CbBMP is more suitable only for tumor detection in an accurate manner. Hence, the prediction is functioned by Eqn. (5).

$$D^* = \begin{cases} malignant & if\ (C=0) \\ Benign & if\ (C=1) \end{cases} \quad (5)$$

Besides these, the trained brain MRI images have additional features: tissue swelling, blood clots, etc. These features all are extracted in the feature analysis process. Then during the tumor detection process, the exact tumor was predicted with a high exactness rate.

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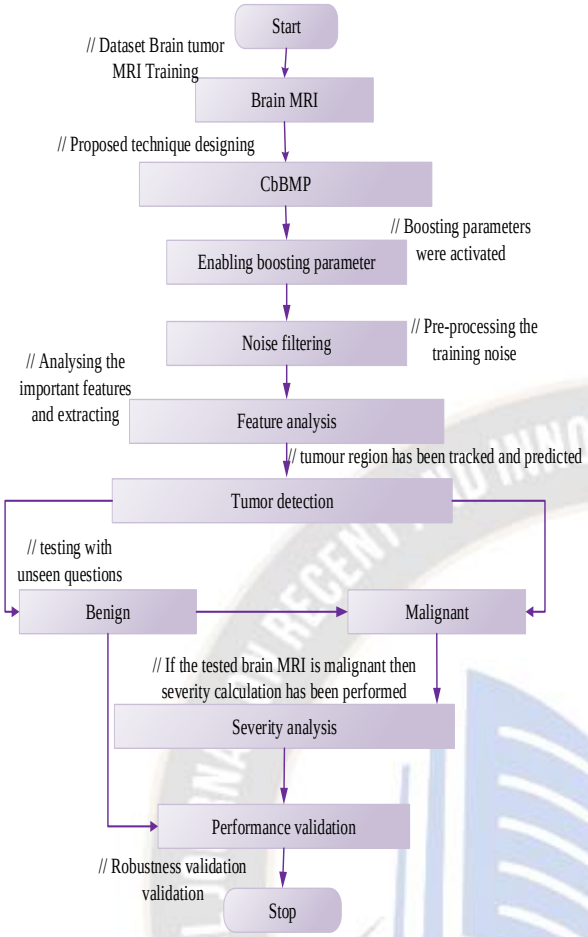


Fig.4CbBMP Workflow

The step-wise working of the designed novel framework is described in fig.4, and the pseudo-code is described in algorithm .1. Moreover, the database has been taken into consideration of 80:20, that is, training 80% and testing 20%. During the testing process, tumor detection has been executed on the basis of malignant and benign. Also, the severity score has been measured for the malignant cases.

Algorithm: 1 CbBMP

Start
{
$\text{int } B_t = 1,2,3,4,5....n;$
// database initialization
Pre-processing ()
{
$\text{int } K, A, u, r;$
// initializing pre-processing variable
$K \rightarrow B_t - noise \quad features$
//here, the noise features are eliminated by the boosting parameter
}
Feature analysis ()_
{
$\text{int } s, C, Y;$
// initializing feature analysis variable
$C(B_t) = extrcat(s[B_t])$
// meaningful features were extracted
}
Tumor prediction ()
{
$\text{int } D^*;$
// initializing the prediction variable
if $(C = 0)$
{
Malignant
}else (normal)
}
}
stop

V. RESULTS AND DISCUSSION

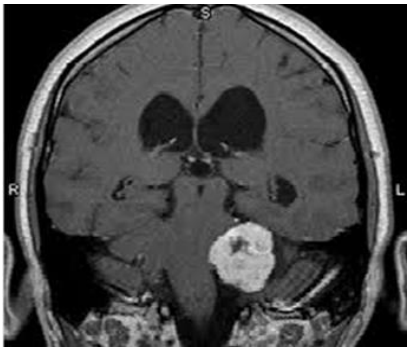
The planned design is executed in the MATLAB environment and running on the windows 10 platform. Initially, 10,000 brain MRI images were gathered and imported into the system containing both normal and abnormal images. The dataset considered in this present study is the brain tumor kaggle database. The parameter specification is tabulated in table.1.

Table.1 Execution parameter description

Parameter specification	
Platform	MATLAB
version	R2020b
Operating system	Windows 10
Dataset format	Jpeg
Database type	Image MRI
No. of samples	10000

5.1 Case study

To check the processing procedure of the designed novel CbBMP, some samples were taken and each process step was executed. Hence, the gained outcomes are described as follows,



(a)

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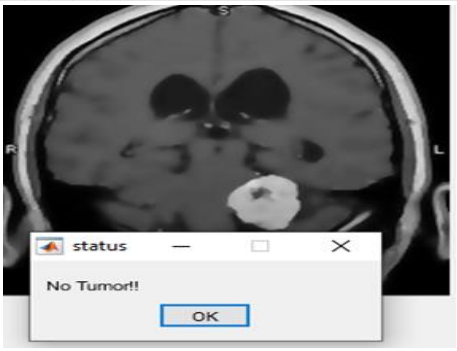
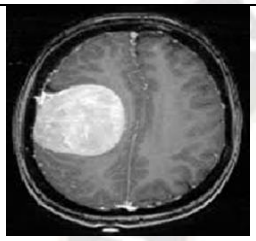
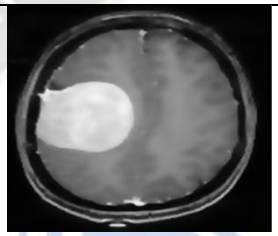
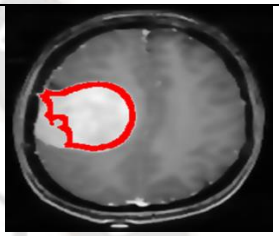
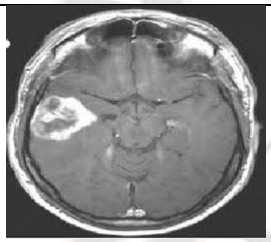
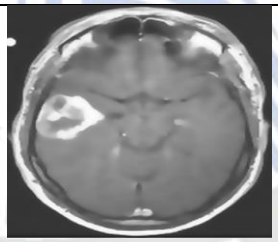
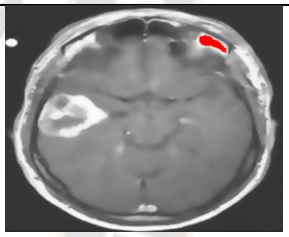
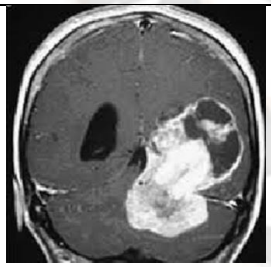
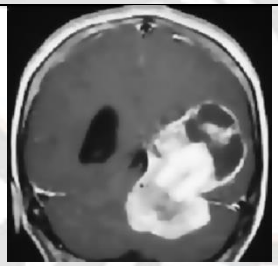
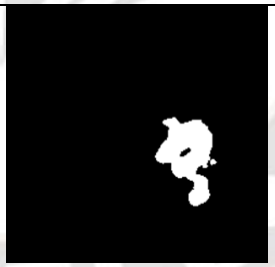
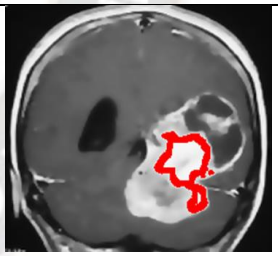
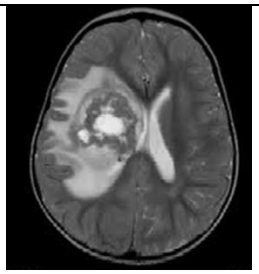
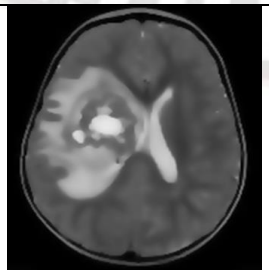
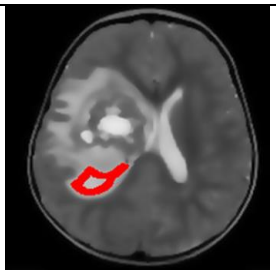


(b)

Fig.5 Normal Brain MRI a) input image, b) filtered image

The imaging results for the standard MRI brain image are described in fig.5. Here, fig.5 b) describes the filtered image. After the noise removing function, feature analysis has been performed. The affected region has been tracked, tumor affected regions are not present, so it is described as no tumor.

Table.2 Input and testing Results

Samples	Input images	Filtered images	Feature analysis (tumor region tracking)	Prediction outcome	Severity(%)
1					90
2					15
3					70
4					40

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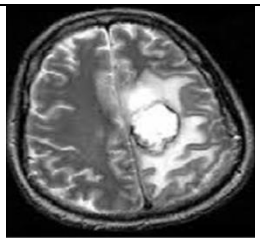
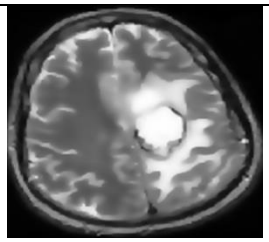
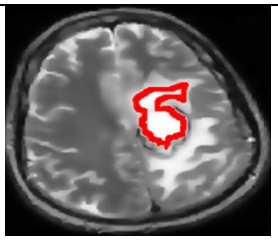
5					80

The testing outcomes of the different 5 samples are described in table.2. The imaging outcomes that are present in table.2 are filtered image, tumor region tracking, and tumor prediction. Besides, if the predicted region is classified as malignant, then the severity range has been measured.

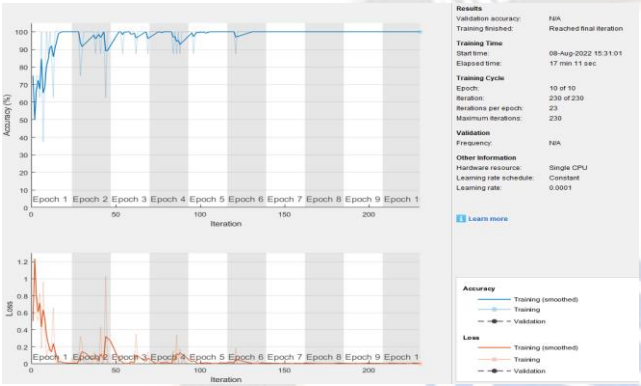


Fig.6 Accuracy and Loss validation

The accuracy and loss parameters are measured in the form of training and validation during the training process described in fig.6.Here, the validation accuracy range has reached the 100% this show, and the model canexactly predict the tumor. In addition, the loss validation has recorded the 0%. It has been verified that the designed model has recorded less misclassification scores, as defined in fig.6. To find the true and false scores confusion matrix defined in fig.7.

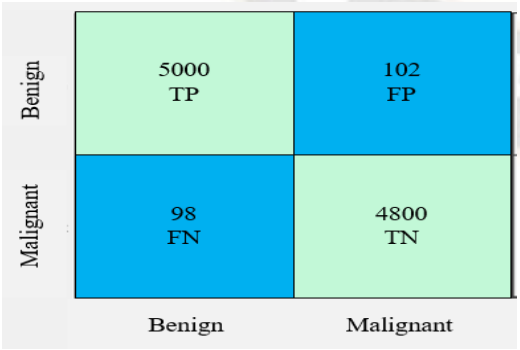


Fig.7 confusion matrix

5.2 Performance assessment

To check the need of the presented model in the diagnosis prediction framework, the performance analysis has been conducted with different existing models, such as autoregressive Convolution neural Framework (ACNF) [29], Hyper-column convolutional network (HCN) [30], softmax, K-nearest model (KNM), Multi-objective Support vector and model (MSVM) [31].

The parameters considered to value the created design's effectiveness are prediction accuracy, F-score, recall, and precision.

The success of the designed model has been verified by the outcome statistics. Hence, the performance parameter validation has been conducted.

The metric accuracy is measured for the exact tumor detection or classification purpose. Hence, the parameter accuracy has been validated in terms of positive and negative cases as well as true and false classes.

$$Accuracy = \frac{t_n + t_p}{t_n + t_p + F_n + F_p} \quad (6)$$

Here, the true negative score has been described as t_n ,true positive value is defined as t_p , and a false negative score is determined as F_n and F_p described false positive score. Hence, the parameter accuracy has been estimated by Eqn. (6).

In addition, to know the exact prediction in the form of positive classed and the exact classification score, the precision parameter was calculated by Eqn. (7).

$$Pr\,ecision = \frac{t_p}{F_p + t_p} \quad (7)$$

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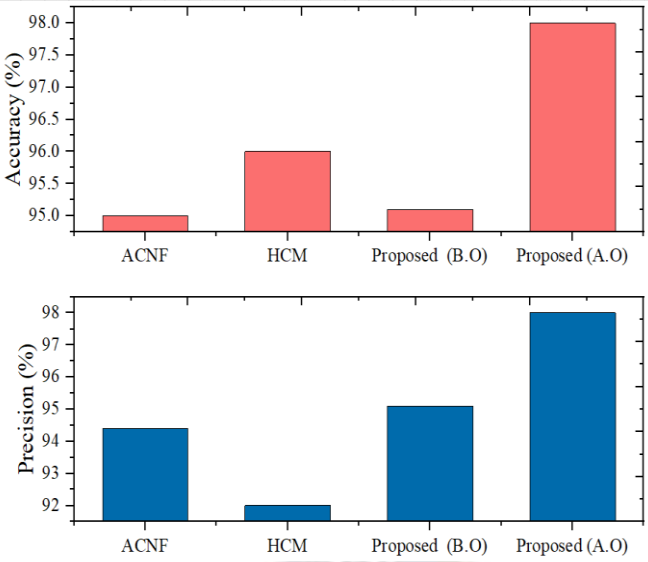

Fig.8 Precision and accuracy Assessment

The model ACNF has employed a 94.4% precision and 95% accuracy score. Then, the HCM approach gained a 92% precision and 96% detection exactness score. The designed novel CbBMP has recorded a high tumor prediction exactness score of 98% and precision of 98%. Before incorporating the chimp model, the prediction exactness has been minimized; hence the recorded precision value is 95.1% and accuracy 95.1%. The statistics of accuracy and precision are defined in fig.8.Here, B.O represents before optimization, and A.O is denoted after optimization.

To measure the stability range of classification with the occurrence of false negative cases, the recall has been measured by Eqn.(8). In addition, recall validation has offered the sensitivity score for the designed classification model.

$$recall = \frac{t_p}{F_n + t_p} \tag{8}$$

To gain mean recall performance and precision score, the F-measure parameter was estimated by eqn.(9). It has provided the overall exactness score by incorporating the false and true class prediction.

$$F-measure = \frac{2 * recall * precision}{recall + precision} \tag{9}$$

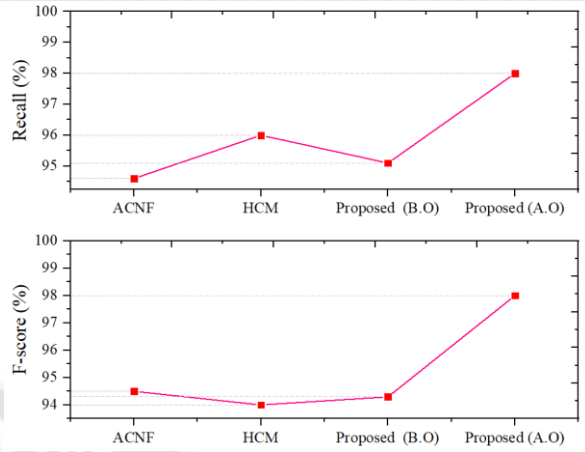

Fig.9 Validation of recall and F-measure

The ACNF model has gained a 94.5% F-score and a recall value of 94.6%. Also, the approach HCM has recorded recall measure as 96% and F-value as 94%. Considering these, the proposed method is measured under dual phases before and after incorporating the chimp solution. Before incorporating the chimp solution, the gained f-score was 94.3%, and recall was 95.1%. After involving the chimp function, 98% f-score and 98% recall was reported, as described in fig.9.

Table.3 Comparison of statistics

	F-score (%)	**Recall (%)**	**Precision (%)**	**Accuracy (%)**
ACNF	94.5	94.6	94.4	95
HCM	94	96	92	96
Proposed (without optimization)	94.3	95.1	95.1	95.1
Proposed (with optimization)	98	98	98	98

5.3 DISCUSSION

From all the performance validation, the novelCbBMP has reported the most satisfactory outcome because of the hybrid function process that is boosting and optimal function in the multilayer perceptron. Here, the performance was validated two ways before and after incorporating the chimp model to measure the necessity of the optimal solution in the neural boosting model. Moreover, the overall robustness of the designed novel mechanism is detailed in the table.4

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Table.4 overall performance of CbBMP

Performance of CbBMP(%)	
F-score	98
Recall	98
Precision	98
Accuracy	98
Error rate	2
Time	2s

To find the robustness of the designed model more accurately, some other techniques were also adopted and compared with some key metrics like error rate, accuracy, and time, which are explained in fig.10. To find the misclassification outcome, the error score has been measured, compared to other models the novel CbBMP has described the less misclassification rate.

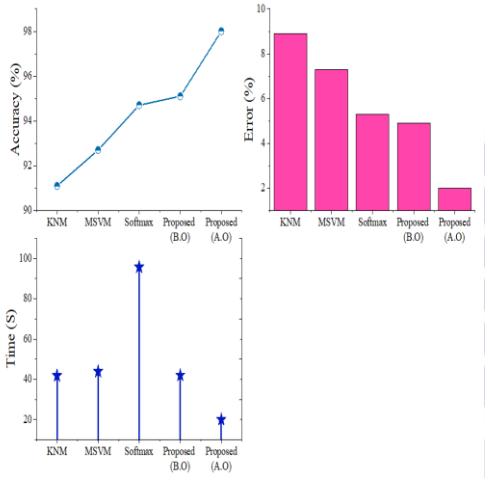

Fig.10 Robustness validation

In addition, to validating the designed model's computation cost, execution time has been found and compared with other recent conventional models. In that, the novel CbBMPhas described the less execution time that is 20%. Also, before applying, the chimp fitness 42s has required to complete one execution. These metrics have verified the efficiency and suitability of the designed model in the medical field.

VI. CONCLUSION

For detecting the brain tumor with a high exactness score, the present research has introduced a novelCbBMP, which includes boosting function, feature analysis, and optimal detection. Moreover, these combined function processes have helped earn the most satisfactory brain tumor prediction rate from the MRI images. Hence, the proposed framework's recorded exactness score for the brain tumor forecasting process is 98%. Compared to conventional models,4% of the exactness score has been maximized. Moreover, the proposed system is tested in two cases before and after incorporating the chimp function. Hence, the recorded misclassification score is 4.9% before incorporating the chimp fitness solution. After executing the chimp function in the designed boosting deep networks, the recorded error score is 2 %. Hence, the chimp function has minimized 2.9% of the misclassification score. Thus, the designed detection mechanism is suitable for the tumor diagnosis process in the medical field. However, the introduced model is unsuitable for all problems; it can only detect the brain tumor accurately. In the future, designing the multi-objective system along the proposed mechanism will afford the finest multi-disease prediction outcome.

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