The Seybold Report

ISSN 1533-9211

DOI 10.17605/OSF.IO/3VGCR

AN OPTIMIZED INTELLIGENT SEVERITY ANALYSIS FRAMEWORK FOR BRAIN LESION PREDICTION

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Abstract

Brain lesion forecasting is the most trending study in the medical industry because of this disease severity rate. Several intelligent prediction models existed to offer the finest brain lesion prediction outcome. However, a suitable outcome is not attained because of its poor image quality. Usually, the Magnetic resonance image (MRI) is high in noise content, which maximizes the prediction complexity. These drawbacks resulted in low prediction exactness and severity calculation scores. So, the current work aimed to develop a novel Dove-based multilayer perceptron Severity analysis (DbMPSA) framework for improving the disease severity analysis rate. Initially, the MRI images were preprocessed, and the meaningful features were extracted; then, the disease region was tracked and segmented. Finally, the severity rate was measured based on the affection range. Subsequently, the presented model has attained a high exactness score in specifying the severity and segmentation.

Keywords: Brain Lesion, Severity Classification, Multilayer Perceptron, Disease Region Segmentation, Feature Extraction.

1. INTRODUCTION

The irregular tissues that grow within the brain near dopaminergic neurons are called Brain lesions [1]; it directly impacts regular life. These aberrant tissues have the propensity to develop brain erraticism and induce head tension [2].

Hence, stress disrupts human functions by causing numerous brain problems [3].

Indicators of such illnesses include vertigo, fainting episodes, headache, and paralysis [4].

However, the presence of tumours in essential areas can be treated with the use of other therapeutic methods such as medication [4], radiation therapy [5], and chemotherapies [6].

Furthermore, in the year 2019, it was expected that roughly 86 thousand instances of neurological symptoms would be found in the United States among about 700 thousand individuals with neurological problems [7].

ISSN 1533-9211

DOI 10.17605/OSF.IO/3VGCR

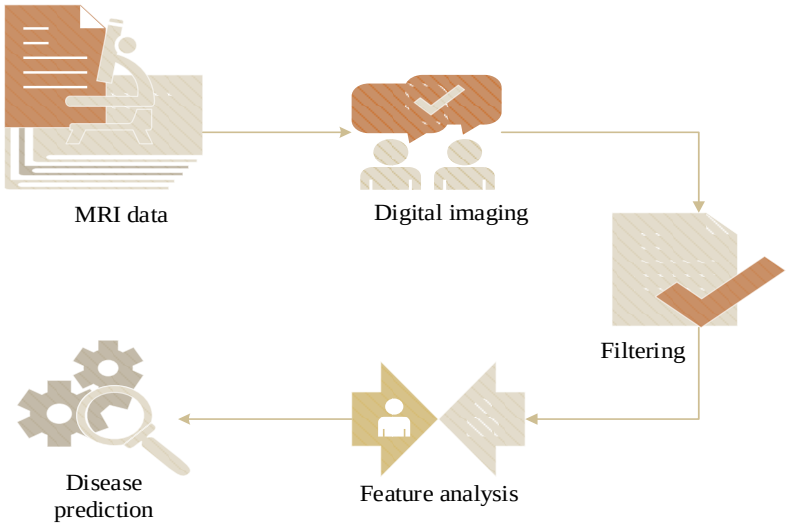

Fig. 1 Digital imaging system

Computerized 2D and 3D delineation of brain abnormalities can accomplish the results more quickly and provide accurate detection for subsequent lesion analysis and monitoring. The digital imaging system is defined in fig. 1. Recent research has focused on applying deep networks to medical uses [8, 9]. The size, shape, tumour region, and proximity closeness of the tumour are now at the top of the priority list, evaluating cerebrum cancers somewhat problematic [10]. It is difficult to detect brain tumours in the initial stages due to the inability to determine their exact size [11].

If a brain tumour is detected at an undeniably early stage, then the death rate may be reduced through effective treatments [12]. Considering these, the imaging application was introduced for brain lesion detection [13]. X-pillar was the most effective and widely used technique for brain tumour regions [14].

Current detection methods rely on conventional systems depending on human existence [15], which increases the possibility of false-positive results for detecting brain cancers [16]. Current techniques and strategies for eradicating cancers and their progeny have become profoundly alien [17, 18]. Methods of image analysis can be used to detect brain diseases.

Image feature analysis approaches transform images into the foreground and apply structure to these to produce redesigned images [19]. This assessment will consider methods to detect brain cancers using image processing techniques. In recent, several disease detection research works, such as Gaussian procedure [21], Decision tree [22], transfer learning [25], etc., have existed to predict the exact disease region from the brain MRI images. In that, some approaches have gained the finest disease region tracking accuracy.

However, the severity finding of the tracked diseases part is not existed because of the image complexity. So, the present study has aimed to design the severity analysis system based on the optimized intelligent mechanism. Finally, the improvement and the need for the designed framework are verified by performing comparative studies.

ISSN 1533-9211

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The major contributions of this current study are elaborated as follows,

- The brain MRI images were trained to the system to test the designed system, which contains both normal and abnormal images.
- Consequently, a novel DbMPSA was framed with the required feature analysis and severity prediction parameters
- Primarily, the noise features were neglected in the preprocessing layer and entered the classification layer
- Henceforth, present features were extracted, and the affected region has been segmented
- Finally, the disease type was specified, and the severity rate was validated and compared with other models in terms of Dice, precision, positive predicted score (PPS), accuracy, false predictive score, recall, true positive Score (TPS), f-measure and false positive Score (FPS).

The current work paper is presented in the form of recently associated literature in 2nd section, and the problems that the conventional model faces are exposed in section. 3. Then the solution for the defined problems is elaborated in section. 4. The validation results of the novel solutions are discussed in section. 5. Finally, the research paper is concluded in the 6th section.

2. RELATED WORKS

Some recent work associated with brain tumour prediction systems is described as follows;

The MRI images are more complex because of the noisy feature. Considering that, Xiaoran Chen et al. [21] have implemented a local Gaussian procedure in the lesion prediction framework to reduce computation and algorithm complexity. Hence, this disease prediction model has gained a reduced computational score, and high detection score was gained. However, the resource usage cost was maximized because of the additional noise removal features in the Gaussian filter.

Javaria Amin et al. [22] have surveyed the brain lesion prediction system. Hence, the models like neural networks and optimization have been considered in this research. By the performance validation, it has been verified that the deep networks have earned the finest disease prediction outcome than the other model. However, it has recorded more time than the machine learning models for predicting the disease-affected region.

A decision tree with principle component analysis has been introduced by D. Jude Hemnath et al. [23] for segmenting the affected part from the brain MRI images. Here, the principle components features were activated to remove the raw dataset's noise features. In addition, the decision scheme has been utilized to decide whether the tracked region is normal or the affected region. However, the average detection rate has been measured, and the filtering process has taken more time to execute.

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Some effective disease prediction models for imaging systems are more complex in design. So, Md KhairulIslam et al. [24] have designed the light weighted disease analysis framework based on the K-means algorithm and principle components methods. To track the disease-affected region template-based model was utilized based on the super pixel features. Moreover, to train the database, artificial networks were utilized. Finally, the detection complexity was reduced. However, if the data is complex, it takes more time to execute.

The effective deep network as the transfer learning has been implemented by Andrés Anaya-Isaza et al [25], forecasting the disease region with a high exactness score. Henceforth, the filtering function was executed using the component analysis scheme. Hence, the designed transfer learning with the component analysis model is more sufficient to train a large number of data and also record the finest prediction score. However, this model has earned the widest design complexity score.

3. SYSTEM MODEL AND PROBLEM STATEMENT

Different neural networks have implemented brain lesion or tumour detection frameworks with optimization strategies. However, the severity analysis model has not been elaborated on as much. Also, finding the MRI image's severity rate is difficult in many cases because of the complex data [20]. The results and drawbacks of the conventional image processing model are defined in figure 1. Here, the traditional image model analysis has fewer features that have tended to cause poor outcomes in different stages. Hence, finding the disease severity is more complicated in many medical imaging studies.

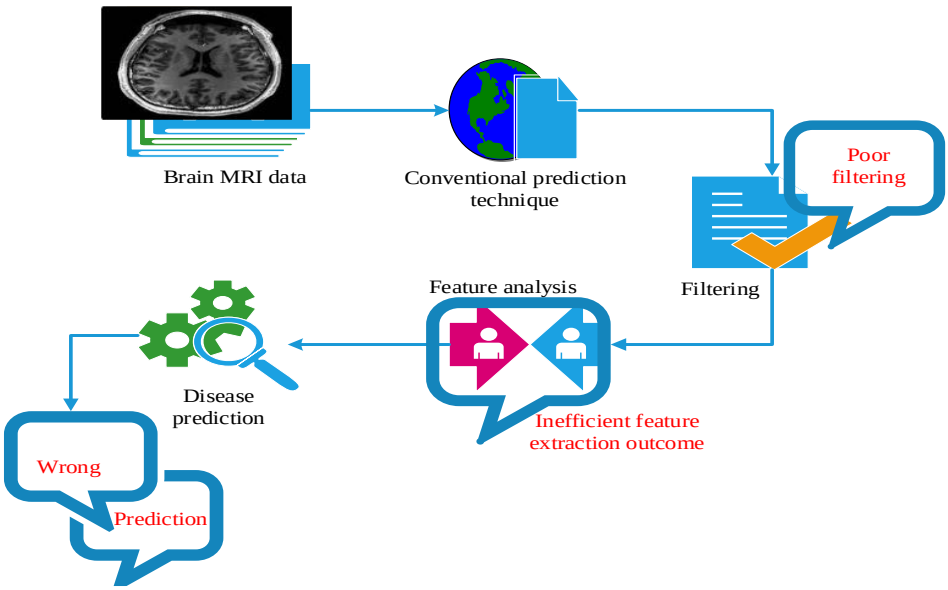

Fig. 2 Problems in conventional prediction system

But, severity prediction is the most important module for digital medical imaging application and medical researchers. Hence, these objectives were adopted for this present study to address

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the described issues in the past disease prediction models. Here, the severity was predicted based on matching original and affected brain features.

4. PROPOSED METHODOLOGY: DbMPSA

A novel Dove-based multilayer perceptron Severity analysis (DbMPSA) framework has been proposed for segmenting and analyzing the severity range of the brain lesion. The MRI dataset has been considered to check the efficiency of the designed severity analysis system. Initially, the MRI images were preprocessed and given to the classification module then feature analysis and segmentation functioned optimally. Finally, the severity of brain lesion has been measured to enrich the disease prediction system. Subsequently, the parameters were calculated and compared with other models. The novel DbMPSA is figured in fig. 2.

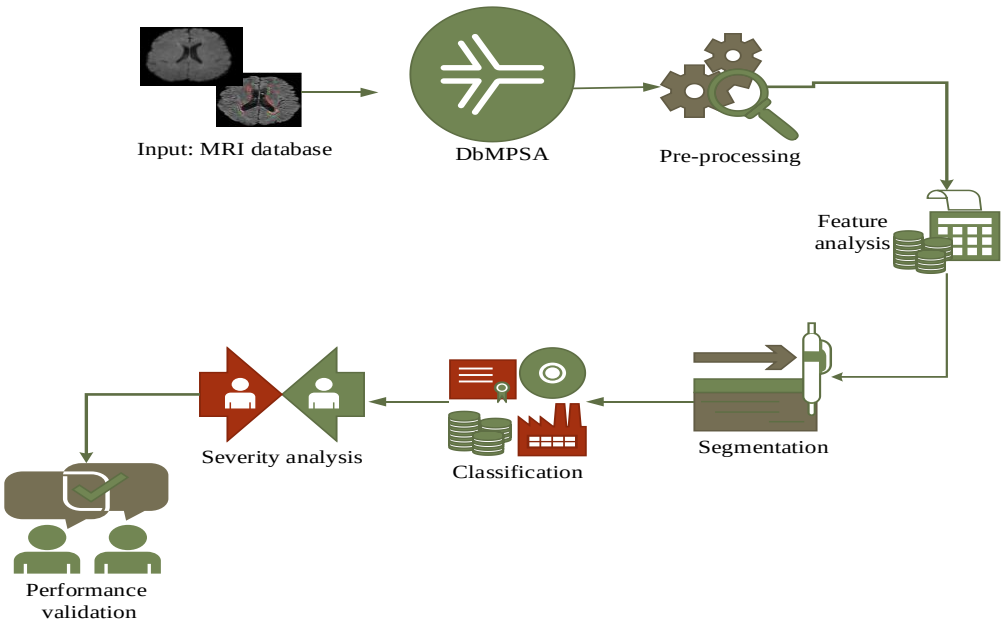

Fig. proposed DbMPSA architecture

The need of this presented framework for the medical application and the improvement score over than the conventional model is justified by analyzing the performance metrics and comparison validation.

4.1 Process of the proposed methodology

The designed model has five layers: the data training phase, hidden layer, classification modules and output layer. Moreover, it is processed using the dove swarm function principle [29] and the multilayer perceptron intelligence model [30]. The deep, intelligent model called multilayer perceptron is utilized to afford the finest filtering outcome. Here, the filtering process was processed in the DbMPSA's hidden layer.

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DOI 10.17605/OSF.IO/3VGCR

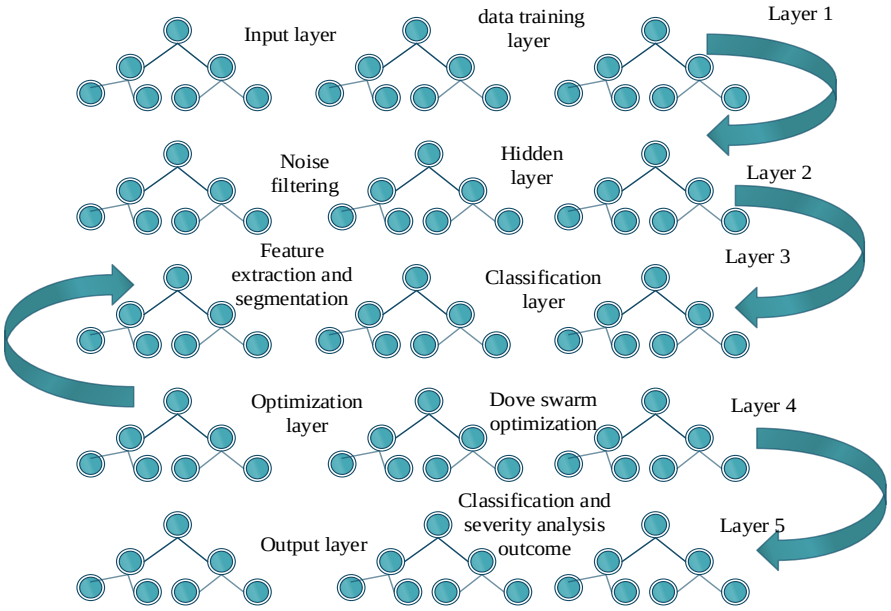

Fig. 4 Processing Layers of DbMPSA

Then the feature analysis and segmentation are carried out in the classification phase. Here, the dove fitness tuned the classification parameters that afforded the tuned prediction outcome. The novel DbMPSA functioning layers are described in fig. 4.

4.1.1 Data training and preprocessing

In the primary phase, several brain lesion MRI images were gathered and imported into the python environment. Moreover, the data training function is executed using Eqn. (1).

$$F(b) = b\{1,2,3,4,5,6..n\} \quad (1)$$

The MRI brain lesion database is represented as b then the training function is defined $F(b)$ and $1,2,3,4..n$ determines the n number of data samples.

$$V = b[(r,e) - e] \quad (2)$$

Moreover, the preprocessing variable is V, the raw data containing both normal and noise features. Hence, the noise features are defined and the normal features are described r. By executing the Eqn. (2) the noise variables were eliminated from the imported data.

4.1.2 Feature extraction

The ordinary image data is rich with high and low-range pixels, which has determined several rich features. Hence, processing the entire features might take a long to complete the task, which has tended to maximize the algorithm complexity. Considering this, feature extraction

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ISSN 1533-9211
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is the main part of multimedia applications. Moreover, the feature extraction process is defined using Eqn. (3)

$$Y_f = \frac{b_m - b_l}{n_f}(j-1) \quad (3)$$

The feature extraction variable is determined as Y_f, meaningful features are represented as b_m, and meaningless features are described b_l. By processing the Eqn. (3) the meaningless features were eliminated, and the required features were extracted. The n_f determines the n features count, and the iteration count is defined as $j-1$.

4.1.3 Disease tracking and segmentation

To find the severity score of the disease affection range segmentation is the most required task for the multimedia application considering this segmentation function was executed in the image processing domain. Here, the disease tracing function was processed using the dove position behaviour, equated in Eqn. (4).

$$T_d = b + \beta(Y_f) \quad (4)$$

The disease tracing variable is determined as T_d and β denotes the finest solution of the optimal dove algorithm. The disease features were stored in the β variable. During the execution, the disease features were traced from the trained data by matching the stored disease features.

4.1.4 Classification and severity probability

The classification process is executed in dual cases 0 and 1; if the segmented images are specified under the 0^{th} class, then it is considered normal. If the segmented images are specified in the first classes, it is defined as a disease-affected region.

$$C_b = \begin{Bmatrix} if\,(T_d = 0) & Normal \\ f\,(T_d = 1) & abnormal \end{Bmatrix} \quad (5)$$

Once the segmented part is classified as a disease, the severity analysis process is initiated to measure the disease affection severity range. Here, the classification process was equated in Eqn. (5).

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Algorithm: DbMPSA
start
{
int $b = 1,2,3...n$;
// dataset initialization
Preprocessing ()
{
int V, r, e;
//Preprocessing variables were initialized
$V(b) = e - database$
// eliminating noise features
}
Feature extraction ()
{
int Y_f, b_m, n_f, b_l;
// feature extraction variables were initialized
$Y_f \rightarrow b_l - b$
// Extracting meaningful features
}
Disease tracking and segmentation ()
{
int T_d, β;
// initializing feature tracing variable
$segment \rightarrow \beta(Y_f)$
// Disease region was segmented
}
Classification and severity probability()
{
int C_b;
// Classification variable was initialized
$if\ (T_d = 0)$
{
normal
}else (abnormal)
} $Severity = affected \quad region / entire \quad region$
}
stop

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The defined mathematical formulations are illustrated as pseudo-code, described as algorithm 1.

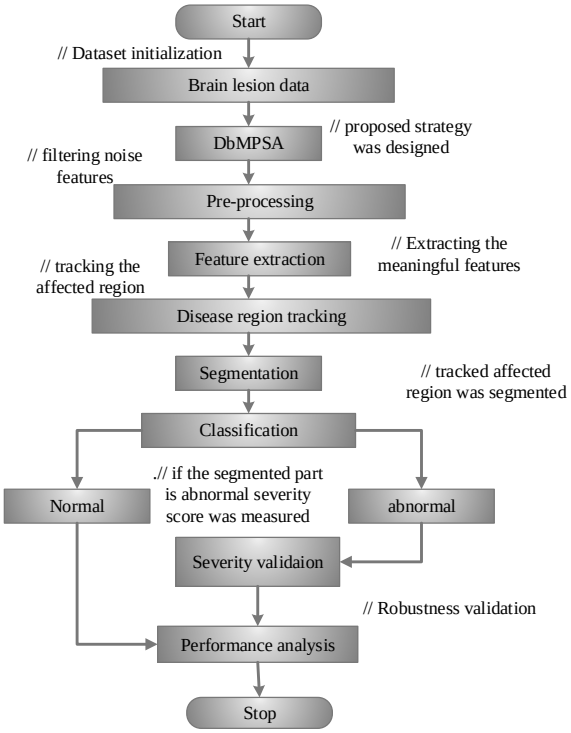

Fig. 5 Flow of DbMPSA process

The flow and the step process of this disease classification and the severity estimation framework are diagrammatically visualized in fig. 5. After processing the described steps, the performance of the novel DbMPSA has been valued by different classification metrics.

5. RESULTS AND DISCUSSION

The novel DbMPSA model is validated in the python programming platform and executed in the windows 10 framework. The database considered for this testing validation is MRI brain lesion, which contains both normal and abnormal data.

Table. 1 Specification of Execution parameters

Parameters description	
Programming environment	Python
Database	MRI brain lesion data
Dataset format	Image
Operating system	Windows 10
Total images count	253
Deep Network	Multilayer perceptron
Optimization	Dove swarm

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ISSN 1533-9211
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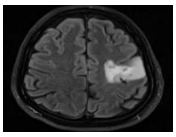
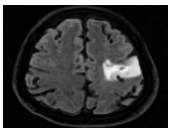
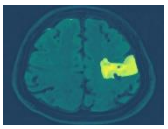
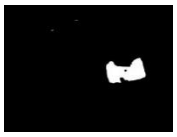
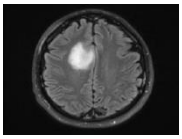
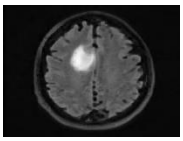
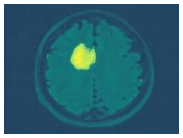
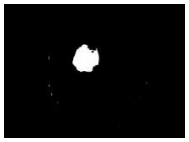
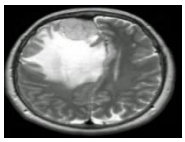
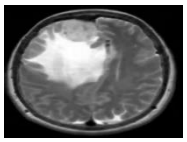
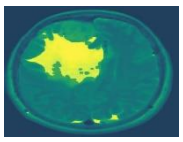
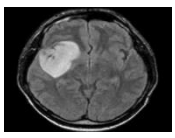
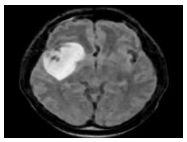
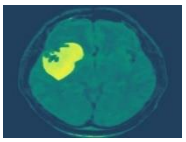
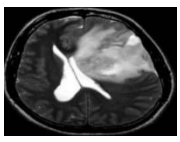
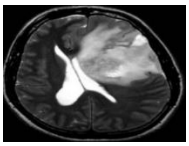
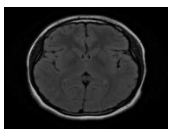
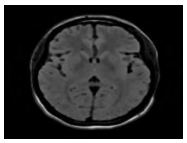
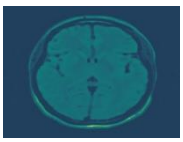
The disease-affected region was traced and segmented then the severity probability range was measured based on the segmented images. The execution parameter specification is described in table. 1.

5.1 Case study

To check the functioning performance of the designed mechanism, some test validations were executed and the outcomes were described in the systematic way, which is defined in table. 2. Hence, for the test validation brain lesion database was adopted from the kaggle site, it contains total 253 images. In that 98 images are normal images and 155 images are tumor images. In addition, images that consider for training is 78 normal images and 124 brain lesion images. Also, the images that utilized for testing is 20 normal images and 31 abnormal images

Table 2: Testing outcome

samples	Input images	Preprocessed images	Feature analysis (tracking outcome)	Segmented	Severity (%)
1					0.048
2					0.035
3					0.14
4					0.058
5					0.199
Normal image					0

ISSN 1533-9211

DOI 10.17605/OSF.IO/3VGCR

The robustness of the designed model was determined by evaluating the validation graphs with two metrics: correct prediction and wrong prediction. Hence, the correctly predicted count for the normal class brain is 19, and the recorded wrong prediction is 1. Same, the earned exact forecast for the abnormal classes is 31, and the wrong prediction is 0. This has verified that this model is suitable for brain lesion segmentation with less miss classification rate.

r) s)

t) u)

Fig. 6 Testing outcome of normal image: r) input image s) preprocessed image, t, feature extraction outcome, u) segmented outcome.

The proper working function of the designed approach is valued by testing the implemented mechanism with normal images. Hence, the testing outcomes for the normal images are illustrated in fig.6. Also, fig.6 u) exposed the segmented results; there is no segmented region, so the severity is 0. It has represented this tested image has no disease features.

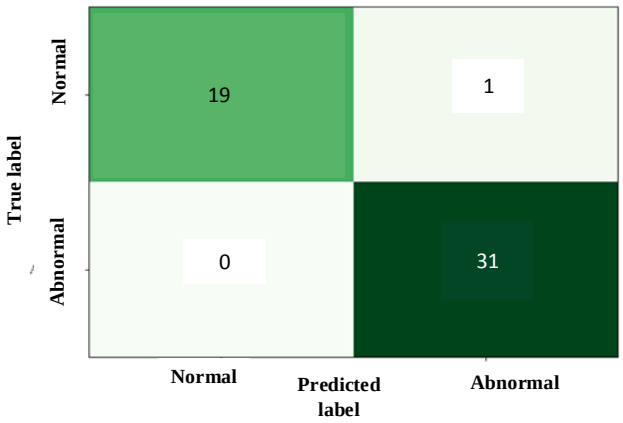


Fig. 7 confusion matrix

The classification or detection outcome was attained in the form of positive and negative scores for both true and false classes. Hence, the positive and negative scores in both true and false classes were organized in the form of a confusion matrix, illustrated in fig.7.

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5.1 Performance Assessment

The improvement score of the designed novel DbMPSA was justified by calculating the chief metrics like Accuracy, F-score, precision and sensitivity score taken for the validation. Also, the recently associated models that were taken for analyzing the performance improvement are the Convolution layer (CL) [26], Fully Connected Convolution layer (FCCL) [26], Decision Tree (DT) [28] and Adaboost Model (AM) [28].

Precision: To determine the Positive score of the disease classification process, the precision performance metrics were validated using Eqn. (6).

$$\Pr ecision = \frac{T_p}{F_p + T_p} \tag{6}$$

The CL model scored a precision score of 94.37%, the FCCL mechanism recorded 95.48% precision, AM recorded 94% precision, and the approach DTM earned a precision rate of 88%.

Accuracy: To find the exactness rate of the disease region segmentation and the severity calculation, the accuracy parameter was measured by Eqn. (7). This metric has afforded the robustness value of the designed model. In addition, the Accuracy is measured by taking the average score of the positive and negative scores of the prediction.

$$Accuracy = \frac{T_n + T_p}{T_p + T_n + F_p + F_n} \tag{7}$$

The exactness score recorded by the existing models are defined as follows, CL gained 97.79% accuracy, FCCL model earned 91.21% accuracy, AM scored the

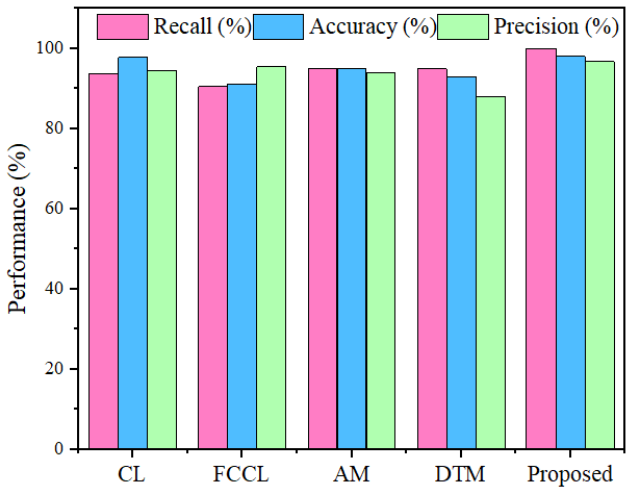

Fig. 8 performance evaluation

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The number of correct positive predictions from the total positive detection is measured using recall metrics. Hence, this positive prediction outcome has provided the overall testing performance. Moreover, the sensitivity is validated by Eqn. (8).

$$Sensitivity = \frac{T_p}{F_n + T_p} \tag{8}$$

The sensitivity score earned by the model CL is 93.78%, the FCCL model reported the sensitivity score as 90.48%, AM scored 95% sensitivity and the DTM gained a sensitivity score of 95%. Hence, the evaluation of Accuracy, precision and recall is defined in table. 3 and fig. 8.

Table. 3 validation of Accuracy, recall and precision

Efficiency validation			
	Recall (%)	**Accuracy (%)**	**Precision (%)**
CL	93.78	97.79	94.37
FCCL	90.48	91.21	95.48
AM	95	95	94
DTM	95	93	88
proposed	100	98.03	96.8

F-measure: The recall metrics determined the mean range of true and false scores. Hence, the f-measure is the average prediction statistics of false and true scores, equated in Eqn. (9).

$$F\_measure = \frac{2 \times sensitivity \times \Pr ecision}{sensitivity + \Pr ecision} \tag{9}$$

Hence, to validate the F-score performance, a few existing associated models were taken, such as partial tree (PT) [27], Random Forest (RF) [27], Naive Bayes (NB) [27], Rep Tree (ReT) [27], and Random Tree [27].

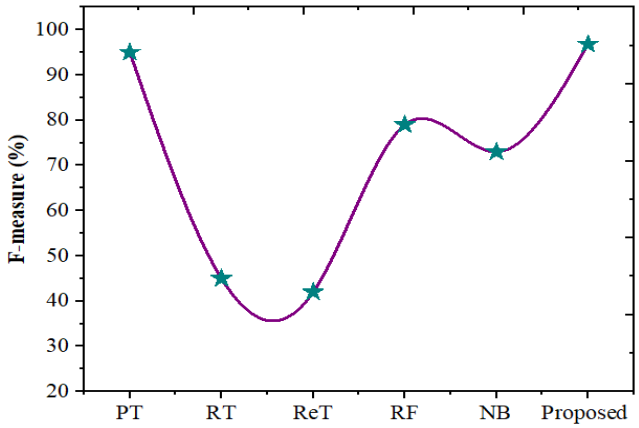

Fig. 9 F-measure validation

ISSN 1533-9211

DOI 10.17605/OSF.IO/3VGCR

Here, the PT approach scored the F-value as 95%, RF recorded the F-value as 79%, ReT achieved a 42% F-score, RT attained a 45% F-score, and the model NB gained the F-value as 73%. These statistics are exposed in fig. 9.

In addition, to find the exact detection stability range, the prediction exactness was calculated in different cases that are Positive-predicted Score (PPS), Negative-predicted Score (NPS) and Dice Coefficient (DC). Hence, to perform this validation, some of the recent studies were adopted, such as U-Net [31], Fluid Attenuated Model (FAM) [31] and Attention Model (AM) [31]. Moreover, the comparison statistics were described in table. 3 and fig. 10.

Table. 3 Prediction Score statistics

Prediction statistics			
	DC (%)	**PPS (%)**	**NPS (%)**
U-Net	94.9	93	99
FAM	82	91	99.5
AM	82	79	99
Proposed	96.8	96.8	100

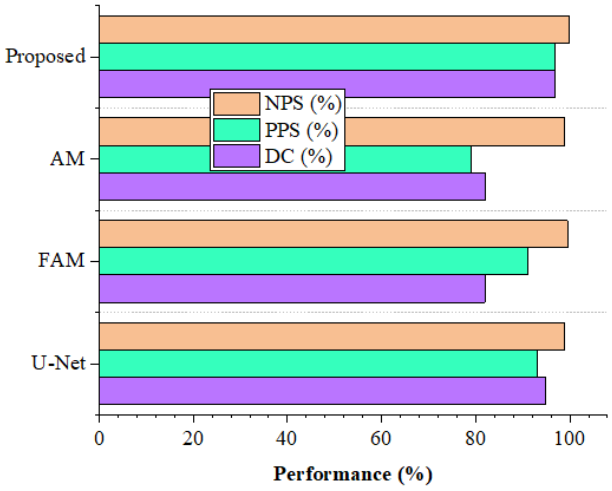

Fig. 10 Prediction robustness

Dice: The DCS was measured to measure the segmentation exactness score in the overlap classes. Hence, gaining the highest dice score has revealed the stability of the DbMPSA. Hence, dice statistics were measured to measure the proposed system robustness in failure cases. Besides, the PPS and NPS were calculated to find the right prediction percentage of each class.

5.3 Discussion

The validated performance parameters proved that the designed novel DbMPSA scored the best disease segmentation and classification outcome. It has been verified that the presented DbMPSA is highly suitable for the disease diagnosis and the severity finding problem. Hence, the presented research's significance has provided the disease-affected region's severity rate. It helps to find suitable medical support for the specific disease.

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ISSN 1533-9211
DOI 10.17605/OSF.IO/3VGCR

Table. 4 Overall performance

Performance of DbMPSA	
Efficiency parameters	**Performance (%)**
Precision	96.8
Accuracy	98.03
Recall	100
Dice	96.8
F-score	96.8
PPS	96.8
NPS	100
TPS	100
FPS	0.05

The overall performance was defined in table. 4. In prediction parameters, the designed model has scored the optimum consequence, which revealed the outstanding performance of the novel DbMPSA.

6. CONCLUSION

A novel DbMPSA framework was implemented in this present study for measuring the severity level of the tumor from the trained brain MRI. Initially, the noise features were analyzed and eliminated from the trained MRI image data then the error-free data was considered as the classification layer's input. Here, the Dove's best solution is utilized to trace and segment the tumor spot with high exactness score. After that, based on the disease affected region from the entire region, disease severity was measured. Subsequently, the gained tumor segmentation accuracy is 98.03%, compared to the conventional model, tumor prediction score was improved by 1%. Also, the recorded DC is 1, compared to the traditional schemes 2% of DC was improved. However, sampling features are not incorporated in this present study, which might results in overfitting. In future, designing the sampling features along with this proposed model will give the better results for all king of MRI database.

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