Abstract: Automated brain tumor detection and segmentation are crucial in medical diagnostics as they give details about functional structures and also potential unusual tissue that is required to define surgical strategies. Segmentation of images is one of the most difficult issues in the area of MRI scan analysis research. However, due to low contrast, automatic tumor segmentation, accuracy issues, and ill-defined boundaries remain difficult. For the prevention of brain tumors, an investigation was developed for implementing a novel framework. To overcome the problem faced by traditional existing techniques, this paper proposed an automatic brain tumor segmentation and detection system using the proposed dense convolution neural network without human intervention, where an intrinsic set of features are extracted to perform the classification task. The main aim of this paper is to segment the tumor portion from the affected MRI using a novel clustering approach. Moreover, a lot of scholars have researched the diagnosis of brain tumors, yet the accuracy-based performance metric in diagnosis results is low. A deep learning framework is proposed to evaluate brain disease more accurately using a Black Widow Optimization driven Dense Convolution Neural Network (BW-DCNN). The various performances are assessed, and the results are compared to those of other existing classifiers and approaches.

Keywords: Brain tumour, MRI, BW-DCNN, Accuracy, Existing techniques.

I. INTRODUCTION

An appealing method for improving human perception is image processing. The abnormal growth of cells in the human brain is known as a brain tumor. The most popular MRI procedure uses radio wave energy pulses to create images of the brain that can be used to diagnose patients and provide detailed information [1] [2]. The primary pre-processing step for the identification of brain tumors is segmentation [3] [4]. It enhances the effectiveness and precision of brain tumor automatic detection. When analysing medical images for timely and effective treatment planning, digital image processing plays a critical role [5]. Any image processing software’s primary goal is to use image data to extract the necessary attributes so that a machine can use them to create the final product [6] [7]. Any image processing application’s fundamental goal is to use image data to extract the necessary attributes, which can then be used by a machine to make the correct diagnosis.

Pre-processing (image denoising, enhancement, etc.), feature extraction, segmentation, and classification are the most frequently used stages of digital image processing to partially or fully automate the task of detecting brain tumors [8] [9]. Radiologists use magnetic resonance imaging, a precise imaging technique, to create images of organs and tissues. Strong magnetic fields, radio waves, and electric field gradients are used in MRI instead of the ionizing radiation used in CT and X-rays. The brain is a significant organ that is made up of a variety of components, including white matter (WM), grey matter (GM), background and cerebrospinal fluid (CSF) [10] [11]. The brain’s general functions are controlled. The cell growth become not normal called as brain tumors if number of cells multiplies uncontrollably. wherein the abnormal cells are controlled while the cells grow and multiply uncontrollably. The following categories are then assigned to it: Benign and Malignant [12] [13].

A benign tumor does not spread quickly and doesn’t harm the surrounding good tissue. Second tumor malignant means advanced of cancer getting bad over time and kills the patient. Only when the necessary features are carefully chosen and extracted will the image segmentation be more accurate and efficient. Because of the decreased complexity, segmentation computation time is also decreased. MRI can produce precise images of the brain and is non-invasive [14] [15]. As a result, it is frequently employed in the early stages of tumor characterization and diagnosis. Automatic tumor grading and segmentations obtained from MRI is more advantageous for hospital usage. Segmenting brain tumor by MRI is used for giving data about tumor, like size and shape. Discriminative models, which automatically extract and select imaging features during model training, deep learning with CNN is a promising machine learning approach. The contribution of this article,
The brain tumor MRI is given as data, it is pre-processed and the noise is removed using gaussian measure and CLAHE.

After removal of noise the data is segmented by rough c-means clustering and the segmented data is classified through the DCNN, to enhance it BW is added and the data is classified.

The classified data is evaluated through performance measures, accuracy and loss is mainly assessed to present the significance of presented device.

This study is divided into sections: part 2 discusses the results and an examination of relevant current research using the provided model. Section 3 describes the recommended technique for the task, which is then tried with and analysed. Section 4 discusses the work's results and the comparison of them. Section 5 concludes the work.

II. LITERATURE REVIEW

This article addresses the literature evaluations connected to brain tumour detection and segmentation are listed below.

Sajid, S., et.al., [16] (2019) have described brain tumor segmentation and detection within MRI image by deep learning. If assessing the label output, submitted hybrid (CNN) convolutional neural network using patch like approach and making both contextual and local information. In pre-processing step, images normalised then bias-field corrected and feed forward pass via CNN, first processing step have small false-positives around head portion deleted and whole part inserted in the proposed method.

Deepak, S. and Ameer, P.M., [17] (2021) have proposed automated categorization of brain tumor from MRI using CNN. For medical image classification, support vector machine (SVM) and convolutional neural network (CNN) features proposed in this paper. Machine learning algorithm CNN extracts features based on brain MRI images.

Amin, J., et.al., [18] (2020) have demonstrated convolutional neural network-based tumour types based on DWT fuse of MRI sequences. The tumour region is segmented using a global thresholding method, which is then fed into a proposed convolutional neural network (CNN) model to differentiate tumour and non-tumor regions. It may be extended in the future to incorporate the fusion of additional techniques, including PET and CT scans, in order to analyze categorization findings.

Ozyurt, F., et.al., [19] (2019) have reported brain tumor diagnosis determined by convolutional neural network with neutrophilic professional maximum fuzzy sure efficiency. This paper suggested a hybrid approach that makes use of convolutional neural networks and neurophysics. Primary aim is distinguishing amongst malignant and benign tumour regions in areas segmented from brain images.

Harish, P. and Baskar, S., [20] (2020) have advocated MRI-based brain tumor identification and categorization utilizing a quicker R-CNN and Alex Net model. This study presents a new framework for MRI-based tumour detection and classification. This paper proposed a deep learning technique which is a relatively new and very reliable technique for the task of segmenting and classifying images. When compared to previous approaches, the proposed innovative architecture has the greatest detection and classification efficiency.

Sert, E., et.al., [21] (2019) have presented single image ultra-resolution relying highest fuzzy entropy classification and CNN are 2 new methods for tumour diagnosis. For tumour images, high - resolution methodologies are favoured as a supplement to get rid of these issues. For the purpose of segmenting brain tumours on an MRI image, the suggested method makes use of (MFES) maximum fuzzy entropy segmentation and (SISR) single image super resolution.

Saba, T., et.al., [22] (2020) Recently submitted brain tumor detection utilizing a mix of handmade and deep learning features. The Grabbing cut approach is utilized in the suggested study to correctly segment the real symptoms lesion, and the course of learning is carried over to the visual-geometry-group (VGG-19) for collecting the factors mixed by physically constructed (texture, form) using the sequential approach.

Khan, H., et.al., [23] (2020) demonstrated stacking handcrafted traits and a convolutional neural network for IoT-enabled brain tumor identification. This research proposes completely automated brain tumor segmentation utilizing a revolutionary cascade technique that intelligently mixes handmade characteristics with CNN.
Sun, J., et.al., [24] (2019) have proposed drrnet: Deep residual refinement networks for automated brain tumor identification. For the segmentation of brain tumors, this paper suggested a brand-new automatic 3D CNN method. In the decoder, we also use densely connected fusion blocks.

Wang, W., et.al., [25] (2020) have recommended Classification of tumors, convolutional neural network learning techniques are implemented with extracting features. This research model’s primary purpose is to segment and identify MRI brain tumors. convolutional layer employed to enhance recognizing efficacy and rate, and combine artificially selected features.

III. PROPOSED METHODOLOGY

A brain tumor is one of the most dangerous diseases today, and focusing on its early detection is critical for concentrating mortality rates. Without requiring human intervention, a reflex brain cancer spotting and partition system based on a proposed dense convolution neural network is presented, in which an intrinsic set of items is removed to perform the classification task. The main objective of this work is to use a novel clustering approach to segment the tumor portion of the affected MRI. Furthermore, even though many scholars have studied the diagnosis of brain tumors, the accuracy-based performance metric in diagnosis results is low. As a result, a deep learning framework is proposed to evaluate brain disease more accurately using a Black Widow Optimization-driven Dense Convolution Neural Network to address this issue and several other challenges identified in the research gap (BW-DCNN). The suggested block diagram’s general design is shown in the figure below.

![Figure 1: Layout of the proposed methodology](image)

3.1 Pre-processing using Gaussian filter and clahe:

The GF is a 3D complexity manipulator that is applied to remove noises and soften the pictures. convolution of the image \(y(y,x)\) of size \(n \times m\) with a function of \(f(y,x)\), denoted by \(y(y,x) \ast f(y,x)\), is given by (1)

\[
y(y,x) \ast f(y,x) = \sum_{p=-b}^{b} \sum_{q=-c}^{c} y(p,q) f(y-p,x-q)
\]

(1)

Where \(b\) and \(c\) are given by \(b = \frac{n-1}{2}\) and \(c = \frac{m-1}{2}\). A pictorial representation of (1) is denoted in figure 1. \(f(y,x)\) →Gaussian filter, made by Gaussian distribution in (2):
The GF has two bounds: standard deviation σ and the dimensions of the window. If the image smoothing effect desires to be greater, the rate of σ turns higher. Several instances of filter compete with the removal of ‘salt and pepper’ noise, this filter incorporates and feature extraction upon the SIFT algorithm.

$$f(y, x) = \frac{1}{2\pi\sigma} e^{-\frac{y^2 + x^2}{2\sigma^2}}$$ (2)

Figure 2: A window filter

GF of smoothing are effectual low pass filters from the point of view of frequency and spatial territories, are effective to carry out, and could be utilized sufficiently in sight requests

The output segmented image is enhanced using CLAHE, which has developed a significant output on the health care picture. It is evaluated by separating the pictures into various non-intersecting parts of the same measures. For $512 \times 512$ pictures, to obtain a nice mathematical assessment, the numeral of parts is usually generally chosen to be equivalent to sixty-four by equally separating the picture by eight in all directions. Fig. 1 demonstrates three various communities of parts. The first part, which contains four zones, is the sort of corner region (CR). Another group, which includes 24 fields, is the decree of border regions (BR). Overall zones expect edge zones, pertain to this class. The final part includes all the leftover 36 parts, called the class of inner regions (IR). In this work, initially, a histogram of all provinces is intentional. Following, the individual histogram each histogram is reallocated in a path in such a way that its peak does not go over the limiter. Lastly, CDF of the consequent dissimilarity-restricted histograms are resolute for grayscale mapping. In the CLAHE method, bytes are plotted by chattering the slightly joining the output from the organizing of 4 alongside zone.

3.2 Segmentation using rough c-means clustering:

RCM signifies the concept. C-means are refined by monitoring each cluster, which is considered as an interval or rough set. It is classified as upper and lower BX and BX adit, having the following characteristics. (i) An item $x_k$ may be part of only one lower estimate. (ii) If $x_k$ is in cluster $X$'s BX, then $x_k$ is also in BX. (iii) If $x_k$ is not a section of any lower estimate, it refers to two or more higher approximations. This data contains overlaps between clusters. The axis $\nu_i$ of cluster $U_i$ is assessed as

$$V_i = \begin{cases} 
W_{low} \frac{\sum_{k \in U_i} x_k}{|U_i|} + W_{up} \frac{\sum_{k \in \bar{U}_i \cap \bar{U}_i} x_k}{|\bar{U}_i \cap \bar{U}_i|} & \text{if } \bar{U}_i \neq \emptyset \land \bar{U}_i - \bar{U}_i \neq \emptyset, \\
\frac{\sum_{k \in \bar{U}_i \cap \bar{U}_i} x_k}{|\bar{U}_i \cap \bar{U}_i|} & \text{if } \bar{U}_i \neq \emptyset \land \bar{U}_i - U_i \neq \emptyset, \\
\frac{\sum_{k \in U_i} x_k}{|U_i|} & \text{otherwise,}
\end{cases}$$ (3)

$W_{low}$ and $W_{up} \rightarrow$ The comparative significance of lower and higher estimates. Here, $|\bar{U}_i|$ \rightarrow numeral of models in the lower cluster approximation $U_i$, while $|\bar{U}_i \cap \bar{U}_i|$ \rightarrow numeral structures in the broad border lie between the dual assessments. The algorithm is explained below.

1. Assign initial $\nu_i, c \rightarrow$ clusters.
2. Create individual design $x_k$ to the down approximation $BU_i$ or higher approximation $BU_i, BU_j$ of cluster pairs $U_i, U_j$ by evaluating the variance in its length $d_{ik} - d_{jk}$ from cluster centre pairs $\nu_i$ and $\nu_j$. 

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3. Let $d_{ik} \to$ least and $d_{jk}$ $\to$ next to a minimum. If $d_{jk} - d_{ik} < $ some threshold, then, $x_k \in BU_i$ and $x_k \in BU_j$ and $x_k$ cannot be a member of any lower approximation, else $x_k \in BU_i$ such that distance $d_{ik}$ is least through the $c$ clusters.

4. Evaluate the new mean for individual cluster $U_i$ using Eqn. (1).

5. Reiterate Steps 2-4 until confluence, i.e., there are no longer recent tasks of items.

### 3.3 Classification using Dense BW CNN

Three convolution layers (Conv) of the 3D ConvNet process the input RGB or grey picture patches, which are then followed by a rectified linear unit (ReLU) to increase the resilience and training efficacy of the input range. Conv3D1, Conv3D2, and Conv3D3 are cascaded to generate a broad field-of-view for collecting packed characteristics, with a channel of 52 and a kernel size of 3. MSFC-DenseNet is a densely linked network that uses multiscale convolution layers to collect rich contextual data for stereo matching. It is useful for improving the network's features expressing capabilities and is resilient in ill-posed areas. Unlike the prior study's encoder-decoder structure, MSFC-DenseNet makes many direct connections from every layer to all subsequent layers, enabling picture information to be recovered via reuse of features.

It is defined as a combinational module consisting of three highly interconnected convolutional modules with sizes of $k$, $2k$, and $3k$, accordingly, where $k$ specifies the number of map features created by each densely connected convolutional block. The hyperparameter $k$, which is commonly set to 12, is used to refer to the growth rate. Each block contains a batch normalisation (BN), a ReLU, and a Conv3D with a step of one and buffering of one. To avoid overfitting during training, at the bottom of each block, we include a 0.5-frequency dropout operation. Heavily linked convolutional blocks may produce more obvious characteristics while also increasing the size of the network. A transition layer is located at the bottom of the MSFC-DenseNet and is made up of a convolution layer with a stride of 1 and a kernel size of 3, as well as ReLU. A 3 x 3 convolution layer is used to integrate multiscale spatial information. Pooling lowers the spatial accuracy of feature maps and the sensitiveness of the variance measurement term when contrasted with convolution. After pooling, the linear or deconvolution extrapolation function is employed to enlarge the characteristics map to match its original size. Yet, during training, additional memories and time are often required. As a consequence, the created transition layer is a good alternative for obtaining dense characteristics while keeping spatial resolution. Additional details is shown in Figure 1. Because the suggested patch-based matching model has a total of two channels, the network's input form is $[256, 9, 9, 3]$, where the tensor denotes $[\text{batch size} \ 2, \ \text{height}, \ \text{width}, \ \text{channels}]$. After the convolution processes, the tensor form is changed to $[256, 1, 1, 124]$. To acquire the network forecast of all selected samples for training inside each epoch, we apply the reshaping function to alter the length of the tensor while without changing any of the components. The size of the two-dimensional matrix is $[128, 248]$. The first component of the matrix represents the fixed batch size, while the second component represents the parameter of each sample. Lastly, the matrix is divided into completely linked layers, which are then merged to form a feature vector. The fully connected procedure adds some computing overhead to a single forward pass. As a consequence, the fully linked layer in our network is a superior choice for enhancing matching cost calculation accuracy.

![Figure 3: Structure of dense CNN](image_url)
important methods. BWO an evolutionary algorithm, includes criteria that resemble evolution processes like reproduction, selection, and mutation. The difference among each evolutionary algorithm and the other is made by the variety of criteria. BWO imitates mating behaviour of black widow spiders. This algorithm differs from evolutionary algorithms in several ways, allowing it to perform well in complex issues. The Darwin natural selection theory, described as the idea of adjusting species over time, descent with modification, and the generation of new ones, inspired the BWOA. Although BWO preserves a balance between the discovery and extraction stages, it may be utilized to address a wide range of optimization issues involving many local optimal settings. Figure 4 shows a diagram for the BWO method. The following is a concise summary of the major stages of BWO.

![Flow Chart for BWO Method](image)

**Figure 4: flow chart for BW**

1. **Initial population**

   The black widow spider perceives each problem's potential solution (widow). Every black widow spider shows the contents of the issue parameters. In order to solve benchmark functions, the structure should be treated as an array. The dimensional optimization problem is denoted by the letters $M_v$ and the matrix population by the letters $M_p$. The problem system is evaluated by a widow ($d$), which is an array of $M_v$, as shown below:

   \[
   d = [y_1, y_2, y_3, ..., y_{M_v}] \quad (4)
   \]

   Each variable's floating-point number is $(y_1, y_2, y_3, ..., y_{M_v})$, and the widow fitness is represented as $S$.

   \[
   S = S(y_1, y_2, y_3, ..., y_{M_v}) \quad (5)
   \]

   To begin the optimization problem, the spider's initial population $(P)$ with the candidate matrix size $(M_p \times M_v)$ is created.

2. **Procreate**

   During the conception stage, establish an array named alpha that is as long as a widow arrays and includes randomized integers. Offspring is generated by $\alpha$ and $x_1$ and $x_2$ : parents, $y_1$ and $y_2$ : offspring. Result is calculated and saved.

   \[
   y_1 = \alpha \times x_1 + (1 - \alpha) \times x_2 \quad \text{and} \quad y_2 = \alpha \times x_2 + (1 - \alpha) \times x_1 \quad (6)
   \]

3. **Cannibalism**
There are three varieties of cannibalism. (i) A female black widow consumes her spouse during or after mating (sexual cannibalism). (ii) Strong siblings consume their lower siblings (sibling cannibalism). (iii) Baby spiders may consume the mother spider. The fitness values are used to determine which spiderlings are strong and which are weak.

4. Mutation

Mutation is performed by selecting random Mute pop number of individuals in the population to be mutated. Every solution swap 2 array elements at random. Following mutation, the new population is assessed and saved in the new population, pop3. At last, the new population created by combining pop3 and pop2 migrations, arranged to revert back the better widow of thresholds with dimension Nvar.

IV. RESULTS AND DISCUSSIONS

The results of the proposed and enforced automated brain tumour identifying and segmenting system are discussed in this section. When compared to the current algorithm, proposed algorithm performance is examined. Sensitivity, precision, specificity, f-measure, accuracy, recall, NPV, MCC, FPR, FNR are performance matrix. The previous algorithms such as DCNN, DNN and DBN are analyzed and compared with the presented BW-DCNN. Metrics of performances are examined below.

4.1. Metrics for Efficiency

This section describes the suggested model’s efficacy measures, some of which are being verified and evaluated. Mathematical expression of performance measures analysis inserted in the scheduled and existing studies:

- **Sensitivity:**
  It is calculated by dividing the genuine affirmative by the total number of objects in the positive cluster.
  \[
  sensitivity = \frac{TP}{TP+FN} \times 100
  \] (7)

- **Specificity:**
  The specificity is the proportion of persons who test negative for a certain illness in a population of non-infected people. Although some individuals who do not have the illness may test positive, no test is completely reliable (false positive).
  \[
  Specificity = TN \times TN + FP
  \] (8)

- **Accuracy:**
  The terms true positive (TP), false negative (FN), true negative (TN), and false positive (FP) are used to describe the accuracy of the data (FP). HG categorize HG tumors, HG classified LG tumors, LG classified LG tumors, and LG classified HG tumors, represented by the letters TP, FP, TN, and FN.
  \[
  Accuracy = \frac{TN+TP}{TN+FP+TN+FN}
  \] (9)

- **Precision**
  It is referring to the percentage of true positives that are correctly segmented. To put it another way, it’s the number of pixels that make up a cluster and are split into that cluster.
  \[
  Precision = \frac{TP}{TP+FP}
  \] (10)

- **Recall:**
  The recall measurements for the class pituitary tumor were quite high, while meningioma recall measures were extremely low.
  \[
  Recall = \frac{TP}{TP+FN}
  \] (11)

- **F-measure:**
  F-measure is the harmonic mean of precision and recall.
  \[
  F-measure = 2 \times \frac{Precision \times Recall}{Precision + Recall}
  \] (12)

- **NPV:**
  It’s the chance that samples that pass a negative screening test are actually negative. The following expression can be used to compute it:
  \[
  NPV = \frac{TN}{FN+TN}
  \] (13)

- **MCC:**
Mathew’s correlation coefficient (MCC) splits the score into two categories: [1, +1]. The values in this range, in other words around zero, one, and one, indicate random, entirely incorrect, and ideal forecasts, respectively.

\[
 MCC = \frac{TP \times TN - FP \times FN}{\sqrt{(TP+FP)(TP+FN)(TN+FP)(TN+FN)}\times100}
\] (14)

❖ FPR:
The positive proportion is computed using the FALSE negative rate (FNR), however the approach-identified negative is obtained using the Equation below.

\[
 FNR = 1 - Sensitivity
\] (15)

❖ FNR:
The false positive rate (FPR) is used to calculate the ratio of incorrectly identified pixels to correctly detected pixels, and it is calculated using the equation below.

\[
 FPR = 1 - specificity
\] (16)

4.2. Metrics performance analysing existing and proposed approaches

The performance metrics of the presented and present methods are stated in the table below. Performance measures that have been proposed and presently in use of NPV, sensitivity, precision, accuracy, f-measure, recall, MCC, specificity, FPR, FNR. A confusion matrix is to examine sensitivity, accuracy, f-measure, NPV, recall, MCC, specificity, precision, FPR, FNR is shown in the diagrams below. Tables 1 and 2 provide a performance comparison between the suggested and current techniques’ performance metrics.

Table 1: Comparing the efficacy of current and suggested approaches.

<table>
<thead>
<tr>
<th>Algorithms</th>
<th>accuracy</th>
<th>sensitivity</th>
<th>precision</th>
<th>specificity</th>
<th>f-measure</th>
<th>recall</th>
</tr>
</thead>
<tbody>
<tr>
<td>DCNN</td>
<td>0.896039604</td>
<td>0.884615385</td>
<td>0.851851852</td>
<td>0.903225806</td>
<td>0.867924528</td>
<td>0.884615385</td>
</tr>
<tr>
<td>DNN</td>
<td>0.861386139</td>
<td>0.871794872</td>
<td>0.790697674</td>
<td>0.85483871</td>
<td>0.829268293</td>
<td>0.871794872</td>
</tr>
<tr>
<td>DBN</td>
<td>0.836633663</td>
<td>0.897435897</td>
<td>0.736842105</td>
<td>0.798387097</td>
<td>0.809248555</td>
<td>0.897435897</td>
</tr>
<tr>
<td>Proposed BW-DCNN</td>
<td>0.925742574</td>
<td>0.948717949</td>
<td>0.870588235</td>
<td>0.911290323</td>
<td>0.90797546</td>
<td>0.948717949</td>
</tr>
</tbody>
</table>

Table 2: Performance comparison of purposed and existing methods

<table>
<thead>
<tr>
<th>Algorithms</th>
<th>Performance matrices</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>NPV</td>
</tr>
<tr>
<td>DCNN</td>
<td>0.925619835</td>
</tr>
<tr>
<td>DNN</td>
<td>0.913793103</td>
</tr>
<tr>
<td>DBN</td>
<td>0.925233645</td>
</tr>
<tr>
<td>Proposed BW-DCNN</td>
<td>0.965811966</td>
</tr>
</tbody>
</table>

Table 1 and Table 2 The comparison between the suggested and traditional methods is stated clearly. For overall lines, total amount of member variables and member functions, obtained values through selecting attributes are effective than obtained values through traditional method. Besides that, the proposed approach has a high value for accuracy, f-measure, recall, sensitivity, FPR, NPV, MCC, specificity, FNR and precision. The suggested attribute selection model’s cohesion metric certainly obtains effective rate.
4.2.1. Sensitivity, Specificity and Accuracy:

Fig. 5 depicts the specificity, accuracy, and sensitivity of matrices used for comparing of existing and proposed processes. Figure 8 depicts the sensitivity, accuracy, and specificity of recommended and present processes like DBN, DNN, DCNN, and BW-DCNN. The mentioned method outdoes present strategy of specificity, sensitivity, and accuracy.

![Performance comparison through Sensitivity, specificity and accuracy](image1)

**Figure 5: Performance comparison through Sensitivity, specificity and accuracy**

4.2.2. Precision, recall and F-measure

The previous methods; DCNN, DBN and DNN are compared with the presented method BW-DCNN. The performance of this system is evaluated by some metrics, f-measure, precision and recall. The analysed values are plotted in graph. In figure 6 shows the values plotted, the values of previous methods are lower when compared to present method.

![Comparison with algorithms](image2)

**Figure 6: Comparison with algorithms**

4.2.3. NPV and MCC:

From figure 7, illustrates that the performance of present and previous method using NPV and MCC matrices. The methods are compared and plotted n graph, shows that presented method have greater values than the current devices.

![Comparison with algorithms](image3)
4.2.4. FPR and FNR:

From figure 8, the previous system such as DNN, DCNN and DBN is analyzed through FPR and FNR, compared with present method BW-DCNN. The analyzed performance of presented value of FNR is lower in presented method and FPR is superior than previous methods.

V. CONCLUSION

MR images are used to segment and detect brain tumours in this paper. The proposed method improved the MR image and used global segmentation to segment the tumour. The results of our experiments show that our method is effective at enhancing, segmenting, and extracting the brain tumour from MR images. This paper proposed an automatic brain tumour segmentation and detection system using DCNN without human intervention to overcome the problem faced by traditional existing techniques. The main goal of this paper is to use a novel clustering approach to segment the tumour portion of affected MRI. BW-DCNN is proposed as a deep learning framework for more accurately evaluating brain disease. The accuracy of the presented device is superior than the previous model.
REFERENCE


