Berkeley wavelet transform and improved YOLOv7-based classification technique for brain tumor severity prediction

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ABSTRACT

Abnormality in brain tissues is a life-threatening illness in humans Un-bias to gender and age if it is unrecognized and untreated within time, will lead to severe complications and extreme conditions. The brain tumor is mainly influenced by a variety of unpredicted and unavoidable reasons. Its evaluation, spread pattern, and identification involves complex assignment. Its early grading and the proper classification ensure effective treatment. The proposed work attempts to extract and classify the tumor region using an automatic classification system for magnetic resonance imaging (MRI) brain tumors. A deep learning convolutional neural network-based architecture YOLO is employed to classify and detect the tumor from brain MR images. The proposed method resulted in superior segmentation, and classification performance in terms of subjective visualization and objective metrics as compared to state of art approaches. The proposed YOLO-based method collectively achieved 98.89% classification accuracy on the BRAINIX and Kaggle datasets.

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1. INTRODUCTION

Lots of research has been investigated in the last decade on tumor detection. One of the significant diseases where tumor detection is addressed is the brain tumor. Even though the tumor is not listed in the first position regarding deaths, road accidents take more life than tumors, but the situation in both scenarios is different. Road accidents are preventive, and most of the time, they happen due to human negligence. Some unavoidable situations are also witnessed for road calamities, such as sudden obstacles, failure in mechanism, and many others [1]. In this context, brain tumors can happen due to various reasons such as pollution, stress, family background, and eating habits.

This situation is unavoidable even though many precautions are taken. This type of disease can cause much pain to the sufferer. However, recent technological advancement makes it possible to cure it, if detected at an early stage. It is important to note that it should be detected in its early stage to offer the proper treatment, which is one of the main reasons why lots of research is investigated in this field. In the last decade, a 300% increase in brain tumor cases has been noticed, and according to the data of GLOBOCON 2023 [2]–[5], more than 17.7 million deaths have been registered due to tumor infections. Figure 1 shows the

cases and deaths from 2010 to 2022 and the estimated volume from 2023 to 2040. The death rate will be controlled and reduced to some extent, and the survival rate can increase. If the infection in tissues can be detected in its early stage, it is possible to control and reduce the death rate due to brain tumors [6], [7]. New technological evolutions open new findings and help doctors offer patients more convenient and sound healthcare.



Figure 1. Estimated number of cases and deaths [4], [5]

The tumor is an abnormality growing tissues, and an abnormal enlargement of tissues in brain causes tumor in brain. These tissues have no physiological function and perform no activity in the brain. However, as they increase the volume in the brain, it creates undue pressure on the brain, and so it affects the overall functioning of the brain and causes irregular nerve symptoms [8]. Once the tumor starts developing, they overgrow. If the proper treatment is not offered in time, it becomes dangerous and can take a life. Manual detection from radiologists requires lots of investigations and lots of analysis. In the tumor identification process, every clock of time is essential. If detected and analyzed within the time frame, it becomes easier to offer the proper treatment to the patient [9], [10]. This disease is entirely curative, only timely identification is a significant concern, and hence many researchers are employing their skills to develop new advanced methods for identifying the tumor with improvising performance parameters [11]–[13].

Various imaging modalities are available for capturing tumor information from the brain; the most popular are one of them is computed tomography (CT) and the other one magnetic resonance imaging (MRI). The MRI is highly preferable because of its non-invasive nature, no radiation, and no harm [14], [15]. For identification and detection of location and extract meaningful information from the brain tumor, radiologists perform two main activities: i) Differentiation of the brain MR image characteristics, *i.e.*, unusual (abnormal) or typical (normal); and ii) Classifying abnormal brain tissues into various tumor types (grades) based on their spread.

Based on these activities, brain behavior can be studied and analyzed effectively. The paper briefs, as illustrated, are the literature review discussed in section 2. The proposed method in section 3 and materials in section 4. Results and discussion in section 5. Finally, section 6 gives the conclusion of the proposed system.

2. LITERATURE REVIEW

Based on the severity, *i.e.*, whether the tumor belongs to malignancy or benignity, brain tumors are graded from I-IV typecasts categories by the World Health Organization (WHO). The growth rate of Grade II and IV malignant types of brain tumors have having faster growth rate, compared to other grades. They spread at a higher rate to other body parts and impinge on healthy cells [16]–[19]. Ramamoorthy *et al.* [20] investigated and proposed a technique, consisting of pre-processing using histogram equalization with a learning-based quantization model for detecting tumors in the brain. With this technique, they have achieved, moderate accuracy, precision, and specificity with 93%, 92%, and 94%, respectively. According to Asaf Raza *et al.* [21], traditional machine learning-based classifier requires hand-crafted features, which require a lot of time. So, they investigated and proposed a technique that employs a hybrid deep learning model that effectively detects and classifies three types of brain tumor, namely, glioma, meningioma, and pituitary tumor. According to them, their technique adopts a primary convolution neural network-based architecture, and with this, they claim higher precision and accuracy as well as 100% recall and an F1 score of above 99%.

Salman *et al.* [22] investigated the hybrid methodology of image processing techniques and claimed an accuracy rate of up to 95% for segmentation and separation of an area of interest in brain tumors.

Rasool *et al.* [23] presented a highly efficient hybrid deep learning model, which is can be used for the classification of brain tumors. This method utilizes a new hybrid convolutional neural network (CNN)based architecture to classify brain tumors. The proposed technique compromises on two different scenarios, the first is based on a pre-trained Google-Net model with a support vector machine (SVM) for pattern classification, and the second integrates a finely tuned Google-Net. The first approach tuned the proposed algorithm with improved accuracy to 98.1%, whereas the second approach produced an accuracy of 93.1%.

Ali *et al.* [24] presented an attention-based convolutional neural network approach for the segmentation of brain tumors. This technique is employed with a mechanism for avoiding overfitting. Results of their work have been compared with some of the recent existing proven techniques and have presented quantitative measures with 98%, 98.1%, 99%, and 99.3% of sensitivity, specificity, accuracy, and precision, respectively. According to [25], [26], the present manual methodology employed by radiologists or experts to detect infection in the brain consumes a lot of time and is prone to human errors. This happens due to the enormous volume of cases and depends on the experience of the expert. So, they investigated and assessed the performance of the artificial bee colony (ABC) algorithm for adaptive glioblastoma detection, and their method reached an accuracy for glioblastoma detection up to 93.67%.

False detection of brain tumors leads to wrong medical intervention, which reduces patients' chances of survival. Senan *et al.* [27] have proposed an indigenous method for detecting brain tumor from MRI images using a hybrid technique to fasten the automatic detection of brain tumors. In their research, they incorporated deep learning, traditional machine learning techniques, and SVM as a classification. According to the authors, the deep learning technique based on the AlexNet algorithm and SVM classification exhibits accuracy, sensitivity, and specificity of 95.10%, 95.25%, and 98.50% respectively.

Hashemzehi *et al.* [28] have investigated a new technique for MRI based brain tumor detection, which is based on deep learning using the integration of CNN and neural auto-regressive distribution estimation (NADE). An effective strategy has been planned and showcased by Mittal *et al.* [29] for brain tumor detection and segmentation of tumor, using an enhanced deep learning concept, which is interrogated based on stationary wavelet transform (SWT) and the new growing convolution neural network (GCNN). To prove the validity of the proposed system, the authors have presented performance metrics in terms of accuracy, peak-signal-to-noise ratio (PSNR), and mean squared error (MSE). Accordingly, the combination of SWT and GCNN shows a significant improvement in the segmentation automation process and contributes to the reduction of mean square error compared to conventional CNN methodology. Arunachalam and Sethumathavan [30] introduced an improved YOLO5-based technique for brain tumor detection. The segmentation is achieved using the McCulloch method. The system gives an accuracy of 99.32% and an F1 score of 91.26%.

Babu et al. [31] presented a fully automated system using four four-stage processes. The Curvelet transformation is used in the first step for image de-noising. Artificial bee colony (ABC) optimization is applied to remove infected areas from MRI scans in the next stage. In the third stage, to recover the learning rate, another optimization based on CNN is used. The entire system experimented on BRATS 2013 and 2015 datasets and achieved a classification accuracy of 98.5% and 99.0% for both datasets, respectively. The combination of CNN and Haar wavelet features has been investigated by Dheepa and Shankari [32] for the automatic identification of infected areas from MR images. The validation of the algorithm is experimented with using the BRATS 2018 dataset and achieved an F1 score of 97%, precision of 97%, sensitivity of 96%, specificity of 97%, and accuracy of 96%. Many researchers witness the CNN-based techniques for brain tumor classification, but local background information is restricted in local CNN. This problem is addressed by Sille *et al.* [33] by investigating a deep convolutional generative adversarial network. For validation of the algorithm's performance, the dice score coefficient (DSC), peak-signal-to-noise ratio (PSNR), and structural index similarity (SSIM) are calculated and attained 97% accuracy with loss reduced to 0.012. Reddy and Dhuli [34] proposed a segmentation of brain tumor infection from MR images using a fast-linking modified spiking cortical model (FL-MSCM) and performed the classification using a lightweight convolutional neural network (lightweight CNN) model. The experimental analysis achieved dice similarity coefficient (DSC) and accuracy in classification of 95.7% and 99.58%.

In the literature review discussed above, we have seen various tumor detection and classification methodologies, mostly based on support vector machine (SVM), artificial neural network (ANN), k-nearest neural network (K-NN), and convolutional neural network (CNN). To improve the survival of the patients, Algani *et al.* [35] employed binary gray wolf optimization-convolutional neural network-long short-term memory (BGWO-CNN-LSTM)-based technique and achieved a specificity of 99.54%, recall of 99.23%, and accuracy of 99.74%. The five-stage model for the identification of infected brain areas from MR images is suggested by Ramtekkar *et al.* [36]. In the first stage, pre-processing is performed using a Compound filter.

In the second stage, segmentation is achieved using threshold and histogram techniques. Features are extracted, and optimization of best features is performed in the third and fourth stages using grey level co-occurrence matrix (GLCM), whale optimization, and grey wolf optimization [37]. Finally, CNN is applied for the classification and attains 98.2% detection accuracy.

Despite much research, the existing research work cannot meet the expectations. Hence a new methodology is exigently required by introducing a new algorithm for brain tumor detection. The outcomes of our proposed technique demonstrate the effectiveness and high performance over the other recent work mentioned in the literature. In addition to this, the present work will assist doctors and radiologists in the diagnosis of brain tumors in patient studies in the literature. In addition, this research will uphold doctors and radiologists for automatic diagnosis of brain tumor disease.

3. PROPOSED METHOD

Figure 2 shows various stages used in the proposed system. The proposed system utilizes preprocessing, enhancement, skull stripping, segmentation, extraction of tumor area, feature extraction and selection of relevant features, and finally, classification based on improved deep learning CNN based architecture YOLOv7. The raw images might have unwanted noise and unwanted parts, which are removed at the pre-processing stage. The pre-processing helps in improving the signal-to-noise ratio, without hampering the other regions of the image. The overall clarity of the raw MR images is enhanced by applying the enhancement through adaptive contrast enhancement based on the modified sigmoid function [38], [39].



Figure 2. Steps used in the proposed algorithm

Brain MR images have additional tissues, such as the skull, skin, and fat, which should be removed before the segmentation; otherwise, it will affect the performance of the segmentation. Skull-stripping operation [40] is used to eliminate these tissues. For effective skull-stripping, several methodologies are available. We employed a threshold-based [41] skull-stripping method in our system. Threshold-based skull stripping is straightforward. It simply removes the skull from the brain MRI by setting the threshold value. In our case, we set the threshold value at 0.7, which works fantastically. Even though this additional cerebral tissue (skull) will not affect the result removing this ensures more clarity in the segmentation operation.

Feature extraction is used to reduce image complexity and reduce the burden on the classification system. With feature extraction, tumor detection, and its classification process are more efficient, state-forward, accurate, and efficient. With feature extraction, high-dimension space can be mapped to less-dimension space in linear or non-linear systems. In image processing, especially in medical imaging, essential features such as contrast, shape, texture, and color are extracted to reduce image complexity [42]. Gray level co-occurrence matrix (GLCM) and texture feature are the most widely used image analysis applications

introduced by Haralick *et al.* [43]. Feature extraction is used to reduce the classifier's complexity so classification of an image is simplified and Fastly processed. Without feature extraction and optimization thereof will affect the results badly. The experimental analysis is also performed without feature optimization, and the results yield is not appreciable. The feature extraction process extracts the relevant information from the infected image and gives precise information to the classifier to classify them effectively. In the final results of the classifier, 5% to 10% of the deviation is noticed when performed without the relevant feature extraction. In life-threatening diseases, variation in processing time by some minutes may play a significant and decisive role, but more than this effectiveness and accuracy of the classifier matter an internet of things (IoT).

3.1. Segmentation and morphological operation

MRI image, as a two-dimensional signal can be processed by popular Berkeley wavelet transform (BWT), also described as 2D triadic wavelet transform. In BWT transformation, the mark and selection of the threshold required by the seed point is easily located. BWT smoothens the boundary edges and preserves the information without hampering the outer layer. It is easy outfitting characteristics make BWT the most adoptable wavelet transformation for segmentation operation. The segmentation process is performed layer wise; precise information from the infected tumor image must be connected and recognized correctly. The BWT conducts its operation layer-wise, becoming one of the best methodologies for performing segmentation. The image transformation is easily represented in BWT and is fully orthonormal. This feature encourages easy segmentation of MR images involving complexity. The basis of the transformation operation lies within its mother wavelet transformation β_x^{φ} . As shown in (1), substitute wavelets are produced at various pixel positions in a two-dimensional plane, by scaling and translating the mother wavelet.

$$\beta_x^{\varphi}(s,\tau) = \frac{1}{s^2} \beta_x^{\varphi} (3^s(x-i), 3^s(y-j))$$
(1)

Where s and τ are used as scaling and translation parameters of the transform and β_x^{φ} is the transforming function. The detailed algorithm for the brain tumor segmentation is implemented using BWT and it is described in algorithm 1. The boundary extraction from the brain image area is done using morphological operation. The threshold is used to decide the boundary between the pixel values; First, the image is binarized, *i.e.*, converted into 0's and 1's by selecting a threshold value. Anything above the threshold value will be converted into white pixel or 1 and below it will be converted into 0 from the input MRI gray image having 0-255 levels. Thus, separate regions are formed in the image, separating the infected tissue in the image. The infected tissue is extracted from the image and the image is eroded to remove unnecessary pixels from the tissue.

Algorithm 1. Segmentation using BWT

```
1. Img = Input image;
2. Get size of the image (size)
3. Find size1 = size/3
4. Img1 = Convert Img to square image
5. Img2 = double(Img);
6. Calculate mean of Img2
7. Calculate miniature component of Img2
8. Select Img3 = Img2(1 : size,1 : size) as image with coordinate of miniature component
9. Find Img4 = 3^{floor(\frac{\log(size)}{\log(3)})}
10. Apply resizing as Img5 = imresize(Img,Img4/size);
11. Img6 = Apply decomposition on image Img5
12. Pick decomposition parameters (CON) i = 1 : size(CON, 1)
13. Create coefficients y using the equation y = floor((i - 1)/3);
14. Create coefficients x using the equation x = mod(i - 1, 3);
15. Create coefficients bw using the equation bw = makebw(CON(i,1),CON(i,2));
16. Decompose coefficients using the equation
       decomp(y * size1 + 1: y * size1 + size1, x * size1 + 1: x * size1 + size1) = bwtfilter(lmg6, bw);
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17. Performs BWT decomposition
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3.2. Classification

Classification is executed to extract vital information and findings from medical images. The classification achieves higher accuracy and gives valued information about the affected area by the diseases [44]. The classification complexity reduction and improvement in accuracy are noticed with the help of proper acquisition, enhancement, feature extraction, and feature optimization of the image. The suggested image classification process is shown in Figure 3.



Figure 3. Process of image classification

Popular classification techniques such as support vector machine (SVM), random forest (RF), self-organizing map (SOM), and principal component analysis (PCA) classifiers are unable to support low-resolution images. Earlier work had shown that these classifiers are computationally complex and require large amount of time for convergence when working on larger datasets. These limitations are resolved by using the YOLOv7-based classification method [45], which is proposed in this paper.

Machine learning and deep learning techniques have gained significant popularity for tumor classification. The majority of these methods involve the first step of learning from training models developed from annotated images of large dataset, where they learn about features and patterns of infected tissues. CNN-based architectures such as YOLO and single shot detector (SSD) have shown promising results in brain tumor detection. Computer vision applications use the well-known object detection algorithm YOLO. It is renowned for its real-time performance and speed. YOLO breaks up an input image into a grid of cells, using which multiple bounding boxes and class probabilities for the objects in each cell are predicted. Steps to detect objects using YOLO: i) Obtain a blob from the image since we require fixed-size input. ii) Store the various layers extracted using YOLO in a variable. iii) Forward the variable to the YOLO network and then receive the output. And iv) Store the output in the layer output variable.

The dataset is trained for 160 Epochs with the input image size 224×224 and 0.1 as the initial learning rate for the training purpose. During the training process, standard data increment methods are used. Then the fine-tuning of the network is considered using a 448×448 image size with the initial learning rate changed to 0.001 for 30 epochs, and the training is performed ten times. The detection and identification often require fine-grained visual information; for this purpose, the network's input resolution has been increased from 224×224 to 448×448 . Our final layer effectively forecasts both class probabilities and bounding box coordinates. A linear activation function is employed for the final layer, and leaky rectified linear activation shown in (2) is used for all other layers.

$$\emptyset(x) = \begin{cases} x, & \text{if } x > 0\\ 0.1x, & \text{otherwise} \end{cases}$$
(2)

The YOLO algorithms are strong enough to handle multi-class classification. Image or object detection consists of two tasks: i) image classification and ii) object localization.

Through the image classification algorithms, the type or class of an object is predicted. In contrast, object localization algorithms find the object in the image and represent it with a bounding box. Figure 4 shows the classification, localization, and detection operation of the object or class from a sample input image.

YOLO uses one of the best architectures of neural networks. Due to its simplicity, high accuracy, and high processing speed, YOLO has become a highly preferred object detection model. It predicts a class and the bounding box that defines the object's location on the input image. Each bounding box recognizes four members:

- (b_x, b_y) as the center of the bounding box
- (b_w) as the width of the box
- (b_h) as the box height



Figure 4. Classification, localization, and detection process of the object

In addition to this, it predicts the corresponding number c for the predicted class and the probability of the prediction (P_c). The entire image is divided into a grid, for example, a 3×3 grid. Through the grid, it becomes easy to detect one object per grid cell compared to one object per image. In the next step, each grid cell is described by a vector. For example, in the case of brain MRI image, two classes are defined such as Normal and Abnormal, then it is described as:

$$C_{r,c} = (P_c, b_x, b_y, b_w, b_h, C_1, C_2)$$

where $C_{r,c}$ is represented the corresponding grid cell, for example, the first cell from the 3×3 grid is represented as $C_{1,1}$. P_c is the probability of the object class, b_x and b_y are the coordinates of the center of the bounding box, b_h , and b_w are the height and width of the bounding box relative to the entire image, and C_1 and C_2 are represented for the class, *i.e.* C_1 for the "Normal" and C_2 for the "Abnormal". The value of C_1 and C_2 is 0 and 1, depending on which class represents the bounding box. Algorithm 2, enlists various steps involved in the implementation of YOLOv7, for the detection and classification of brain tumors.

Algorithm 2. Classification using YOLO

- 1. Import the required packages and libraries
- 2. Select threshold value (0.5), box confidence score, and box class probability
- 3. Calculate score, boxes, and classes
- 4. Calculate IoU between two boxes

$$IOU = \frac{Area \ of \ Overlap}{Area \ of \ Union}$$

5. Select non-max suppression

-

6. Select the value of shape (19, 19, 5, 7) randomly and then predict the bounding boxes

$$Y = \begin{bmatrix} P_c \\ b_x \\ b_y \\ b_h \\ b_w \\ C_1 \\ C_2 \end{bmatrix}$$

7. Generate suppressed boxes from the output of CNN

8. Find the prediction for a random volume

9. Apply pre-trained YOLO algorithm on new images

10. Generate the prediction of bounding boxes and save the images (Im1)

11. Get an image and make predictions using the predict function

12. Plot the predictions

3.2.1. Intersection over union

Intersection over union (IoU) is a performance parameter to evaluate how effectively the object is detected. It is the ratio between the ground truth and the predicted bounding box in Figure 5. An IOU value greater than 0.5, called threshold value, is recommended. IoU value less than the threshold value indicates false detection. The lower the value, the higher the false detection rate. For a positive prediction, the IoU value should be > 0.5, and for negative predictions, an IoU value should be < 0.5



Figure 5. Calculation of IoU

4. PROPOSED METHOD

In this paper, two datasets, namely BRAINIX (DICOM) [46] and Kaggle [47], are evaluated. For validating the performance of the proposed method, 165 normal MR brain images and 289 meningioma MR images are used. The ratio of training and testing will be maintained at 80:20 for the evaluation of the proposed system.

5. RESULTS AND DISCUSSION

MATLAB R2020 and Python 3.7 software are used for simulation purposes. The proposed system is evaluated on two different datasets [46], [47]. The dataset comprises non-cancerous (non-meningioma or normal) and cancerous (meningioma) brain MR images. From BAINIX, 134 meningioma brain images and 67 non-cancerous brain images are used and from Kaggle, 155 meningioma brain images and 98 non-cancerous brain images are used. The proposed system correctly detected 286 out of 289 cancerous images and thus gave a 99% classification rate. The proposed system correctly detected 163 non-cancerous images out of 165 images and thus offers a 98.78% classification rate. Hence the proposed system achieved 98.89% of the average classification rate.

The dice coefficient is an important performance parameter whose default value is between 0 and 1. Its value is directly calculated using the formulas and can also be calculated using the Jaccard coefficient index (JCI). The deviation between the source image and the segmented output image is measured through MSE. In our case, MSE is 0.009. The quality of the segmented image is measured based on image intensity. The calculation of image intensity between expert segmentation, *i.e.*, manual segmentation and segmented output using a mathematical notion is known as PSNR. The recommended value of PSNR for better quality in terms of noise is 40 decibels (dB). Our proposed method obtained 54.3 dB PSNR. The comparative analysis of MSE and PSNR is shown in Figure 5. The comparative analysis of MSE and PSNR, as shown in Figure 6, depicted that our proposed system segments the MR images with less noise. We also analyzed MSE and PSNR without a noise elimination step (*i.e.*, pre-processing), and the results were not encouraging. Figure 7 shows the comparisons of MSE and PSNR without pre-processing. The effect of the pre-processing and enhancement step is reflected in the overall performance, depicted in Figures 6 and 7.



Figure 6. Comparison of MSE and PSNR (with pre-processing)



Figure 7. Comparison of MSE and PSNR (without pre-processing)

The total number of correct negative predictions over the total negative cases is known as the specificity [46]. The total number of correct positive predictions over the total number of positive cases is known as sensitivity (Sens) [48]. In other words, the number of cases detected correctly as positive is measured as sensitivity from the total positive cases. For example, suppose sensitivity is 90% out of 100 positive cases. Table 1 enlists various formulae which are used for calculations of parameters of interest. Table 2 shows a comparison of the test performance of proposed YOLOv7 based classifier with different classifiers such as an adaptive neuro-fuzzy inference system (ANFIS), genetic algorithm (GA), and K-nearest neighbors (KNN). Table 3 shows the comparison of the proposed method with other proven methodologies. Even though the results of some of the proven research and proposed method look very close, the approach of YOLO is completely different, and it processes large datasets efficiently.

Table 1. Performance parameter matrices							
Quality parameter (all value in %)	Formula						
Accuracy (Acc)	True Positive (TP) + True Negative (TN) $\times 100$						
Sensitivity (Sens)	$\frac{Total Positive + Total Negative}{True Positive (TP)} \times 100$ $\frac{Total Positive (TP + FN)}{Total Positive (TP + FN)} \times 100$						
Specificity (Spec)	True Negative (TN)						
Precision or positive predictive value (PPV) Recall or pegative predictive value (NPV)	$\frac{Total Negative (TN + FN)}{TP} \times \frac{100}{T00}$ $\frac{TP}{TP + FP} \times 100$						
Relevance factor	$\frac{TN}{TN + FN} \times 100$ Precision × 100						
False negative rate (FNR)	$\frac{Recall}{FN} \times 100$ $\frac{FN}{FN + TP} \times 100$						
False positive rate (FPR)	$\frac{FP}{FP}$ × 100						
Dice similarity coefficient (DSC)	$\frac{FP + TN}{2TP} \times 100$ $\frac{TP + TP}{2TP + FN} \times 100$						

Table 2. Comparison of accuracies in different classifiers

1									
Number of test images (normal =165, abnormal=289)									
Evaluation parameter	ANFIS	GA	K-NN	YOLO (Proposed)					
True negative	72	74	69	77					
False positive	9	5	12	3					
True positive	340	350	338	372					
False negative	22	25	35	2					
Specificity (%)	88.88	93.67	85.18	96.25					
Sensitivity (%)	91.15	93.33	90.61	99.46					
Accuracy (%)	90.74	93.39	89.64	98.89					
Precision or PPV (%)	97.42	98.59	96.57	99.2					
Recall or NPV (%)	68.57	74.74	66.34	97.46					
False negative rate (FNR) (%)	8.84	6.67	9.38	0.53					
False positive rate (FPR) (%)	11.11	6.32	14.81	3.75					
Average dice coefficient index (%)	94.18	95.89	99.49	99.33					
IoU				0.89					

Ref.	Method	Year	Acc. (%)	Sens. (%)	Spec. (%)	IoU
[32]	Deep convolutional generative adversarial neural network	2023	97	NA	NA	NA
[35]	GLCM + CNN	2023	98.2	NA	NA	NA
[20]	Histogram equalization + learning-based neural network	2022	93	92	94	NA
[22]	Hybrid image processing	2022	95	NA	NA	NA
[23]	Pre-trained Google Net with SVM	2022	98.1	NA	NA	NA
[23]	Finely tuneed Google Net	2022	93.1	NA	NA	NA
[25]	ABC	2022	93.67	NA	NA	NA
[26]	Alex Net $+$ SVM	2022	95.10	95.25	NA	NA
[47]	Modified ABC	2022	96	98.9	64	NA
[48]	GLCM + Seg Net + DT	2022	98	NA	NA	NA
[29]	YOLOv7 + McCulloch	2022	99.32	NA	NA	NA
[31]	CNN + haar wavelet	2022	96	96	97	NA
	Proposed BWT + YOLOv7		98.89	99.46	96.25	0.89

Table 3. Comparison of performance parameters with proven methods

6. CONCLUSION

Some of the existing research proposed for classifying and detecting brain tumors are promising but only partially accurate, and complete automation still needs to be included. They vary from image processing and soft computing to deep learning-based methodologies. Some researchers presented performance matrices such as accuracy, specificity, and sensitivity for validation purposes of the algorithm or methodologies. Through accuracy, the total correct predictions over the total used or available data are presented. The specificity matrix can characterize healthy patients, whereas sensitivity gives a characterization of unhealthy patients. These performance matrices play a significant justification for the overall assessment of any proposed algorithm. Almost every researcher has presented and analyzed their works through some performance matrices, so they are used to compare the researcher's work.

Our proposed approach using YOLOv7 extracts and classifies healthy and abnormal brain tissues from MR images with high classification accuracy, and takes less computational time. The complete system is fully automated. This automation supports pathologists in the detection of the tumor region and also helps them to provide early diagnosis suggestions with complete confidence.

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