Scalable Computing: Practice and Experience, ISSN 1895-1767, `http://www.scpe.org`
© 2023 SCPE. Volume 24, Issues 1, pp. 69–80, DOI 10.12694/scpe.v24i1.2088

MULTI-CLASS BRAIN TUMOR CLASSIFICATION AND SEGMENTATION USING HYBRID DEEP LEARNING NETWORK (HDLN) MODEL

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Abstract. Brain tumor classification is a significant task for evaluating tumors and selecting the type of treatment as per their classes. Brain tumors are diagnosed using multiple imaging techniques. However, MRI is frequently utilized since it provides greater image quality and uses non-ionizing radiation. Deep learning (DL) is a subfield of machine learning and recently displayed impressive performance, particularly in segmentation and classifying problems. Based on convolutional neural network (CNN), a Hybrid Deep Learning Network (HDLN) model is proposed in this research for classifying multiple types of brain tumors including glioma, meningioma, and pituitary tumors. The Mask RCNN is used for brain tumor classification. We used a squeeze-and-excitation residual network (SE-ResNet) for brain tumor segmentation, which is a residual network (ResNet) with a squeeze-and-excitation block. A publicly available research dataset is used for testing the proposed model for experiment analysis and it obtained an overall accuracy of 98.53 %, 98.64 % sensitivity and 98.91 % specificity. In comparison to the most advanced classification models, the proposed model obtained the best accuracy. For multi-class brain tumor diseases, the proposed HDLN model demonstrated its superiority to the existing approaches.

Key words: Classification, segmentation, ionizing radiation, proposed methodology, and existing models.

AMS subject classifications. 68T07

1. Introduction. Unnatural and uncontrolled cell development in the brain is known as a brain tumor [13]. It also has the possibility of spreading to other bodily organs and having an impact on human functions [31]. Many different categories exist for classifying brain tumors, including primary and secondary [21]. Primary tumors are those that first appear in the brain [26]. On the other hand, tumors that first develop before spreading to the brain are referred to as secondary tumors [11]. Brain tumor detection and classification can be done using a variety of imaging techniques, but MRI imaging technique is the popular method for brain tumor detection [5]. The frequent kind of brain tumor with glial cell origins is gliomas [25]. The majority of meningioma tumors are benign, a benign tumor called meningioma develops on the membrane [23]. However, the pituitary glands that manage hormones and control bodily processes are where a pituitary tumor originates [35].

From the above information, identifying brain tumors early and classifying them become crucial tasks in case evaluation [16] [7]. In some complex circumstances, the classification stage may also be a difficult assignment for doctors or radiologists [24]. Experts must work on these cases to identify the tumor location and evaluate its tissues in comparison to adjacent regions [15]. To find brain cancer early and in short time, a Computer Aided Diagnosis (CAD) system is required without requiring human participation, because this task takes some time [6].

A subset of machine learning (ML) called deep learning (DL) is focused on hierarchical feature learning and learning data representation [4]. A system of many layers of nonlinear processing identities is used by CNN to extract features [1]. As we go deeper into the network, data abstraction is aided by the fact that the input of one sequential layer becomes the output of the preceding one. CNN's are a class of DL that are frequently employed in the analysis of visual data [18]. They are created to require the least amount of preprocessing possible. The biological processes of the human brain served as its inspiration.

Feature learning and unlimited accuracies are the key benefits of CNNs over standard machine learning and conventional neural networks [33] [10]. Feature learning and unlimited accuracies are improved by increasing

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training samples and result in a more accurate and reliable model [34]. For classifying and segmenting different types of brain tumors, we propose a new HDLC model in this research. Different configurations are used to evolve the network architecture to obtain the most suitable structure. The proposed method adopts the Mask RCNN for different types of brain tumor classification and a SE-ResNet for brain tumor segmentation. The CE-MRI dataset showed the best classification accuracy ever with the proposed model, which is publicly available on figshare.

The main contribution of the research is the following:

- First a local smoothing filter and non-local mean filter are used for prepossessing the MRI images for removing unwanted noise in the image. The image quality and contrast of the image is improved by this stage.
- After the completion of a preprocessing phase the deep learning-based Mask RCNN is used for effective classification. The proposed classification network model is designed for multiple brain tumor classification including pituitary, meningioma, and glioma.
- Then proposed a SE-ResNet for the accurate segmentation of brain tumors. It uses multi-stage architecture and convolution blocks in each stage. The results from this proposed network were more accurate in terms of disease diagnosis.
- The proposed method is evaluated on the publicly accessible database (CE-MRI). The experiments are performed on the Python platform. The proposed approach outperforms the state efficiency for all other approaches, according to the experimental data.

The remaining sections of the paper are divided and structured as follows Literature review is discussed in Section 2 the proposed methodology is presented in Section 3 experimental analysis results of the proposed model and comparison results with other recent state of the art methods are provided in Section 4. Section 5 also gives a conclusion and recommendations for further research.

2. Related Prior Research. In this section, the methods and earlier research for MRI-based segmentation and classification of brain tumors are presented. An innovative deep learning-based model is developed by Kulkarni et al. [14] in this research. This method is developed for the classification of brain tumor diseases. The morphological operations are first applied to the input image after thresholding. The effective features are extracted by CNN. The proposed deep learning model is performed by using a transfer learning approach. The AlexNet model is used for brain tumor classification. GoogLeNet model is used for classifying malignant brain tumors.

The effective hybrid-brain-tumor classification (HBTC) is developed by Nawaz et al. [19] for multiple classifications of brain tumors. The proposed model classifies metastatic (meta), meningioma (menin), glioma, and cystic (cyst) brain tumors in this research. The performance of the brain tumor detection process is enhanced by this proposed network model, and also it reduces the inherent complexity of the process of diagnosing brain tumors. Run-length matrix (RLM), co-occurrence matrix (COM), and gradient feature are recovered from the segmented dataset. To categorize meta, menin, glioma, and cyst tumors, hybrid multi-features were applied, and the nine most optimized features were chosen. These features were then fed to the framework's classifiers, random tree (RT), meta bagging (MB), J48, and multilayer perception (MLP).

The novel deep network model is proposed by Kumar et al. [12] in this research. The vanishing gradient and overfitting problems are resolved by using ResNet-50 and global average pooling. A simulation was run utilizing a dataset of 3064 brain MRI images with three tumors to assess the performance of the proposed model.

The deep learning-based Unet architecture with ResNet50 as a backbone is developed by Sadad et al. [6] for the segmentation of the brain tumor using the Figshare data set. The effectiveness of detection is improved by introducing the preprocessing and data augmentation techniques. Reinforcement learning through transfer learning and evolutionary algorithms are used to classify brain tumors. There is also the use of additional deep learning techniques including InceptionV3, MobileNet V2, DenseNet201, and ResNet50.

The Grab cut method is developed by Saba et al. [22] for effective actual brain tumor segmentation. A serial-based method is used for fine-tuning the transfer learning-based VGG-19 model for extracting the efficient features, then those features are effectively combined with hand-crafted (shape and texture) features. Entropy is utilized to optimize these characteristics for accurate and quick classification, and classifiers are given a

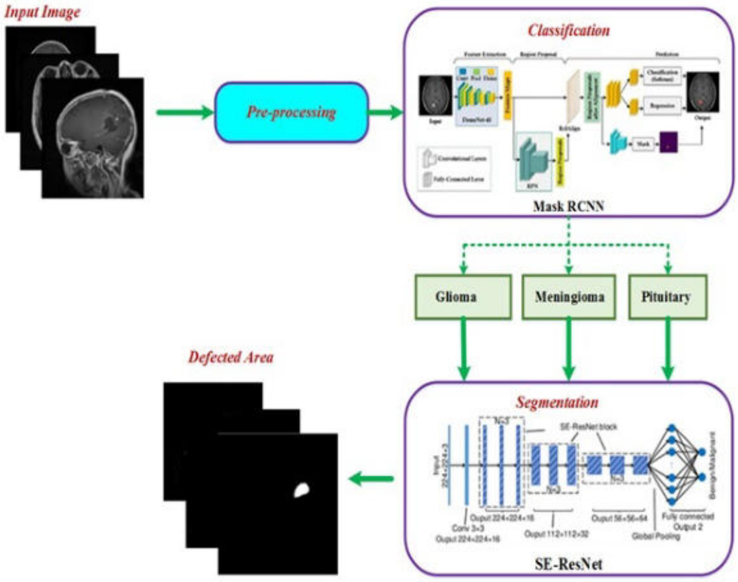

Fig. 3.1: Schematic diagram of the proposed methodology

fused vector as a result. A new hybrid paradigm comprised of a CNN and neural autoregressive distribution estimation (MODE) was proposed by Hashemi et al.[8] in this research. Data acquisition, feature extraction, and classification are the three learning stages this paper indicates for a hybrid architecture. This study's main focus is on automatically predicting the distribution of data and extracting its features in a quick and precise manner.

3. Proposed Methodology. A tumor in the brain is an unexpected lump of flesh in which cells have developed and multiplied uncontrollably. At present, it is a very destructive problem. Because of the complicated nature of the tumor's structure, a timely and accurate diagnosis of brain tumor is essential. The proposed model for identifying brain tumor disease on an MRI consists of the following four fundamental steps: (1) Preprocessing, (2) feature extraction, (3) classification (4) Segmentation, and (5) performance Evaluation.

The first stage is called preprocessing when the images are normalized to produce a uniform contrast. The non-local mean filter and a local smoothing filter are employed for eliminating the noise thus the image can be enhanced. After preprocessing, the effective structural and textual features are extracted by using ResNet-50 for reducing the complexity, and computational cost of the proposed model. The next phase is classification. The multiple brain tumor classification stages such as glioma, meningioma, and pituitary are classified by using a deep learning-based Mask RCNN classifier. Then, the SE-ResNet model is used to segment the defective area. The proposed model's effectiveness is then assessed using test images. The block diagram of the proposed HDLN brain tumor classification is presented in Figure 3.1.

3.1. Problem Statement. Previous deep learning models required numerous steps to analyze the data, and handcrafted features that were retrieved could not guarantee greater classification performance. This illustrates the inadequate nature of automatic learning. Additionally, it performs poorly when there is an unequal distribution of the sample data in a multiclass classification task, which is a problem that is quite common in the medical field. To solve this problem, we propose a new HDLN model for accurate classification and segmentation of multiple brain tumor diseases.

3.2. Image Acquisition. In medical applications, the expansion of 2D images becomes more useful because CE-MRI brain slices often have a small number and a wide slice gap. This study evaluates its methods using 3064 T1-weighted CE-MR images from 233 individuals, which include 930 pituitary, 1426 gliomas, and

Table 3.1: The number of slices and associated patient count for each form of brain tumor (meningioma, glioma, and pituitary) in the dataset.

Category	**Number of Images**	**Patients**
Meningioma	**708**	**82**
Pituitary	**930**	**60**
Glioma	**1426**	**91**
Total	**3064**	**233**

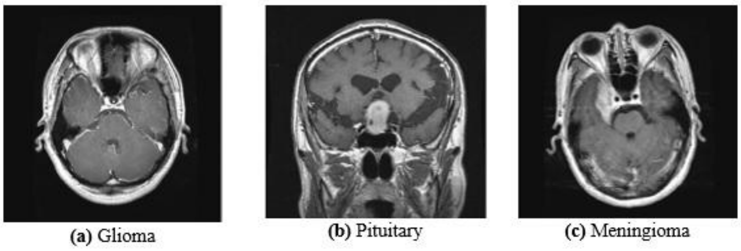
(a) Glioma (b) Pituitary (c) Meningioma

Fig. 3.2: Brain Tumor types

708 meningiomas brain tumors. The radiologist manually defined the tumor boundaries. The 512 × 512 resolution. Mat files used for the dataset images that are accessible on Figshare. A 224 ×224 input layer size was used for designing the proposed framework. Table 3.1 shows the database description, and Figure 3.2 shows the distribution of tumor types.

3.3. Pre-processing stage. The system gathers information about the brain using MRI images as its input. A local smoothing filter and a non-local mean filter are used for preprocessing the MRI images. When photos are compressed or image data is transferred, these filters were employed to reduce any unwanted noise. The image quality and contrast are enhanced during this stage.

3.4. Classification stage. Both pixel-level segmentation and object detection are done by the most recent DL model called Mask-RCNN. It is a faster RCNN extension that can also perform segmentation in addition to localization and classification. Mask-RCNN also separates class prediction from the mask. The segmentation is performed by using the FCN network, which provides a minimal amount of network overhead. Mask- RCNN network is proposed in this research, in this classification network the features are extracted by using DenseNet-41. DenseNet-41 is the feature computation layer of the classification network. DenseNet is the most significant network model of CNN. A collection of dense blocks are present in the DenseNet that are gradually linked to one another using additional pooling and convolutional between succeeding dense blocks. The problem of the top-level key points lacking target location information may be slightly improved by DenseNet by presenting the complicated transformations that accomplish this. DenseNet model reduces the parameters, which lowers the cost. The process of key point propagation is also assisted by DenseNet and it encourages their reuse based on this network is more appropriate for classifying brain tumors. Figure 3.3 illustrates the structure or flow of the proposed classification model. Different networks make up the standard Mask-RCNN network such as a convolutional backbone network, region proposal network, RoI classifier, and bounding box regressor. The following section goes over each stage in great depth.

3.4.1. Feature Extraction. From the input MR images, the effective related features are extracted by the backbone network. Any CNN model that was designed with image analysis might be this network. For a key point extraction, network acquire dependable and more discriminating features. Furthermore, the more computational overhead is required for increasing the depth size of the network and the network weights optimization is more challenging, which could lead to an increasing gradients problem. ResNet model is the backbone network for Mask-RCNN and has been used in previous works in medical image analysis. Although

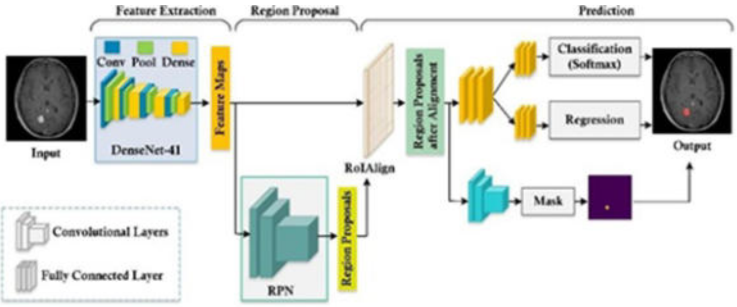

Fig. 3.3: Classification network configuration

the ResNet model has numerous parameters and uses skip connections, this eventually leads to the vanishing gradient problem. A Mask-RCNN with DenseNet framework is implemented in the multi-class classification of brain tumor diseases. The features are more specifically computed by using the DenseNet-41 network. Since the number of dense connections is connected in the DenseNet model. Based on these dense connections, the DenseNet model computes effective set of image features. The initial convolution layer of DenseNet-41 has 24 channels instead of 64, and the kernel is 3 × 3 instead of 7 × 7, resulting in fewer parameters from the actual model. To handle the computational complexity of the network, each dense block's layers are adjusted.

3.4.2. Region Proposal Network. The ROIs are generated by feeding the obtained features to the RPN network in this stage, then the RPN network produces the feature map. The final classification of brain tumors is done by localizing the ROIs to the tumor regions. The sliding window manner is used for scanning the entire image by using 3 × 3 CL in the RPN module for generating the relevant anchors. The image's whole surface is covered by these anchors, which are bounding boxes of various sizes. 20 k anchors of different sizes and scales are present in the RPN network, the whole images are covered by overlapping these anchors with each other. The more tumor-related objects are present in the top anchors, these anchors are chosen using RPN prediction, and bounding box regression is then used to adjust their location and size. Then the classification is performed by passing the several RoIs generation to the next stage.

3.4.3. Bounding Box Regression with RoI Classification. The generated feature map and RoI are sent to this network as input. This network is more sophisticated than the RPN, which only yields two classes, including background and foreground. One of three classes is classified by the proposed RoIs such as pituitary, meningioma, and glioma and the bounding box's size is also increased by this network. From the feature maps, all RoIs are pooled into one fixed size in this stage. For candidate regions with arbitrary sizes, the fixed length of key point vectors is obtained by utilizing the RoIAlign layer for resizing the feature maps. In the RoI pooling layer, misalignment problems are avoided by performing the bilinear interpolation process, which utilizes the quantization operation. Final classification results are obtained by feeding the key points to the classification and regression layer.

3.4.4. Brain Tumor Segmentation using SE-ResNet. The brain tumor is effectively segmented by using the SE-ResNet model in this research. The SE-ResNet ignores the spatial information in favor of examining the dependencies among its convolutional features' channels. Excitation and squeeze operations are present in the SE block that scales the relevance and overall information of each feature map, respectively. The significant information from each channel is extracted by the squeeze operation using global average pooling. A nonlinear function is used by the excitation operation for computing the inter-channel dependencies. Because of its superior ImageNet image classification performance, one of the most popular CNN models is SE-ResNet model. Additionally, SE network is simple to implement because, it only involves adding SE block without altering the structure of the preexisting model. During training, the deep gradient for the seamless transmission is enabled by the residual block, when increasing the network layers in the network. Which is used for effectively training the whole network. The 1D convolutions are used by the proposed network instead of 2D

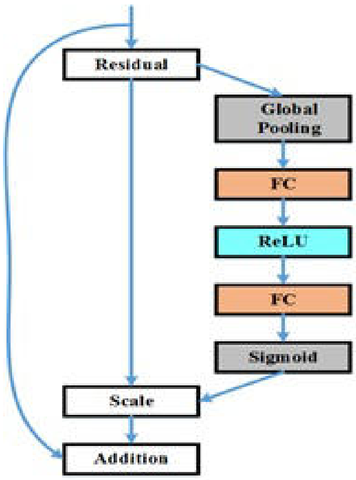

Fig. 3.4: SE-ResNet module structure

convolutions. This is the main difference between the original SE-ResNet and our proposed network model. Figure 3.4 shows the structure of the SE-ResNet model. In this model, the fully connected layer is represented by FC, ReLU and the activation functions are depicted by Sigmoid.

4. Results And Discussion. This research effectively classifies multi-class MRI images. The HDLM is used for the classification and segmentation of the CE-MRI dataset. Multiple classifications of brain tumor diseases are classified by using Mask RCNN. The hybrid SE-ResNet model is developed for the segmentation of multiple brain tumor diseases, where 70% of the dataset was used for training purposes and 30% for testing purposes. The Python platform is used for achieving the classification and segmentation results with computer resources of 8 GB of RAM and an i5 processor. The classification and segmentation performance is increased by adding several approaches to the proposed model.

4.1. Performance Evaluation for Classification. In the deep learning models, the classification performance is analyzed by using a confusion matrix widely. Accuracy, sensitivity, specificity, and precision are used to measure the classification performance of the model. The confusion matrix is used for computing these calculations. All data samples are comprised of True Positive (TP) indices and the model is associated with a specific class for effective classification of the model. Additional samples are available for the True Negative (TN) indices in the confusion matrix. Other successfully determined classes are related to these samples. In the uncertainty matrix, the False Negative (FN) and False Positive (FP) indices represent the classifier's estimated number of incorrect samples.

The confusion matrix is used to retrieve accuracy performance parameters for experimental analysis. By dividing the total value of the confusion matrix by the proportion of true positive and true negative value, Equation 4.1 define accuracy. The confusion matrix factor determines the classifier's performance in the proposed model. Similarly,

$$Sensitivity(Recall) = \frac{TP}{TP + FN} \tag{4.1}$$

$$Specificit = \frac{TN}{N + FP} \tag{4.2}$$

$$Precision = \frac{TP}{TP + FP} \tag{4.3}$$

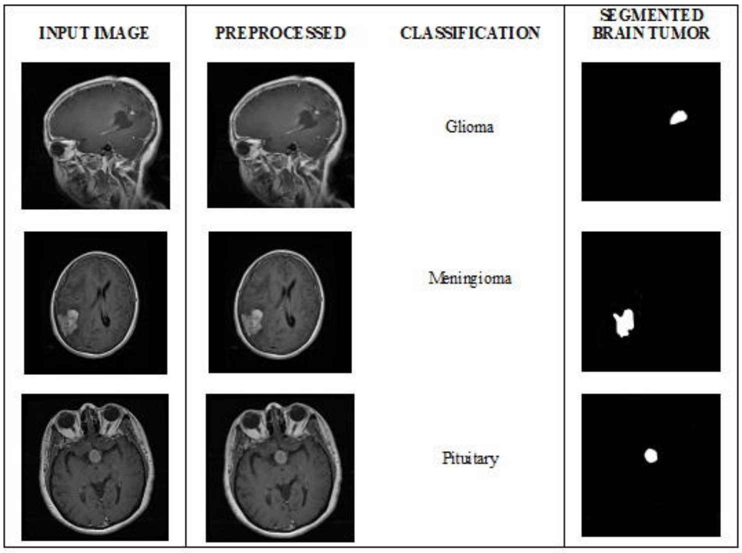

Fig. 4.1: Experimental results of the proposed model

Table 4.1: Performance results for classification of the proposed model

Tumor type	**Accuracy (%)**	**Specificity (%)**	**Sensitivity (%)**	**Precision (%)**
Glioma	**99.34**	**98.65**	**98.79**	**99.02**
Meningioma	**99.23**	**98.87**	**98.45**	**98.98**
Pituitary	**99.32**	**99.23**	**98.69**	**99.04**

$$Accuracy(\%) = \frac{TP + TN}{TP + FN + TN + FP} \tag{4.4}$$

For training, 80% of the data is used and for testing, 20% data is used in the experiment analysis. The ground truth labels and predicted labels are used for evaluation metric computation Similarly, equations 4.2, 4.3, 4.4

4.2. Experimental Results. The multiple classification tasks are performed by using a deep learning-based method. The MRI image classification such as glioma, meningioma, and pituitary are evaluated in terms of performance. All classification tasks are performed by using the HDLN model with the aforementioned network parameters. The experimental results of the proposed model are shown in Figure 4.1.

The extracted accuracy metrics from the confusion matrices are displayed in Table 4.1. The class-wise accuracies, specificities, precisions, and sensitivities of the proposed model is shown in the table. Classification accuracy for meningioma, glioma, and pituitary tumors is 99.23%, 99.34%, and 99.32%, respectively. The performance of the classification results is significantly improved from this observation. The proposed approach provided an overall accuracy, sensitivity, and specificity of 99.23%, 98.64%, and 98.91%. The class-wise performance is determined by employing a small sample of the validation set's images. The multi-class brain tumor classification is effectively performed by the proposed HDLN model.

With 26 epochs and a 0.01 learning rate, the training phase is conducted to achieve higher classification results. For each epoch, the experiment analysis used 31 iterations in total. The training and validation accuracy and loss graph for multiple brain tumor classification is shown in Figure4.2. An accuracy of 99.23% was used to validate the training progress. In the overall training process, 1 min 54 s timing is used for reaching the final iteration. For feature extraction, the two convolutional layers are then applied. Effective feature

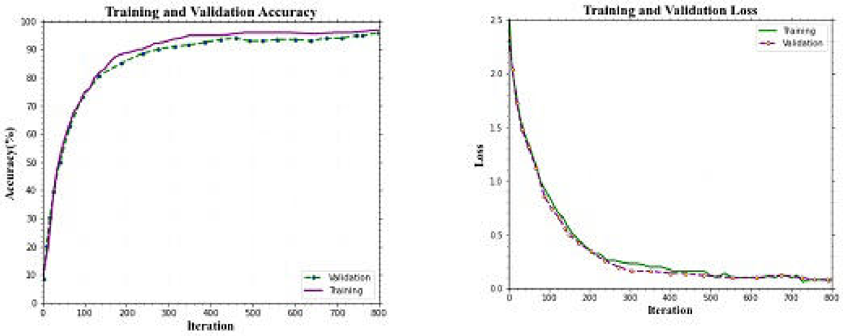

Fig. 4.2: The accuracy and loss of the multi-class classification of brain tumor diseases during training and validation.

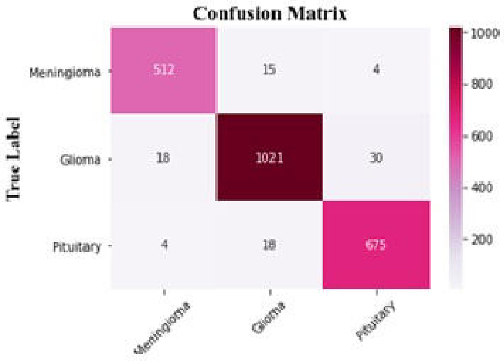

Fig. 4.3: The confusion matrix of the proposed model

extraction improves the validation accuracy during the training phase.

The proposed model's confusion matrix is displayed in Figure 4.3. The predicted values are represented by X-axis and the true labels (ground truth) are represented by Y-axis. The area under the receiver operating characteristic (AUC ROC) curves for different tumor classes in the brain CE-MRI dataset is shown in Figure 4.4.

4.3. Comparative Analysis of Other Classification Models. We compare our proposed model classification results with those from earlier research over the same dataset in this section. The performance result comparison for multi-class classification is shown in Table 3. The proposed Mask RCNN classification network achieves the highest classification results in Table 4.2. 94.82% accuracy is achieved by [30] for the classification of brain tumors using the VGG19 model. In [29], CNN achieves an accuracy of 96.14%. In [2], the authors used transfer learning for feature extraction using a pre-trained GoogleNet model. Three different classifiers are used for the classification of obtained features such as KNN, SVM, and Softmax, 97.1% is achieved by this research. Three alternative processing techniques, including residual blocks, attention modules, and hypercolumn approach were used by the DL model BrainMRNet [32] to classify brain tumors. 97.69% accuracy is achieved by this research for classification. Multilayer perception (MLP) is used to attain effective classification performance [28], and they were able to achieve an accuracy of 98.15%. The higher performance is achieved by the

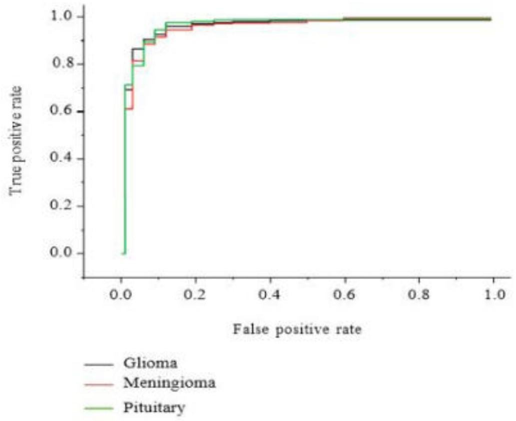

Fig. 4.4: AUC ROC curves of different tumors in the CE-MRI dataset

Table 4.2: Comparison analysis of classification performance

Technique	**Classification model**	**Accuracy (%)**
Swati et al.	**VGG19**	**94.82**
Sultan et al.	**CNN**	**96.14**
Deepak et al.	**GoogLeNet and SVM**	**97.10**
BrainMRNet	**Attention Module Hyper column technique and Residual block**	**97.69**
Proposed classification model	**Mask RCNN (DenseNet-41)**	**99.23**

proposed Mask RCNN classification model than the existing deep learning models and it successfully classifies between multiple classes of brain tumors. The main advantages of the proposed classification network model include the prevention of overfitting and the elimination of any adverse network performance impacts related to the classification process. The features of the tumors are successfully extracted by the proposed model including inter-scale variability, and also the final classification performance is enhanced by the proposed model. While compared to the previous model, the proposed model effectively classifies multiple brain tumor classifications. The proposed method achieves 99.23% accuracy, 99.08% specificity, and 99.12% sensitivity. The proposed model automatically diagnoses and pre-screens the brain tumors due to its high classification accuracy. Figure 4.5 shows the performance evaluation for classification.

4.4. Comparative Analysis of Other Segmentation Models. The proposed model is compared with other segmentation techniques described in this section. The comparative analysis for segmentation models with the average results given in previous research for evaluating the performance.

A quantitative comparison employing various performance measurement parameters, including accuracy, dice score, and mean IoU is displayed in Table 4.3. The RCE technique is proposed by Sheela et al. [28]. The tumor segmentation is done by using fuzzy c-means and an active contour model in this research, an average accuracy of 91% was attained. 0.950 is achieved by [17], and the computation cost is increased due to a large number of parameters in this model. The multi-scale CNN model is developed by [3], and three different spatial scales are used for processing the input MR images using multiple processing routes in this research. They obtained a 0.828 dice score and an average segmentation accuracy of 97.30% respectively. The approach in [18] has a 95.90% accuracy rate and a dice score of 0.955.

While compared to the existing segmentation techniques, the proposed model achieves better performance. The proposed SE-ResNet segmentation model for multi-class brain tumors achieved an overall accuracy of 97.83%, mean IoU of 0.976, and dice score of 0.974. Due to structural complexities, most of the existing model

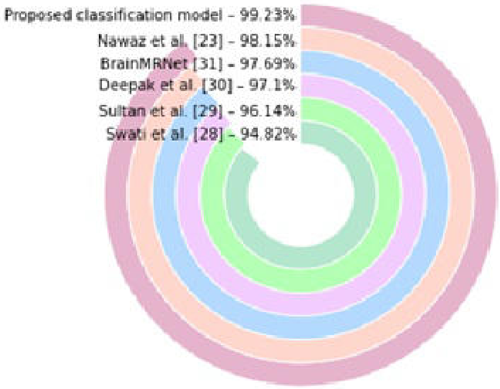

Fig. 4.5: Performance evaluation for classification

Table 4.3: Comparison analysis of classification performance

Technique	**Segmentation Model**	**Dice**	**Mean IoU**	**Accuracy (%)**
Sheela et al.	**Fuzzy-C-Means and Active Contour**	**0.665**	**-**	**91.00**
Masood et al.	**Traditional Mask-R-CNN**	**0.95**	**0.95**	**95.10**
Pernas et al.	**Multiscale CNN**	**0.828**	**-**	**97.30**
Masood et al.	**Mask-RCNN (ResNet-50)**	**0.955**	**0.951**	**95.90**
Proposed Segmentation Model	**SE-ResNet**	**0.974**	**0.976**	**97.83**

like produces only hand-crafted features and these features are not effective for detecting the tumor region[20]. But our proposed model produces effective deep features and these features accurately determine the tumor regions [9]. The entire image is directly processed for the segmentation in some previous approaches, which leads to misclassification as a result of the complex background (e.g., MRI artifacts, brain tissues overlapping with tumor boundaries, etc.), which decreases the segmentation accuracy of the image. A region-based approach is used by this approach in [16] to localize tumors, and tumor segmentation requires further processing. The proposed segmentation model leverages the RoIAlign layer and localized RoIs for segmentation in contrast to previous techniques, which increases the segmentation accuracy and ultimately reduces the segmentation space[27]. Additionally, our proposed model uses fewer computational resources to achieve high performance for multi-class brain tumor segmentation. Performance evaluation for segmentation is shown in Figure 4.6.

5. Conclusions. In this paper, we proposed a novel automatic method for the detection of brain tumor diseases from MRI images. For multi-class brain tumor detection, this research proposes a new HDLN model for automated multi-class classification. The multiple brain tumor disorders including pituitary, meningioma, and glioma are classified by the proposed model using MRI images. A publicly tested dataset (CE-MRI) is employed for testing experimental analysis. First, image pre-processing is achieved in the MRI images by applying to filter for noise reduction and image enhancement. Next, the brain tumor classification is done by using the Mask RCNN model. Then the SE-ResNet model was then used to segment the multiple MRI images. The proposed HDLN model effectively classifies and segments the MRI images with an overall accuracy of 98.53%. Experimental comparisons reveal that the tumor region is more accurately defined by the proposed HDLN model and can function in the proposed network model as a newly developed automatic diagnostic tool. The effective features with an accurate representation of brain tumors are also computed efficiently by the proposed HDLN model while comparing them to the existing models. In the future, we will focus on classifying and segmenting brain tumors using more difficult datasets. To increase the model's accuracy even further, we also want to optimize hyper-parameters and increase training samples.

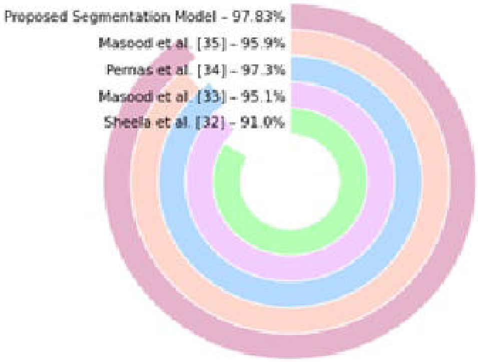

Fig. 4.6: Performance evaluation for segmentation

Acknowledgement. We declare that this manuscript is original, has not been published before, and is not currently being considered for publication elsewhere.

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Edited by: Katarzyna Wasielewska
Received: Dec 30, 2022
Accepted: Apr 8, 2023