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Multi-Graded Brain Tumor Classification Using Yolov7

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***Abstract*— *In recent years, significant progress has been made in the field of diagnosis and classification of brain tumors, mainly attributed to advancements in artificial intelligence and medical imaging. The main objective of this study is to improve the detection and classification of brain tumors by applying and utilizing of artificial intelligence (AI) and recent advancements in medical imaging techniques. Automation of the process of tumor identification and then classification, in addition to tumor grading, will definitely improve all procedures of brain tumor treatment and enhance patient care. The proposed system combines convolutional neural networks (CNNs), which act as extract features, and the You Only Look Once Algorithm (YOLOv7) for effective object identification and accurate classification. The methodology described in this study involves employing a technique of multilayer classification, which integrates three distinct datasets. This comprehensive approach shows an exceptional levels of accuracy and precision. At the initial level, the model attains a 99.78% accuracy in distinguishing between tumor and nontumor cases. At the next level the system accurately sorts types of brain tumors (such, as glioma, meningioma and pituitary tumors) with an average accuracy of 99.35%. Moving on to the final stage it successfully distinguishes between low grade and high grade glioma tumors with a precision of 93.07%. Moreover the model shows accuracies ranging from 99.41%, to 99.61% when classifying types of brain tumors and nontumor cases. The proposed system has the ability to determine the boundaries of the tumor, and thus this has helped in calculating the sizes of tumors with high accuracy.*

Index Terms- *Brain tumor, MRI, Convolutional Neural Network, YOLO, Tumor grading.*

I. INTRODUCTION

In recent years, successful and significant strides have been made in the field of medical image analysis [1,2], particularly in detecting and identifying brain tumors. This progress has been driven by its diverse uses in healthcare for diagnosing diseases [2,3,4]. Adopting this method has transformed the treatment of oncology patients through improved tumor detection techniques, precise mapping of tumor boundaries, and improved operations that reduce damage to brain tissue and ultimately enhance surgical outcomes [5,6,7].

Recent medical research is increasingly depending on different imaging techniques, such as computerized tomography (CT), magnetic resonance imaging (MRI), and diffusion tensor imaging (DTI), which are the backbone of modern medical practices and research [8]. Magnetic resonance

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imaging (MRI) technology provides an outstanding possibility of viewing the structure of the human body and learning about its functions without the need to expose patients to high and harmful radiation [3,9]. One of the most important advantages of MRIs in both detecting and diagnosing brain diseases is its notable ability to highlight the body's tissues, which allows healthcare professionals to examine brain tissue with high accuracy [10].

According to the World Health Organization (WHO), cancer was considered to be the second leading cause of death in 2020, claiming the lives of nearly 10 million people [11]. Cancer cells can be characterized by the rapid growth of these cells, which differ significantly from healthy ones in terms of their proliferation and their ability to harm surrounding healthy tissues. Moreover, cancer can affect any part of the body. Many factors can increase the risk of getting cancer, such as genetics, lifestyle choices, and environmental conditions surrounding the person [12,13,14].

Brain tumor detection and diagnosis pose significant challenges to healthcare professionals, neurologists, and brain surgeons. As a result of the exceptional complexities in this field, this diagnosis, its associated conditions, and the subsequent medical procedures and decisions can have far-reaching effects that significantly impact an individual's quality of life [15]. A comprehensive understanding of the information and results of examinations related to brain tumors is crucial. Additionally, recognizing the importance of MRI examinations in this context will provide an indispensable tool for surgeons and doctors specializing in brain diseases. Furthermore, acquiring a deeper understanding of the methods and approaches utilized to classify and grade brain tumors will enhance our ability to characterize these growths with high accuracy and effectiveness [16].

Convolutional neural networks (CNNs) have emerged as a substantial and vital advance in medical computer vision technologies that have fundamentally transformed the field of identifying and classifying brain tumors [17]. CNNs show tremendous capabilities in extracting features from diverse medical images with particular emphasis on complex details and patterns that are usually hidden or not clearly visible from those images provided by MRI scans [18,19]. CNNs show apparent superiority in those tasks related to image classification in general, especially when it comes to processing grid data and recognizing patterns in those images [20]. For classification, typical CNN models like AlexNet, GoogleNet, VGG, and ResNet are dedicated to classification by concatenating fully-connected layers with the different classifiers [21]. Moreover, CNN models pre-trained on image datasets clearly facilitate and simplify fast and accurate classification and help identify and grade various pathological conditions, such as brain tumors, with high accuracy, reducing the need for surgery [22,23].

The You Look Only Once (YOLO) algorithm represents a significant computer vision advancement, enabling high-speed, real-time object detection and precise location. This speed and accuracy make YOLO a precious and reliable tool for image analysis in critical situations where rapid and accurate diagnosis is essential [19،24]. The YOLO algorithm has proven very useful in various medical and healthcare settings. Rapid detection can help radiologists and healthcare professionals in identifying different tumors and plan appropriate treatment and medical interventions at the right time and in the right circumstances [1,25].

Brain cancer is categorized into two grades, each with its own characteristics and treatment methods. Primary brain tumors originate within the brain, while secondary brain tumors are cancers spread to the brain via other parts of the body [26]. These tumors can be either non-cancerous (benign) or cancerous (malignant) [27].

Primary brain tumors are categorized based on the cells they impact, like gliomas, meningiomas, or pituitary adenomas [28,29]. Gliomas are growths that develop from glial cells, which serve as cells surrounding and safeguarding neurons in the brain [28,30,31]. Meningiomas are neoplasms originating from the meninges, the membranes that protect and envelop the brain and spinal cord. Pituitary adenomas are neoplasms that develop within the pituitary gland, a diminutive endocrine gland near the

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cranial base responsible for regulating many hormones [29].

The primary contribution of this research pertains to the formulation of an innovative approach that integrates CNN for feature extraction alongside YOLO, a state-of-the-art technique for object detection. The implementation of this methodology yields exceptional levels of precision and success in recognizing brain tumors. This work demonstrates notable progress in brain tumor identification and classification by integrating the CNN/YOLO approach and fine-tuning. These methodologies are essential quantitative instruments for healthcare professionals, augmenting the precision of diagnostic procedures and treatment strategies. Additionally, this research presents and employs an all-encompassing tumor grading system, resulting in a more accurate assessment of tumor aggressiveness and providing significant utility for healthcare professionals. Also, we will conduct a comparative analysis of the outcomes obtained from the proposed model compared to previously recommended methodologies.

The structure of this research article is as follows: Section II provides an overview of the relevant literature. Section III presents an overview of the dataset employed in the research. Section IV provides a comprehensive overview of the suggested methodology. Section V provides a discussion of the research results and further analysis. The conclusions are presented in Section VI.

II. RELATED WORKS

Indeed, several studies have made notable contributions in a collective effort to advance brain tumor diagnosis using artificial intelligence (AI) and medical imaging. Khawaldeh et al. [32] introduced a CNN-based model focusing on three classes: healthy, low-grade tumor, and high-grade tumor, using a dataset of 587 MR images from 130 patients. This work focuses on the utilization of Convolutional Neural Networks (ConvNets) for automated and accurate grading of glioma tumors. Thus, the study needs to expand the scope to classify other types of tumors. Similarly, Soltaninejad et al. [33] proposed an approach for glioma tumor classification, combining feature extraction with a CNN and a random forest classifier. The FCN is used to include the tumor region and exclude unnecessary processing of other parts of the brain. The training dataset included 30 MR images, with 20 representing high-grade gliomas and 10 low-grade gliomas. Kaldera et al. [34] utilized a CNN for classification and a Faster R-CNN for segmentation, aiming to reduce computational demands while maintaining accuracy. They worked with 257 images, with 218 assigned to the training set. Even though the proposed model achieves accepted accuracy, it needs further validation and testing on a larger dataset to assess the generalizability of the proposed CNN and Faster R-CNN models. Toğaçar, M. [35] introduced a modified CNN model created for the classification of images. The model is employed exclusively to classify cases as tumors or not. The model's innovation lies in its emphasis on the pertinent region within MR images through attention modules. The dataset of images comprises a total of 253 images. The dataset has a total of 155 tumors and 98 normal samples. The study mentions that the low resolution of the dataset used may have prevented higher results. Kang et al. [36] employed pre-trained CNN models as feature extractors, focusing on the support vector machine (SVM) classifier. They worked with three datasets, including distinct tumor and non-tumor classes and multiple tumor categories. A hybrid scheme for brain tumor classification was applied in such a way that pre-trained CNN models to extract the deep features from brain MR images and ML classifiers to classify brain tumor type effectively. Rinesh et al. [37] proposed a hybrid approach using a multilayer neural network and optimized k-means clustering for feature extraction. They utilized an open-access dataset with 250 brain tumor images partitioned for training and testing. This study analyzes brain tumor localization by performing different operations on hyperspectral images. The tumor is located using a combination of k-nearest neighbor and k-means clustering algorithms. Özkaraca et al. [38] proposed a modified modular deep learning model that retains the existing advantages of known transfer learning methods such as DenseNet, VGG16, and basic CNN architectures in the classification process of MR images

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and eliminates their disadvantages. The study suggests that intensive use of layers and training the model without relying heavily on transfer learning methods can lead to improved performance.

In contrast, much literature focuses on employing the YOLO algorithm for brain tumor classification. Safdar, M.F. et al. [39] emphasized the significance of selecting appropriate data augmentation techniques for medical imaging classification. The proposed model is designed to diagnose low-grade glioma using the YOLOv3 model. The study indicated that the augmentation process by rotation at 180° and rotation at 90° yielded the most favorable outcomes as data augmentation methods. The study did not explore the impact of augmentation methods on other grades of glioma tumors. Montalbo, F.J.P., et al. [40] employ transfer learning and fine-tuning on a YOLOv4-Tiny model to perform the detection and identification of brain tumors. This work has certain caveats in terms of having bounding boxes to detect tumors. The use of bounding boxes still limits the precise selection of tumors compared to a segmentation approach. In the same way, Kumar, N.S. et al. [41] explored the utilization of YOLOv4 for brain tumor classification. Their implementation using Darknet and the Tesla T4 GPU achieved an impressive classification accuracy of over 97%. Many challenges were mentioned in the study when working with medical image analysis, particularly in the context of orientation, size, shear, and dataset preprocessing. Paul, S. et al. [42] proposed a hybrid approach using YOLOv4 for training and YOLOv5 for testing, achieving about 88–90% precision rates. Their model demonstrated accurate recognition of three brain tumor classes with accuracy rates of 98.07% for BraTS 2020 and 97.04% for BraTS 2019 with minimal computational complexity. The study relies on free-of-charge resources like Google Colab, which limits the scope of experiments due to time constraints and resource availability. Also, hyperparameter tuning and exploration of various optimizers were not extensively performed in the study. Kang M. et al. [43] introduced an enhanced YOLO architecture that combines the YOLO architecture with reparametrized convolution based on channel shuffle (RCS). The study focused on reducing the computational and memory demands of the convolutional layer. In order to reduce inference time, the number of the original nine anchors was decreased to four; this modification affected the ability to detect small objects.

These mentioned studies collectively contribute to advancing brain tumor classification through various approaches and datasets, aiming to improve the accuracy and efficiency of tumor diagnosis.

III. DATA SETS

This research utilizes three different datasets acquired through a comprehensive collection process involving many sources, such as public hospitals, private medical institutions, and radiology laboratories. Two of these datasets are publicly available online, such as the BR35H dataset [44] and the CE-MRI dataset [45], while the third dataset is collected and labeled especially for the study. These datasets are considered a diverse collection of MR images in various views with variant tumor and nontumor cases. Having such a wide range of MR images will help with a lot of the problems that come up when trying to make automatic diagnoses that are accurate and precise. Next, we conducted pre-processing on our datasets. The primary objective of the BR35H dataset is to train the network to distinguish between tumor and nontumor cases and evaluate the system's ability to accurately differentiate between instances with tumors and cases without tumors. The second dataset, known as CE-MRI, comprises magnetic resonance imaging (MRIs) of three distinct tumor forms, namely meningioma, glioma, and pituitary tumors. The primary objective of this dataset is to differentiate between the three specified categories of cancers. Finally, the system undergoes extensive testing using datasets that skilled radiologists and doctors have examined and labeled. This testing is conducted to assess the system's performance at three levels of diagnosis. *Fig. 1* illustrates various MR images depicting different brain tumor types, whereas Table I illustrates the three dataset classifications. An augmentation is developed to enhance the diversity of tumor cases, given the limited number of MR

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slices and the limited variability observed in the labeled images, specifically to evaluate glioma tumor grades. Table II shows the data augmentation techniques that were employed in the study.

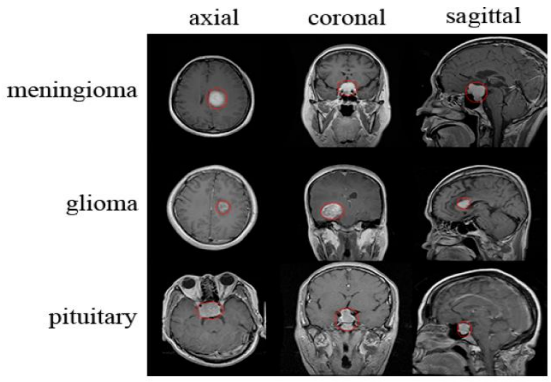

FIG. 1. DATASET SAMPLES ILLUSTRATES VARIOUS MR IMAGES DEPICTING DIFFERENT BRAIN TUMOR TYPES [42].

TABLE I. DATASETS CLASSIFICATION

Dataset	Description
BR35H	**1500** MR images of tumor cases
	1500 MR images of non-tumor cases
	Total images: 3000
CE-MRI	**1426** MR images for Glioma tumor cases
	708 MR images for Meningioma tumor cases
	930 MR images for Pituitary tumor cases
	Total images: 3064
Manually Labeled Dataset	**855** MR images for Glioma tumor cases
	690 MR images for Meningioma tumor cases
	530 MR images for Pituitary tumor cases
	300 MR images for non- tumor cases
	Total images: 2375

TABLE II. DATA AUGMENTATION TECHNIQUES THAT WERE EMPLOYED IN THE STUDY

Data Augmentation Technique	Applied Approach
Blurring	3Px and 5Px
Adding Noise	3% and 5%
Flip Image Vertically	180º
Flip Image horizontally	180º

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IV. METHODOLOGY

The identification of brain tumors has been extensively studied and documented in numerous academic studies within the literature. A significant portion of these investigations primarily focus on the detection and existence of the tumor. Certain classifications of tumors focus mainly on their types without placing much emphasis on the specific location of the tumor or estimating the tumor's measurements.

Despite some limitations in previous studies, our research endeavors focused on improving our methodology, reducing the time of the training period, and enhancing performance, particularly in the context of degenerative glioma tumors or the corresponding grades.

The current study aims to do this for the three most common types of brain tumors: pituitary, meningioma, and glioma tumors, using MR images that have been labeled by an expert radiologist from a publicly available dataset and a private dataset gathered from hospitals. *Fig. 2* presents the proposed system stages and explains how each block of the system's three stages performs its function. The system block diagram is illustrated in *Fig. 3*, which also presents an overview of the achievements made by each system component.

In order to extract features, the image underwent preprocessing and was subsequently forwarded to CNN. The CNN was employed to identify the most generic characteristics, starting with an initial convolutional layer. The output of the convolution layer was afterward fed to a max pooling layer to decrease the spatial data size for the following layer. The process of max-pooling involves the selection of the highest value among the components or pixels within the region of the feature map encompassed by the filter. After that, a pooling layer and another convolutional layer were added. Eventually, the output reached a softmax-activated layer. The softmax-activated layer takes in a vector of raw scores or logits. These logits are often the output of the preceding layers in the neural network, and they represent the unnormalized scores associated with each class. In the early stages, CNN filters can capture edges, corners, and textures. As we go further into the network, filters become more specialized. They recognize more complicated patterns, including forms, object fragments, and texture combinations. Intermediate characteristics are mixtures of fundamental features from preceding levels. More complex elements like object components and texturing affect filters at deeper levels. Recognizing complete items or scenes requires these properties.

CNNs have scale and translation invariance. They can distinguish features and objects independent of size or position in the image. Due to standard weights in the convolutional layers, the network may learn features that work throughout the input space.

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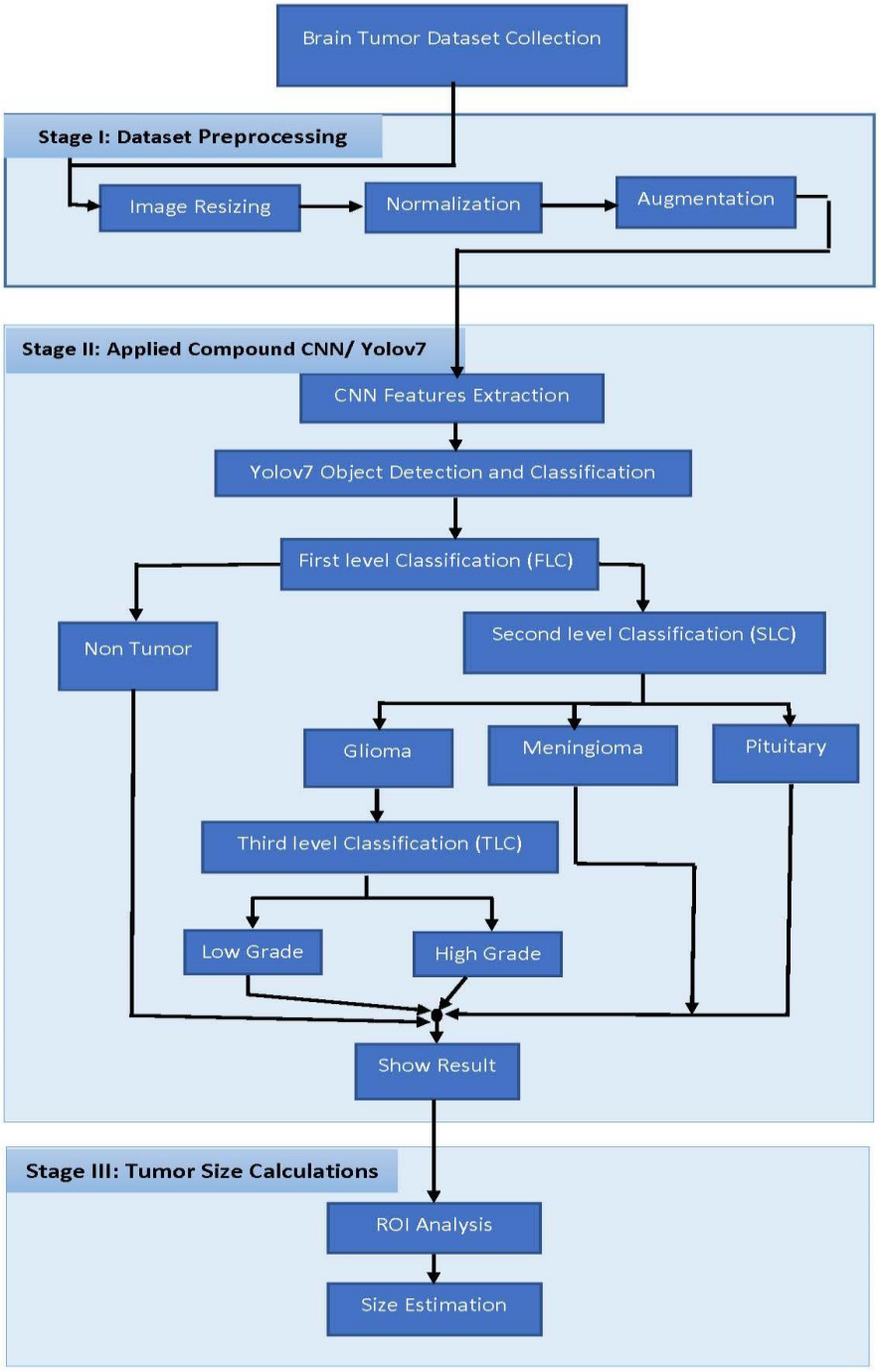

FIG. 2. PROPOSED SYSTEM STAGES.

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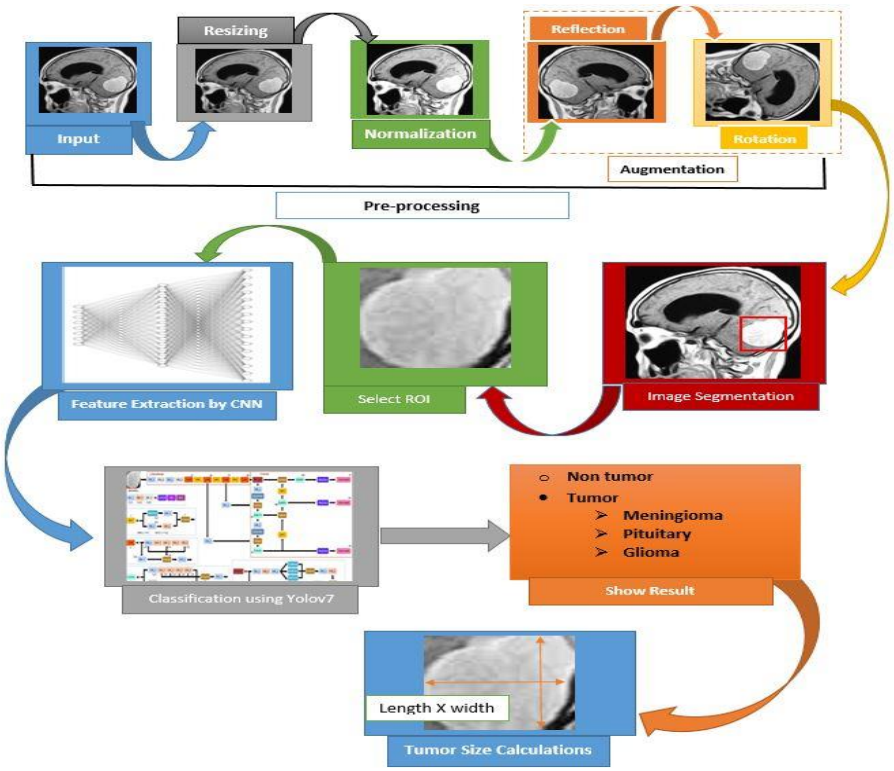

FIG. 3. SYSTEM BLOCK DIAGRAM.

Referring to *Fig. 3*, the algorithm that implemented in proposed system is presented below:

Step 1. Load the dataset of tumor images and corresponding labels

Step 2. Preprocess the images:

- Resize the images to a proper size (224*224)
- Normalize the pixel values to a suitable range [0, 1] or [-1, 1].
- Apply data augmentation techniques, i.e., rotation, flipping, and scaling to increase dataset diversity.

Step 3. Convert annotations to YOLO format:

- Calculate normalized bounding box coordinates:
  - For each bounding box, determine the center coordinates (center_x, center_y) and the width and height
    (width, height) of the box.
  - Normalize the coordinates and dimensions by dividing them by the image size.
  - Divide center_x and width by the image width, and divide center_y and height by the image height.
- Assign a class index to each bounding box.
  - Determine the class index for each bounding box based on whether it represents a tumor or the background.
  - Assign a class index of 0 to the bounding boxes representing the background, and assign a class indexof 1 to the bounding boxes representing tumors or any other relevant class.

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- Save annotations in YOLO-readable format:
  - For each bounding box, create a line in the annotation file in the following format: class index, center_x, center_y, width, height.
  - Replace "class index" with the assigned class index for the bounding box.
  - Replace "center_x", "center_y", "width", and "height" with their corresponding normalized values calculated in step 1.
  - Repeat this process for all bounding boxes in the dataset, appending each line to the annotation file.

Step 4. Implement CNN Feature Extraction

- Choose a CNN architecture: Select a compound CNN architecture (ResNet), this architecture balances complexity and efficiency for feature extraction.
- Pretrain the compound CNN:
  - Download pre-trained weights (ImageNet weights for ResNet).
  - Load the weights into the CNN architecture.

Step 5. YOLOv7 Training

- Apply YOLOv7 architecture: Adjust YOLOv7's network architecture parameters to match the desired class count and anchor box configuration.
- Convert annotations for YOLOv7:
  - Use anchor box clustering techniques to determine anchor box sizes suitable for dataset.
  - Convert annotations to YOLOv7-compatible format (class index, normalized bounding box coordinates, anchor box index).
- Prepare training and validation datasets:
  - Split the dataset into training and validation sets.
  - Organize data in YOLO format: text files with one row per ground-truth bounding box.
- Training YOLOv7:
  - Implement a custom YOLOv7 training script.
  - Monitor loss and other evaluation metrics during training to assess model performance.
  - Adapting learning rates, batch sizes, and data augmentation techniques to achieve best model performance.

Step 6. Fine-tuning and Iteration

- Model fine-tuning: Based on evaluation results, fine-tune the compound CNN and YOLOv7 models for improved accuracy.

Step 7. Evaluate the trained model

- Iterate over the testing set: For each image in the testing set
  - Forward propagate the image through the CNN
  - Compute the feature maps at the desired layer(s)
  - Extract the features and pass them through the YOLO model
  - Obtain the predicted bounding boxes and class probabilities
  - Compare the predicted outputs with the ground truth labels
- Compute evaluation metrics such as accuracy, precision, recall, and F1 score

Step 8. Perform additional post-processing

- Visualize the detected tumors with bounding boxes on test images

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- Calculate additional metrics or generate visualizations

V. RESULTS AND ANALYSIS

In this work, MATLAB 2021a was run on a personal computer equipped with a Core i7 processor from the 10th generation, 32 gigabytes of random access memory (RAM), an NVIDIA GeForce 1060 graphics card with 6 gigabytes of memory, a one-terabyte solid-state drive (SSD), and a 64-bit version of Windows 10. to run all of the simulations and carry out all of the analysis.

The proposed system utilized a comprehensive dataset, which was precisely selected and carefully categorized for our research purposes. In order to ensure the representation of a broad and diverse range of cases, the MR image selection process involved careful examination. Our work involves an inclusive method of data collection and selection to classify brain tumors at multiple levels. These levels, namely:

- First-Level Classification (FLC)
- Second-Level Classification (SLC)
- Third-Level Classification (TLC)

As for the first level of classification (FLC), the 3000 images of brain tumors in the publicly available Br35H dataset will be used. Each dataset folder contains a cumulative total of 1500 MR images. A case containing tumors is categorized in one of the two folders dedicated to cases that do not involve tumors. Behind that, we will compare our results to those of other systems that use the same dataset to see how similar they are. *Fig. 4* depicts the confusion matrix for this phase, while Table III lists all evaluation metrics utilized during the testing phase for FLC. Also, the accuracy and losses curves of the system are illustrated in *Fig. 5*.

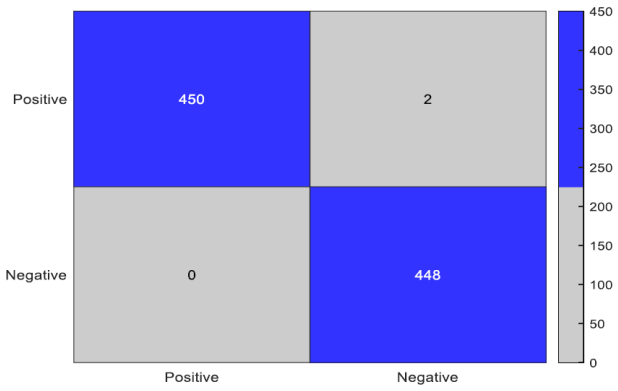

FIG. 4. CONFUSION MATRIX FOR FLC BY USING BR35H DATASET.

TABLE III. VALUES OF THE EVALUATION METRICS USED THROUGHOUT THE TESTING PHASE FOR FLC

Metric	Value
Accuracy	**0.9978**
Precision	**0.9956**
recall	**1.00**
F1-Score	**0.9978**

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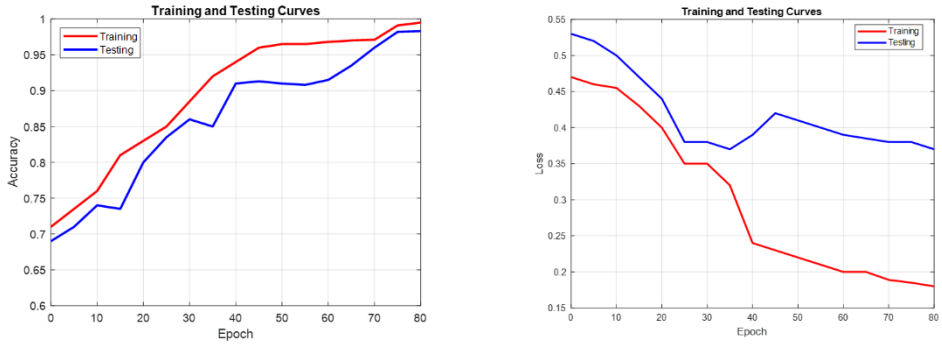

FIG. 5. ACCURACY AND LOSSES FOR THE SYSTEM IN FLC.

The results indicate that the FLC model demonstrates a high level of accuracy in its predictions for nearly all instances. The system successfully attains a low incidence of false positives. It demonstrates a high level of accuracy in correctly identifying all positive instances, with no instances being falsely classified as negative. Notably, the model exhibits a remarkable ability to avoid classifying any positive cases as negatives, demonstrating its strong recall capability. This indicates a commendable equilibrium between precision, which measures the accuracy of positive predictions, and recall, which measures the system's ability to identify all positive occurrences accurately. Comparisons have been made between the proposed work and other models utilizing the same dataset for FLC, as shown in Table IV.

TABLE IV. COMPARISON BETWEEN THE PROPOSED METHOD AND OTHER MODELS UTILIZING THE SAME DATASET FOR FLC

Model	Methodology	Number of MR images in Dataset	Accuracy Average (%)	Precision Average (%)	Recall Average (%)	F1-Score Average (%)
[46]	Enhanced CNN	(7023) images	97.84	97.85	97.85	97.90
[47]	Enhanced CNN	(3100) images	99.1	98.9	89.6	98.6
[48]	InceptionV3	(7023) images	97.12	97.97	96.59	-
[49]	CNN and GLCM	(3000) , (3073) images	98.22	98.2	98	98
[50]	ResNet50	(3000) , (253) images	99.33	98.93	98.67	99.33
[51]	Enhanced CNN	(3064) images	98.99	98.90	98.91	99.04
Proposed Method	**CNN\YOLO**	(3000) images	**99.35**	**99.56**	**100**	**99.78**

By proceeding to the second level of classification (SLC), the CE-MRI dataset is expanded to include a total of **3064** images, which signifies the increasing intricacy of our classification endeavor. As part of this larger collection, the CE-MRI dataset includes **1426** images of glioma tumors and **708** images of meningioma tumors. Furthermore, **930** images of pituitary tumors enrich this level, encapsulating the multifaceted nature of brain pathologies. However, dataset diversity inherently introduced a spectrum of challenges, encompassing differences in image dimensions, resolutions, and inherent qualities. *Fig. 6* depicts the confusion matrix pertaining to this particular phase, whilst Table V provides a comprehensive list of evaluation metrics employed throughout the testing process for SLC.

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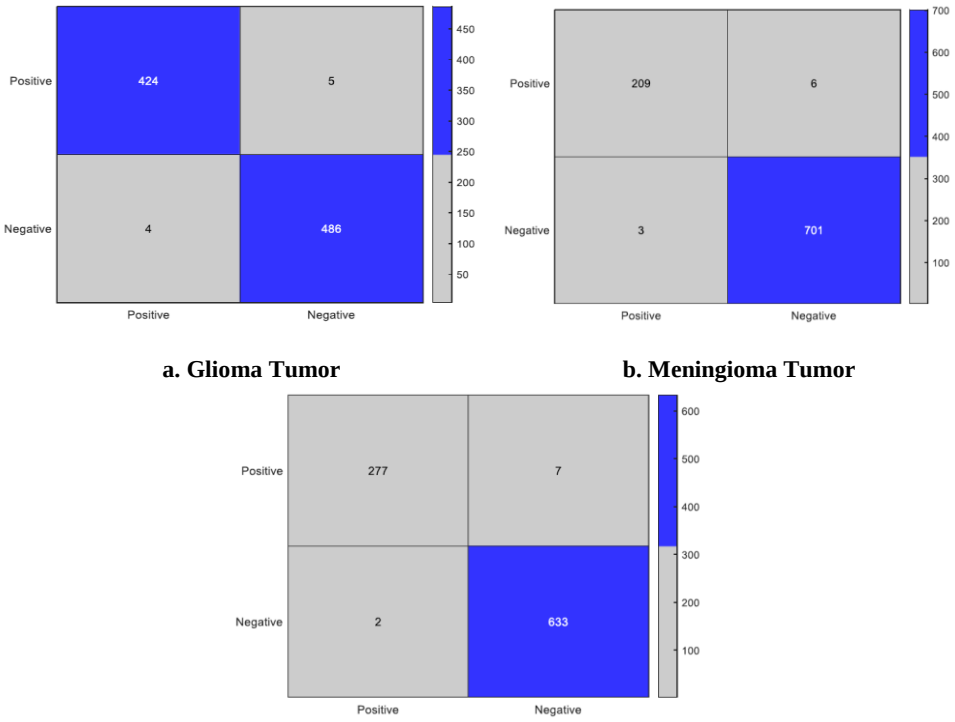

a. Glioma Tumor **b. Meningioma Tumor**

c. Pituitary Tumor

FIG. 6. CONFUSION MATRIX FOR GLIOMA, MENINGIOMA, AND PITUITARY TUMORS FOR SLC.

TABLE V. EVALUATION METRICS FOR SLC

Tumor type	Accuracy	Precision	Recall	F1-Score
Glioma	99.24%	99.30%	99.07%	99.19%
Meningioma	99.02%	97.21%	98.58%	97.89%
Pituitary	99.78%	100%	99.28%	99.64%
Average	99.35%	98.84%	98.98%	98.91%

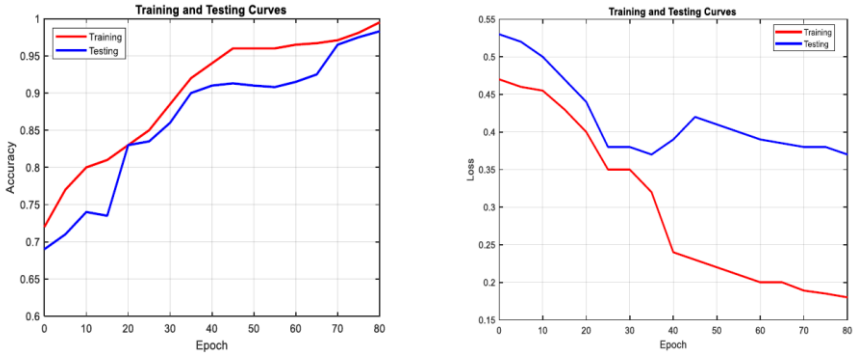

FIG. 7. ACCURACY AND LOSSES FOR THE SYSTEM IN SLC.

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TABLE VI. COMPARISON BETWEEN THE PROPOSED METHOD AND OTHER MODELS UTILIZING THE SAME DATASET FOR SLC.

Model	Methodology	Number of MR images in Dataset	Accuracy Average (%)	Precision Average (%)	Recall Average (%)	F1-Score Average (%)
[52]	ResNet50	(3064) images	99.00	99.00	99.00	99.00
[53]	Inceptionresnetv2	(2475) images	98.91	98.28	99.75	99.00
[54]	Optimized CNN	(2870) images	98.70	98.30	98.60	98.60
[55]	(CNN) VGG19	(3064) (3073)	94.82	89.52	-	91.73
Proposed Method	**CNN\YOLO**	(3064)	**99.35**	**98.84**	**98.98**	**98.91**

Considering the results shown in Table V, *Fig. 7*, and Table VI, it is proposed that the SLC model exhibits a remarkable level of performance across multiple evaluation metrics. The high accuracy score signifies that the model made accurate predictions for almost all cases. The method effectively achieves a low rate of false positives. Furthermore, the precision, recall, and F1-Scores imply that when the model identified a positive instance, it was highly reliable, had a minimal rate of false positives, and reflected the model's ability to provide precise and reliable predictions for capturing all instances of the positive class in the dataset.

Regarding the third level of classification (TLC), which is the highest level in our hierarchical classification system. Our dataset comprises **3395** MR images, including **1250** images representing glioma tumors (875 for training and 375 for testing), **975** images representing meningioma tumors (683 for training and 292 for testing), **770** images representing pituitary tumors (539 for training and 231 for testing), and an additional **400** images representing non-tumor cases (280 for training and 120 for testing). Table VII shows the parameters (Tp, Tn, Fp, and Fn) during the TLC's testing phase.

TABLE VII. ELEMENTS FOR PERFORMANCE METRICS FOR TLC

Tumor Type	Origin Images	TP	FP	TN	FN	Total
Glioma	375	372	3	640	3	1018
Meningioma	292	290	4	722	2	1018
Pituitary	231	230	5	782	1	1018
No_tumor	120	120	6	892	0	1018

TABLE VIII. ELEMENTS FOR PERFORMANCE METRICS FOR LOW-GRADE AND HIGH-GRADE GLIOMA IN TLC

Glioma Tumor Grade	Origin Images	TP	FP	TN	FN
Low Grade	184	173	15	176	11
High Grade	191	176	11	173	15

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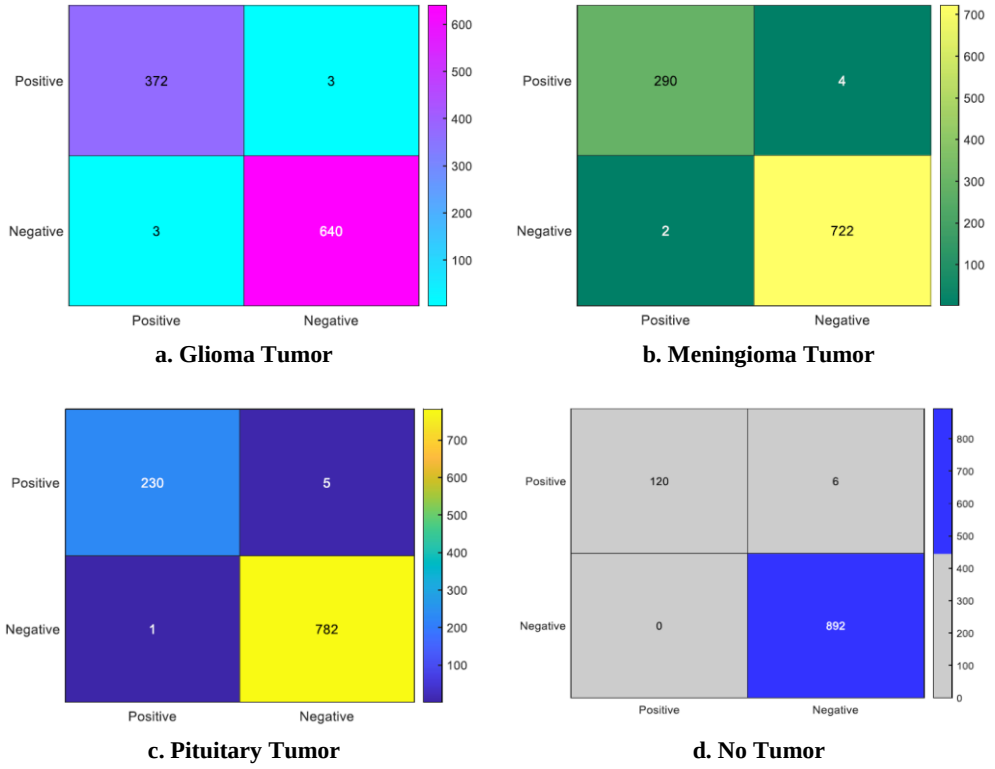

a. Glioma Tumor **b. Meningioma Tumor**

c. Pituitary Tumor **d. No Tumor**

FIG. 8. CONFUSION MATRIX FOR GLIOMA, MENINGIOMA, AND PITUITARY TUMOR AND NONTUMOR FOR TLC.

TABLE IX. EVALUATION METRICS FOR TLC

Tumor type	Accuracy	Precision	Recall	F1-Score
Glioma	99.41%	99.20%	99.20%	89.80%
Meningioma	99.41%	98.64%	99.32%	98.98%
Pituitary	99.41%	97.87%	99.57%	98.71%
No_tumor	99.61%	95.24%	100%	97.56%

TABLE X. EVALUATION METRICS FOR GLIOMA TUMOR GRADING FOR TLC

Glioma Tumor Grade	Accuracy	Precision	Recall	F1-Score
Low Grade	93.07%	92.02%	93.91%	92.98%
High Grade	93.07%	94.12%	92.04%	92.85%

The previously mentioned results in Tables VII, VIII, IX, X and *Fig. 8* showed significant success in classifying and distinguishing various tumor types and glioma tumor grading, each exhibiting distinct characteristics. The results highlight the model's exceptional ability to identify and categorize various medical conditions accurately.

The model exhibits consistent overall accuracy for low-grade and high-grade glioma tumor classifications. The model accurately recognizes both tumor classes, as seen by the excellent accuracy,

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recall, and F1-Score values. These conclusions imply that the model supports differentiate between low-grade glioma and high-grade glioma tumors. Finally, *Fig. 9* illustrates an example of the system's output for TLC for three different tumor cases.

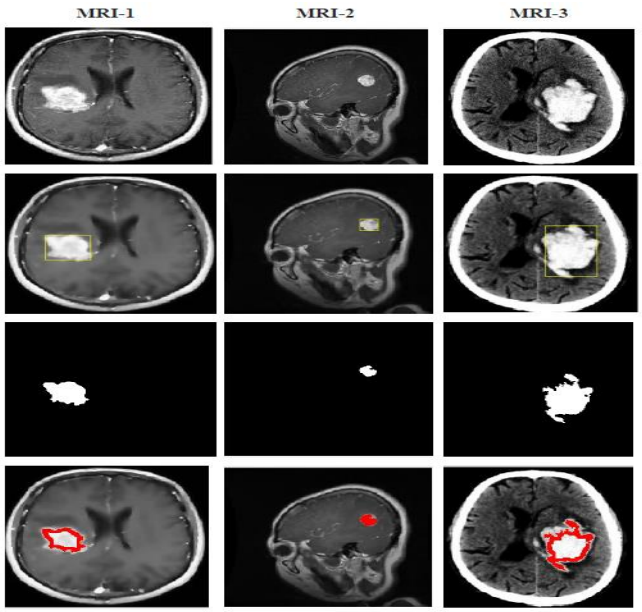

FIG. 9. AN EXAMPLE OF THE SYSTEM'S OUTPUT FOR TLC FOR THREE DIFFERENT TUMOR CASES.

VI. CONCLUSIONS

This study introduced an enhanced brain tumor classification approach, which employed a combination of the Convolutional Neural Network (CNN) for feature extraction and YOLOv7 for tumor classification. The proposed mythology proved to achieve accurate detection of multiclass brain tumors, specifically meningioma, glioma, and pituitary tumors, in addition to classifying low grade and high grade glioma tumor. The proposed model was carefully optimized through fine tuning and parameter adjustment. The model is designed to have three different levels of classification. The first level of classification (FLC) will classify the incoming MR images as clear images or tutorized ones. The second level of classification (SLC) will be responsible for classifying the images into three types of brain tumors (Glioma, Meningioma, and pituitary). The third stage is responsible for classifying the glioma tumor into high-grade glioma (HGG) and low-grade glioma (LGG). Comparative evaluation with existing models, detailed in Tables IV and VI, underscores the superior predictive performance of our proposed architectures. These comparisons were conducted using the same datasets and tumor types and differed primarily in their architectural designs. The achievement of an accurate estimation of glioma tumor grades enhances the understanding of different tumor malignancy levels. This holds significant implications for developing personalized treatment strategies and determining patient prognosis. The results showed high accuracy, providing healthcare professionals with a reliable tool for quickly classifying and characterizing brain tumors. The accumulation of YOLOv7 for object recognition and tumor location has revolutionized brain tumor classification, improving accuracy and precision using MRI. The integration of CNN and YOLOv7 enables a comprehensive view of brain tumors, accurately classifying tumors and identifying tumor borders to help surgeons plan treatments and minimize damage to healthy brain tissue. In future work, we can enhance the system's capability to detect and classify multiple tumor masses; it is crucial to develop advanced techniques tailored specifically for this task. Moreover, the system can perform early detection of tumor recurrence, thereby

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enabling it to recognize indications of recurrence at an earlier stage compared to conventional MRI scans and to identify small changes in MRI scans over time.

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