

Deep Learning Based Method for Brain Tumor Detection

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Abstract: Brain cancer is characterized by the uncontrolled proliferation of distorted brain cells, which replace normal ones and impair cognitive functions, making it a highly dangerous disease for adults. Variations in magnitude, mass, texture, and position add to the complexity of diagnosing and treating these tumors. Physicians can utilize techniques based on computational intelligence to assist in the identification and classification of brain tumors. Numerous methods, including image filtering utilizing the PNLN filtering approach and snake segmentation for tumor identification, are proposed in earlier study. Transfer learning is employed for classification, using a model that combined VGG16 and CNN architectures. Python is used to implement the model, and evaluation indicators are utilized to assess the outcomes. When it comes to brain tumor identification, the suggested model outperforms current machine learning methods in terms of accuracy.

Keywords: Brain Tumor, Snake Segmentation, PNLN Filter, VGG16, CNN

1. Introduction

The brain and spinal cord are crucial for regulating a wide range of biological processes, including information integration, organization, analysis, decision-making, and commanding. The human brain was highly complex due to its intricate physical structure. Disorders affecting the CNS, such as stroke, infections, brain tumors, and migraines, pose significant problems in terms of diagnosis, evaluation and treatment development (Islam et al., 2021). Brain tumors, which result from the abnormal growth of brain cells, present particular challenges for early diagnosis. Magnetic resonance imaging, or MRI, is still a challenging and error-prone manual procedure for detecting brain cancers. To comprehend the impact of benign and malignant tumors on health, it is essential to distinguish between them. Slow, restricted, benign growths are less harmful, but they could still be harmful if they invade important organs or tissues. Aggressive malignant tumors have the ability to invade neighbouring tissues and spread by metastasizing. For prompt intervention and the preservation of the complex functioning of the human brain—a wonder that creates the fabric of human experience—it is essential to comprehend the onset and function of these tumors. An aberrant cell aggregation in the brain is called a brain tumor. These tumors can develop from the brain tissue or move to the brain through metastasis, which is the process by which malignant cells from other regions of the body migrate to the brain. The identification of brain tumors requires a thorough process that frequently includes imaging procedures and a biopsy to determine the nature and stage of the tumor.

Brain tumors must be diagnosed quickly and accurately in order to plan treatments effectively and enhance patient outcomes. (Rammurthy & Mahesh, 2020a). Nonetheless, radiologists sometimes encounter considerable obstacles while analyzing images in such situations. The traditional method of diagnostic assessment is mainly based on their skills and their subjective evaluation of images, performed manually. Discrepancies in the skills of practitioners and the intricacy of brain tumors may give rise to variability in diagnostic accuracy (Kabir, 2020). Diagnosis and treatment planning depend mainly on clinical and radiological data, while MRI is the dominant imaging method for brain malignancies. The multi-sequential, multi-parametric, and multi-planar imaging abilities of MRI make it a must-have instrument that allows thorough examinations of brain lesions. MRI data, thanks to their ability to provide different views of the brain, are now a highlight for computational research (Li et al., 2019). However, conventional imaging methodologies have their drawbacks, such as difficulties with tumor size determination, tumor grading, and evaluation of treatment effects. Innovations in imaging acquisition are being developed to improve lesion definition and facilitate therapy evaluation. In addition, it is noticeable that sophisticated image analysis methods, which are based on substantial data in radiological images, are on the rise (Hossain et al., 2021). Shape-based features can be derived from cortical or hippocampal lobes, but they often fail to take into account the interconnections across the whole brain, and this can possibly be the source of the inaccurate results. Additionally, features that are broken down by area might not be sufficient because pathological developments might differ from the independent, data-driven assumptions that are already in place. Moreover, although voxel-wise features provide thorough information, their enormous size may have a negative impact on the classification process (Rammurthy & Mahesh, 2020b).

AI is a branch of information technology focused on enabling computers to replicate human cognition, enabling them to learn, reason and solve problems based on different information. AI has emerged as a crucial diagnostic and screening technique for brain cancers. Given the complexity and intricacy of brain tumor surgery, it presents a promising area for further integration of AI (Kesav & Jibukumar, 2021). Although many attempts have been made to create precise and trustworthy techniques for classifying brain tumors, a key issue still remains the considerable variation in tumor shape, texture, and contrast among individuals. AI subsets ML and DL are revolutionizing neurosurgical techniques. (Khan et al., 2022). Thanks to AI, neurosurgeons now have more confidence in diagnosing brain tumors, knowing that advanced algorithms assist in their decision-making. Deep learning, especially neural networks play an important role by delivering highly promising results (Han et al., 2019). CNNs (Convolutional neural networks) are particularly effective at learning features offering remarkable precision. There are numerous deep learning applications in use today, including those for pattern recognition, localization of objects, speech identification among others.

The architecture of a basic CNN comprises an input layer, many hidden layers for extricating features and an output layer, culminating in a fully connected layer. (Dandil & Karaca, 2020). Convolution, Convolution, rectified linear unit (ReLU), and pooling layers are examples of hidden layers in neural networks. Convolution layer extract features from incoming data by carrying out fundamental convolution computations. (rectified linear unit), and pooling layers are examples of hidden layers in neural networks. Convolution layer extract features from incoming data by carrying out fundamental convolution computations. As hidden layers deepen, they progressively extract distinct features, transitioning from concrete to abstract representations. ReLU layers employ activation functions for nonlinear computation, facilitating complex mapping relationships (Özyurt et al., 2019). Pooling layers, typically employing average or max pooling, are crucial despite selecting only one outcome from a set, as they maintain invariance, reduce parameters, cut computational costs, and mitigate overfitting in deep learning. sequence performs the same operation based on the previous computation's outcome (Raut et al., 2020). However, due to the reliance on past data, RNNs

struggle with addressing long-term dependencies. To overcome this limitation, some researchers suggest LSTMs as a solution. LSTM is an improved version of RNN capable of handling and predicting substantial events in time series data with long-term dependencies and intervals. Document summarization, picture analysis, speech recognition, handwriting identification, and music synthesis are just a few of the tasks it has been effectively used for. (Patil & Hamde, 2020). Unlike traditional RNNs, LSTM incorporates a “cell” to regulate the relevance of the input data. When data is received, LSTM assesses it according to predetermined standards. Only the data that the algorithm deems useful is retained after the forget gate selectively eliminates unnecessary information. This concept forms the foundation of LSTM's effectiveness in addressing long-term dependency issues and achieving acceptable performance (Turk et al., 2022).

2. Literature Review

(Lamba et al., 2024) introduced a new integrated method using advanced AI techniques. This technology showed remarkable potential for accurately identifying important features in input data, helping medical professionals detect abnormal cell growth in the brain. They create an automated approach for identifying brain cancers using publicly accessible brain MRI datasets [17]. To improve the image quality and maintain consistency, data augmentation was applied. This method employed a 16-layer VGG model through transfer learning reducing the workload for medical experts in making accurate diagnoses. To improve diagnostic speed and accuracy, critical features were identified and supervised learning using linear SVM was applied. The proposed model outperformed the established methods with 99.09% precision, 99.02% specificity, 98.87% accuracy, 98.73% sensitivity, and 98.91% F1-score.

(Naim et al., 2024) sought to create a precise method for identifying and categorizing brain tumors, or BT. applying methods from deep learning and machine learning [18]. By merging three merged datasets, the system was created to classify both brain tumor and healthy data. This work adopted several variants of ConvNets to achieve a satisfactory level of outcomes. As per the findings, the unification of ConvNet and LSTM proved to be the most successful, with an accuracy of 0.984, compared to other variants. A hybrid network was created by combining the models using ensemble learning to further enhance performance, which led to a notable improvement with an accuracy of 0.988.

(Pedada et al., 2023) proposed an improved U-Net architecture leveraging residual networks. For more precise outcomes, this system used sub-pixel convolution in the decoding part and employed intermittent shifting in the encoding part [19]. Convolution of subpixels, compared to conventional convolutional resizing offered improved modeling capability with additional parameters, while maintaining the same computational complexity and avoiding issues with de-convolution overlap. The devised U-Net framework's efficiency level was tested using BraTS 2017 and 2018. The framework, respectively yielded 0.934 and 0.922 accuracies on these datasets. Furthermore, the tumors are separated into three groups: EC (enhancing core), WT (total tumor), and TC (tumor core). The suggested U-Net model performed better than the current techniques, according to the experimental data.

(Dharshini et al., 2023) put forth a hybrid version of a DL oriented framework to localizes tumors in brain area. This framework unified ConvNet and BAT (bat algorithms) to improve the speed and accuracy of brain tumor identification using medical imaging techniques including CT (computed tomography) scans and MRI. [20]. The technique involved identifying tumor features such as size, shape, and functional characteristics by mapping its contours and boundaries. These features helped classify and determine the tumor's significance, which could be visualized through color-coded labels to indicate different levels of tumor severity. While the bat algorithm improves the CNN's parameters for improved performance, the CNN was

trained to recognize patterns and features suggestive of a malignancy. This integrated approach offered a promising way to support clinical teams in diagnosing brain tumors more effectively.

(Chattopadhyay & Maitra, 2022) proposed a system based on CNNs to distinguish brain tumors from 2D MRI data. Deep learning techniques and traditional classifiers come next. [21]. To make the framework's training effective, a diverse set of MRI imagery were used with varying tumor sizes, locations, shapes, and intensity levels. Additionally, they incorporated an SVM classifier and tested many activation functions (such as softmax, RMSProp, sigmoid, etc.) to validate this method. This implementation was carried out using TensorFlow and Keras in Python, which provided an efficient environment for fast development. With 0.997 accuracy, the CNN model outperformed the findings of earlier exploration in this field.

(Koshti et al., 2022) sought to create a web application that could be used in medical facilities to help identify brain cancers using MRI scans [22]. This was accomplished by creating a CNN model that correctly identified whether an uploaded brain MRI scan revealed tumorous activity. The use of transfer learning helped boost the framework's training efficiency. The partitioning of the dataset provided three subsections: training, testing, and validation, using an 80:10:10 proportion. The framework was trained for twelve times, and callbacks were implemented to automate the model saving process. The test accuracy was found to be 0.97. This trained model will be integrated with the web application via an API. The web application provided users with four main routes: a welcome page containing system information, a page with medical information and awareness about brain tumors, and additional functionalities to be detailed in the application.

(Dipu et al., 2021) showed a technique developed using some DL oriented algorithms for localizing objects. This was done to autonomously finding and categorizing brain tumors. [23]. Different versions of Yolo, Faster-RCNN, and Detectron2 were among the seven neural network-based techniques that were used. 641 MRI scan pictures from the BraTs were used to train the system. YOLO V5 outperformed the other models in the evaluation, achieving the highest mAP@0.5 marked as 0.957. YOLO V3 Pytorch, on the other hand, scored 84.30%, the lowest accuracy. Deploying these frameworks in actual world could transform neuroscience by providing medical professionals with an efficient, computerized mechanism for identifying tumors.

(Maharjan et al., 2020) aimed to solve the overfitting issue and facilitate multi-class classification in order to increase classification accuracy [24]. It includes regularization techniques and a CNN with an advanced softmax loss function. By examining the likelihood scores of categorized data and the associated run time, classification accurateness and operation slot were assessed. When tested on many MRI image samples, the system achieved higher accuracy and shorter processing times compared to existing solutions. Specifically, the presented system showed a 2% improvement in accuracy and a reduction in processing time by 40 to 50 milliseconds compared to other current methods.

(Siar & Teshnehlal, 2019) employed CNN to find cancers in MRI pictures of the brain. Initially, CNN was used on the images, and several classification techniques were used to assess its effectiveness [25]. The accuracy of the RBF (Radial Basis Function) classifier was 97.34%, the DT classifier was 94.24%, and the Softmax Fully Connected layer was 98.67%. Apart from precision, the functionality of the network was assessed using universal indicators. Among the classifiers the Softmax function showed the highest accuracy in the CNN based on testing image data. The suggested approach, which integrated CNN with feature extraction techniques, attained a test accuracy of 0.992. Physicians were greatly assisted in identifying and treating brain cancers by this increase in diagnostic precision, which ultimately improved patient care.

3. Research Methodology

The model that has been presented is the transfer learning technique, which combines CNN and VGG16. An explanation of the diverse operations of the devised framework is provided here:

Input MRI image and Pre-process

The input is magnetic resonance imaging, which is first pre-processed with a Gaussian filter. This filter will lessen the image's noise. This filter, also referred to as a smoothing operator, renders photos non-blurry. It eliminates fine visual details that are naturally present. The GF (Gaussian function) that describes the noise's probability distribution is referred to as its impulse response. It eliminates Gaussian noise effectively. This filter has a GF of a specified standard deviation and is linear and lower pass.

Segmentation

The snake segmentation technique will be used to divide the magnetic resonance imaging image into the brain region. Due to its reliance on sequential scanning, this approach aims to capture maximum probable edges of the imagery. An adjustable main contour curve $C(s)$ is constructed in the image space using the SAC approach [6–8], and an energy function (EF) is suggested to characterize the form of the area in accordance with the internal and external power. The features of curve help to determine the first one and the attributes of image assist in describing the external energy including curvature, curve length, etc. EF is diminished to converge the $C(s) = (x(s), y(s), s \in [0, 1])$ toward the border of the target area, while adhering to the constraints imposed by both energy terms.

$$E(C) = \int_0^1 \alpha E_{int}(C(s)) + E_{img}(C(s)) + \gamma E_{con}(C(s)) ds \quad (1)$$

Three components make up EF: E_{con} , which displays the constrained energy; E_{img} , which displays the image energy, which is determined by the required position attributes, like edges; and E_{int} , which displays the internal energy to preserve the curve's continuity and regularity. Given that geometric constraints are taken into consideration. the SAC method is helpful. The main goal is to extract the closed borders without sacrificing image quality. There are still certain restrictions, though. The region is difficult to tackle owing to its reliance on the prime contour. The effectiveness of the control points in view of placement, structure, and quantity depends on the selection of an optimal prime contour.

Filtering

The PNLM (Parallel Non-Local Mean) filter, a more sophisticated form of the conventional non-local mean filter, can be used to successfully remove a particular kind of noise seen in MRI scans. When compared to the conventional NLM approach, the PNLM approach yields a lower MSE (Mean Squared Error) value. It provides greater efficiency than typical methods by effectively computing weighted averages according to proximity by computing pixels in parallel and evaluating patches throughout the whole picture. Given a noisy discrete scan $u = \{u(i) | i \in I\}$, the evaluation of the predictable value $NL[u](i)$ for i is provided as:

$$NL[u](i) = \sum_{j \in I} W(i, j) u(j) \quad (2)$$

The weights $\{W(i, j)\}$ are determined by considering the correlation among pixels (i, j) . ensuring they adhere to the conditions $0 \leq w(i, j) \leq 1, w(i, j)$. The resemblance between two pixels is estimated using the strength profiles of their surrounding zones, denoted as $u(N_i)$ and $u(N_j)$. Here, $u(N_k)$ represents the brightness level vector for a predefined square zone

positioned at k pixel. The following measurement of the diminishing function of Euclidean distance is used to calculate the resemblance:

$$\|u(N_i) - u(N_j)\|_2^2, a \quad (3)$$

where $a > 0$ and denotes the Gaussian kernel's SD. When ED is used in noisy surroundings, the following issues are raised:

$$E\|u(N_i) - u(N_j)\|_2^2, a = \|u(N_i) - u(N_j)\|_2^2, a + 2a^2 \quad (4)$$

ED preserves the degree of correlation between pixels, and this similarity further establishes the method's resilience. A significant amount of weight is placed on the average of the pixels in a neighborhood with a similar gray level. These weights can be expressed as follows:

$$W(i, j) = \frac{1}{z(i)} e^{-\|u(N_i) - u(N_j)\|_2^2, a / h^2} \quad (5)$$

at which $Z(i)$ is standardized value

$$Z(i) = \sum e^{-\|u(N_i) - u(N_j)\|_2^2, a / h^2} \quad (6)$$

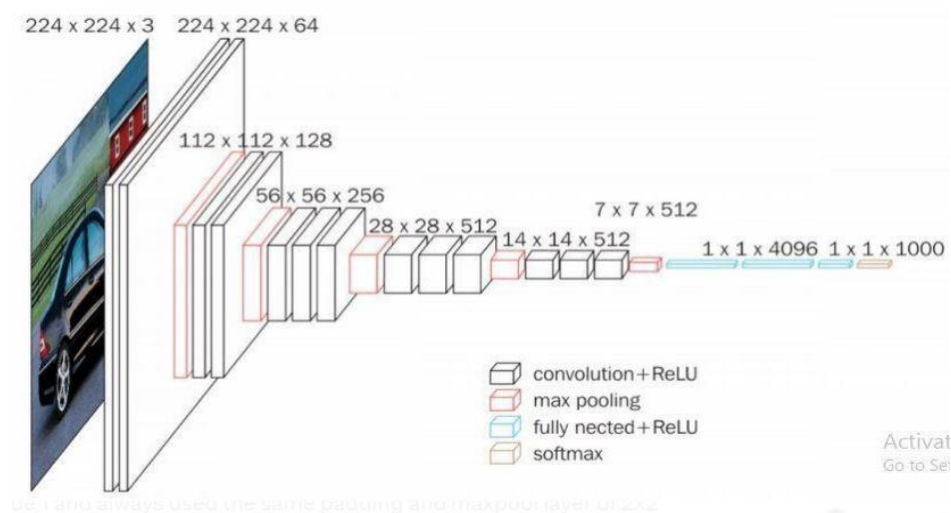
where "h" serves as a mark of filtration. This metric constrains the regression of the exponential function, and h denotes the degree of filtering. It aids in managing EF regression since the weights' regression resembles a function of EDs.

Classification

The VGG16 and CNN models are combined in the transfer learning model to predict the tumor type. The CNN model is utilized for training, with the VGG16 serving as the foundation model.

Figure 1

VGG16 Model Architecture

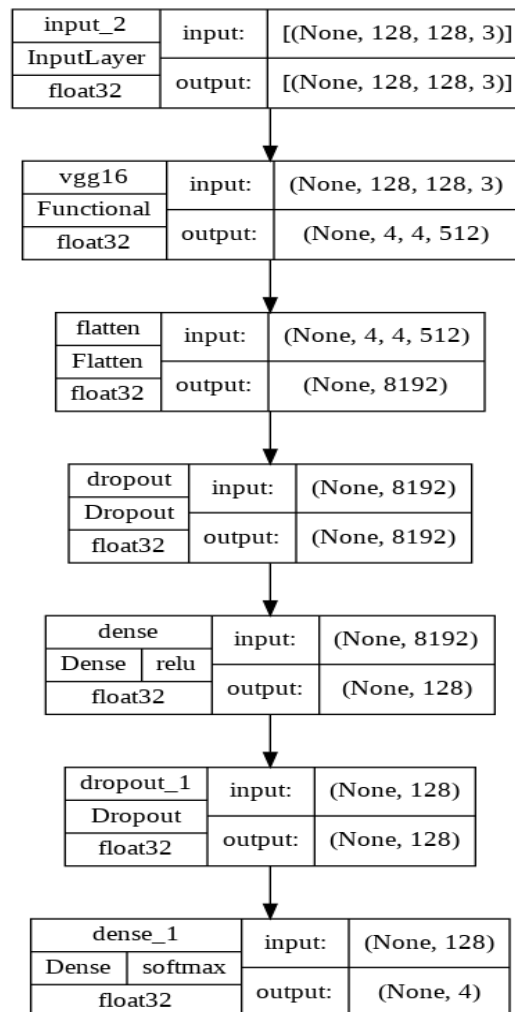


The characteristics of VGG16 Model are:

1. This model consists of sixteen layers, each of which contains weights. Three thick layers, five MP layers, and about thirteen convolutional layers are present. However, there are only sixteen layers of weight.
2. Three RGB channels are used as input in this model, which has a tensor size of 224, 244.
3. This model has few hyper-parameters and employs max-pool layers of 2x2 filters with stride 2.
4. VGG-16 is computationally demanding, needing a large amount of memory and computing power, especially during training, because of its depth and quantity of parameters.
5. In terms of parameter count, VGG-16 is one of the bigger models, with about 138 million parameters.
6. Three FC layers contain three convolutional layers: 4096 channels are available for 1000-way ILSVRC classification in primary two, the last leads. As so, there are a thousand channels. The last one is known as the "soft-max layer."

Figure 2

Design of the Presented Transfer Learning Architecture



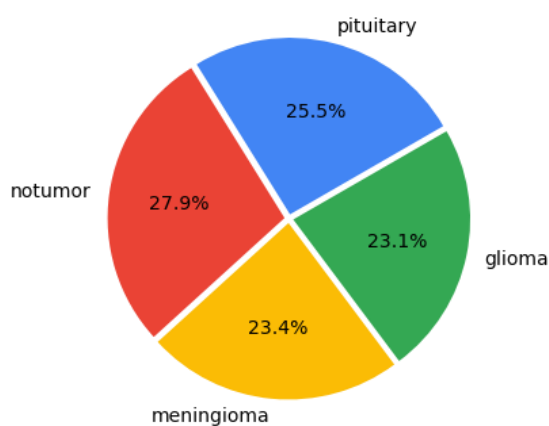
4. Result and Discussion

This work concentrates on identifying tumors in brain using the transfer learning strategy. The dataset for this work is sourced from Kaggle which includes various forms of

brain tumors. The data collection consists of approximately 5700 which are utilized for both training and testing purposes. To test the frameworks, accuracy, precision, and recall are taken into account.

Figure 3

Class Allocation in the Dataset



According to the shown image, there are 4 classes in the dataset with the data found with only small differences among them in terms of class allocation where each class corresponds to around 25 to 30% of the total data.

Figure 4

Representative Imagery

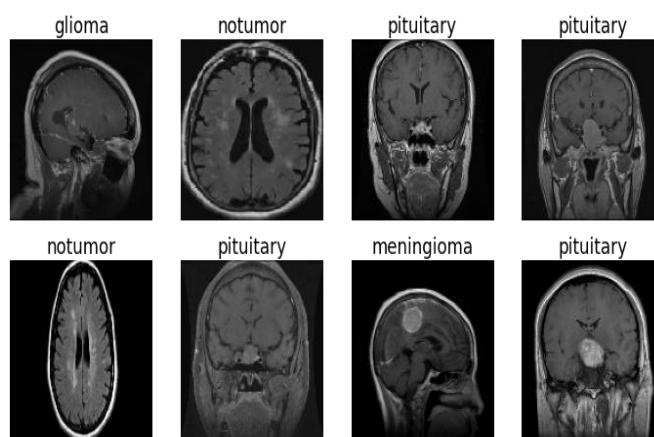


Figure 4 displays the brain tumor dataset's example images. Each class's sample image that is utilized for training is displayed.

Figure 5

Training Accuracy of Proposed Model

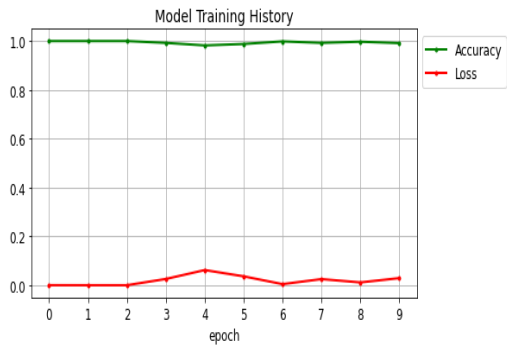
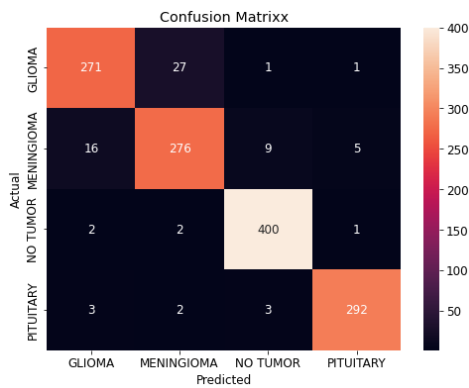


Figure 5 illustrates how the proposed strategy reduces loss to 3 to 4 percent while maintaining training accuracy of approximately 96 percent. The training shows how effective the new strategy is.

Figure 6
Confusion Matrix



The proposed method's confusion matrix, along with the predicted and actual values, is displayed in Figure 6. The classes are reasonably balanced at the time of prediction, and overfitting is not a problem.

Table 1
Outcome Assessment

Model	Accuracy	Precision	Recall
Random Forest	66 Percent	56 Percent	66 Percent
SVM	77.59 Percent	78 Percent	78 Percent
KNN	69.88 Percent	70 Percent	70 Percent
Proposed Model	91 Percent	91.2 Percent	92 Percent

Figure 7
Result Analysis of Proposed Model

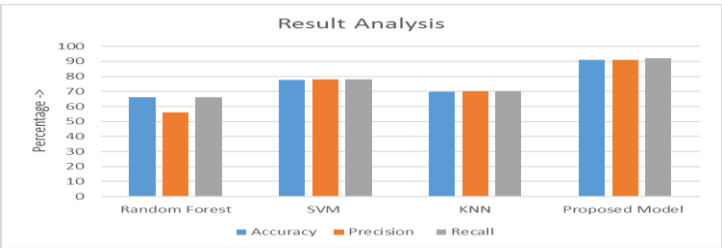


Figure 7 assess the outcomes of the newly devised framework against three standard approaches. The reliability of the proposed model is demonstrated by its up to 95 percent accuracy; the KNN, Random Forest, and SVM models' respective accuracy for brain tumor identification is 69.88, 66 percent, and 77.59 percent.

5. Conclusion

This paper concludes that brain tumor detection is a problem effectively solved using artificial intelligence. The brain tumor detection technique consists of various stages, including data preprocessing, segmentation and classification. The PNLM algorithm is used to preprocess the data by removing Rician noise from the images. Snake-based segmentation helps in selecting the region of interest. For classification, transfer learning is applied by combining the VGG19 model with a CNN model. The accuracy of the suggested transfer learning model is 96%. The model's test results show 95% accuracy, 94% precision, and 95% recall. The study compares RF, SVM, and KNN against the new framework. The accuracy of the suggested model is up to 15% higher than that of these models. For better brain tumor identification in the future, a hybrid transfer learning model may be created.

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