Proceedings of the 2023 International Conference on Machine Learning and Automation
DOI: 10.54254/2755-2721/35/20230397

Brain tumor malignancy classification using improved VGG16 based on MRI images

Jinru Han

School of Electronic Information and Electrical Engineering, Shanghai Jiao Tong University, Shanghai, 200240, China

hjr1219@sjtu.edu.cn

Abstract. This study introduces a method based on Magnetic Resonance Imaging (MRI) images and Convolutional Neural Networks (CNN) to categorize the malignancy of brain tumors. The major goal of this research is to develop an accurate and reliable model that aids in tumor early identification, leading to better patient outcomes. Specifically, first, the MRI images undergo preprocessing, which includes intensity normalization and random brightness and contrast adjustments for data augmentation. Next, the Visual Geometry Group (VGG16) model serves as a baseline, enhanced with flatten, dense, and dropout layers. Transfer learning is applied to leverage pre-trained features from VGG16, improving the generalization capability of model. A sizable collection of brain MRI pictures is used to train the model. The experimental outcomes on the MRI dataset illustrate the efficacy of the suggested model. The CNN-based approach achieves high accuracy in classifying brain tumor malignancy based on MRI images, indicating its potential in medical image analysis and its significance in early tumor detection and diagnosis. The proposed model serves as a valuable tool for healthcare professionals, aiding in well-informed decisions and providing an ideal medical approach for early detection of brain tumors. This research opens avenues for future work in medical imaging and deep learning, paving the way for improved treatment and diagnosis of brain tumors.

Keywords: brain tumor, Convolutional Neural Networks, MRI Images, transfer learning.

1. Introduction

A tumor is characterized by an anomalous accumulation of cells, leading to the formation of a tissue mass. It occurs due to the uncontrolled proliferation of cells within the body [1]. Tumors can be categorized into two main types: malignant and benign tumors. Malignant brain tumors have the propensity to infiltrate neighboring tissues as a result of their aggressive growth, making them distinct from benign brain tumors. Therefore, primary malignant brain tumors have a poor prognosis. It can severely affect cognitive function and reduce overall quality of life [2]. Notably, the field of brain tumor examination has successfully incorporated the fundamentals of medical image analysis. Particular focus has been placed on magnetic resonance images to simplify basic procedures such as extraction, segmentation and classification. These advances have automated key steps. This enables close and efficient detection of tumors [3]. The field of brain tumor analysis encounters significant challenges arising from the unpredictable and irregular characteristics of brain tumors, such as their random sizes, shapes, and locations. Moreover, due to the enormous volume of data that necessitates processing, the

DOI: 10.54254/2755-2721/35/20230397

manual partitioning of tumors becomes a time-consuming, labor-intensive, and subjective task. This combination of factors culminates in a reduction in the accuracy of the analysis process.

There are two main categories of segmentation of brain tumors algorithms: traditional machine learning techniques and deep learning methods. Sharma et al. delved into the examination and evaluation and comparison of the effectiveness of Multi-Layer Perceptron (MLP) and Naive Bayes for pattern classification tasks [4]. They emphasized the efficacy of neural networks in handling complex mappings. In addition, they demonstrated the application of probability-based Naive Bayes classification in the challenging task of exact rule modeling. Abd-Ellah et al. proposed a computer-aided diagnosis system [5]. This system utilizes K-means clustering for Magnetic Resonance Imaging (MRI) image segmentation. Additionally, features are extracted by Discrete Wavelet Transform as well as reduced using Principal Component Analysis. Support Vector Machine two-stage classification method was applied to a non-standard MRI database for tumor detection. Myneni et al. implemented the identification of brain tumor cells using Support vector machine (SVM) classifier [6]. In addition, they used Naive Bayes classifier and Random Forest to compute and compare the results. Siddique implemented the detection task based on Visual Geometry Group (VGG16) classification model which showed excellent performance [7]. Kanade extended the Probabilistic Neural Network (PNN) algorithm [8]. Furthermore, brain tumor segmentation was accomplished using multiple CNNs [9]. Additionally, Ahmmed et al. employed a combination of Artificial Neural Networks and Support Vector Machines for brain tumor classification [10]. The integration of artificial neural networks greatly reduces the error in the learning process. However, since the method uses a relatively limited number of images, questions have arisen about its applicability to datasets with many images.

The main goal of this study is to create a detection model for accurately classifying brain tumor malignancy based on MRI images using convolutional neural networks (CNN). Specifically, first, in the preprocessing stage, images are normalized while random brightness and random contrast are applied. The images are stochastically processed to achieve data augmentation. Second, the VGG16 model is used as a baseline being used to construct the detection model. Flat, dense and culling layers are introduced to construct the improved VGG16. Third, transfer learning is introduced to enhance the generalization performance of the model. The model is then trained on the training set before having its performance evaluated on the test set. Fourth, the role of the culling layer is analyzed by evaluating the accuracy and loss. Finally, the study discusses the limitations encountered during the experiments and provides potential future directions for the improvement and application of the method. The proposed framework can serve as a practical system, offering physicians an optimal medical approach for the early detection of brain tumors.

2. Methodology

2.1. Dataset description and preprocessing

For this study, a composite dataset is used that combines three distinct datasets: figshare, Br35H, and SARTAJ dataset. The primary emphasis is on brain tumor classification employing MRI scans [11]. The dataset is made up of a total of 7023 human brain MRI images, which have been carefully balanced and categorized into four distinct classes: meningioma, glioma, pituitary, and no tumor. The class distribution is visually depicted in Figure 1. The main objective is to classify the MRI images from the dataset into these four specified classes.

Notably, the images in this dataset exhibit variations in size. As a crucial step in data preprocessing, all images are uniformly resized to 128x128 pixels, as illustrated in Figure 2. Following that, data augmentation techniques are employed to enrich the dataset's diversity. Brightness and contrast adjustments are applied by introducing random factors to the pixel intensities, thereby introducing variability in the appearance of the images. After augmentation, pixel value normalization is performed to standardize the dataset, enabling smoother training of the deep learning model.

DOI: 10.54254/2755-2721/35/20230397

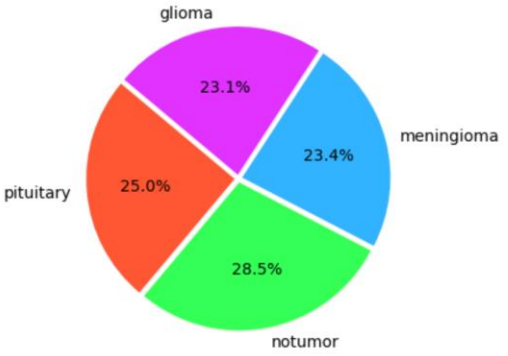

Figure 1. Class distribution of MRI dataset.

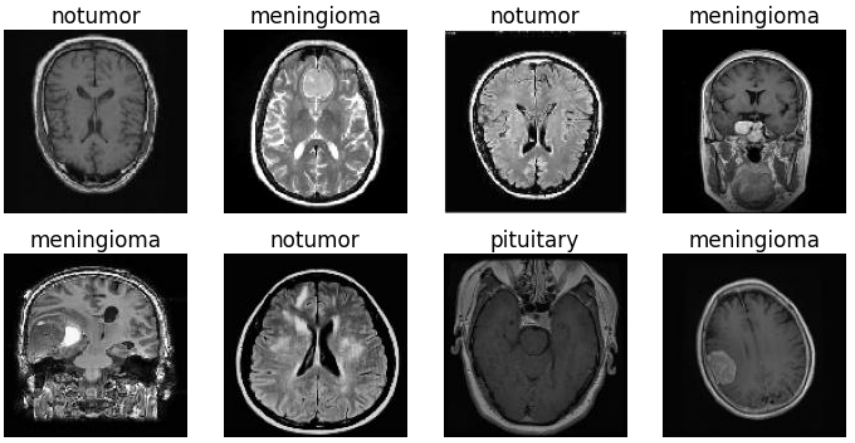

Figure 2. Images from MRI dataset after resizing.

2.2. Proposed approach

This work uses MRI images to build a deep learning model that accurately classifies the aggressiveness of brain tumors. In this study, an improved VGG16 is constructed by combining a custom-designed CNN with a migration-learning VGG16.The proposed method utilizes the pre-trained features of the VGG16 and enhances them with a customized CNN. Thereby the improved VGG16 can effectively extract and utilize spatial features in MRI images. Data preprocessing includes normalization and data enhancement for better generalization. The model architecture includes convolutional and fully connected layers as well as ReLU activation to achieve accurate brain tumor classification by fusing these techniques. Figure 3 below illustrates the architecture of the system.

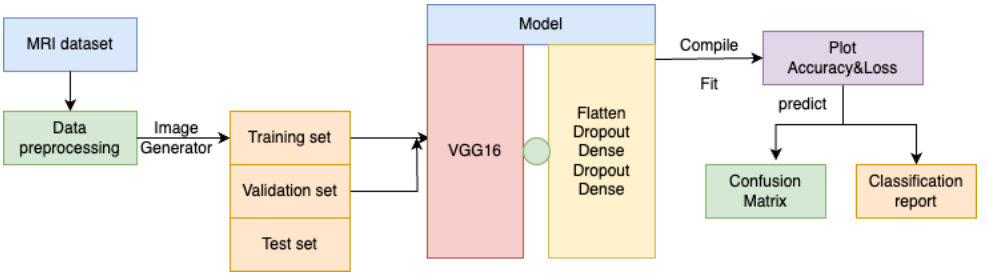

Figure 3. The overall pipeline.

DOI: 10.54254/2755-2721/35/20230397

2.2.1. Improved-VGG16. The original architecture of the VGG16 model comprises 16 layers, 13 of which are convolutional layers and 3 of which are dense layers. For the purpose of brain tumor classification in this study, only the convolutional layers of VGG16 are utilized as a feature extractor, while the 3 dense layers are replaced. This transfer learning approach capitalizes on the pre-trained weights and feature extraction capabilities of the original VGG16 model to enhance brain tumor classification. The replacement of the dense layers involves several steps. Firstly, a flatten layer is introduced to preserve the spatial information extracted by the convolutional layers and so the 3D output can be converted to 1D vector., which is essential for forwarding the features to subsequent fully connected layers. Subsequently, a dropout layer is incorporated to mitigate overfitting issues, and the dropout rate is 0.2. Following that, a fully connected layer consisting 256 units and activation of ReLU is introduced to perform feature transformation and dimensionality reduction. This enables the network to learn higher-level representations and uncover relationships among the extracted features, with the ReLU activation facilitating the model's ability to capture non-linear patterns in the data, enhancing its expressiveness. Furthermore, another dropout layer is added to further address overfitting concerns, and its dropout rate is 0.4. In the end, the model incorporates a dense layer with 4 units, catering to the unique categories within the dataset, and utilizes a softmax activation function. This configuration empowers the model to generate a valid probability distribution across the 4 possible classes. The specific architecture of the model is visually depicted in Figure 4, providing a clear representation of its structure and layers.

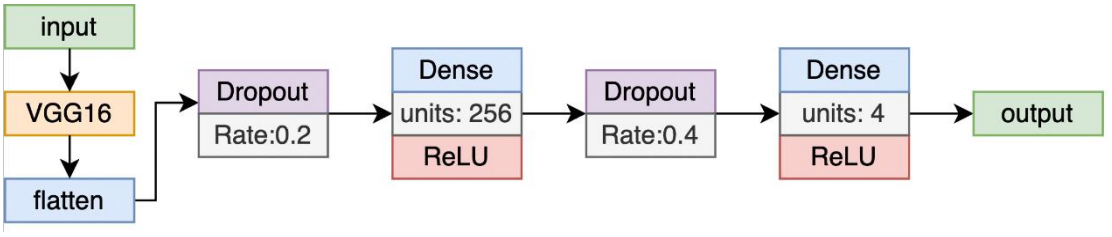

Figure 4. The pipeline of the improved-VGG16.

2.2.2. Loss function. The selection of an appropriate loss function is of paramount importance in the training process of CNN models. For this brain tumor classification task, the sparse cross-entropy loss function for categories is used. The cross-entropy loss' importance comes in its capacity to measure the discrepancy between the model's projected probability distribution and the actual probability distribution (ground truth) of the target labels. It quantifies how well the model's predicted probabilities match the actual class labels, and the sparse categorical cross-entropy function is designed to handle integer target labels efficiently without the need for explicit one-hot encoding. Minimizing the sparse categorical cross-entropy loss encourages the model to produce high probabilities for the correct class and lower probabilities for incorrect classes. The sparse categorical cross-entropy loss is mathematically defined as follows:

$$Loss = -\sum_i y_i \cdot log\, p_i \tag{1}$$

The above formula denotes the Sparse Categorical Crossentropy loss, where y_i signifies the actual label of the *i*-th class and p_i illustrates the predicted label of the *i*-th class.

2.3. Visualization

In this paper, two composite plots are constructed to show the model fitting results. The initial graph displays the accuracy and loss of the model at various time points on both the validation and training datasets. This analysis allows comparison of models with different architectures on the categorization of brain tumors dataset. In addition, the study examines the improved VGG16 model in detail. It used the trained VGG16 model to predict the test set data and computed classification reports based on the predictions. In addition, a confusion matrix was constructed to compare the results with the true labels.

DOI: 10.54254/2755-2721/35/20230397

The confusion matrix is visualized as a heat map. Finally, an image is randomly selected from the class and a saliency map is used to highlight the key points that affect the model output.

2.4. Implemented details

During the implementation of the proposed model, several crucial aspects are emphasized. Initially, for hyperparameters, a learning rate of 0.0001 is established, and it is reduced by a factor of ten when observing a plateau in the validation loss. The batch size of the model if 20, and the model undergoes 10 epochs of training using an RTX3090 GPU Compute Engine. The Adam optimizer is selected due to its effectiveness in managing gradient descent in high-dimensional spaces. To enhance the dataset's diversity and mitigate overfitting, techniques to augment data are employed which involve random adjustments in contrast, brightness, and normalization of the input images. By exposing the model to various perspectives and scales of facial images during training, its robustness and generalization capabilities are improved. Furthermore, Tensorboard callbacks are integrated to monitor the validation loss and log records for visualization. These careful considerations ensure the model's optimal performance and efficiency during training and evaluation.

3. Result and discussion

In the subsequent steps, the improved-VGG16 model is analyzed on the test dataset, and a comprehensive evaluation of the results was conducted. The test dataset comprised 562 images evenly distributed across the four classes. Predictions were made on this dataset, and a detailed examination was performed using a confusion matrix and a classification report. The analysis encompassed studying the variations in accuracy and loss during the model's training on both the training and validation datasets. Furthermore, a thorough investigation was carried out on the prediction accuracy, shedding light on its performance. Additionally, a comparative study was conducted between the model with and without a dropout layer after the flatten layer. This comparison aimed to explore the discrepancies in accuracy and loss between the two models and provide insights into the possible contributing factors.

Figure 5 and Figure 6 present the accuracy and loss curves of the model lacking a dropout layer after the flatten layer on both the training and validation datasets, while Figure 6 displays the same curves for the previously created model. The training of model-1 initiates with an accuracy of 0.82 on the training set and demonstrates rapid improvement, eventually converging to approximately 0.99. In contrast, model-2 begins with an accuracy of 0.79 and steadily increases, with both models achieving similar final accuracies on the training set. However, model-1 slightly improves from 0.91 and fluctuates around 0.95, while model2 exhibits continuous improvement from 0.79, ultimately reaching around 0.97 on the validation set. Likewise, both model-1 and model-2 demonstrate a reduction in loss on the training set, starting from higher values and converging to approximately 0.03, indicating a progressive fit to the training data and a decrease in the gap between predicted values and ground truth labels. However, the validation loss of model1 starts higher and fluctuates, stabilizing around 0.19, whereas model-2's validation loss decreases from its initial higher value to around 0.21.

Based on the comparison of accuracy and loss, it can be inferred that model1 exhibits signs of overfitting, while model-2 effectively mitigates this issue by incorporating a Dropout layer. In conclusion, the first model performs well on the training set but shows indications of overfitting on the validation set. Conversely, the second model effectively addresses overfitting through the addition of a Dropout layer, leading to enhanced overall performance on the validation set. Monitoring accuracy and loss on both training and validation sets during model training aids in optimizing the model and fine-tuning hyperparameters for improved performance.

DOI: 10.54254/2755-2721/35/20230397

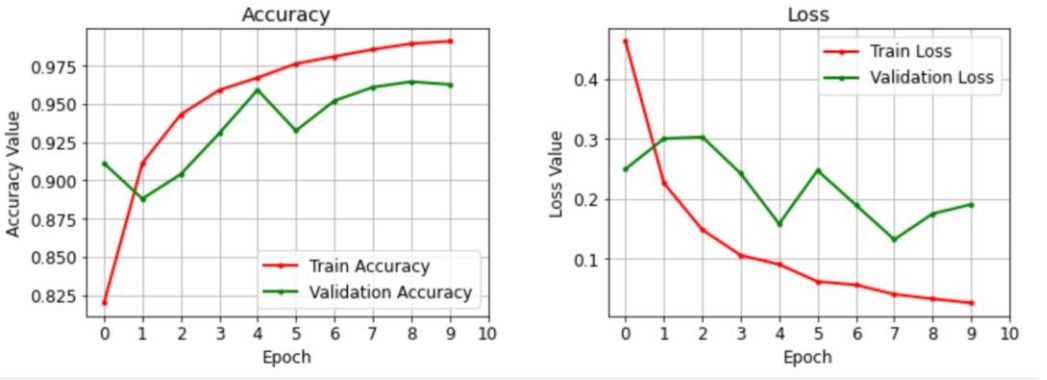

Figure 5. The results of model without dropout layer (model-1). The left is Accuracy curve while the right is Loss.

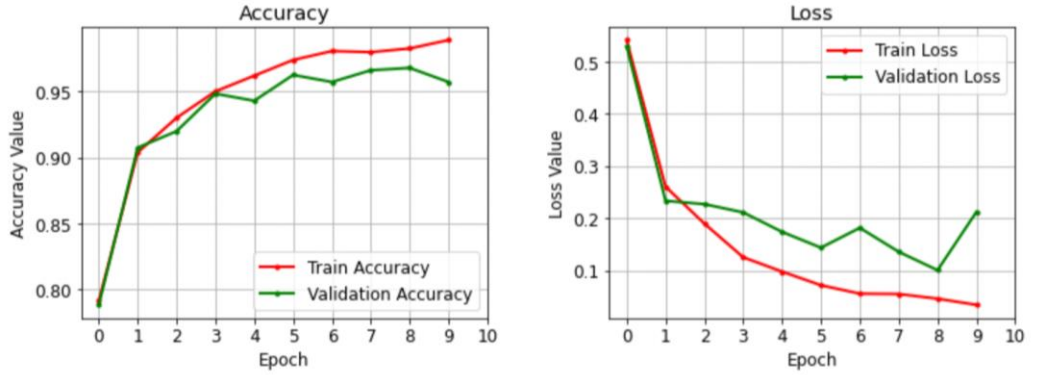

Figure 6. The results of model with dropout layer (model-2). The left is Accuracy curve while the right is Loss.

The confusion matrices of the two models are illustrated in Figure 7 and Figure 8. The observation is that the first model exhibits high precision (close to 1) for the classes "glioma," "pituitary," and "notumor," but relatively lower precision of approximately 0.83 for the "meningioma" class. Additionally, the recall for the "glioma" class is relatively lower, at around 0.81. After calculating, model1's overall accuracy is approximately 0.95. Comparatively, model-2 outperforms model-1 in terms of recall , precision, as well as f1-score for all classes, and overall accuracy of approximately 0.96. Surprisingly, despite the higher accuracy on the training set, model-1 shows a lower overall accuracy on the test set, which further supports the suspicion of overfitting in model-1. Furthermore, it is noteworthy that both models perform exceptionally well on the "notumor" class concerning recall, precision, and f1-score. This may be attributed to slight class imbalance in the dataset, with "notumor" having more samples compared to "glioma," potentially influencing the model's performance and leading to lower precision and recall for the "glioma" class.

DOI: 10.54254/2755-2721/35/20230397

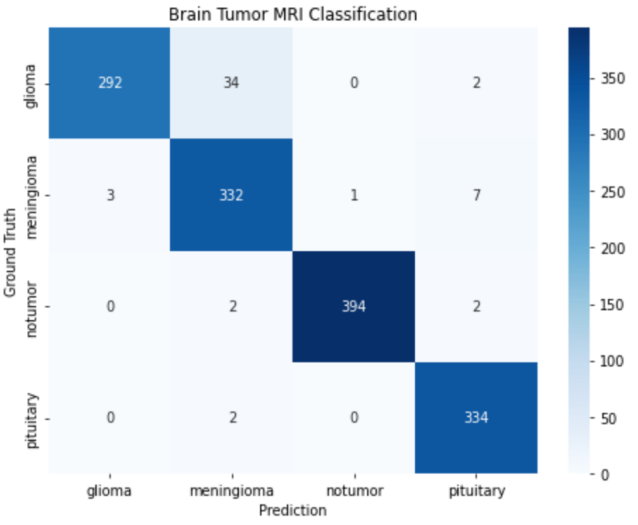

Figure 7. The model's confusion matrix without a dropout layer (model-1).

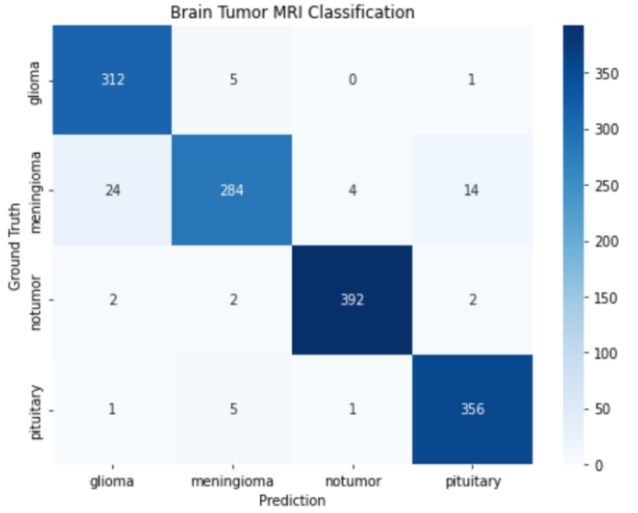

Figure 8. The model's confusion matrix with a dropout layer (model-2).

4. Conclusion

Automated brain tumor classification methods provide intuitive diagnosis. This research introduces an enhanced VGG16 model for automated categorization of brain tumors in MRI images. There are several critical steps in the suggested technique. First, the MRI images undergo a preprocessing step that includes intensity normalization, random brightness and contrast adjustments to enhance the data. Second, the VGG16 model is used as a basis. And the flat, dense and culling layers are integrated to further enrich the architecture. Transfer learning is used to leverage the existing feature extraction capabilities of the VGG16 model to enhance the overall generalization of the model. Subsequently, training is performed on an extensive dataset of brain MRI images to achieve accurate classification of tumor malignancy. The experimental outcomes shows that the enhanced VGG16 model achieves a general categorization accuracy of 96%, an F1 score of 0.96, and precision of 0.96. The outcomes show how highly reliable and durable the suggested brain tumor detection system is. The created method is anticipated to play a significant role in helping doctors diagnose brain tumors early on and treat them quickly and effectively. In the future, it is planned to extend the method proposed in this study to 3D brain scanning. Accurate tumor localization is achieved using the improved VGG16 model. This

DOI: 10.54254/2755-2721/35/20230397

progress is anticipated to significantly enhance both the accuracy and applicability of the proposed framework. Ultimately, it will benefit patients by facilitating early detection and improving treatment strategies.

References

[1] Ratan R Sharma S Sharma S K 2009 Brain tumor detection based on multi-parameter MRI image analysis ICGST-GVIP J 9(3): pp 9-17

[2] Schwartzbaum J A Fisher J L Aldape K D Wrensch M 2006 Epidemiology and molecular pathology of glioma Nature Clinical Practice Neurology 2(9): pp 494-503.

[3] Chahal P K Pandey S Goel S 2020 A survey on brain tumor detection techniques for MR images Multimedia Tools and Applications 79: pp 21771-21814.

[4] Sharma K Kaur A Gujral S 2014 Brain tumor detection based on machine learning algorithms International Journal of Computer Applications 103(1).

[5] Abd-Ellah M K Awad A I Khalaf A A Hamed H F 2016 Design and implementation of a computer-aided diagnosis system for brain tumor classification in 2016 28th International Conference on Microelectronics (ICM) IEEE pp. 73-76.

[6] Myneni S Y Rajagopal S K Maddipatla S C Priya S S 2021 Machine Learning based Brain Tumor Diagnosis and Stage Detection in 2021 5th International Conference on Information Systems and Computer Networks (ISCON) IEEE pp. 1-5.

[7] Siddique M A B Sakib S Khan M M R Tanzeem A K Chowdhury M Yasmin N 2020 Deep convolutional neural networks model-based brain tumor detection in brain MRI images in 2020 Fourth International Conference on I-SMAC (IoT in Social, Mobile, Analytics and Cloud) (I-SMAC) IEEE pp. 909-914.

[8] Kanade P B Gumaste P P 2015 Brain tumor detection using MRI images Brain 3(2): pp 146-150.

[9] Lang R Zhao L Jia K 2016 Brain tumor image segmentation based on convolutional neural network in 2016 9th International Congress on Image and Signal Processing, BioMedical Engineering and Informatics (CISP-BMEI) IEEE pp. 1402-1406.

[10] Ahmmed R Swakshar A S Hossain M F Rafiq M A 2017 Classification of tumors and its stages in brain MRI using support vector machine and artificial neural network in 2017 International Conference on Electrical, Computer and Communication Engineering (ECCE) IEEE pp. 229-234.

[11] 2023 Brain Tumor MRI Dataset https://www.kaggle.com/datasets/masoudnickparvar/brain-tumor-mri-dataset.