International Journal on Recent and Innovation Trends in Computing and Communication
ISSN: 2321-8169 Volume: 11 Issue: 9
Article Received: *25 July 2023* ***Revised:*** *12 September 2023* ***Accepted:*** *30 September 2023*

Brain Tumor Detection and Classification Using Hybrid VGG-XGB model

Dr.B.Kalaavathi[1*]
Professor, School of Computer Science and Engineering
Vellore Institute of Technology,
Vellore, India
kalaavathi.b@vit.ac.in

B.Sridhevasenaathypathy[2]
Student B.Tech CSE-AI&ML , School of Computer Science and Engineering
Vellore Institute of Technology,
Chennai
sridhevasenaathypathy.b2021@vitstudent.ac.in

Serena Janny[3]
The Harker School
San Jose, CA, USA
serenajanny06@gmail.com

Abstract—To avoid potential fatalities, it is vital to diagnose brain tumors at its earlier stage itself. Tumors vary widely in shape, size, and location and this makes accurate segmentation and classification difficult even with significant efforts in this field. Therefore, a hybrid method for classifying brain tumors called the hybrid VGG-XGBoost (hybrid VGG-XGB) model is proposed in this work. The K-means technique is used to extract significant characteristics from brain tumor images after they have first been improved using contrast-limited adaptive histogram equalization (CLAHE). Then, for extracting the high-level features segmented regions, VGG-19 model has been used and for classification process, XGBoost supervised learning technique has been utilized. As evidenced by criteria like precision, recall, F1-score, kappa score, and the confusion matrix, our novel approach outperformed baseline models and produced excellent results with a 98% accuracy rate. The suggested methodology for brain cancer diagnosis in healthcare systems is recommended by us, based on highly predictive outcomes

Keywords-brain tumor; segmentation and classification; xgboost; MRI; machine learning.

I. INTRODUCTION

More than 200 different types of tumors can afflict humans; they are referred to as benign or malignant neoplasms in medical terminology. Brain tumors are considered severe diseases where abnormal growth of brain tissue causes abnormalities in brain function (American Cancer Society). The number of persons who have died from brain tumors has increased by 300% in the last three decades, according to the National Brain Tumor Foundation (NBTF). According [20], untreated brain tumors can result in death. Due to their intricacy, brain tumors can be difficult for medical professionals to diagnose and treat.

The prognosis of patients with brain tumors is greatly influenced by early diagnosis and therapy commencement due to the reason that it requires surgery, brain tumor biopsies are more difficult than biopsies of other body areas. Thus, it is imperative to develop an alternative technique for precise diagnosis that does not require surgery. The most effective and widely used method for identifying brain cancers is magnetic resonance imaging (MRI) [19].

Furthermore, as it has less dimensional inaccuracy, radiation exposure to patients is reduced, and there are no adverse effects, it is thought to be superior to computed tomography (CT). The field of neuroscience places great importance on brain tumors since timely detection can save lives (Islam et al., 2021). There is still need for progress in terms of classification speed and accuracy, despite the wide range of techniques available for detecting abnormalities in brain magnetic resonance imaging.

It is getting harder and harder to analyze and extrapolate medical data using traditional methods as a result of its increasing bulk. There's a fresh motivation for scientists to improve current approaches for more comprehensive clinical research [8]. Early cancer detection and localization are critical for the success of cancer therapy. In medical imaging, better clinical identification done by segmentation along with the structures that are complex are reported.

When the quantity of images increases, the radiologist manually evaluates each image to determine the tumor's size. This could lead to an inaccurate assessment. An automated approach is required because medical picture evaluation and classification are subject to human mistake [17]. In order to provide patients with the best chance of recovery, prompt and accurate detection of brain tumors is crucial for directing effective treatment plans.

Machine learning approaches, particularly supervised learning, have shown promise for significant increases in speed and accuracy in the classification of brain tumors. Supervised learning algorithms may be trained to recognize intricate patterns and traits that are suggestive of brain tumors as precisely as possible by using labeled data that contains both tumor and non-tumor occurrences.

With this method, precise diagnosis is not only made easier, but the model's comprehension is also expanded to include previously unstudied cases. For the process of brain tumor classification, a supervised learning method namely, XGBoost has been implemented.

The following are the contributions made by this work:

- To suggest the Hybrid VGG-XGBoost (hybrid VGG-XGB) model as a hybrid model for categorizing the brain tumors.
- The VGG-19 model is utilized to extract high-level features from the segmented regions and apply the K-means technique for feature extraction. XGBoost classifier is then used to carry out the classification process.
- To assess the performance of the proposed model by utilizing various parameters like Precision, Accuracy, Recall, F1-Score, Confusion matrix, and Kappa Score.

The organization of this paper is organized as follows: A recent study has been discussed in Section 2 that has utilized a variety of models for identifying brain tumors in magnetic resonance imaging (MRI). A detailed explanation of the suggested work has been provided in Section 3. In Section 4, the evaluation matrices and the outcomes of the selected dataset were discussed. This paper is concluded in the Section 5.

II. LITERATURE SURVEY

Deep transfer learning architectures' efficacy in brain tumor diagnosis was the focus of a study conducted [7]. This study used the InceptionV3, VGG19, DenseNet121, and MobileNet transfer learning architectures. [6] The Transformer module (TM) and the self-attention unit (SAU) in a hybrid deep learning strategy to classify various cancers in MR images. This innovative approach combines local and global information to produce fine-grained characteristics through the use of a cross-fusion process.

The lightweight and optimized version of deep transfer learning (iResNet) helps to overcome the problem of overfitting. A brain tumor detection method was proposed that demonstrated high sensitivity and specificity [4]. However, the limitation of this study was set to use only a small dataset which may not represent the entire population. In [5] proposed two deep learning models were proposed for identifying binary and multiclass brain tumors, but the limited amount of accurately annotated data was still a challenge.

A brain tumor segmentation technique called attenuation residual U-Net was presented [3]. The learning and retrieval module's adaptive feature processing leads to better segmentation outputs, which in turn provide better tumor lesions. However, computational source constraints lead to the loss of context-related information about the tumor lesion sections.

A system for automatically classifying brain tumors using machine learning networks was created [1] to distinguish between images of high- and low-grade glioma cancer. The brain and other central nervous system malignancies were classified by the scientists using an extreme gradient boosting model, which had 90% and 95% accuracy rates, respectively.

As a part of his Deep Learning approach, [2] a multi-path-way Convolution Neural Network design for segmenting and classifying the brain tumors. Three different types of model branches are combined by utilizing the max-pooling and a single convolution layer in which every model branch will have two max-pooling convolution layers that are in different sizes.

By using the substantial collection of brain tumor pictures, [9] addressed the challenging issue of identifying brain tumors in MRI scans. Also, the author demonstrated the procedure of applying transfer learning technique for optimizing the cutting-edge YOLOv7 model thereby improving its capacity to identify gliomas, meningiomas, and pituitary brain tumors.

Brain cancers can now be accurately classified using a unique deep learning method based on transfer learning, according to [8].Rebuilding the transfer learning architecture, fine-tuning, and substantial pre-processing are all part of their new approach. Additionally, Xception, ResNet50V2, InceptionResNetV2, and DenseNet201 were among the transfer learning techniques they used.

III. MATERIALS AND METHODS

The suggested Hybrid VGG-XGB model for classifying brain tumors is covered in detail in this section.

3.1. Dataset

The Magnetic Resonance Imaging (MRI) dataset, which contains images from brain MRI scans, was used in this work [18]. This database contains 3264 MRI images that have been classified as tumors or non-tumors. The testing results included images of 74 pituitary tumors, 105 no tumors, 115 meningiomas, and 100 gliomas. Images of 822 meningiomas, 826 pituitary tumors, 827 gliomas, and 395 no tumor were taken into consideration for evaluating the model.

3.2. Overview of the work

First, input MRI pictures are processed using the CLAHE approach to improve the images. K-means is then used to carry out the segmentation process. Subsequently, VGG-19 is used for feature extraction, and the XGBoost classifier is used for final classification. This results to the categorization of meningioma, pituitary tumor, glioma, and no tumor. After classification, the process's overall effectiveness can be determined through performance evaluation. Figure 1 demonstrates this technique.

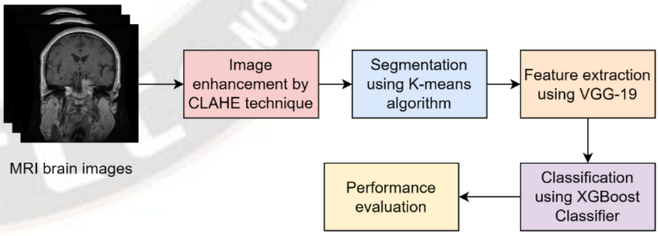


Figure 1. Flow of proposed Hybrid VGG-XGB model

3.3. Image Enhancement using CLAHE

Convolutional linear adaptive histogram equalization, or CLAHE, was applied to enhance the visual appeal of the images [17]. Pre-processing techniques such as CLAHE may conceivably improve the visibility and clarity of skin lesions. A narrow, reliable, and contrast range can be produced by CLAHE when the bilinear thresholding, and bilinear interpolation are used. Different sized pictures are collectively used and the feature values will be varied when they bilinear are extracted from different sized photographs. The pixel size of the image was decreased to 768 by 576 using this procedure. A resolution of 768 by 576 pixels was ideal for preserving every bit of information from the original shot. The photos can now go to the segmentation process.

3.4. Segmentation using K-means algorithm

The K-means technique is utilized to achieve image segmentation subsequent to image enhancement. To separate or categorize data into k different categories, a method called K-means can be used. Since k is not a negative number, it must be positive. When comparable data are clustered together to create a cluster, the sum of squares of the distances between the data points and the centroids of each cluster decreases. In short, the k-means clustering algorithm is the method of choice for data classification.

K-means clustering approach is simple to comprehend. We will consider that there are k clusters, and that the centroid of each cluster is represented by the integer k. The initial centroids can come from the first k items or they can be chosen at random. In any case, they have to originate from the same set. Following that, the K-means algorithm will proceed through the three stages listed below until it finds convergence:

Continue until the object move group is stable.

1. Find the coordinate of the centroid.
2. Calculate the separation between each object and the centroids.
3. Sort the items according to the shortest distance (find the nearest centroid).

3.5. Feature extraction using VGG-19

In several tasks related to disease diagnosis and prediction, deep learning has been widely used recently [12][13][14]. The issue of disappearing gradients in deep convolutional neural networks was suggested to be resolved by the VGG-19 model. Deep neural networks are well recognized for having a huge number of parameters, which enables them to extract complicated patterns and pictures from the input data.

Since the vanishing gradient problem occurs, deep network training is extremely difficult. The gradients that backpropagate across the layers experience a considerable decrease, which causes this issue. The network's capacity to learn with maximum effectiveness is put to the test by this problem. Feature engineering in our suggested approach makes use of VGG19.

3 fully connected (FC) layers and 16 convolutional layers make up a 19-layer deep neural network known as VGG-19 [16]. The ImageNet dataset, which has over a million photos divided into a thousand classifications, was used in its creation to classify images.

Uing this network's architecture and design, greater complexity in picture data categorization is feasible which places max pooling layers with a 2 × 2 window size and a 2-pixel stride after the convolutional layers of VGG19, which use 3 × 3 filters with a 1-pixel stride. This VGG19 model uses the rectified linear unit (ReLU) activation function in its fully connected and convolutional layers. The definition of the convolution operation for an input feature space I of dimensions $W \times H$, utilizing a filter L of size $M \times M$ over a location (m, n), is:

$$O(m,n) = \sum_{a=1}^{M} \sum_{b=1}^{M} I(m+a-1, n+b-1) \times L(a,b) \quad (1)$$

Where the output at position (m, n) is denoted by O(m, n). L denotes the filter used in the convolution procedure. The ReLU function is widely employed in deep learning models because to its computational efficiency and real-world efficacy[15]. VGG19 uses max pooling layers and convolutional layers with ReLU activation functions to extract features and lower spatial dimensionality. Finally, the fully linked network layers also make use of ReLU activation mechanisms. The activation function of ReLU applied to FC layers for feature extraction over an input m is as follows:

$$ReLU(x) = \max(0, x) \quad (2)$$

Figure 2. Illustrates VGG19 architecture for extracting feature from FC-7 and FC-8 layers.

The total number of 4096 x 25 learnable weights and 4096 x 1 bias is computed to make a initial fully connected layer and to mitigate the dropout rate of 50% observation of implementing dropout layer has been observed between the fully connected layers. Figure 2 illustrates the VGG19 architecture for feature engineering. There are a total of 1000 by 4096 learnable weights in the final layer. At the FC7 layer, the activation-resulting feature map measures 1 × 1 × 1000, while at the FC8 layer, it measures 1 × 1 × 4096.

Feature Concatenation

By emphasizing the highest value in a new equation, feature concatenation is a method that combines two feature spaces into a single vector. It increases prediction and training times while also increasing accuracy. Z_3 or the composite vector, is defined as the maximum value obtained from $Z_1 \in FV1$ and $Z_2 \in FV2$, provided that Z_3 is unique and does not include any duplicate components. The dimensions of the feature vector Z_3 are $FV1 \times 4096$ and $FV2 \times 1000$, making it a composite object. Presented below is the concatenated feature map:

$$\widetilde{Z_3} = Z_3 \leftarrow \max(Z_1, Z_2)\ \&\ Z_3 \in not\ repeated \quad (3)$$

3.6. Classification using XGBoost

XGBoost classifier is used for MRI image classification when the feature map from the previous phase is obtained. XgBoost is a reliable method for classification and [11]. The framework fits residual values with iterative decision trees, improving efficiency and performance. It is based on gradient boosting.

Since XgBoost estimates the loss function using a Taylor expansion rather than Friedman's gradient boosting, it produces a better trade-off between bias and variance. This frequently results in fewer decision trees needed for more accuracy. The representation of XgBoost is seen in the graphic below.

Assuming that a sample set has m features and n samples, it may be expressed as

$$G = f(x_s, y_s) \times g(G_t) \quad (4)$$

In this case, t denotes the true value and s the eigenvalue. After adding together, the outcomes of K trees, the final projected value is calculated and expressed as follows.

$$y_g = \sum_{k=1}^{n} f(x_s), f_k \in F \quad (5)$$

In which F denotes a set of decision trees, each of which is specified as follows:

$$F = \{f(x) = w_q(x)\}\{q: R^m \to T, W \in R^T\} \quad (6)$$

In XgBoost, one tree's weight is represented by the value of (x), whereas the weight of the leaf nodes is represented by $wq(x)$. Consider a tree with T leaf nodes overall, with q the arrangement connecting a sample to its corresponding leaf node. Based on this, the total of all the leaf node values in each tree represents the expected value of XgBoost. Through learning, these k trees are guided toward this model in order to minimize the target function below.

$$L^g = \sum_{g=1}^{n} I(y_g, y_g^*) + \sum_{k=1}^{n} \partial(f_k) \quad (7)$$

When it comes to statistical analysis, loss is the discrepancy between the real and estimated values. Logarithmic loss, square loss, and exponential loss are among the several types of loss functions that are commonly used. To prevent overfitting, regularization W is used to calculate the decision tree penalty. Here is the formula for W:

$$\partial(f_k) = ɯT + \frac{1}{2}\alpha\|ɯ\|^2 \quad (8)$$

The number of leaf nodes, or T, that are present in the regular term is one hyper-parameter that controls the complexity of the model. The penalty coefficient, denoted by the letter, is usually a constant value for a given leaf weight w. A new tree is created to accommodate the residuals from the previous round, and the model's complexity is frequently determined empirically during the training phase. As a result, the equation for the model with t trees added is as follows:

$$y_s^g = y_s^{g-1} + f_k(x_s) \quad (9)$$

The final objective function is obtained:

$$obj - function = -\frac{1}{2}\sum_{t=1}^{T}\frac{G_t}{H_t+\mu} + \rho T \quad (10)$$

To minimize model complexity, regularization to the standard function using XgBoost is typically employed, and first and second derivatives are utilized to fit the residual error. To reduce computing and overfitting, this method additionally allows for column sampling and comparatively, this produces a greater number of hyper-parameters than gradient-boosting decision trees (GBDT), but fine-tuning them works differently.

IV. RESULT AND DISCUSSION

The effectiveness of the suggested hybrid VGG-XGB model is assessed quantitatively using a range of measures, including sensitivity, F1-score, accuracy, recall, and precision. In order to calculate four metrics, four primary indicators must be considered: the percentage of healthy cases correctly classified (false positives, FP); the percentage of healthy cases incorrectly classified (false negatives, FN); the percentage of unhealthy cases correctly classified (true negatives, TN); and the percentage of unhealthy cases incorrectly classified (false positives, FP). Various factors, including as accuracy, precision, recall, and F1-score, are used as assessment indicators to analyze how well different models perform. These measurements came from the data of right and wrong detections. Equations (11) through (14) provide an expanded computation of the measures for multi-class activities utilizing macro averages, which may help with understanding.

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad (11)$$

$$Precision = \frac{TP}{TP+FP} \quad (12)$$

$$Sensitivity/recall = \frac{TP}{FN+TP} \quad (13)$$

$$F1 - score = \frac{2 * Precision * Recall}{Precision + Recall} \quad (14)$$

The suggested work is evaluated by comparing its performance to current methods, namely the Support value-based deep neural network (SDNN) [10] and the 2D Convolutional Neural Network (2DCNN) [19].ReNet50V2 [8].

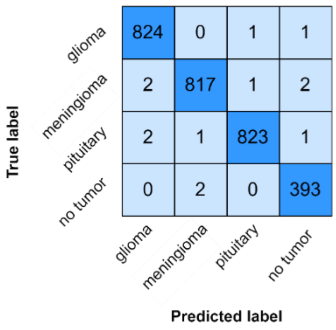
TABLE 1: COMPARISON OF THE PROPOSED WORK WITH THE OTHER STATE OF ART MODELS

Algorithms/parameters	**2DCNN**	**SDNN**	**ResNet50V2**	**Proposed hybrid VGG-XGB model**
Accuracy (%)	94.2	95.3	96.1	98.0
Precision(%)	89.23	92.56	93.3	96.34
Recall(%)	91.87	93.45	93.3	94.39
F1-score (%)	90.53	93.00	93.3	96.87

Examining the classification context for brain tumors as presented in Table 1 will help determine how effective the proposed effort is. The proposed hybrid VGG-XGB model outperforms the prior models with the following impressive results: 98.0%, 96.34%, 94.39%, and 96.87% for accuracy, precision, recall, and F1-score, respectively. This improved performance is evidence of the hybrid model's effectiveness, which includes feature extraction via the VGG-19 convolutional neural network and final classification using the XGBoost classifier.

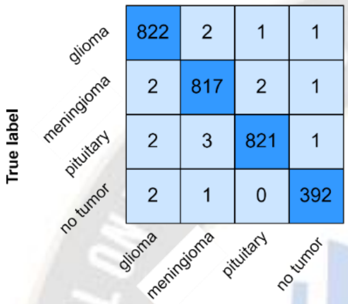
Compared to the other models, 2DCNN, SDNN, and ResNet50V2, the Proposed Hybrid VGG-XGB model excels in providing higher accuracy, which is crucial in medical image analysis, where misclassification can have significant consequences. The improved precision and recall also indicate a better balance between correctly identifying tumor regions and minimizing false positives and false negatives, which are essential for clinical accuracy.

Confusion matrix: A confusion matrix, in the context of artificial intelligence, is a matrix that displays the efficiency of relevant algorithms. Each row in the matrix represents the actual (true) value of instances, whereas each matrix column represents the predicted number of instances. We can ascertain whether the results are ambiguous or whether the classes overlap thanks to this matrix, which lives up to its name. Decreasing the modeling process's false positive and false negative results is crucial for medical research. Figure 3 - Figure 6 illustrates how false positive and false negative rates affect an organization.



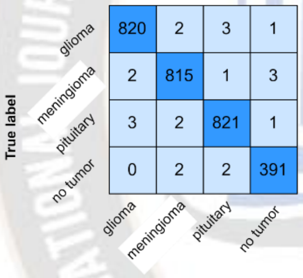
True label \ Predicted label	glioma	meningioma	pituitary	no tumor
glioma	824	0	1	1
meningioma	2	817	1	2
pituitary	2	1	823	1
no tumor	0	2	0	393

Figure 3. Confusion matrix for proposed hybrid VGG-XGB model



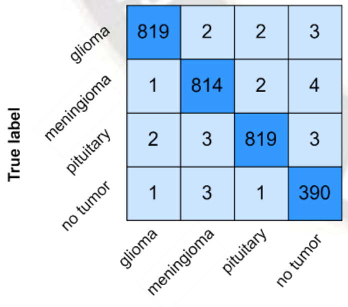
True label	glioma	meningioma	pituitary	no tumor
glioma	822	2	1	1
meningioma	2	817	2	1
pituitary	2	3	821	1
no tumor	2	1	0	392

Figure 4.Confusion matrix for ResNet50V2



True label	glioma	meningioma	pituitary	no tumor
glioma	820	2	3	1
meningioma	2	815	1	3
pituitary	3	2	821	1
no tumor	0	2	2	391

Figure 5. Confusion matrix for SDNN



True label	glioma	meningioma	pituitary	no tumor
glioma	819	2	2	3
meningioma	1	814	2	4
pituitary	2	3	819	3
no tumor	1	3	1	390

Figure 6:Confusion matrix for 2DCNN

Kappa score: The kappa score is a metric used to assess the degree of agreement between the predicted and observed outcomes of a classification model while accounting for the potential that the observed agreement is the product of pure chance. The scale goes from -1 to 1, with 0 denoting chance agreement, 1 denoting total agreement, and -1 representing total disagreement.

$$Kappa\ score = \frac{P_o - P_e}{1 - P_e}$$

In which P_o represents the observed agreement, and P_e represents the expected agreement.

$$P_o = \frac{TP + TN}{TP + TN + FP + FN}$$

$$P_e = \frac{(TP + FP)}{(TP + TN + FP + FN)}$$

TABLE 2: COMPARISON OF PROPOSED WORK'S KAPPA SCORE WITH THE OTHER MODELS

Model	Kappa score
2DCNN	95.34
SDNN	96.67
ResNet50V2	97.12
Proposed hybrid VGG-XGB model	98.36

The Table 2 provides a comparison of various models based on their Kappa scores, which serve as an indicator of their classification performance for tumor region segmentation. It is evident that all the models have achieved high Kappa scores, signifying their effectiveness in accurately classifying tumor regions in medical images. Remarkably, the Proposed hybrid VGG-XGB model stands out with the highest Kappa score of 98.36. This hybrid model likely combines the strengths of both VGG, a well-established CNN architecture, and XGBoost, a powerful gradient boosting algorithm.

VGG excels at extracting intricate and hierarchical features from medical images, enabling accurate segmentation of tumor regions. Its deep convolutional layers provide exceptional feature representation, capturing fine details crucial for precise classification. Also, XGBoost is renowned for its robustness in handling complex, high-dimensional data, making it an ideal choice for the final classification step. The combination of these techniques seems to result in superior classification accuracy, demonstrating the advantages of model fusion in brain tumor classification.

CONCLUSION

Artificial intelligence and machine learning are essential to the healthcare industry, especially when it comes to imaging-based illness identification. Using MRI data, this study presented a novel method for segmenting and classifying brain tumors: the hybrid VGG-XGB model. MRI brain images were enhanced using the CLAHE approach, and relevant features were extracted using the K-means algorithm, segmented using VGG-19, and classified using XGBoost. With 98.0% accuracy, 96.34% precision, 94.39% recall, and 96.87% F1-score, respectively, the experimental findings demonstrated outstanding performance, surpassing the state-of-the-art techniques at this time. These outcomes highlight how well our approach works to identify anomalies in MRI brain scans.

ACKNOWLEDGMENT

The author would like to appreciate the effort of the editors and reviewers. This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

REFERENCES

[1] K. R. Bhatele and S. S. Bhadauria, “Machine learning application in Glioma classification: review and comparison analysis,” Arch. Comput. Methods Eng., vol. 29, no. 1, pp. 247–274, Jan. 2022. doi.org/10.1007/s11831-021-09572-z

[2] A. Das, S. K. Mohapatra, and M. N. Mohanty, “Design of deep ensemble classifier with fuzzy decision method for biomedical image classification,” Appl. Soft Comput., vol. 115, no. 108178, p. 108178, Nov.2022. doi.org/10.1016/j.asoc.2021.108178

[3] J. Zhang, X. Lv, H. Zhang, and B. Liu, “AResU-Net: Attention residual U-Net for brain tumor segmentation,” Symmetry (Basel), vol. 12, no. 5, p. 721, Apr. 2020. https://doi.org/10.3390/sym12050721

[4] M. K. Islam, M. S. Ali, M. S. Miah, M. M. Rahman, M. S. Alam, and M. A. Hossain, “Brain tumor detection in MR image using superpixels, principal component analysis and template based K-means clustering algorithm,” Mach. Learn. Appl., vol. 5, no. 100044, p. 100044, May. 2021. https://doi.org/10.1016/j.mlwa.2021.100044

[5] M. S. I. Khan et al., “Accurate brain tumor detection using deep convolutional neural network,” Comput. Struct. Biotechnol. J., vol. 20, pp. 4733–4745, Aug. 2022. https://doi.org/10.1016/j.csbj.2022.08.039

[6] S. Tabatabaei, K. Rezaee, and M. Zhu, “Attention transformer mechanism and fusion-based deep learning architecture for MRI brain tumor classification system,” Biomed. Signal Process. Control, vol. 86, no. 105119, p. 105119, Jun. 2023. https://doi.org/10.1016/j.bspc.2023.105119

[7] M. M. Islam, P. Barua, M. Rahman, T. Ahammed, L. Akter, and J. Uddin, “Transfer learning architectures with fine-tuning for brain tumor classification using magnetic resonance imaging,” Healthcare Analytics, vol. 4, no. 100270, p. 100270, Sept. 2023. https://doi.org/10.1016/j.health.2023.100270

[8] M. A. Talukder et al., “An efficient deep learning model to categorize brain tumor using reconstruction and fine-tuning,” Expert Syst. Appl., vol. 230, no. 120534, p. 120534, May. 2023. https://doi.org/10.1016/j.eswa.2023.120534

[9] A. B. Abdusalomov, M. Mukhiddinov, and T. K. Whangbo, “Brain tumor detection based on deep learning approaches and magnetic resonance imaging,” Cancers (Basel), vol. 15, no. 16, Aug. 2023. https://doi.org/10.3390/cancers15164172

[10] B. Raghuram and B. Hanumanthu, “Brain tumor image identification and classification on the internet of medical things using deep learning,” Measur. Sens., vol. 30, no. 100905, p. 100905, Sept. 2023. https://doi.org/10.1016/j.measen.2023.100905

[11] K. Shaheed, Q. Abbas, A. Hussain, and I. Qureshi, “Optimized Xception learning model and XgBoost classifier for detection of multiclass chest disease from X-ray images,” Diagnostics (Basel), vol. 13, no. 15, Aug. 2023. https://doi.org/10.3390/diagnostics13152583

[12] L. Alzubaidi et al., “Review of deep learning: concepts, CNN architectures, challenges, applications, future directions,” J. Big Data, vol. 8, no. 1, p. 53, Mar. 2021. https://doi.org/10.1186/s40537-021-00444-8

[13] Z. Zhao et al., “Conventional machine learning and deep learning in Alzheimer’s disease diagnosis using neuroimaging: A review,” Front. Comput. Neurosci., vol. 17, p. 1038636, Feb. 2023. https://doi.org/10.3389/fncom.2023.1038636

[14] M. Attique Khan et al., “Classification of positive COVID-19 CT scans using deep learning,” Comput. Mater. Contin., vol. 66, no. 3, pp. 2923–2938, Dec. 2021. https://doi.org/10.32604/cmc.2021.013191

[15] B. Lu et al., “A practical Alzheimer’s disease classifier via brain imaging-based deep learning on 85,721 samples,” J. Big Data, vol. 9, no. 1, Oct. 2022. https://doi.org/10.1186/s40537-022-00650-y

[16] F. Mohammad and S. Al Ahmadi, “Alzheimer’s Disease Prediction Using Deep Feature Extraction and Optimization” Mathematics, vol. 11, no. 17, p. 3712, Aug. 2023. https://doi.org/10.3390/math11173712

[17] C.-J. Tseng and C. Tang, “An optimized XGBoost technique for accurate brain tumor detection using feature selection and image segmentation,” Healthcare Analytics, vol. 4, no. 100217, p. 100217, Dec. 2023. https://doi.org/10.1016/j.health.2023.100217

[18] Sartaj, 2020, “Brain tumor classification (MRI) [Data set]”. Available at: https://www.kaggle.com/datasets/sartajbhuvaji/brain-tumor-classification-mri?select=Training.

[19] S. Saeedi, S. Rezayi, H. Keshavarz, and S. R Niakan Kalhori, “MRI-based brain tumor detection using convolutional deep learning methods and chosen machine learning techniques,” BMC Med. Inform. Decis. Mak., vol. 23, no. 1, p. 16, Jan. 2023. https://doi.org/10.1186/s12911-023-02114-6

[20] Y. Meng, C. Tang, J. Yu, S. Meng, and W. Zhang, “Exposure to lead increases the risk of meningioma and brain cancer: A meta-analysis,” J. Trace Elem. Med. Biol., vol. 60, no. 126474, p. 126474, Jul. 2020 https://doi.org/10.1016/j.jtemb.2020.126474