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DEEP LEARNING-GUIDED GENOMIC PROFILING FOR BRAIN TUMOR SUBTYPING USING HYBRID FEATURE SELECTION AND ENSEMBLE CLASSIFICATION

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SUMMARY

The problem of brain tumors is a range of different subtypes, which have a variety of clinical forms, and the diagnosis and treatment of tumors is a challenging task. This paper introduces a hybrid deep learning system that combines genomic profiling with MRI image analysis to provide an effective brain tumor subtyping. The framework is initiated by the preprocessing of MRI images, which is followed by grayscale conversion and noise reduction as done by Fast Non-Local Means (FNLM) filtering. This will aid in ensuring that important structural data is retained with minimal irrelevant noise. To conduct segmentation, the UNet++ framework is used, which is the best-performing architecture in medical image analysis. UNet++ enhances the conventional UNet by adding embedded skip routes, which allows a more productive information exchange between encoder and decoder networks, improving the accuracy of segmentation. The extraction of features is conducted by a local binary pattern (LBP), Gray-Level Co-occurrence Matrix (GLCM), and Discrete Wavelet Transform (DWT). These methods are able to reproduce both the frequency domain and textural characteristics of the tumor areas. The variables are further narrowed down to the most relevant ones by the Minimum Redundancy Maximum Relevance (mRMR) algorithm, thus only the most relevant features are taken in the classifier. The classification is done by an improved variant of the AlexNet that is optimized with the addition of batch normalization, global average pooling, and local response normalization parameters to minimize overfitting and maximize learning effectiveness. The model postulated in this study has a high performance of 99.79

%accuracy, 96.82 %sensitivity, 98.32 %specificity, and 98.61 %precision. These findings indicate the effectiveness of the hybrid approach, combining handcrafted characteristics and deep learning in early and confident brain tumor subtyping, which has considerable potential to enhance the level of diagnostic accuracy and individual treatment approaches in neuro-oncology.

Key words: *UNet++, genomic profiling, feature selection, deep learning, brain tumor classification, MRI Segmentation, alexnet.*

INTRODUCTION

The complex pathophysiology of the brain tumor, high mortality, and inconsistent reaction to therapy are a serious public health problem [1]. Many cell types of the brain are the source of these tumors, divided into several types, including gliomas, meningiomas, and pituitary adenomas, each of which is [2] with unique molecular, physical, and clinical features. The process of brain tumor sub-availability is important to diagnose the disease, guide surgical and medical intervention, and enable personal treatment strategies. The accurate sub-availability allows physicians to differentiate between tumors of low and high grade, predict the progression of the disease, and select appropriate methods such as radiotherapy, chemotherapy, or targeted molecular remedies. Traditional clinical procedures, such as visual inspection of biopsy and MRI scans, rely more on radiologist expertise and histopathological assessment [3]. Being effective, these methods are naturally subjective and can be limited by sampling errors, inter-supervision variability, and delay in diagnosis. In addition, tumor inequality faces additional challenges, as the same type of tumors can display separate genetic and phenotypic characteristics. This variability underlines the importance of integrating advanced computational methods for more consistent and accurate tumor classification.

Examination of an early brain tumor is crucial because it can result in more effective treatments, faster recovery procurement, and higher opportunities for survival. When the tumors are seen early, doctors have more options for treating them before they become fatal. However, traditional methods that require manual scanning of the brain can be slow and sometimes miss small or hidden signs of the tumor. Artificial intelligence (AI), especially in the analysis of medical images, can now be identified with faster and more accurate detection of brain cancer. AI tools can also detect small changes in an MRI scan that may be difficult for the human eye to see [5]. These technologies are helping doctors to diagnose brain tumors with more confidence. As the research continues, combining AI with information about a patient's genes can quickly and more powerfully and personally identify.

Medical imaging analysis has changed as a result of recent developments in Deep Learning and Artificial Intelligence (AI). MRI scans can provide valuable features, and especially impressive skills are shown in this regard, which enable tumors with high -performance tumors and enabling subtypes [6]. Moreover, radiogenomics, an emerging field that combines imaging features with genomic profiles, has shown the promise of identifying nuclear signatures in a non-invasive way [7]. By combining radiological patterns with gene expression and transformation data, researchers can gain a more comprehensive understanding of the life of the tumor. In this regard, hybrid models that combine the Deep Shrimony with the handcrafted feature extraction, anesthetic classification, and enhanced facility selection algorithms techniques [8]. These models can capture both low-level image texture and high-level semantic features, enhancing the model's ability to differentiate tumor subtypes with high precision. Such integration not only improves classification accuracy but also supports early and reliable diagnosis, which is critical for patient survival and quality of life. Therefore, brain tumor subtyping in Figure 1 using a multidisciplinary approach that combines MRI imaging, genomics profiling [4] [9], and AI-driven analytics represents a powerful direction in modern neuro-oncology [10]. It paves the way for personalized medicine, reduces diagnostic uncertainty, and enables timely therapeutic decision-making.

Figure 1. Block diagram using DL architecture for brain tumor subtyping

There are five parts in this study, it introduces the problem of brain tumor diagnosis and explains how AI, especially deep learning, can support faster and more accurate detection compared to traditional methods. he second provides a detailed review of past research; this review gap sets the stage for the proposed work. The suggested hybrid technique is explained in the third. The best features are selected after MRI images have been cleaned and segmented and features have been retrieved using texture and wavelet methods. These are fed into an improved AlexNet model. The fourth presents and analyzes the results, where the hybrid model achieves high accuracy (99.79%) and outperforms several popular deep learning models on the BraTS2020 dataset. Finally concludes that combining handcrafted and deep features with genomic profiling can offer powerful tools for doctors, making brain tumor subtyping.

Key Contributions:

1. Proposed a hybrid deep learning model of genomic profiling and MRI image analysis to subtype brain tumors.
2. Selections of features improved by using mRMR and better AlexNet to classify brain tumors more accurately.
3. Reached 99.79% accuracy and high performance on the BraTS2020 dataset, and it was better than other models.

The paper is structured in the following way: the Introduction explains the necessity of proper brain tumor subtyping, the drawbacks of the current diagnostic tools, and proposes AI and deep learning as the remedies to the problem. The Literature Review shows the work that has been done previously on the deep learning approaches to the classification of brain tumors and outlines the gaps in the knowledge. The Proposed Methodology describes the hybrid deep learning architecture of the genomic profiling and MRI analysis, including the description of working preprocessing, segmentation (with the UNet++), feature extraction, and classification with an improved AlexNet structure. The Dataset section will provide information about the BraTS2020 dataset, its modalities, and the type of tumors that were used to evaluate the models. Experimental Setup and Evaluation describe the implementation of metrics of performance and comparing the performance of various models. The section Results and Discussion give and analyses the performance of the model in segmentation and classification. Last but not least, the Conclusion is a summary of major findings, possible clinical implementation, and a recommendation of future research.

LITERATURE REVIEW

The use of sophisticated deep learning methods, especially modified and pre-trained CNNs, in the context of medical imaging has been the subject of many research throughout the last ten years in Table 1. These approaches have been extensively used for tasks such as classification, segmentation, and diagnostic image analysis across a variety of modalities. While many of these works addressed different tumor types and imaging datasets, our review is limited to those studies that utilized the same MRI dataset relevant to our current investigation. Despite significant progress, the challenge of achieving fully automated and reliable brain tumor segmentation remains unsolved, largely due to the variability and limitations of manual and semi-automated methods.

Rasool et al. [11] suggested a dual-path CNN method for MRI image-based brain tumor classification. Their method compared two variations: one pipeline involved using GoogleNet as a feature extractor followed by classification through a Support Vector Machine (SVM), the other, however, made use of a Softmax layer together with a modified version of GoogleNet. According to the assessment, the hybrid model that included GoogleNet and SVM outperformed the fine-tuned model, which had an impressive accuracy of 93.1%, reaching 98.1% accuracy.

Building upon the same architecture, Raza et al. [12] introduced DeepTumorNet, a customized CNN model tailored for brain tumor classification. By modifying the standard GoogLeNet replacing its final five layers with fifteen specifically designed layers and employing a leaky ReLU activation the model demonstrated superior results. DeepTumorNet demonstrated near-perfect precision, recall, and F1-score performance, testing using a publically accessible dataset of brain MRI images and obtaining 99.67% accuracy, significantly outperforming traditional models such as ResNet50 and MobileNetV2.

Díaz-Pernas et al. [13] took a multiscale deep learning approach inspired by the human visual system. Their model processed brain MRI slices from sagittal, coronal, and axial planes without requiring pre-segmentation or skull stripping. Applied to a dataset of over 3,000 images from 233 patients, the system demonstrated high classification performance, with an overall accuracy of 97.3%, showcasing its robustness and adaptability across anatomical views.

In another contribution, Sadad et al. [14] used a ResNet50 backbone together with the U-Net architecture to segment tumors. Through extensive preprocessing and data augmentation, they enhanced the learning process. By combining reinforcement learning and evolutionary algorithms with transfer learning, the study successfully improved tumor classification, the best reported accuracy of 99.6% was attained by NASNet.

Biswas and Islam [15] adopted a more traditional hybrid approach that integrated image preprocessing, feature extraction using 2D wavelet transforms, and dimensionality reduction via Principal Component Analysis (PCA). The Levenberg–Marquardt approach was used to train an artificial neural network (ANN) for classification. Their framework achieved 95.4% accuracy, supported by high sensitivity and specificity, indicating effective generalization.

Renugadevi et al. [16] proposed a multi-stage system that addressed segmentation, tumor grading, and survival prediction. Using the UNet++ architecture for segmentation, they extracted radiomic features and applied synthetic oversampling (SMOTE) and adaptive sampling techniques to address class imbalance. The Stochastic Gradient Descent (SGD) classifier achieved 96% accuracy in tumor grading, while XGBoost performed best for survival prediction with the lowest mean squared error among the evaluated methods.

Expanding beyond imaging, Thakur et al. [17] presented a hybrid model for classifying cancer based on gene expression data that combines CNNs and Recurrent Neural Networks (RNNs). Features were initially extracted using VGG16 and VGG19 architectures and then passed through the hybrid model for classification. Their results, with accuracies of 97.8% and 99.4% across two datasets, and low MSE values, accentuate the model's proficiency in managing high-dimensional genomic data.

In a similar direction, Dixon et al. [18] developed an ensemble learning model that fused features extracted by CNNs with those derived from a Vision Transformer (ViT). This model integrated both deep and hand-crafted features such as texture descriptors like Haralick and Local Binary Patterns (LBP) along with ViT-based embeddings. The ensemble demonstrated consistent performance improvements across public and private datasets in ablation studies.

Gu and Ren [19] contributed a machine learning framework that employed multiple feature selection techniques, including PCA, Gini index, and mutual information, followed by classification using algorithms like Gaussian Process Classifier (GPC), Decision Trees, and K-Nearest Neighbors (KNN). The combination of PCA and GPC yielded the most promising results, significantly improving performance compared to using raw features alone.

Lastly, Arora and Lamba [20] proposed a 3D MRI-based method for tumor detection and localization. After denoising and segmenting the images using a convolutional radial basis function network, feature extraction was performed via a belief neural network integrated with reinforcement learning. Their model achieved a 97.57% accuracy rate and enabled precise tumor localization across all three anatomical planes, confirming its utility in semantic segmentation applications.

The analyzed literature indicates that the classification of brain tumors with the help of deep learning has made a great leap in advancement, and such methods as CNNs, UNet, and ResNet50 prove to be successful. Accuracy has also been enhanced by hybrid approaches where different architectures, feature extraction strategies and machine learning classifiers are used. Although such improvements have been made, there are still some obstacles to overcome, especially in the realization of completely automated and accurate segmentation and classification of various subtypes of tumors. Combining imaging and genomic data has not been well exploited, even though some studies have looked into this, and has not been fully exploited to achieve best classification results yet. The current research provides answers to

these gaps by developing a hybrid deep learning model, which integrates MRI-based segmentation with UNet++ and genomic profiling and feature selection models (mRMR), as a more valid and reliable means of brain tumor subtyping. The suggested methodology will increase the accuracy of the diagnosis, decrease the influence of subjective experience, and offer a powerful tool of individualized treatment approach in neuro-oncology.

Table.1 Existing method for classifying brain tumors

Reference	Technique Used	Accuracy	Limitations
[11]	Hybrid CNN with GoogleNet + SVM/Softmax	98.10%	Limited to predefined CNN structures
[12]	DeepTumorNet (Modified GoogLeNet with 15 new layers, Leaky ReLU)	99.67%	High model complexity
[13]	Multiscale CNN inspired by Human Visual System	97.30%	No preprocessing, may impact generalization
[14]	U-Net with ResNet50 + evolutionary algorithms + RL	99.6%	IoU lower (0.9504), model dependency
[15]	ANN with wavelet transform + PCA	95.40%	Relies heavily on preprocessing and handcrafted features
[16]	UNet++ + PCA + Tree-based + ML classifiers	96% (SGD)	Requires complex multi-stage training
[17]	RNN-CNN with VGG16/VGG19 features	99.4%	High training time and computational cost
[18]	ViT + CNN (weighted ensemble)	Not specified	Accuracy not clearly quantified
[19]	GPC with PCA + Gini + Mutual Info	Up to 294.31% improvement	Limited to gene expression data
[20]	Convolutional radial function + belief neural networks	97.57%	High RMSE (55.56), AUC and Dice score lower

PROPOSED METHODOLOGY

The suggested method is broken down into five phases, as Figure 2 shows. The BraTS2020 dataset was used to gather 155 slices of brain tumor images originally. When the image was converted to grayscale, a filter was used to eliminate the noise. The best features were chosen from the hybrid feature selection process using the Minimum Redundancy Maximum Relevance (mRMR) approach. Following the assignment of these characteristics, classification enhanced the hybrid AlexNet classifier. Tumor aggressiveness will also be revealed.

Dataset

In medical imaging, the Multimodal Brain Tumour Segmentation Challenge 2020 dataset (BraTS2020) is widely used for brain tumour segmentation and classification [21][22]. A number of modalities are utilized to get brain MRI images, including FLAIR, T1, T2, and T1-CE (Contrast Enhanced) imaging. An MRI image sample for each modality is shown in Figure 2. A different modality scans and highlights different areas of the brain tumor. There are 155 slices in each MRI modality's volume. Four categories were identified using the tumor sub-regions' segmentation annotation labels: enhancing tumour (ET), peritoneal oedema (ED), necrotic/non-enhancement tumour (NCR/NET), and background (0). BraTS2020 has subsets for testing and training; in the former, the brain scan tumor areas are identified by 369 instances with ground truth annotations. On the other hand, the testing subset is specifically designed to test and assess the performance of different models and algorithms and lacks any ground truth annotations.

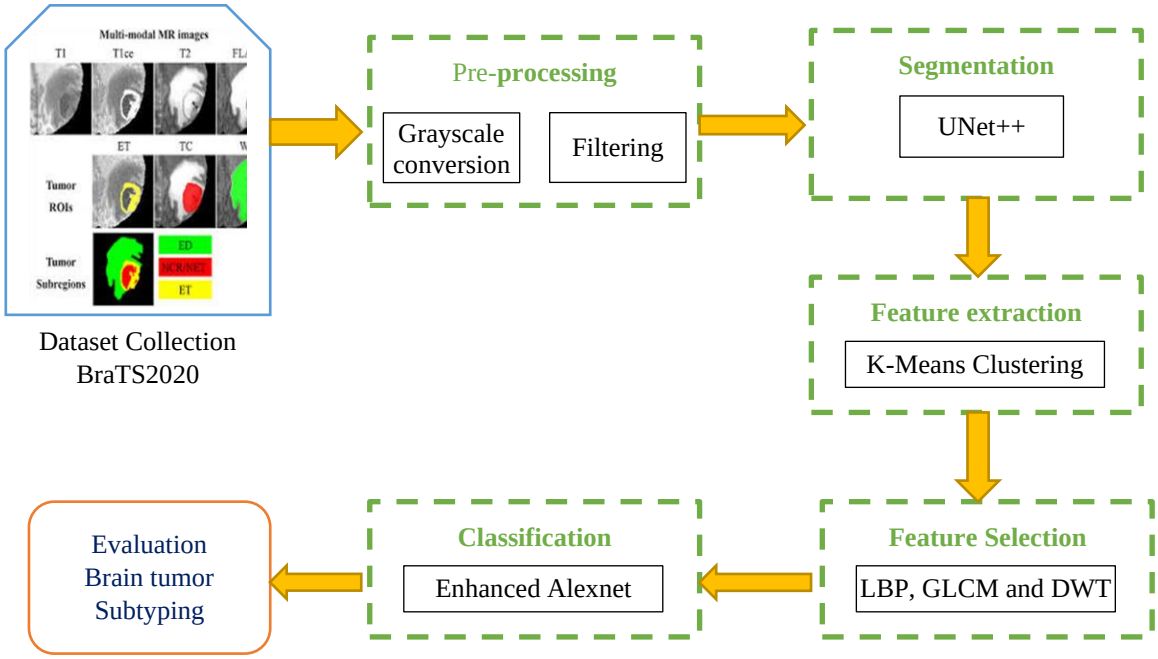

Figure 2. Proposed methodology

Pre-Processing

Pre-processing, which improves detection accuracy by eliminating extraneous components from MRI scans, an important step in diagnosing brain tumors is examining adjacent tissues or blood vessels. To ease processing and lower data needs, the photos are first transformed to greyscale in order to remove unnecessary information. The FNLM filter [23] is then used to eliminate noise, which is very useful for maintaining image structure while lowering noise.

Grayscale Conversion

Greyscale conversion reduces processing and storage needs, which improves the efficiency of the analysis that follows. To increase the machine learning algorithms' processing time, the additional black background in each MRI modality must be eliminated [24]. Consequently, the size of every image is shrunk from 240 × 240 × 155 to 128 × 128 × 128. Increasing the size of the dataset was an additional objective of the data augmentation. Then, 10% is utilized for testing, 10% for validation, and 80% of the improved dataset is utilized for trained.

Filtering

By weighting pixel values according to their Euclidean distance, the FNLM filter preserves important edge information, in contrast to traditional filters that could blur the entire image. Both qualitative and quantitative assessments have shown that this method, which is now possible because of improvements in computing power, is successful in improving image clarity in eq. (1):

$$N_L[i](M) = \sum N \epsilon i \, W(M,N) i(N) \quad (1)$$

where, W (M, N): weight of the pixels M&N, ranges between 0≤W (M, N) ≤1 and ΣW (M, N)$N \in i$=1.

Eq. (2) determines weight W (M, N) with respect to the similarity of pixels M and N, where i(N) and i(M) represent the intensity of pixels N and M, respectively.

$$W(M,N) = \frac{1}{Z(M)} e - \frac{\|P(X_m) - P(X_n)\|}{D^2} \quad (2)$$

where, the normalization coefficient, Z (M), is found using Eq. (3), and the pixel vectors for M and N are XM and XN.

$$Z(M,N) = \sum N\, e - \frac{[P(X_m) - P(X_n)]^2}{D^2} \quad (3)$$

In Eqs. (2) and (3), the amount of noise that is removed is determined by the coefficient D, which is usually a constant equals the standard deviation. A higher D value increases image smoothing and enhances noise removal effectiveness.

Algorithm 1: Preprocessing pseudocode

Input: RGB_MRI_Image

Output: Preprocessed_Image

1. Convert RGB_MRI_Image to Grayscale_Image

2. For each pixel M in Grayscale_Image:

    Initialize Z(M) = 0, NL(M) = 0

    For each pixel N in neighborhood of M:

      Compute patch distance: d = ||P(XM) − P(XN)||²

      Compute weight: W (M, N) = exp (−d / D²)

      Update normalization: Z(M) += W (M, N)

    For each pixel N:

      NL(M) += [W (M, N) * i(N)] / Z(M)

3. Return NL(M) as Preprocessed_Image

The algorithm 1 here in described is a preprocessing pseudocode that is used to turn a 3D RGB MRI image to a grayscale image as well as remove noise with fast non-local means (FNLM) filter. It first transforms the input RGB MRI image in grayscale making the data easier to analyze. The algorithm also uses the Euclidean distance of the target pixel and its neighbors to decide which pixels in the grayscale image are similar to each other. Each pixel is assigned a weight in relation to a neighboring pixel depending on this distance with nearer pixels getting higher weights. Such weights are then normalized in order to make the processing consistent. Lastly, a denoised image is created by means of the weighted pixel values, the output is provided as that. It is also effective in eliminating noise that is not relevant but maintains the significant structural information in the MRI image hence this is appropriate to be followed by the segmentation and classification activities.

Segmentation

For semantic segmentation tasks deep learning is being used in medical image analysis was selected by the UNet++ architecture. UNet++ is built around the encoder and decoder. The encoder component intensifies channel numbers while carrying out a contracting route similar to the UNet, which results in each level down sampling the spatial resolution of the feature map. UNet++ uses many nested decoders in place of the conventional UNet decoder [25]. The model is trained using the preprocessed 128 x 128 x 128 photos as input. Two 3∗3 kernel convolutions with the activation function ReLu (rectified linear unit) are used in the contraction approach. Figure 2 shows how UNet++ uses layered dense skip connections to link encoder and decoder sub-networks at multiple layers to improve segmentation accuracy. Information transfer between the two sub-networks is substantially improved by this novel technique.

Feature Extraction

An integral part of classification is featuring extraction. The categorisation performance is greatly influenced by the important aspects of the photos. Colour, size, and structure are used to categorise objects as either global or local. While colour and texture are particular, their structures are universal. In order to group the brain areas using an optimised k-means clustering algorithm, to categorize the images in this research, deep and artisan characteristics were acquired. Choosing the ideal clusters value for the k-means clustering procedure is referred to as optimised. This optimisation method aids in classifying the various brain regions as well as the tumour portion.

Assuming N×N means for the local window size, the result is as

$$s(i,j) = \sum_{k=i-Nj}^{i+Nj} \sum_{i=j-Nj}^{j+N} h(k,l).I(k,l) \quad (4)$$

$$d_{kj} = \sqrt{(i-k)^2} + (j-l)^2 \quad (5)$$

Feature Selection (FS)

The FS is an essential task that eliminates noisy, unnecessary, and redundant data to lower the amount of features. Selecting the characteristics that best depict each tumor is one step in the image processing process. The initial phases (optimisation, segmentation, and morphology) determine how accurate the feature selection. Consequently, the objective of feature selection algorithms is to minimize the size of an image while preserving its most significant characteristics. To produce more effective feature vectors, three algorithms LBP, GLCM, and DWT were used in this investigation. To produce representative characteristics which, help in the early identification of brain tumors, the fused feature is a contemporary, potent, and effective technique.

Using the LBP, which characterizes the texture of 2D surfaces, features are first selected. Each iteration of the method uses a 5 × 5 size, selects a center pixel, and analyzes it using Equation (6). For each central pixel, the program substitutes neighboring pixels and a radius of 24 adjacent pixels. 203 features are selected and saved in a feature vector after the procedure is performed for every pixel in the image.

$$LBP_{R,P} = \sum_{P=0}^{P-1} S(g_p - g_c)2^p s(x) = \begin{cases} 0, & x < 0 \\ 1, & x \geq 0' \end{cases} \quad (6)$$

where the target pixel (center) and surrounding pixels' gray values, the radius for neighbouring areas, and the number of neighbours are denoted by P, R, and c, respectively.

Second, the GLCM is used for feature selection, which is an effective technique for selecting textural characteristics from brain tumor regions. The GLCM method is derived from the grey levels of the brain tumor position shows a variety of compositional levels. The method separates coarse and smooth zones based on regional data. Pixels with nearby values are found in the smooth region, whereas pixels with diverging values are found in the coarse area.

Thirdly, characteristics from the ROI are selected by the DWT. Square mirror filters divide the input signals into two signals to match the low- and high-pass filters. For each image, the algorithm generates 12 features: three detailed parameters and approximation parameters. While high-pass filters (LH, HL, and HH) produce three characteristics as detail coefficients (horizontal, vertical, and diagonally, correspondingly), low-pass filters (LL) produce approximations factors.

To create highly effective features that can accurately diagnose the tumor, the features of the three approaches are finally hybridized into a single feature vector.

The procedure of fusing the characteristics selected from the three methods is shown in Figure 3. Each image represents 228 features as all the features are merged into a single feature vector.

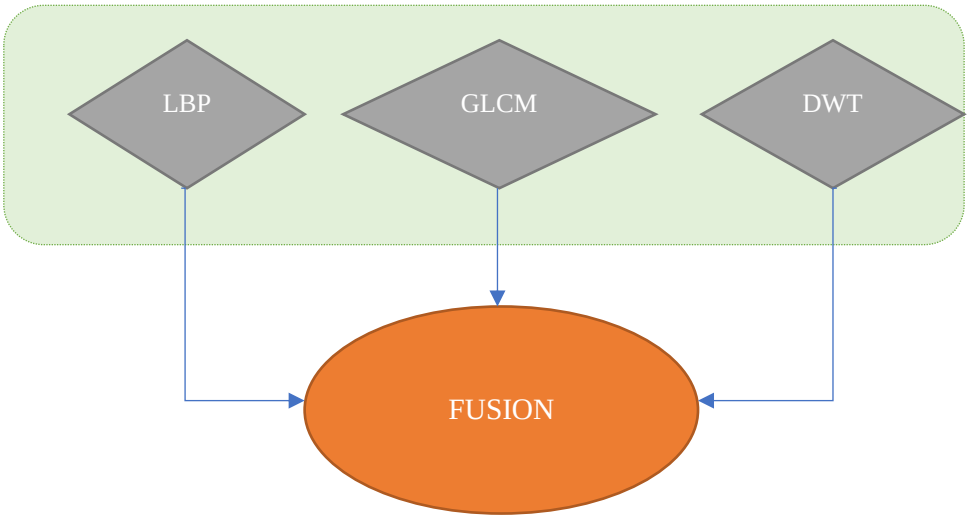

Figure 3. Fusion process

Classification

Following the FS, the ASA is used as an input for a hybrid AlexNet classifier that receives the chosen features. The complex details of medical images may not be sufficiently captured by handwritten functions, which are time-consuming, are often necessary for conventional algorithms. The requirement for human feature engineering can be reduced by using DL models like AlexNet, which can automatically identify significant features. To identify brain tumours, the improved AlexNet output layer employs a SoftMax classifier. In the end, the suggested classifier increases classification accuracy while effectively detecting brain tumours. Figure 4 is a flowchart that illustrates the technique that has been proposed.

The components of AlexNet are as follows: five convolutional layers, two normalization layers, figure 5 shows three max-pooling layers, a softmax layer, and two completely connected layers. Each convolution is followed by ReLU activation. With padding, the real result is 227 × 227 × 3, even though the input size is normally 224 × 224 × 3. The model has more than 60 million parameters.

Enhanced AlexNet

Three fully connected (FC) layers constitute the architecture, five convolutional layers, and many layers for normalizing and pooling, which processes input images with dimensions of 227 × 227 × 3. In order to overcome problems like gradient vanishing and enable quicker convergence during training, the ReLU activation function is utilised throughout. By training only, a fraction of neurones in each iteration, dropout reduces overfitting in the FC layers and enhance the network's capacity for generalisation.

The following are some ways that the improvements detailed in this study vary from the current AlexNet categorisation system.

- Convolutional layers were included into the AlexNet architecture to improve image categorization by using max-average pooling methods and maintaining responsive local regions.
- A global average pooling layer that preserves the final features while drastically lowering overfitting. The ultimate outcome is unaffected by the lack of many network variable computations, which enhances network performance.
- Lastly, to prevent some extra numerical problems and remove neurone saturation, a local response normalisation (LRN) the convolutional layer was supplemented with another layer. As seen in Figure 3, post-convolution BN layers were forwarded to the next network layer.

The convolutional layer's output is as follows:

$$X_j^1 = f\left(\sum_{a=1}^{N} W_j^{I-1} * Y_a^{I-1} + b_j^i\right) \quad (7)$$

where, on layer L, the j-th feature map is denoted as X_j^1. N represents all of the characteristics on layer I-1, bji represents the bias for layer l's j-th feature map, (*) indicates convolution, and YaI-1 is layer I-1's feature map. $W_j^{I-1}1$ represents on layer I-1, the jth kernel. The size of the feature map is decreased by pooling layers, and the last layer classifies using the SoftMax function:

$$ReLU(X) = \begin{cases} 0, & X < 0 \\ X & X \geq 0, \end{cases} \quad (8)$$

$$SoftMax(X_i) = \frac{e^{x_i}}{\sum_{y=1}^{m} e^{xy}} \quad (9)$$

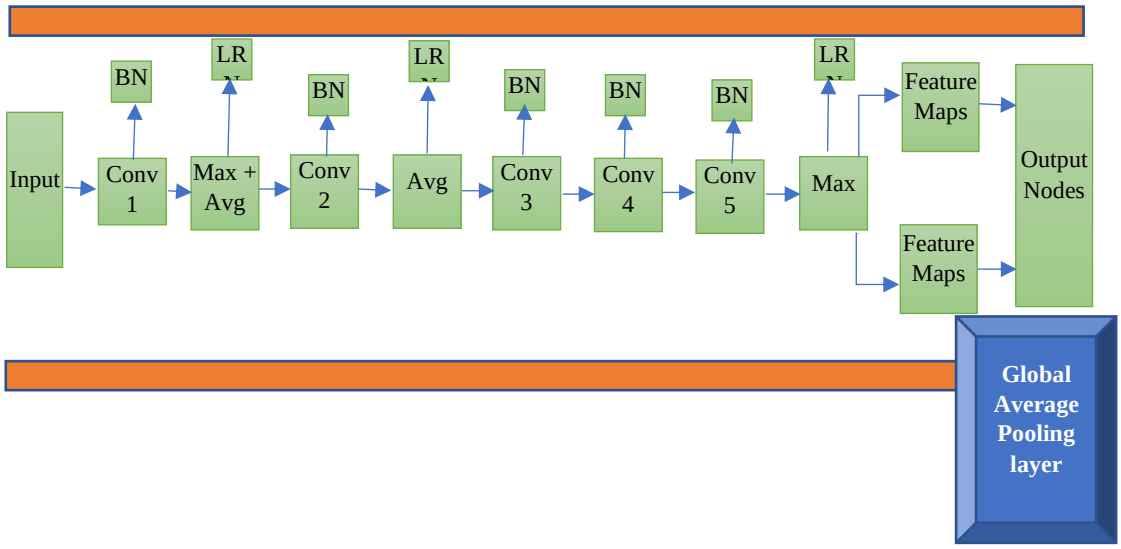

Figure 4. Enhanced alexnet

where, the number of classes and the input data are denoted by m and Xi, respectively. AlexNet employs parameters to modify the mean and variance to normalize features.

$$P_i = \varphi \tilde{t_i} + \beta \quad (10)$$

$$\tilde{t_i} = \frac{t_i - \mu}{\sqrt{\sigma^2 + \gamma}} \quad (11)$$

where, the symbols σ and μ stand for variance and mean, respectively. The parameter for feature extraction is γ, which is a constant. To minimize classification errors and improve the parameters to improve accuracy and reduce error rates, this optimization modifies β and ϕ.

This algorithm 2 gives the steps in training the improved AlexNet model in brain tumor classification. It starts with the AlexNet layer activation and image preprocess with filters and grayscale conversion of the MRI images. The partition is split into training and to make the data more sufficient, synthetic data is generated. It is then refined on the improved AlexNet architecture. The algorithm then follows forward propagation in every iteration and the training data is used to modify the weights of the model according to the predictions. After every iteration, the accuracy of the model is determined and the ultimate accuracy is determined after the completion of the training loop. The process makes the model learn effectively and is able to classify the brain tumor images effectively.

Algorithm 2: Pseudocode of the Enhanced AlexNet [46]

AlexNet layers are initialized

MRI image preprocessing (filtering, grayscale conversion)

Data on partitions

Set up the model and train it

Labeled_Data, Enhanced_AlexNet, Train_Model

Construct synthetic samples and supplement data

Generate_Synthetic_Data (Labeled_Data) = Synthetic_Data

Modify the concept

Model_Tuned = Fine_Tune_Model (Enhanced_AlexNet, Labeled_Data)

Perform the primary training loop

From 1 to the Total_Iterations, for every iteration:

Proceed with Forward Propagation (Unlabeled_Data, Model_Tuned)

Modify the model according to the prediction

Determine and evaluate correctness

Determine_Accuracy (Unlabeled_Data, Model_Tuned) = accuracy

Assess the finished model

Calculate_Accuracy = Final_Accuracy

Evaluation Metrics

This research uses assessment measures to assess the suggested model. The accuracy measure evaluates the predicted quality of the suggested model. It calculates the proportion of accurately predicted events, as a percentage of the total number of occurrences in the dataset, including true positives (TP) and true negatives (TN). Precision is the percentage of times the model produced an optimistic estimate. The percentage of all positive cases that were TP forecasts is known as recall. The F1 score is a representation of the harmonic mean calculated from the accuracy and recall scores. A model's F1-score is higher when it consistently exhibits high recall and accuracy levels. In the following equation, false positives are represented by FP, false negatives by FN, true positives by TP, and true negatives by TN.

Accuracy

The performance of a classifier model in the training stage is assessed using a statistic termed classification accuracy. It calculates the number of positive and negative situations there are in the training set that were properly categorized. The proportion of samples that are not used in the training process is the typical definition. Equation (12) represents the training accuracy in relation to this:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \quad (12)$$

Precision

Precision is expressed in Equation (13) and quantifies accuracy in predicting positive results for all expected positive samples.

$$Precision = \frac{TP}{TP + FP} \tag{13}$$

Recall

The percentage of properly anticipated positive samples among all positive samples is termed as the recall, sensitivity, or true positive rate. This may be seen in Equation (14):

$$Recall = \frac{TP}{TP + FN} \tag{14}$$

Specificity

Measure's ability to correctly identify non-cancer (healthy) samples.

$$Specificity = \frac{TN}{TN + FP} \tag{15}$$

RESULTS AND DISCUSSION

Software Details

The deep learning models were trained in Python 3.8, and trained with the help of TensorFlow (v2.5.0) and Keras (v2.4.3) as well as NumPy (v1.19.2) and OpenCV (v4.5.2) used as extra libraries to process images and extract features. The training was done using an NVIDIA RTX 3090 hardware with 24 GB of VRAM and using CUDA 11.2 and cuDNN 8.1 to speed up deep learning tasks. The training environment was based on the operating system that operates on Linux (Ubuntu 20.04), which makes it efficient in managing data pipelines. Accuracy, precision, recall, specificity, and F1-score were the measures used to assess the performance and the hybrid model yielded impressive results, with accuracy, sensitivity, specificity, and precision of 99.79%, 96.82%, 98.32%, and 98.61%respectively.

Results Of Unet++ Segmentation

After preprocessing, training, validation, and testing datasets comprising 80%, 10%, and 10% of the BraTS2020 MRI images have been separated separately. The UNet++ architectural model trained the MRI images. UNet++ is compared against UNet, Attention UNet, and ResNet50 segmentation models. The performance measurements were determined using the TP, FP, TN, and FN parameters of the confusion matrix. Accuracy, Sensitivity Specificity, and Precision were the measures used to assess the segmentation results. Using Equations (1), (2), (3), and (4), they are measured. According to Table 2, UNet++ achieved the highest accuracy, precision, sensitivity, and specificity values, which are 98.42%, 0.9947, 0.9858, and 0.9789, respectively.

Table 2. Comparison of the segmentation methods

Approach	Accuracy (%)	Sensitivity (%)	Specificity (%)	Precision (%)
UNet	97.76	96.81	94.21	93.25
Attention Unet	96.54	96.25	97.25	96.26
UNet++	98.56	99.47	98.62	97.36

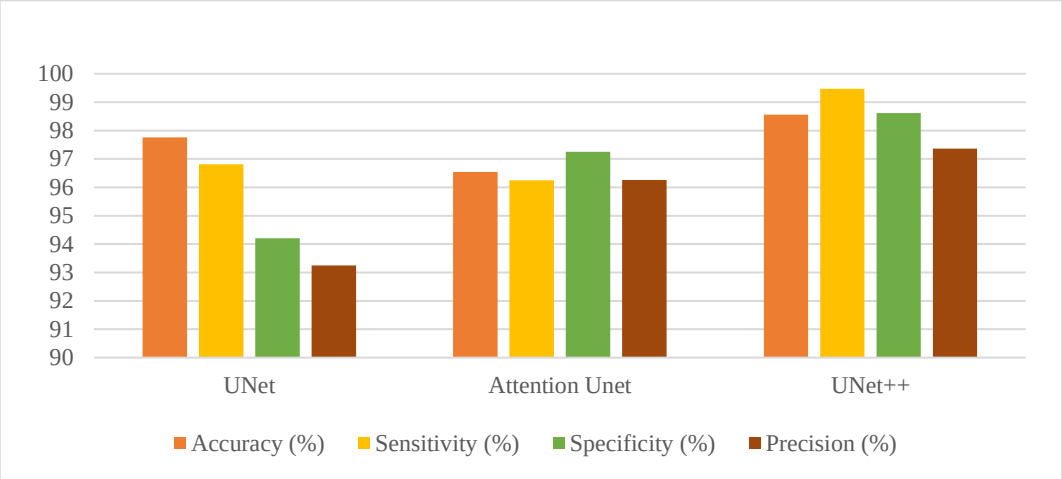

Figure 5. Segmentation

Comparative Analysis Classification

The recommended strategy accomplishes the maximum accuracy of 99.76% among the compared models, as demonstrated in Figures 3,4,5,6 and Table 3, demonstrating its better capacity to detect affirmative cases accurately. Additionally, the suggested approach shows a significant increase in sensitivity (96.73%) and specificity (98.76%), demonstrating its efficacy in accurately recognising negatives as well as finding true positives. At 97.61%, respectively, the precision values are likewise noticeably high, demonstrating the suggested method's resilience in producing consistent and trustworthy classification findings.

Table 3. The suggested algorithm's comparison with existing techniques

Approach	Accuracy (%)	Sensitivity (%)	Specificity (%)	Precision (%)
SVM	92.75	90.79	92.53	91.24
CNN	94.65	92.25	94.73	93.92
DCNN	95.60	92.17	95.31	94.42
RestNet50	98.90	93.96	97.21	96.21
Proposed	99.79	96.82	98.32	98.61

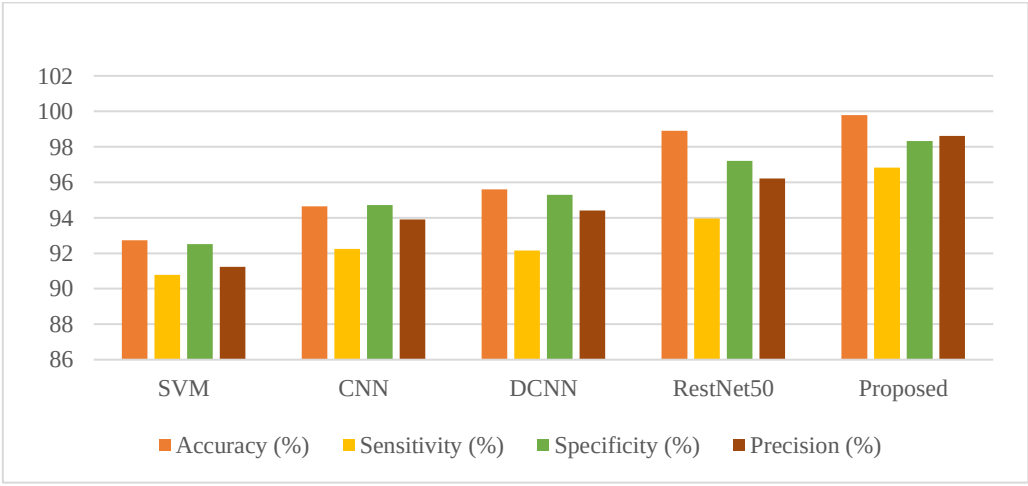

Figure 6. Classification

In order to create a rich feature vector for tumour classification, suggested a hybrid brain tumor multi-classification architecture that extracts deep hidden features and texture using three learning modules. These modules are then coupled by a feature weighing scenario. The models' attempts at integration quantitatively show that our ensemble technique is superior (accuracy ≥ 99%) for both datasets, as

indicated in Table 3.

The model's combined ViT and texture characteristics surpass the others, with an overall accuracy of ~ 95%, based on the later study of ablation methods that break down the ensemble model in various scenarios.

Ablation Study

The reason behind the ablation study was to test the effect of the key components on the performance of the final model. The research experimented the relevance of feature selection with the mRMR technique that when omitted the accuracy dropped to 96.55% with a baseline accuracy of 99.79%. The model performance of the UNet++ in terms of segmentation was also compared to the simple models such as UNet and Attention UNet. The top result of 98.56 was reached by UNet++ and its removal increased the segmentation accuracy by 2-3%. Also, there was a loss of accuracy of 1.8% when genomic profiling was not included as an input score, which revealed the importance of combining both the genomic information and MRI analysis in enhancing the subtyping of the brain tumors.

CONCLUSION

The paper describes a hybrid deep learning model that will utilize genomic profiling and MRI image analysis to perform accurate subtyping of brain tumors. The proposed method was very successful, and the results were impressive: an accuracy of 99.79, a sensitivity of 96.82, a specificity of 98.32, and a precision of 98.61 are the best possible results that can be achieved with the help of UNet+ solution, feature selection by means of the mRMR approach, and classification with the help of an improved version of AlexNet. These results highlight the possibility of integrating deep learning with genomic data as the solution of producing high-quality, early, and specific brain tumor diagnostics. This hybrid model combines the best ability to improve diagnostics but also provides useful information on specific treatment plans when dealing with neuro-oncology. The combination of the handcrafted element and the deep learning plays a significant role in getting over the constraints of the traditional approaches which are typically reliant on human expertise and are more likely to have subjective errors. Future directions include additional optimization of the model through additional refined feature selection methods and consideration on the possibility of using multi-modal data available through the various imaging modalities to create better classification. Moreover, adding to the data more types of tumors and the population of patients would strengthen the model and its external validity. A next step that might be beneficial is to investigate the real-time clinical use of this hybrid model in making treatment decisions and predicting patient outcomes. Besides, combining the additional genomic information which may include epigenetic alterations or single-cell sequencing may enhance the quality of tumor subtyping and further understanding of the molecular events underlying tumor heterogeneity.

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