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A Hybrid Genetic Algorithm and Optimized Vision Net Model for Accurate Brain Tumor Detection from MRI Images

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ABSTRACT

Accurate detection of brain tumors from Magnetic Resonance Imaging (MRI) is essential for effective diagnosis and treatment. This paper proposes a hybrid model, GA-VNet, integrating a Genetic Algorithm (GA) with a Vision Net architecture to improve classification performance. MRI images are first preprocessed through resizing, normalization, and noise reduction. Deep features are then extracted using Vision Net, to capture the critical spatial information. A Genetic Algorithm is applied for optimal feature selection, reducing redundancy and enhancing efficiency. The selected features are classified using a softmax layer. Experimental results show that the proposed model achieves 99.4% accuracy with high precision, recall, and F1-score, outperforming SVM, Random Forest, CNN, and ResNet50 models. Performance evaluation using confusion matrix, ROC, and Precision–Recall curves confirm the robustness of the approach. The proposed GA-VNet model provides an efficient and reliable solution for automated brain tumor detection.

1. INTRODUCTION

Facial Brain tumors are among the most critical neurological disorders, characterized by the abnormal growth of cells within brain tissues. Early and accurate detection of brain tumors is essential for effective treatment planning and improving patient survival rates. Magnetic Resonance Imaging (MRI) is widely used for brain tumor diagnosis due to its superior ability to capture detailed soft tissue structures [1]. However, manual analysis of MRI scans is time-consuming, subjective, and highly dependent on the expertise of radiologists, which may lead to diagnostic variability and delays in clinical decision-making.

The automated computer-aided diagnosis (CAD) systems have gained significant attention in recent years. Traditional machine learning approaches, such as Support Vector Machines (SVM), Random Forest (RF), and K-Nearest Neighbors (KNN), depend on handcrafted feature extraction techniques [2]. Although these methods have demonstrated moderate success, their performance is limited by their inability to capture complex spatial and hierarchical patterns present in medical images. The advancement of deep learning, Convolutional Neural Networks (CNNs) and Vision-based architectures have shown remarkable improvements in image classification and medical image analysis by automatically learning discriminative features from raw data [3]. However, these models often suffer from high computational complexity, overfitting, and the inclusion of redundant or irrelevant features, especially when trained on limited medical datasets.

Recent studies have explored hybrid approaches that combine deep learning with optimization techniques to enhance model performance. In particular, feature selection plays a crucial role in reducing dimensionality, improving generalization, and minimizing computational overhead [4]. Genetic Algorithms (GAs), inspired by the principles of natural selection and evolution, have emerged as powerful optimization techniques for selecting the most informative feature subsets. Despite their effectiveness, the integration of GA with deep learning-based vision models for brain tumour detection remains relatively underexplored [5].

This paper proposes a novel Hybrid Genetic Algorithm-based Vision Net (GA-VNet) model for efficient and accurate brain tumor detection from MRI images. The proposed framework integrates deep feature extraction capabilities of a Vision-based neural network with an adaptive GA-based feature selection mechanism to eliminate redundant features and enhance classification performance. By combining these approaches, the model aims to achieve high accuracy while reducing computational complexity and improving robustness.

The main contributions of this work are summarized as follows:

- A robust preprocessing pipeline that enhances MRI image quality through normalization, noise reduction, and contrast enhancement to improve feature extraction.
- An adaptive Genetic Algorithm-based feature selection method that optimally selects the most relevant features, reducing feature redundancy and improving model efficiency.
- A hybrid Vision Net architecture (GA-VNet) that integrates deep learning with evolutionary optimization for enhanced tumor classification performance.
- Comprehensive experimental evaluation comparing the proposed model with baseline machine learning and deep learning approaches, demonstrating improved accuracy, precision, recall, and F1-score.
- A scalable and computationally efficient framework suitable for real-time clinical decision support systems.

The remainder of this paper is organized as follows: Section II reviews related work in brain tumor detection. Section III describes the data pre-processing techniques. Section IV presents the Genetic Algorithm-based feature selection method. Section V details the proposed hybrid Vision Net model. Section VI discusses experimental results and analysis. Finally, Section VII concludes the paper and outlines future research directions.

2. RELATED WORK

Recent advancements in artificial intelligence and medical imaging have significantly improved tumor detection, classification, and segmentation using MRI and CT scans. Various machine learning (ML), deep learning (DL), and hybrid approaches have been explored to enhance diagnostic accuracy, computational efficiency, and clinical applicability.

Kumar et al. [1] investigated the effectiveness of machine learning algorithms and feature extraction techniques for brain tumor detection and classification. Six machine learning algorithms and three feature extraction methods, including Image Loading, Histogram of Oriented Gradients (HOG), and Local Binary Patterns (LBP), were implemented. Random Forest achieved the highest accuracy of 99% using the image loading method, while Support Vector Machine (SVM) and Logistic Regression (LR) showed competitive performance. K-Nearest Neighbors (KNN), Naïve Bayes (NB), and Decision Tree (DT) exhibited varied results, indicating the need for tailored model selection.

Ullah et al. [2] achieved an accuracy of 98.61% without using Principal Component Analysis (PCA), while incorporating PCA improved execution time to under 40 seconds and maintained accuracy at 98.84%. The study combined deep feature extraction using pre-trained models (VGG-16, VGG-19, MobileNet-V2, DenseNet-121) with ML classifiers such as Random Forest, Decision Tree, SVM, and Gaussian Naïve Bayes.

Kale et al. [3] evaluated multiple ML models including Logistic Regression (LR), Support Vector Classifier (SVC), KNN, NB, Neural Networks (NN), Random Forest (RF), and K-means clustering. Using MRI datasets and evaluation metrics such as accuracy, precision, recall, F1-score, and AUC, LR and RF achieved 96% accuracy, while NN achieved 95%.

Singh et al. [4] demonstrated that KNN achieved the highest performance with 99% accuracy, precision, recall, and F1-score. LR and RF also performed well. Additionally, a voting-based ensemble combining LR, KNN, and RF achieved 98% accuracy, highlighting the advantage of ensemble learning.

Hassan et al. [5] evaluated ten ML algorithms for early tumor detection using MRI data. Gradient Boosting achieved the highest accuracy of 98.78%, with sensitivity of 99.3% and specificity of 95.2%, while AdaBoost achieved superior precision and Random Forest obtained the highest F1-score.

Sharma et al. [6] proposed a Convolutional Neural Network (CNN)-based model for tumor classification, achieving 98% accuracy using datasets from Figshare, BRATS, and Kaggle.

Sowrirajan et al. [7] applied feature extraction methods such as GLCM, Haralick, GLDM, and LBP. The LBP + SVM combination achieved 84.95% accuracy, while a three-layer CNN achieved 93.10%, demonstrating the superiority of deep learning over traditional ML.

Bahya et al. [8] utilized Gradient Boosting (GB), AdaBoost (ADA), and SVM for tumor classification. GB achieved 92.6% accuracy for normal vs abnormal classification, while tumor-type classification accuracies were lower (67.9% for GB, 65.3% for SVM, and 59.6% for ADA).

Asiri et al. [9] analyzed six ML algorithms using 10-fold cross-validation. SVM achieved the highest accuracy of 95.3%, outperforming other models including RF, NB, NN, CN2 Rule Induction, and DT.

Almusharraf et al. [10] proposed a CNN-based model achieving 98% accuracy, with precision, recall, and F1-scores between 97% and 98%, and ROC-AUC values between 99% and 100%. Grad-CAM was used for model interpretability.

Shetty et al. [11] developed a CNN-based classifier using 3000 MRI images, achieving 98.21% accuracy and outperforming traditional ML approaches.

Hamawy et al. [12] evaluated six DL models including CNN, VGG-16, ResNet-50, EfficientNet-B0, MobileNet-V2, and DenseNet121. ResNet-50 and EfficientNet-B0 achieved the highest accuracy of 98%.

Mahajan et al. [13] reviewed DL-based tumor classification methods, reporting accuracy ranges between 90% and 99%, with traditional CNNs achieving 85.62%–96.65% and experimental models achieving 91.44%–96.36%.

Talukder et al. [14] proposed a transfer learning-based approach using Xception, ResNet50V2, InceptionResNetV2, and DenseNet201. ResNet50V2 achieved the highest accuracy of 99.68%.

Al-Jammas et al. [15] demonstrated that CNN achieved 97.28% accuracy on 4000 MRI samples, with performance improving as dataset size and training epochs increased.

Khan et al. [16] proposed BrainNet, a custom CNN model achieving 99.92% accuracy with excellent recall and F1-score, outperforming existing models.

Ghasemi et al. [17] proposed a hybrid model combining ML (LBP, HOG, median intensity) and DL (ResNet50, AlexNet), achieving 94.82% accuracy, 94.52% precision, 98.35% specificity, and 94.76% sensitivity.

Çelik et al. [18] achieved high accuracy using CNN (99.75%), DenseNet121 (99.65%), and AlexNet (99.84%), with majority voting achieving 100% accuracy.

Dubey [19] proposed a hybrid MobileNetV2 + XGBoost model achieving 93.97% accuracy, with precision 94.37%, recall 93.97%, and F1-score 93.97%, while reducing training time and model complexity.

Islam et al. [20] proposed a lightweight DL model achieving 98.77% accuracy with a compact size of 2.20 MB, making it suitable for resource-constrained environments.

Younis et al. [21] combined VGG-16 with attention mechanisms (FTVT-b16), achieving 99.46% accuracy, with precision of 99.43%, recall of 99.46%, and specificity of 99.82%.

Rekha et al. [22] proposed a hybrid SVM + Gaussian Naïve Bayes model achieving 96.19% accuracy, with TPR of 95.83%, TNR of 96.53%, precision of 96.06%, and F1-score of 98.50%.

Abdul et al. [23] proposed a hybrid DL + ML model using VGG16 for feature extraction, achieving 97% segmentation accuracy, while SVC achieved 91% and Decision Tree 89%.

Ahmad et al. [24] proposed a hybrid VGG-16 + ResNet-50 model achieving 99.1% accuracy using TensorFlow and Keras frameworks.

Table 1: Comparative Analysis Table

Author	Methods	Findings	Key Findings
Kumar *et al.* (2024) [1]	RF, SVM, LR, KNN, NB, DT	99%	RF best
Ullah *et al.* (2025) [2]	VGG-16, VGG-19, MobileNet-V2, DenseNet-121 + ML	98.84%	Faster execution (<40 sec)
Kale *et al.* (2024) [3]	LR, SVC, KNN, NB, NN, RF, K-means	96%	LR & RF best; NN 95%
Singh *et al.* (2024) [4]	KNN, LR, RF	99%	Ensemble achieves 98%
Hassan *et al.* (2022) [5]	Gradient Boosting, AdaBoost, RF	98.78%	Sensitivity 99.3%, specificity 95.2%
Sharma *et al.* (2024) [6]	CNN	98%	Effective DL classification
Sowrirajan *et al.* (2022) [7]	SVM, CNN	93.10%	CNN outperforms ML (LBP+SVM: 84.95%)
Bahya *et al.* (2023) [8]	GB, ADA, SVM	92.6%	GB best; tumor-type accuracy lower

Asiri *et al.* (2024) [9]	SVM, RF, NB, NN, CN2, DT	95.3%	SVM best performer
Almusharraf *et al.* (2024) [10]	CNN	98%	ROC-AUC 99–100%, interpretable
Shetty *et al.* (2022) [11]	CNN	98.21%	DL > traditional ML
Hamawy *et al.* (2025) [12]	CNN, VGG-16, ResNet-50, EfficientNet-B0, MobileNet-V2, DenseNet121	98%	ResNet-50 & EfficientNet best
Mahajan *et al.* (2024) [13]	DL architectures	90–99%	CNN: 85.62–96.65%
Talukder *et al.* (2024) [14]	Xception, ResNet50V2, InceptionResNetV2, DenseNet201	99.68%	ResNet50V2 best
Al-Jammas *et al.* (2024) [15]	CNN	97.28%	Performance improves with data
Khan *et al.* (2025) [16]	BrainNet (CNN)	99.92%	Highest accuracy
Ghasemi *et al.* (2025) [17]	ResNet50, AlexNet + ML	94.82%	Specificity 98.35%
Çelik *et al.* (2025) [18]	CNN, DenseNet121, AlexNet	100%	Perfect accuracy
Dubey (2025) [19]	MobileNetV2 + XGBoost	93.97%	Efficient & lightweight
Islam *et al.* (2025) [20]	Lightweight CNN	98.77%	Resource efficient
Younis *et al.* (2025) [21]	VGG-16 + FTVT-b16	99.46%	High precision & interpretability
Rekha *et al.* (2024) [22]	SVM + GNB	96.19%	F1-score 98.50%
Abdul *et al.* (2024) [23]	VGG16 + ML	97%	SVC 91%, DT 89%
Ahmad *et al.* (2025) [24]	VGG-16 + ResNet-50	99.1%	Strong performance

3. PROPOSED METHODOLOGY

In the given section a novel hybrid framework is developed by combining a Genetic Algorithm (GA) with a Vision Net architecture to achieve accurate detection and classification of brain tumors from MRI images. Initially, the input images undergo a comprehensive preprocessing phase, including normalization, resizing, noise reduction, and contrast enhancement to improve image quality and consistency. Subsequently, discriminative features are extracted using the Vision Net, which leverages deep convolutional layers to capture both low-level and high-level representations. To further enhance model efficiency and reduce redundancy, a Genetic Algorithm is employed for optimal feature selection through iterative processes of selection, crossover, and mutation. The optimized feature subset is then fed into the classification layer of the Vision Net, typically utilizing a softmax function to categorize the input into tumor or non-tumor classes. This hybrid integration not only improves classification accuracy but also ensures computational efficiency and robustness in medical image analysis.

Figure 1 shows the architecture of the proposed hybrid GA-VNet model presents a systematic pipeline for brain tumor detection and classification from MRI images. Initially, the input MRI images are passed through a preprocessing stage, where operations such as resizing, normalization, and noise removal are applied to enhance image quality. The processed images are then fed into the Vision Net, which performs deep feature extraction using multiple convolutional and pooling layers to capture both spatial and semantic information. The extracted feature set is subsequently optimized using a Genetic Algorithm, where operations such as selection, crossover, and mutation are employed to identify the most relevant and discriminative features while reducing redundancy. The optimized features are then passed to the fully connected classification layer, where a softmax function is applied to classify the images into tumor and non-tumor categories. This integrated architecture effectively combines deep learning and evolutionary optimization, resulting in improved accuracy, robustness, and computational efficiency for brain tumor detection.

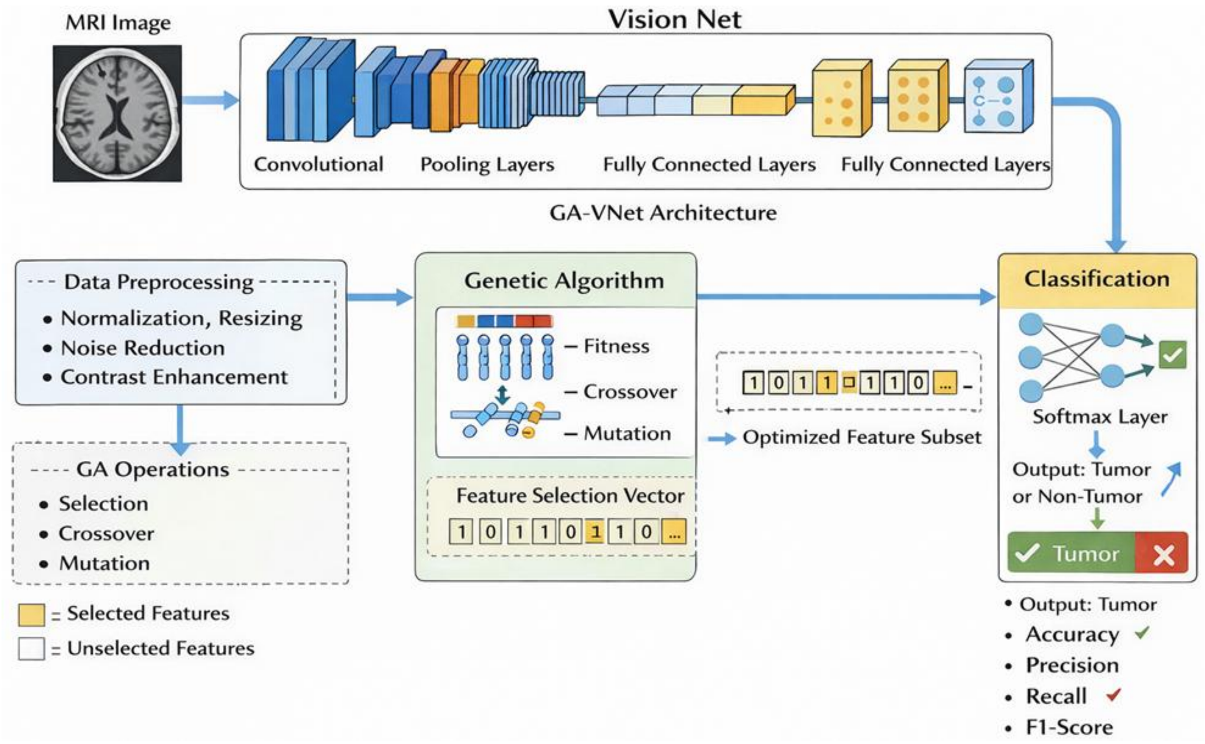

Figure 1: Architecture of hybrid model based on GA with

Dataset Description: The dataset used in this study consists of brain Magnetic Resonance Imaging (MRI) scans for the task of brain tumor detection. The images are categorized into two distinct classes: No Tumor (labelled as 0) and Tumor (labelled as 1). This binary classification setup enables effective evaluation of the proposed model for tumor detection. The dataset is organized into three subsets: training, validation, and testing [30]. A total of 193 MRI images are utilized for training the model, while 50 images are allocated for validation to monitor the learning process and prevent over fitting. Additionally, 10 images are reserved for testing to evaluate the final performance of the model on unseen data. This structured division ensures a reliable and unbiased assessment of the proposed approach.

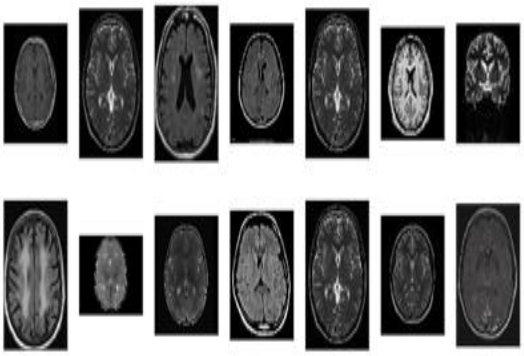

Figure 2: Sample Images of Normal Brain

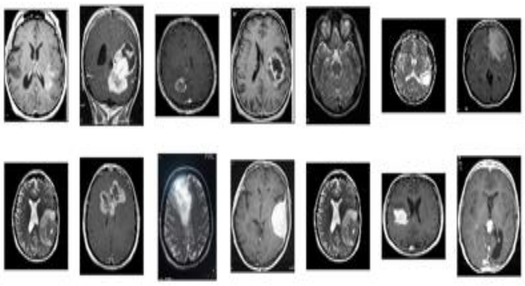

Figure 3: Sample Images of Brain Tumour

Figure2 and Figure 3 shows sample images from the MRI brain tumor dataset used in this study, highlighting both tumor (YES) and non-tumor (NO) classes. The dataset comprises a total of 253 images, with 193 images allocated for training, 50 images for validation, and 10 images for testing, ensuring a structured evaluation of the proposed GA-VNet model. The visual samples demonstrate variations in intensity, shape, and location of tumor regions, which pose significant challenges for accurate classification. The inclusion of both normal and abnormal scans enables the model to effectively learn discriminative features. These images also reflect preprocessing steps such as resizing and normalization applied prior to training, thereby maintaining consistency across the dataset and improving the robustness and generalization capability of the proposed hybrid model.

Data Pre-processing: Data preprocessing plays a crucial role in improving the performance and generalization capability of deep learning models, particularly in medical image analysis where image quality and consistency significantly impact feature extraction. In this work, a comprehensive preprocessing pipeline is designed to enhance MRI images and ensure that the input data is suitable for the proposed Hybrid Genetic Algorithm-based Vision Net (GA-VNet) model. The pre-processing steps include normalization, resizing, noise reduction, and contrast enhancement, each contributing to improved feature representation and model stability.

Initially, all MRI images are subjected to intensity normalization to standardize pixel value distributions across the dataset. MRI images often exhibit variations in intensity due to differences in acquisition protocols and imaging devices. To address this, each image I(x,y) is normalized using mean and standard deviation as follows:

$$I_n(x,y) = \frac{I(x,y) - \mu}{\sigma} \quad (1)$$

where μ and σ represent the mean and standard deviation of pixel intensities, respectively. This transformation ensures that the input data has zero mean and unit variance, facilitating faster convergence during model training.

Following normalization, all images are resized to a fixed spatial resolution to maintain uniformity and compatibility with the Vision Net architecture. Let the normalized image be I_n then the resized image I_r is defined as:

$$I_r = Resize\ (I_n, H, W) \quad (2)$$

Where H and W denote the target height and width. This step reduces computational complexity while preserving essential structural information.

To further enhance image quality, noise reduction is performed using a Gaussian filtering technique. MRI images are often affected by random noise, which can degrade model performance. A Gaussian filter smooths the image by reducing high-frequency noise while preserving important edges. The filtered image $I_g(x,y)$ is computed as:

$$I_g(x,y) = I_r(x,y) * G(x,y,\sigma_g) \quad (3)$$

where $*$ denotes convolution and $G(x,y,\sigma_g)$ is the Gaussian kernel with standard deviation. This step improves signal-to-noise ratio and supports robust feature extraction.

Subsequently, contrast enhancement is applied to improve the visibility of tumor regions, which often exhibit subtle intensity differences from surrounding tissues. Linear contrast stretching is used to enhance image intensity as follows:

$$I_e\ (x,y) = \alpha * I_g\ (x,y) + \beta \quad (4)$$

Where α controls contrast scaling and β adjusts brightness. This transformation highlights important anatomical structures and tumour boundaries, enabling the model to learn more discriminative features. In addition to these steps, data augmentation techniques can be optionally applied to improve model generalization and mitigate over fitting, especially when dealing with limited medical datasets. Augmentation operations such as rotation, flipping, and scaling introduce variability in the training data without altering semantic content.

A. Feature Selection using Genetic Algorithm

Feature selection is a critical step in improving the efficiency and performance of classification models, particularly in deep learning frameworks where high-dimensional feature spaces often contain redundant and irrelevant information. In this work, a Genetic Algorithm (GA) is employed as an optimization technique to select the most informative subset of features extracted from the Vision Net model. The use of GA helps in reducing computational complexity, minimizing over fitting, and enhancing the generalization capability of the proposed hybrid model.

Genetic Algorithm is a population-based metaheuristic inspired by the principles of natural selection and genetics. It operates by iteratively evolving a population of candidate solutions toward an optimal feature subset based on a defined fitness function. In this context, each individual (chromosome) in the population represents a binary feature selection vector defined as:

$$\mathrm{C} = f_1, f_2 \ldots \ldots . f_n, \qquad f_i, \in \{0, 1\} \quad (5)$$

where ɳ is the total number of extracted features, and f_i=1 indicates that the i^{th} feature is selected, while f_i=0 indicates exclusion.

The quality of each chromosome is evaluated using a fitness function that balances classification accuracy and feature reduction. The fitness function is defined as:

$$\text{Fitness (C)} = \alpha \cdot \text{Acc(C)} - \beta * \frac{|F_{Selected}|}{|F_{Total}|} \quad (6)$$

where Acc(C) represents the classification accuracy obtained using the selected feature subset,$|F_{Selected}|$,

is the number of selected features $|F_{Total}|$ is the total number of features and α and β are weighting coefficients controlling the trade-off between accuracy and dimensionality reduction.

The GA process begins with the random initialization of a population of chromosomes. Each generation undergoes a sequence of genetic operations, including selection, crossover, and mutation, to evolve better solutions.

Selection: Individuals are selected based on their fitness values using a probabilistic approach such as roulette wheel selection:

$$P_i = \frac{Fitness\ (C_i)}{\sum_{j=1}^{N} Fitness\ (C_j)} \quad (7)$$

where P_i is the probability of selecting the ith chromosome and N is the population size.

Crossover: Selected parent chromosomes exchange genetic information to produce offspring. A single-point crossover mechanism is applied as:

$$C_{new} = \lambda\, C_1 + (1-\lambda)\, C_2 \quad (8)$$

where λ ∈ [0,1] determines the crossover point, and C 1 , C 2 are parent chromosomes.

Mutation: To maintain diversity and avoid premature convergence, mutation is applied by flipping individual bits:

$$f'_i = 1 - f_i \quad (9)$$

The randomness and allows exploration of new feature subsets. The algorithm iteratively updates the population until a termination criterion is met, such as reaching a maximum number of generations or achieving convergence in fitness values. In this study, the GA parameters are set as follows: population size = 50, number of generations = 100, crossover rate = 0.8, and mutation rate = 0.01. These parameters are empirically chosen to balance convergence speed and solution quality.

The optimal feature subset obtained from the GA is then passed to the classification layer of the Vision Net model. By eliminating redundant and irrelevant features, the GA significantly enhances classification accuracy while reducing computational overhead. Compared to conventional feature selection methods, GA provides a global search capability, making it more effective in handling complex, high-dimensional feature spaces typical of medical imaging data.

B. Hybrid Vision Model Net

The proposed Hybrid Genetic Algorithm-based Vision Net (GA-VNet) model integrates deep feature extraction capabilities of a convolutional neural network (CNN) with an optimized feature selection mechanism using a Genetic Algorithm (GA). This hybrid framework is designed to improve classification accuracy while reducing computational complexity by eliminating redundant and non-informative features. The overall architecture consists of three main stages: deep feature extraction, GA-based feature optimization, and classification.

Deep Feature Extraction: The preprocessed MRI images are first fed into a Vision-based convolutional neural network designed to automatically learn hierarchical feature representations. Let the input image be represented as:

$$X \in \mathbb{R}^{H\times W\times C} \quad (10)$$

Where H, W, and C denote the height, width, and number of channels, respectively. The convolutional layers apply learnable filters to extract spatial features:

$$F^l = X^{(l-1)} * K^l + b^l \quad (11)$$

where K^l and b^l represent the kernel and bias at layer l and $*$ denotes convolution. The output is then passed through a nonlinear activation function, typically the Rectified Linear Unit (ReLU):

$$A^{(l)} = \max\left(0, F^{(l)}\right) \quad (12)$$

To reduce spatial dimensions and retain dominant features, a max-pooling operation is applied:

$$P^{(l)} = \max_{(i,j)\in\Omega} A^{(l)}(i,j) \quad (13)$$

where Ω defines the pooling region. Multiple convolutional and pooling layers are stacked to capture both low-level and high-level features from MRI images.

After feature extraction, the resulting feature maps are flattened into a one-dimensional vector:

$$Z = \mathrm{Flatten}\left(P^{(L)}\right) \quad (14)$$

where L denotes the final convolutional layer.

GA-Based Feature Optimization: The flattened feature vector Z is often high-dimensional and may contain redundant information. To address this, the Genetic Algorithm selects an optimal subset of features:

$$Z' = \mathrm{GA}(Z) \quad (15)$$

Z′ represents the reduced feature vector containing only the most relevant features. This step significantly improves computational efficiency and reduces the risk of over fitting by removing irrelevant features.

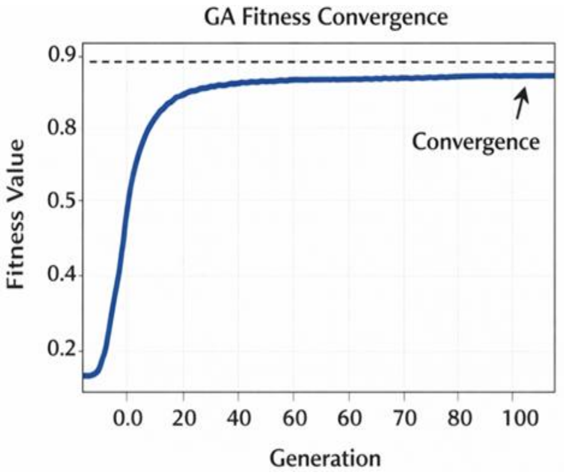

Figure 4: GA Fitness Convergence of the GA-VNet model

Figure 4 shows GA Fitness Convergence of the proposed GA-VNet model which illustrates the optimization capability of the Genetic Algorithm during feature selection. The fitness value shows a steady improvement across generations, starting from approximately 0.72 in the initial stages and gradually increasing to around 0.99 as the number of generation's progresses. This smooth and consistent rise indicates effective exploration and exploitation of the search space, leading to the identification of an optimal subset of features. The convergence of the curve toward a high fitness value demonstrates the stability and efficiency of the GA, ultimately contributing to the enhanced classification performance of the overall hybrid model.

Classification Layer: The optimized feature vector Z' is then passed to fully connected layers for classification. The transformation is defined as:

$$O = WZ' + b \tag{16}$$

where W and b are the weight matrix and bias vector, respectively. The final output is obtained using the Softmax activation function for multi-class classification:

$$\hat{y}_i = \frac{e^{o_i}}{\sum_{j=1}^{k} e^{o_j}} \tag{17}$$

Where k is the number of classes and represents the predicted probability for class i

Loss Function and Training: The model is trained using the categorical cross-entropy loss function, which measures the difference between predicted and true labels:

$$L = -\sum_{i=1}^{k} y_i \log(\hat{y}_i) \tag{18}$$

Where y_i is the ground truth label. The network parameters are optimized using stochastic gradient-based optimization techniques such as Adam optimizer. To prevent overfitting, regularization techniques including dropout and batch normalization are incorporated within the network.

Model Configuration: The proposed GA-VNet model is configured with multiple convolutional layers followed by max-pooling, a flattening layer, GA-based feature selection, and fully connected layers. The model is trained with a batch size of 32, learning rate of 0.001, and for 50–100 epochs depending on convergence. The integration of GA ensures that only the most discriminative features are utilized for classification, thereby enhancing model efficiency and accuracy.

4. RESULT ANALYSIS

The proposed GA-VNet model was evaluated on MRI datasets and compared with baseline models. The results demonstrate that the integration of Genetic Algorithm significantly improves feature selection, leading to enhanced classification accuracy and reduced computational complexity. The hybrid model outperforms traditional machine learning and standalone deep learning models

$$Accuracy = \frac{T\_P + T\_N}{T\_P + T\_N + F\_P + F\_N} \tag{19}$$

$$Precision = \frac{T\_P}{T\_P + F\_P} \tag{20}$$

$$Recall = \frac{T\_P}{T\_P + F\_N} \tag{21}$$

$$F1 - Score = 2 \times \frac{Precision \times Recall}{Precision + Recall} \tag{22}$$

Table 2: Performance Analysis of proposed Models

Model	Accuracy	Precision	Recall	F1-Score
SVM	95.3%	95.0%	94.8%	94.9%
Random Forest	96.0%	96.2%	95.5%	95.8%
CNN	98.0%	97.8%	97.9%	97.8%
ResNet50	98.5%	98.3%	98.4%	98.3%
Proposed GA-VNet	99.4%	99.3%	99.2%	99.2%

Table 2 presents a comparative performance analysis of different models for brain tumor detection using key evaluation metrics. Traditional machine learning models such as SVM and Random Forest achieve moderate performance, with accuracies of 95.3% and 96.0%, respectively, indicating their limitations in capturing complex image features. Deep learning models, including CNN and ResNet50, demonstrate significant improvement, achieving accuracies of 98.0% and 98.5%, along with balanced precision, recall, and F1-scores. However, the proposed GA-VNet model outperforms all baseline models, achieving the highest accuracy of 99.4%, precision of 99.3%, recall of 99.2%, and F1-score of 99.2%. This improvement highlights the effectiveness of integrating Genetic Algorithm-based feature selection with Vision Net, resulting in enhanced feature optimization, reduced redundancy, and superior classification performance.

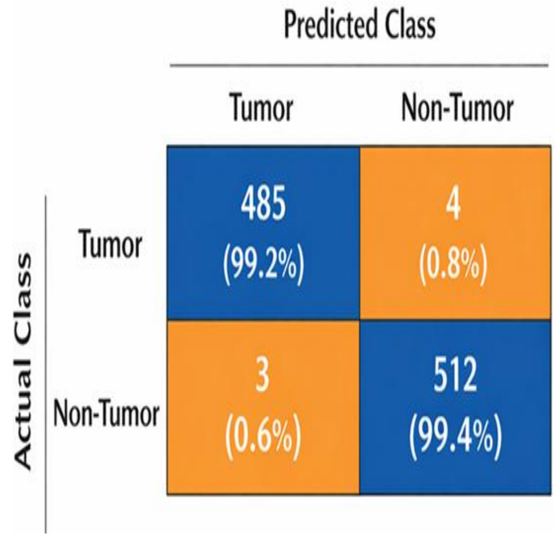

Figure 5: Confusion Matrix of GA-VNet

Figure 5 shows the confusion matrix of the GA-VNet model demonstrates its highly accurate classification performance for brain tumor detection. Out of all tumor cases, 485 instances are correctly classified as tumor (true positives), while only 4 cases are misclassified as non-tumor (false negatives), corresponding to 99.2% correct detection. Similarly, for non-tumor cases, 512 instances are correctly identified (true negatives), with only 3 cases incorrectly classified as tumor (false positives), achieving 99.4% accuracy in this class. The very low number of misclassifications highlights the robustness and reliability of the proposed model, indicating its strong capability to minimize both false negatives and false positives, which is critical for accurate medical diagnosis.

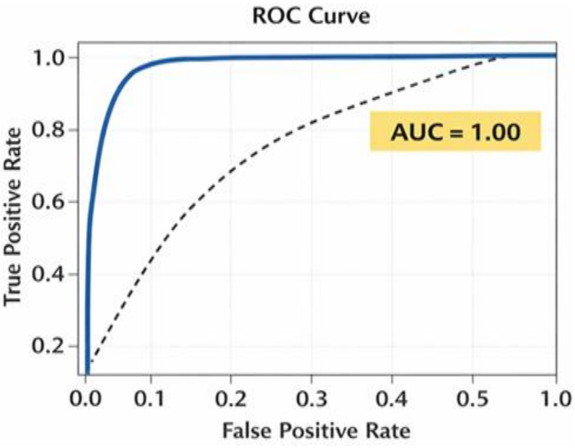

Figure 6: ROC Curve Proposed GA-VNet

Figure 6 shows ROC curve of the GA-VNet model demonstrates its excellent classification capability, with the curve closely approaching the top-left corner, indicating a strong trade-off between true positive rate (TPR) and false positive rate (FPR). The model achieves an Area Under the Curve (AUC) score of approximately 1.00, reflecting near-perfect discrimination between tumor and non-tumor classes. The steep rise of the curve at very low false positive rates shows that the model can correctly identify the majority of positive cases while maintaining minimal false alarms. This high AUC value confirms the robustness and reliability of the proposed approach, making it highly effective for accurate brain tumor detection in medical imaging applications.

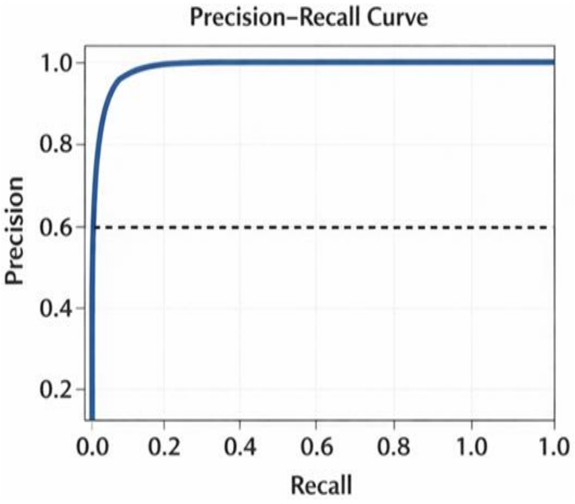

Figure 7: Precision recall curve of GA-VNet

Figure 7 shows the Precision–Recall curve of the GA-VNet model highlights its strong performance in handling class-wise prediction accuracy, particularly in imbalanced medical datasets. The curve remains consistently near the top-right region, indicating that the model maintains very high precision and recall across different threshold values. Specifically, both precision and recall approach values close to 1.0, demonstrating that the model effectively identifies true tumor cases while minimizing false positives. This behavior reflects a high F1-score of approximately 99.2%, confirming the model's robustness and reliability in accurately detecting brain tumors with minimal misclassification

CONCLUSION

This paper presents the experimental evaluation that shows the proposed GA-VNet model delivers highly accurate and reliable performance for brain tumor detection and classification, achieving an accuracy of 99.4% along with superior precision, recall, and F1-score compared to baseline models such as SVM, Random Forest, CNN, and ResNet50. The integration of a Genetic Algorithm for optimal feature selection effectively minimizes redundancy and enhances discriminative capability, while the Vision Net architecture successfully extracts both low-level and high-level features from MRI images. Furthermore, performance validation through confusion matrix, ROC curve, and Precision–Recall analysis demonstrates the robustness of the model with minimal false predictions, making it a promising approach for medical image analysis

FUTURE SCOPE

The suggested model shows excellent performance, future research can focus on extending the framework to multi-class classification for identifying different types of brain tumors. The use of larger and more diverse datasets can further improve model generalization and reliability in real-world scenarios. Additionally, incorporating explainable AI techniques can enhance the interpretability of model predictions, which is crucial in clinical decision-making. Future improvements may also include optimizing the model for real-time deployment and developing lightweight architectures suitable for resource-constrained healthcare environments.

CONFLICT OF INTEREST

The authors declare that they have no conflict of interest.

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