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OPTIMIZED DEEP LEARNING FRAMEWORK FOR BRAIN TUMOR CLASSIFICATION USING GENETIC ALGORITHM-DRIVEN HYPERPARAMETER SELECTION

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Abstract

Early and precise brain tumor detection is crucial to optimal treatment planning and patient outcome. Traditional MRI diagnosis tends to be time-consuming and subject to interobserver variations. For accurate and efficient diagnosis, we outline a deep learning framework with incorporation of Convolutional Neural Networks (CNN) coupled with Genetic Algorithm (GA)-assisted hyperparameter optimization for brain tumor automatic classification. The model is trained on a dataset of 7,023 MRI scans into Glioma, Meningioma, Pituitary, and No Tumor classes. For enhanced model robustness, Brain Data Augmentation (BDA) methods, such as affine transformation and intensity normalization, were performed. GA was used to tune important hyperparameters like learning rate, batch size, and epochs for training to enable better convergence and reduce overfitting. The VGG-16 model optimized showed a classification accuracy of 99%, with better sensitivity and specificity by tumor type. Confusion matrix analysis also proved that there was little misclassification, especially between tumors with similar morphology. This work highlights the potential of AI-based diagnostic platforms in neuro-oncology as a precise, reproducible, and efficient tool for the detection of brain tumors. Upcoming studies will investigate multi-modal image fusion, deep ensemble learning, and explainable AI methods for improving clinical relevance and decision support systems.

Keywords:
Brain tumor classification, Convolutional Neural Networks (CNNs), Genetic Algorithm (GA), Magnetic Resonance Imaging (MRI), Deep learning, Hyperparameter optimization.

1. Introduction

Brain tumors are abnormal growths of brain or adjacent tissue cells and are classified as benign or malignant. They can result in severe health complications such as neurological dysfunction, mental impairments, and death. The World Health Organization ranks brain tumors as one of the top cancer-related death-causing disorders throughout the world. The key components for achieving successful treatments and better results require early diagnosis together with precise tumor classification [1].

The physial consequences of brain tumors spread to the emotional sphere and psychological condition of patients. Multiple symptoms including headaches as well as seizures and vision problems and cognitive decrease dramatically diminish the quality of life and produce long-term disability. Brain tumor diagnosis creates major emotional burdens and financial distress for families because families need immediate and precise medical verification [2].

The current diagnostic techniques in medicine bring about results through scanning methods including Magnetic Resonance Imaging (MRI) and Computed Tomography (CT) scans. MRI stands out because of its advanced soft tissue contrast capabilities that create detailed images of brain anatomy which serves to detect tumors and all other surrounding abnormalities. The emergency medical capabilities of CT scanners contrast with their limited performance when viewing soft tissues although they maintain crucial diagnostic role in emergency rooms [3].

Brain tumor classification systems show high complexity which adds difficulty to diagnostic procedures. Brain tumor diagnosis becomes more complex since physicians need accurate classification because different brain tumors have varying characteristics and treatment methods among the 120 distinct types. When a diagnosis fails to match the correct treatment another patient receives inappropriate healthcare which produces unsatisfactory treatment results [4]. This challenge underscores the need for advanced diagnostic tools that can improve accuracy and consistency.

Recent developments in artificial intelligence (AI), especially machine learning and deep learning, hold great potential. Convolutional Neural Networks (CNNs) have proven very successful in interpreting medical images, detecting patterns hard for the human eye to spot. Current deep learning models, however, struggle with hyperparameter tuning and extracting the right features, typically resulting in underperformance [5]. Traditional optimization techniques like Stochastic Gradient Descent (SGD) [6] and Adam may not always converge to the best solutions, limiting their effectiveness [7].

This study overcomes these limitations by combining Genetic Algorithms (GAs) with deep models. GAs, drawing from natural selection, search for optimal hyperparameters and feature subsets, improving the performance of CNN-based classification models for brain tumors. By using GAs, this work attempts to enhance diagnostic accuracy, minimize overfitting, and yield a more solid framework for MRI-based brain tumor detection.

Despite the developments in imaging technologies and AI, accurate and timely classification of brain tumors is still a major challenge. Image interpretation variability, complexity of tumor types, and shortcomings of current deep learning models restrict consistent and dependable diagnoses. Improved techniques are needed with a high demand to improve diagnostic accuracy and decrease dependence on subjective human interpretation.

Existing deep learning models for brain tumor classification usually lack good hyperparameter tuning and feature selection, resulting in poor performance. Traditional optimization methods such as SGD and Adam are commonly adopted but may not always yield the best performance. This research addresses this gap by investigating the combination of Genetic Algorithms (GAs) to optimize deep learning models to enhance their accuracy and resilience in brain tumor classification.

Table [1] shows accuracy, sensitivity, and specificity to classify normal and abnormal brain MR images. VGG-16 with AQO model performed exceptionally well in abnormality detection, with 97.46% sensitivity, 96.89% accuracy, and 98.2% specificity for normal [8].

Table 1 Performance Comparison of Deep Learning Models in Brain Tumor Classification

CNN Model	Class	Accuracy (%)	Sensitivity (%)	Specificity (%)
VGG-16 with AQO	Normal	96.89	97.46	98.9
	Abnormal	97.52	99	98.2

This research has significant implications for both medical diagnostics and AI applications in healthcare [9]. By improving the accuracy and efficiency of brain tumor classification, the study aims to:

- Enable faster and more reliable diagnoses.
- Reduce the workload of medical professionals by automating routine tasks.
- Improve patient outcomes through early detection and personalized treatment plans.

The research examines significant obstacles associated with deep learning model utilization for brain tumor identification through Genetic Algorithm implementation. The main research investigation determines the way Genetic Algorithms modify Convolutional Neural Network (CNN) model performance. This research evaluates how GAs enhances the hyperparameter optimization process of CNN brain tumor detection systems. The research studies how Genetically Altered features affect MRI-based diagnosis of brain tumors through classification accuracy analysis and how GAs affect the optimization of CNN parameters for brain tumor identification. The research wants to demonstrate how GAs resolves traditional optimization challenges including suboptimal convergence and overfitting in optimization processes.

This study has three main research objectives. The research optimizes deep learning models through VGG-16 implementation of Genetic Algorithms for adjusting hyperparameters and selecting features [10]. The research evaluates how GA-optimized models function to prevent overfitting while improving generalization potential of networks. A performance analysis between GA-optimized and conventional deep learning models happens utilizing standard evaluation metrics including accuracy and F1-score and precision and recall. Assessment of these objectives supports the creation of precise robust tools for brain tumor diagnosis which improves clinical practice outcomes.

This research expands AI and medical imaging literature by presenting a new optimization strategy for deep learning model development. The discovered results demonstrate practical value for medical applications since they provide both superior brain tumor identification precision alongside more effective processing. This research addresses existing method limitations to create enhanced diagnostic equipment which results in superior patient results.

This study focuses on optimizing three CNN architectures VGG-16 using Genetic Algorithms. The research is conducted on a dataset of MRI images for brain tumor classification, with performance evaluated using metrics like accuracy and F1-score. According to our paper, Section 2 covers related work, Section 3 describes the proposed brain tumor classification model, Section 4 presents experimental results, and Section 5 concludes the study.

2. Related Work

Deep learning has revolutionized medical diagnostics, offering precise and automated solutions for disease detection [11]. This literature review discusses key studies in medical imaging and deep learning, highlighting advancements and gaps in research.

CNNs are widely used in medical image analysis due to their ability to detect patterns in images. Abdusalomov et al. [12] utilized a fine-tuned YOLOv7 with CBAM and SPPF+, achieving a 99.5% detection rate, though challenges remain in detecting small tumors. Ahmed et al. [13] proposed a hybrid model combining Vision Transformers with GRU, outperforming traditional methods with high accuracy and real-time diagnostic potential. Celik & Inik [14] integrated CNNs with classical machine learning techniques, attaining a 97.15% accuracy rate while focusing on efficient computation. Khairandish M et al. [15] combined Full Resolution Convolutional Networks with SVM for brain tissue classification, demonstrating high clinical applicability. Rastogi D et al. [16] employed generative models with CNNs, achieving up to 96.11% accuracy using ResNet50 and Xception, highlighting the effectiveness of deep CNNs in tumor detection.

Further research has optimized specific tumor classifications, such as Lakshmi Prasanthi & Neelima [17], who developed a hybrid deep learning model for glioma detection, achieving 96.63% precision. Umarani et al. [18] enhanced brain tumor segmentation using U-Net with self-attention mechanisms, surpassing existing techniques in accuracy but requiring real-time applicability improvements.

Kilicarslan et al. [19] explored nutritional anemia detection using a GA-CNN model, achieving 98.5% accuracy, with potential extensions to other health-related conditions. Ibrahim et al. [20] introduced a quantum-inspired genetic algorithm for efficient feature selection, improving medical classification accuracy to over 98%. AbdulRazek et al. [21] tackled data augmentation limitations using a GAN-GA model, improving medical image quality by 6.8%, offering potential for real-time applications. Dar & Ganivada [22] demonstrated the effectiveness of MobileNet with genetic algorithms for breast ultrasound classification, enhancing early detection. Gasmi et al. [23] proposed an ensemble of Vision Transformers and EfficientNet-V2, achieving 95% classification accuracy for brain tumors.

Several studies have explored hybrid approaches and transfer learning to optimize medical image classification. Balamurugan & Gnanamanoharan [24] developed a segmentation technique combining genetic algorithms with fuzzy C-means, achieving 99.33% accuracy. Gencer K, Gencer G (2025) [25] introduced hybrid machine learning models for multi-type brain tumor classification, emphasizing improved feature extraction. Wageh et al. [26] utilized transfer learning with deep learning architectures, achieving 99.7% accuracy across two brain tumor datasets. Chhabra & Kumar [27] fine-tuned a VGG16 model for pneumonia detection, attaining 93.6% accuracy and highlighting the impact of data augmentation. Sorour et al. [28]employed the VGG16 model to classify medical images for brain tumors and Alzheimer’s disease, achieving strong performance across multiple conditions.

Other research has focused on hyperparameter optimization and explainability in AI models. Basha et al. [29] combined VGG16 with transfer learning, achieving 99% accuracy for brain tumor detection and segmentation. Lakide et al. [30] improved lung cancer classification accuracy using a modified ResNet50 architecture, obtaining 98.1% precision. Oladimeji & Ibitoye [31] integrated CBAM with ResNet50 for better feature representation, enhancing brain tumor classification. M et al. [32] incorporated Grad-CAM with ResNet50, achieving 98.52% accuracy while improving model interpretability. Sowrirajan et al. [33] leveraged VGG16 for MRI-based brain tumor classification, achieving 98% accuracy and proposing comparisons with other deep learning models.

Optimization techniques help improve the performance of deep learning models. Genetic Algorithms (GAs) have been used to fine-tune CNNs by selecting the best parameters. A study by Pérez-Núñez et al. [34] optimized CNNs with GAs to detect breast cancer in mammograms, leading to higher accuracy compared to standard CNN models.

Brain tumors differ from other diseases like lung disease, breast cancer, and Alzheimer’s due to their irregular shapes, varying textures, and overlapping features in MRI scans, making classification more challenging. Genetic Algorithms (GA) are needed to optimize hyperparameters, improve model generalization, and enhance feature extraction, ensuring higher accuracy in distinguishing between similar tumor types.

Our study aims to address this gap by applying advanced deep learning techniques specifically for brain tumor identification.

Most of the medical research adopts datasets that are limited in samples and share common patterns thus prone to overfitting issues. The model indicates good performance when handling training datasets without showing adequate results for fresh clinical examples. The model's generalization capabilities will improve through our research by combining extensive datasets with diverse content. Our method trains on multiple MRI scan types to create a system that enhances the practice of brain tumor diagnosis. The high accuracy rates of certain deep learning systems make them difficult to use clinically because of their demanding computational requirements. The research explores precision vs performance efficiency through parameter tuning of CNNs by Genetic Algorithms. The model execution will deliver satisfactory results while using minimal hardware power requirements.

Medical imaging benefits considerably from deep learning thanks to CNNs together with optimization methods and ensemble learning approaches. Brain tumor detection methods face continuing problems with limited datasets together with issues related to computational speed and model application scope. The research expands previously performed experiments by applying Genetic Algorithms to optimize CNN parameters for brain tumor identification. This research work addresses the critical gaps found in earlier studies to help develop better practical medical diagnostic equipment.

3. Materials and Methods

In this section organized methodology for brain tumor classification which promotes dependable model development. The methodology encompasses five distinct steps including Data Collection followed by Preprocessing and then Feature Extraction along with Selection before Model Development before Validation. Every step strengthens the classification system in terms of accuracy and efficiency and clinical implementation capabilities thus creating a strong dependable process.

3.1 Process Modeling

This part describes the methodology adopted for brain tumor classification through deep learning approaches, classification using deep learning techniques. The process includes data collection, preprocessing, model training, and evaluation.

3.1.1 Data Collection

To obtain a complete representation of brain tumors the first operation requires acquiring MRI datasets from various sources. The team has assembled publicly accessible datasets as well as medical institution collaborative data [35].

Table 2 Dataset Collection

Attribute	Details	Attribute	Details
Total Images	7,023 MRI brain images	**Classes**	Glioma, Meningioma, Pituitary, No Tumor
Dataset Sources	figshare (Glioma)	**MRI Imaging Planes**	Axial: Topdown view
	SARTAJ (Corrected Glioma)		Sagittal: Side view
	Br35H (No Tumor)		Coronal: Front view
Training Set	Glioma: 300	**Testing Set**	Glioma: 1,311
	Meningioma: 306		Meningioma: 1,311
	No Tumor: 405		No Tumor: 1,311
	Pituitary: 300		Pituitary: 1,311
Image Intensity	Hyperintensity: Bright abnormal regions	**Key Features for Tumor Classification**	**Glioma:** Glial cell tumors, common in frontal/temporal lobes
	Hypointensity: Dark normal/necrotic tissue		**Meningioma:** Protective layer tumors, welldefined
			Pituitary: Near pituitary gland, base of brain
			No Tumor: Normal scans for comparison

3.1.2 Data Augmentation

The application of different data augmentation methods helps both increase the diversity of datasets and strengthen generalization abilities of models. All images receive fixed dimensions before processing by the system.

The model receives images with (224x224 pixels) uniform size to maintain consistency and learns tumor recognition through random rotations presented at different orientation angles. The model gains resistance to diverse tumor placement locations through the addition of flipping operations both horizontally and vertically. Random zooming techniques add distance variations to the data which helps the model maintain its independence from tumor size.

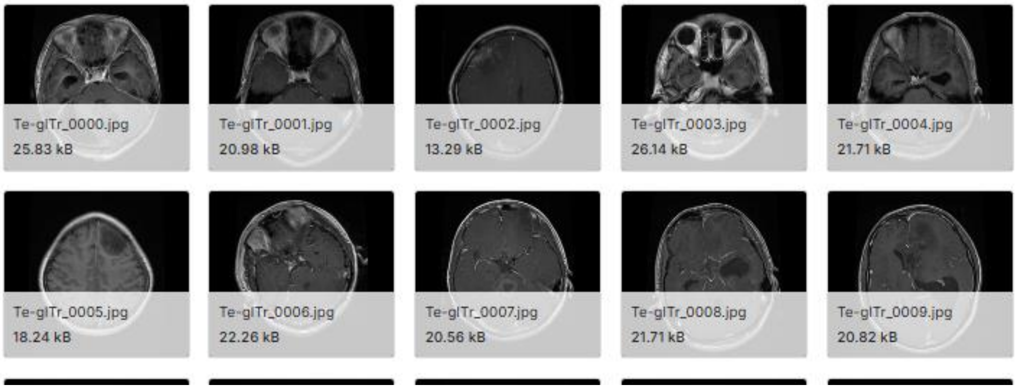


Figure 1 Augmented Dataset

3.1.3 Data Split

The dataset contains three sections to optimize training along with the evaluation process. An amount of 50% from the training set allows the model to identify patterns which reveal brain tumor attributes. The validation set with 25% of the data performs parameter optimization to prevent training overfitting. The testing set delivers unbiased model performance evaluation by including 25% of the data which has never been shown to the model.

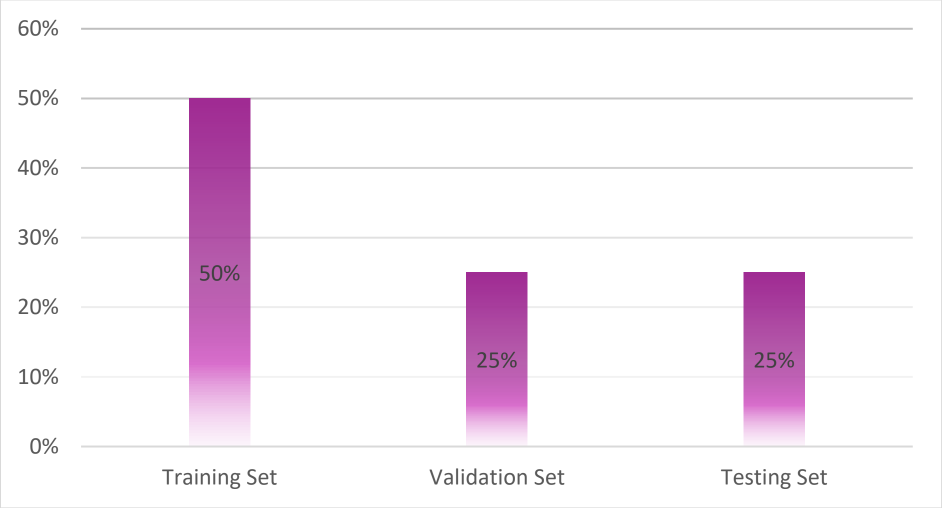


Figure 2 Dataset Splitting

3.1.4 Image Rescale

All images require normalization of pixel intensity values through rescaling until they span either the [0,1] or [-1,1] range. Model training convergence becomes faster because of normalization which results in better overall performance.

3.1.5 Deep Learning Model Training

The deep learning model receives the final images as input after technicians apply all previously discussed techniques. A final check includes verifying the images use correct tensor format as well as applying relevant preprocessing steps necessary for the selected model architecture.

3.1.6 Hyperparameter Selection using Genetic Algorithm

The deep learning model reaches optimal performance through the implementation of hyperparameter selection performed by Genetic Algorithms. Genetic Algorithms enable an efficient search of hyperparameter space which results in better model performance.

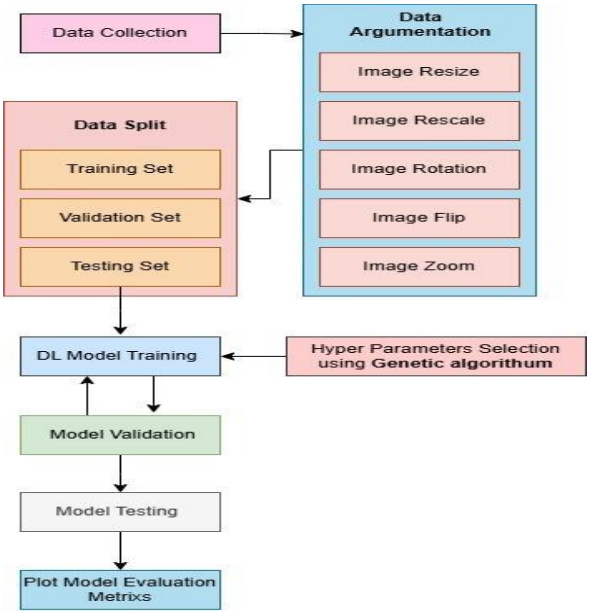


Figure 3 Flow chart of our proposed study

3.1.7 Preprocessing Steps

Our data preprocessing included directing images into orderly folders and keeping file paths within a data frame before separating the images into training and validation and test splits. Data augmentation processes which included rescaling and flipping along with rotation were used to boost model effectiveness while normalization optimized convergence time and maintained data stability.

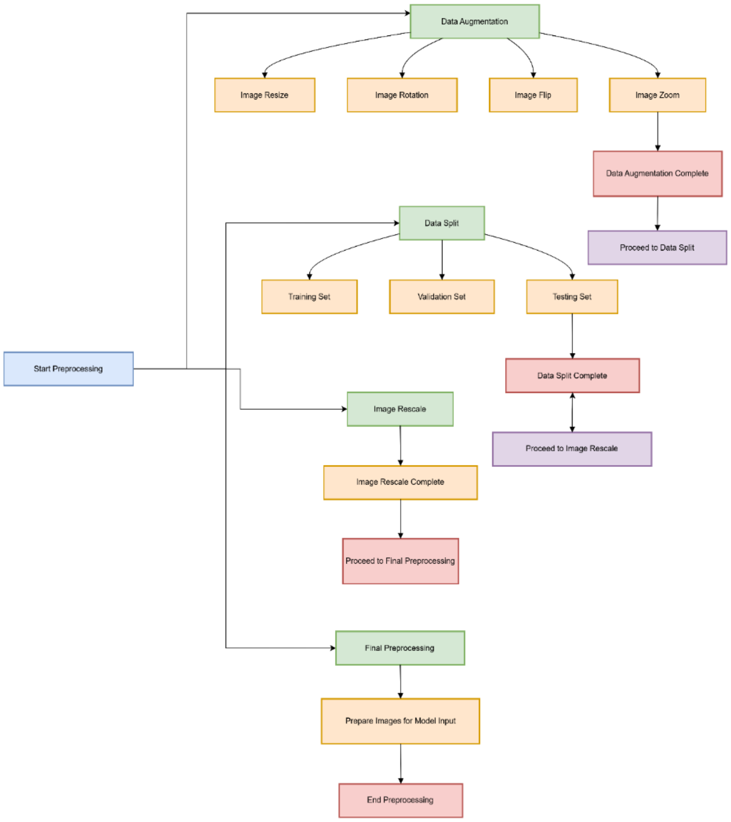


Figure 4 Preprocessing Steps

3.2 Hyperparameter Selection Techniques

Our brain tumor classification methodology utilizes Genetic Algorithms (GAs) as an efficient tool to select the best hyperparameters which will enhance deep learning model performance. Traditional methods for modelling medical imaging data such as Grid or Random Search are considered computationally costly because of their complexity. GAs enables the adaptive search of hyperparameter combinations through which they maintain exploration-exploitation balance for maximizing classification accuracy. A population of potential hyperparameter sets that contains learning rate, batch size and network architecture runs as the process's first step. Each set is evaluated based on classification accuracy using k-fold cross-validation. The best-performing sets undergo selection, crossover, and mutation to refine hyperparameters iteratively. This ensures convergence toward optimal values, improving the model's ability to classify brain tumors from MRI scans.

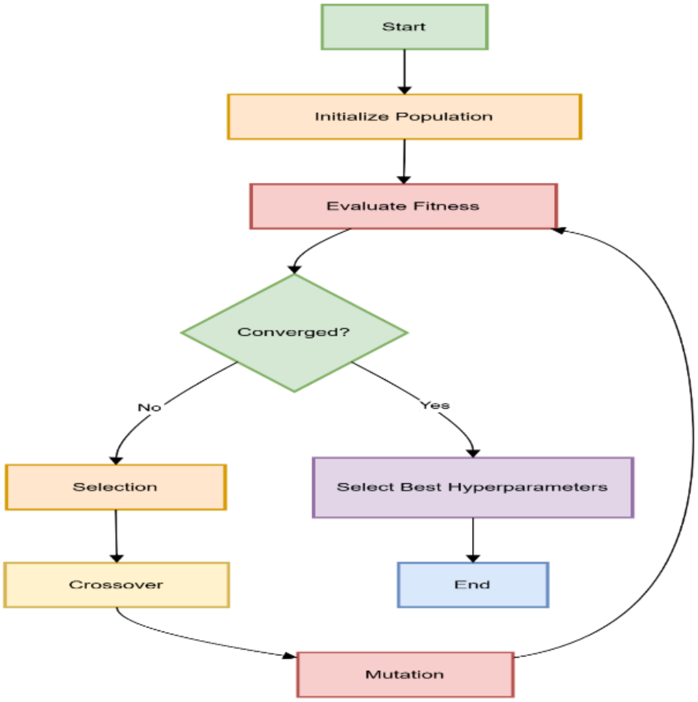


Figure 5 Feature Selection Diagram

3.3 VGG16 and Genetic Algorithm (GA)

This study classifies brain tumor MRI images into four categories using a CNN built on VGG16 with custom layers. A Genetic Algorithm (GA) optimizes hyperparameters like learning rate, optimizer, epochs, and batch size through selection, crossover, and mutation. GA iteratively refines the best performing combinations, enhancing model accuracy and efficiency.

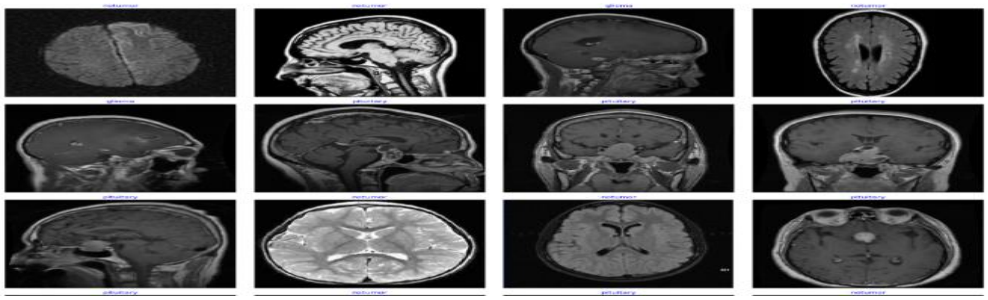


Figure 6 Image preprocessing

The dataset is split into training, validation, and testing sets. Image preprocessing includes normalization and data augmentation techniques like rotation, shifting, and zooming for training, while validation and test sets are only rescaled. The model, built on VGG16, replaces the top layers with custom layers: a GlobalAveragePooling2D layer, a fully connected layer with 128 neurons and ReLU activation, and a softmax output layer for fourclass classification. Compiled with the Adam optimizer (learning rate 0.01) and categorical crossentropy loss, the model is trained for 30 epochs, tracking accuracy and loss for both training and validation sets.

After training, the model achieves a 99% test accuracy, with strong performance in the "No Tumor" and "Pituitary" categories. However, it struggles to distinguish between Glioma and Meningioma, likely due to data imbalances or similarities between these classes. Genetic algorithmbased hyperparameter optimization improves training efficiency and overall performance. Future enhancements could include additional data augmentation, finetuning VGG16, or exploring alternative architectures.

Table 3 Algorithm of CNN + Genetic Algorithm (GA)

```
Input:
    Abnormal A segmented Brain MR data
    Normal N segmented Brain MR data
Processing:
    Step 1: Apply BDA data augmentation:
        Augment both abnormal and normal images (rotate, flip)
    Step 2: Preprocess the augmented data:
        Normalize pixel values of augmented images to [0, 1]
    Step 3: Initialize the Genetic Algorithm:
        Define population size P, generations G, mutation rate M, and crossover rate C
        Initialize the candidate solutions (hyperparameters)
    Step 4: Run Genetic Algorithm to find optimal hyperparameters for CNN:
        Select, crossover, and mutate the population to find the best hyperparameters
        Evaluate CNN performance for each set of hyperparameters
    Step 5: Define and train the optimized CNN model:
        Use the optimal hyperparameters found by the GA
        Train the CNN with augmented data (from BDA)
    Step 6: Evaluate the trained CNN model:
        Evaluate performance on validation or test data
Output:
    Trained CNN model with optimized hyperparameters for classifying brain MRI images as normal or abnormal
```

The proposed algorithm, shown in Table [3], integrates a Convolutional Neural Network (CNN) with a Genetic Algorithm (GA) to enhance brain MRI image classification. The process begins with data augmentation techniques like rotation and flipping to improve model adaptability. Images are then normalized and preprocessed for CNN training. GA is applied to optimize hyperparameters by evolving multiple configurations through selection, crossover, and mutation. Once the best combination is found, the CNN is trained on the augmented data and tested on unseen samples. This approach improves classification accuracy by leveraging GA to finetune the CNN's performance.

4. Results

The research utilizes Genetic Algorithms (GA) combined with Convolutional Neural Networks (CNNs) for improving Magnetic Resonance Imaging (MRI) scans classification into brain tumors. GA optimizes the base architectural features of VGG16 through a hyperparameter adjustment process that includes learning rate modifications and batch size and dropout rate adjustments to enhance both accuracy and system robustness. The performance assessment employs accuracy as well as sensitivity and specificity together with precision and F1score. The analysis of visual data through accuracy tables and learning curves and confusion matrices reveals positive effects on performance from GA based optimization methods. The next sections present methodologies for preprocessing data and methods to select hyperparameters in addition to the evaluation procedures.

4.1 Hyperparameter Tuning Process

The section presents groups of hyperparameters including batch size together with optimizer type and learning rate and epochs which were implemented for experimental training of the model. Each "individual" refers to one combination of these parameters:

4.1.1 Individual 1

The results for Individual 1 highlight the model's effectiveness in brain tumor detection. Trained with a batch size of 32, the Adam optimizer, and a learning rate of 0.0001, the model achieved stable learning over 20 epochs, balancing efficiency and accuracy.

a) Accuracy Trends

The accuracy graphs show steady improvement over 17.5 epochs, with training accuracy reaching 100% and validation stabilizing at 95%, ensuring strong generalization for brain tumor detection.

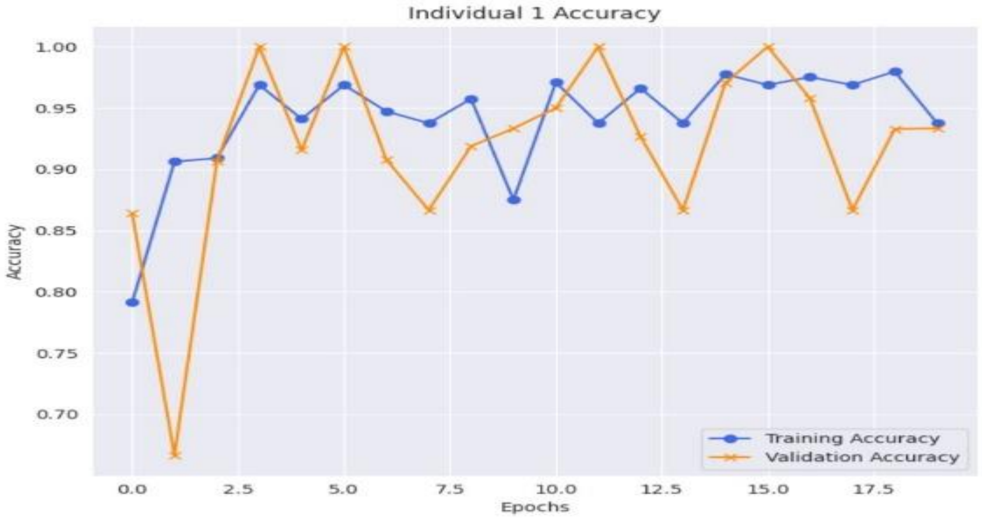


Figure 7 Individual 1Accuracy Trend

b) Loss Trends

The loss graphs show a steady decrease in training loss, indicating effective learning. Validation loss remains low, confirming minimal overfitting and consistent tumor detection accuracy.

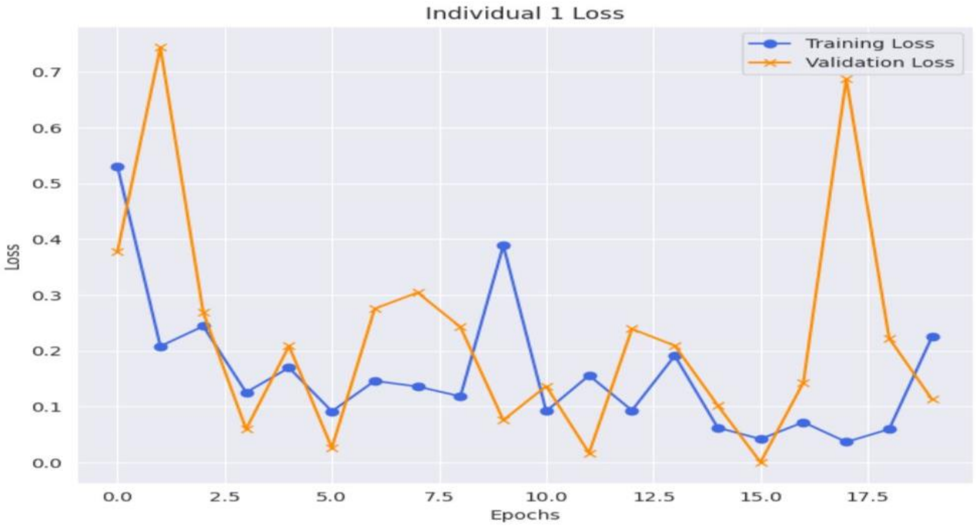
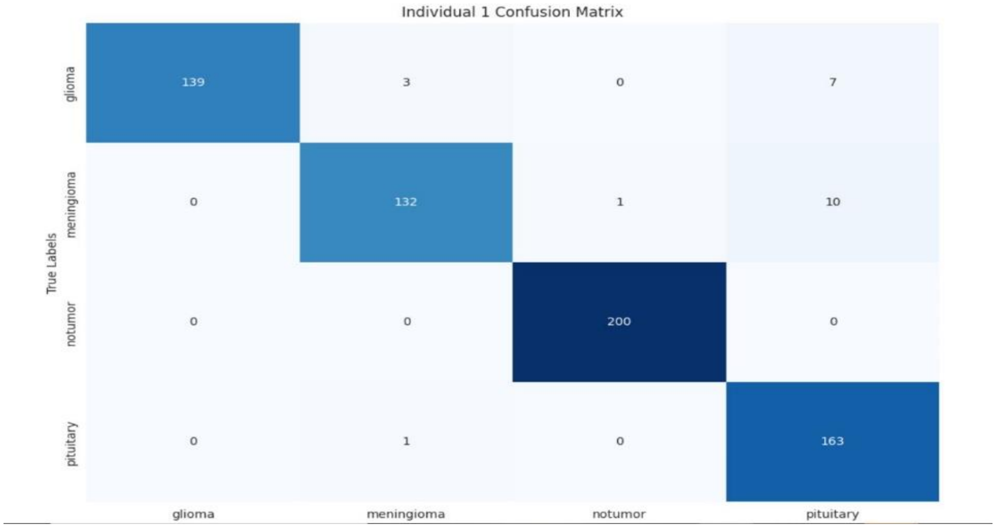


Figure 8 Individual 1 Loss Trend

c) Confusion Matrix Analysis

The confusion matrix shows strong classification performance. Glioma was correctly identified in 139 out of 149 cases, meningioma in 132 cases, and pituitary tumors in 163 out of 164 cases. All "No Tumor" cases were perfectly classified, demonstrating the model's reliability in distinguishing tumor types with minimal errors.



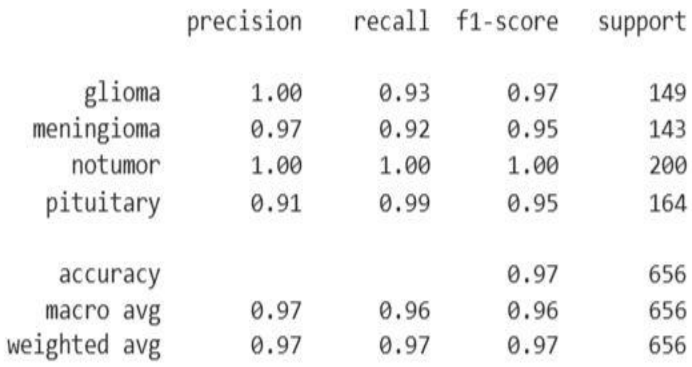
	glioma	meningioma	notumor	pituitary
glioma	139	3	0	7
meningioma	0	132	1	10
notumor	0	0	200	0
pituitary	0	1	0	163

Figure 9 Individual 1 Confusion Matrix

d) Performance Metrics Table

The performance metrics highlight the model's accuracy. Glioma achieved a precision of 1.00 and recall of 0.97, while meningioma had a slightly lower recall of 0.91. "No Tumor" cases were classified perfectly

(1.00 across all metrics). Pituitary tumors showed strong performance with a recall of 0.99 and an F1score of 0.95. With an overall accuracy of 97%, the model proves highly reliable for brain tumor detection.



```
              precision    recall  f1-score   support

      glioma       1.00      0.93      0.97       149
  meningioma       0.97      0.92      0.95       143
     notumor       1.00      1.00      1.00       200
   pituitary       0.91      0.99      0.95       164

    accuracy                           0.97       656
   macro avg       0.97      0.96      0.96       656
weighted avg       0.97      0.97      0.97       656
```

Figure 10 Individual 1 Performance Metrics

4.1.2 Individual 2

Individual 2 is a model that has been set up with specific training settings: it uses a batch size of 64, the Stochastic Gradient Descent (SGD) optimizer, a learning rate of 0.01, and it trains for 25 epochs.

a) Accuracy Trends

The accuracy graph shows the model's performance during training and validation. Training accuracy rises to 90%, indicating effective learning. However, validation accuracy peaks at 70%, suggesting the model performs well on training data but struggles with unseen data.

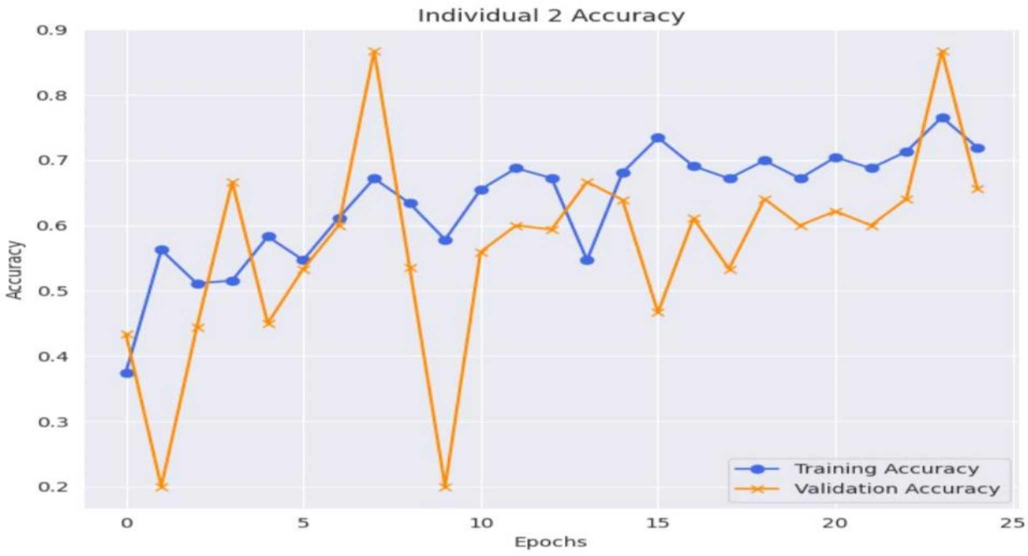


Figure 11 Individual 2 Accuracy Trend

b) Loss Trends

The loss graph shows the model's error over time. Training loss decreases, indicating improvement. However, validation loss initially drops but may level off or rise later, suggesting possible overfitting.

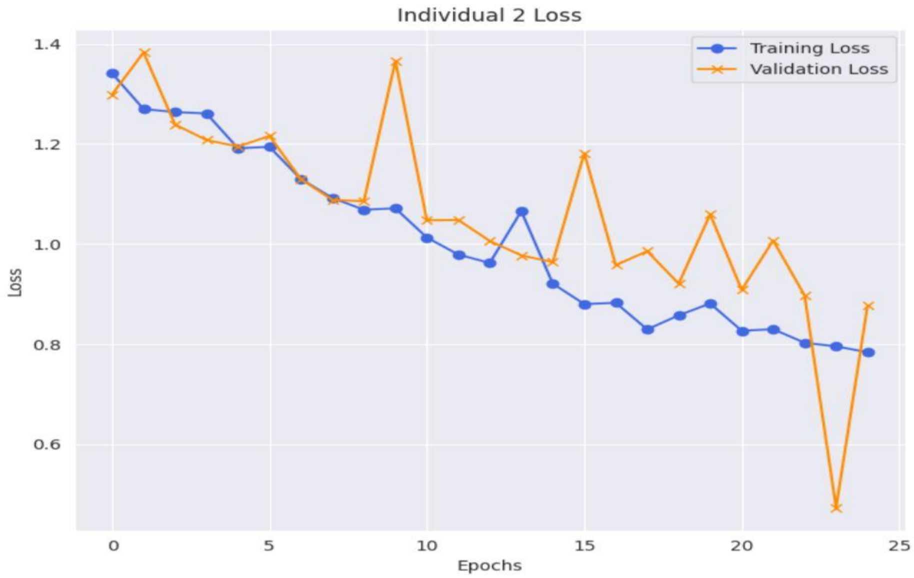
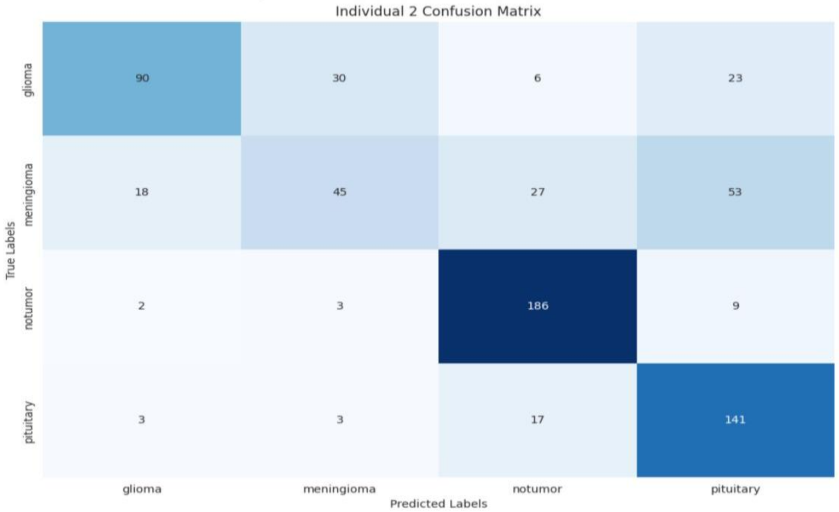


Figure 12 Individual 2 Loss Trend

c) Confusion Matrix Analysis

The confusion matrix shows how well the model classifies brain tumors. It correctly identified 30 gliomas but misclassified several others, highlighting areas for improvement in distinguishing tumor types.

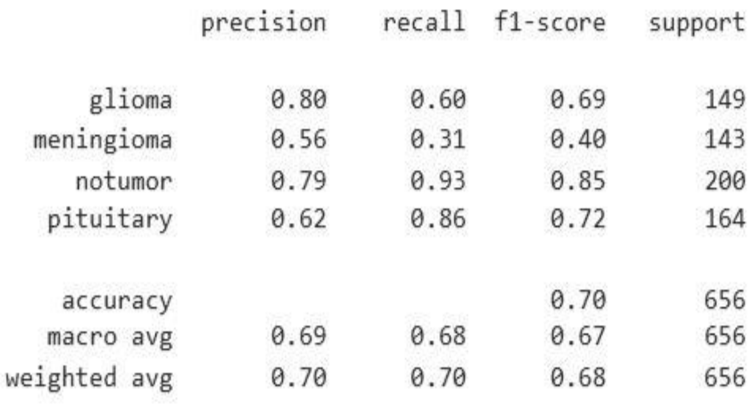


	glioma	meningioma	notumor	pituitary
glioma	90	30	6	23
meningioma	18	45	27	53
notumor	2	3	186	9
pituitary	3	3	17	141

Figure 13 Individual 2 Confusion Matrix

d) Performance Metrics Table

The classification metrics summarize the model's performance. Gliomas have 80% precision but only 60% recall, meaning many actual cases were missed. The overall accuracy is 70%, with strong performance for notumors but needing improvement in identifying meningiomas.



```
              precision    recall  f1-score   support

      glioma       0.80      0.60      0.69       149
  meningioma       0.56      0.31      0.40       143
     notumor       0.79      0.93      0.85       200
   pituitary       0.62      0.86      0.72       164

    accuracy                           0.70       656
   macro avg       0.69      0.68      0.67       656
weighted avg       0.70      0.70      0.68       656
```

Figure 14 Individual 2 Performance Metrics

4.1.3 Individual 3

Individual 3 is a model configured with a batch size of 128, the RMSprop optimizer, a learning rate of 0.001, and it trains for 30 epochs.

a) Accuracy Trends

The accuracy graph shows the model's performance during training and validation. Training accuracy improves to 90%, indicating effective learning, while validation accuracy reaches 78%, suggesting lower generalization to new data.

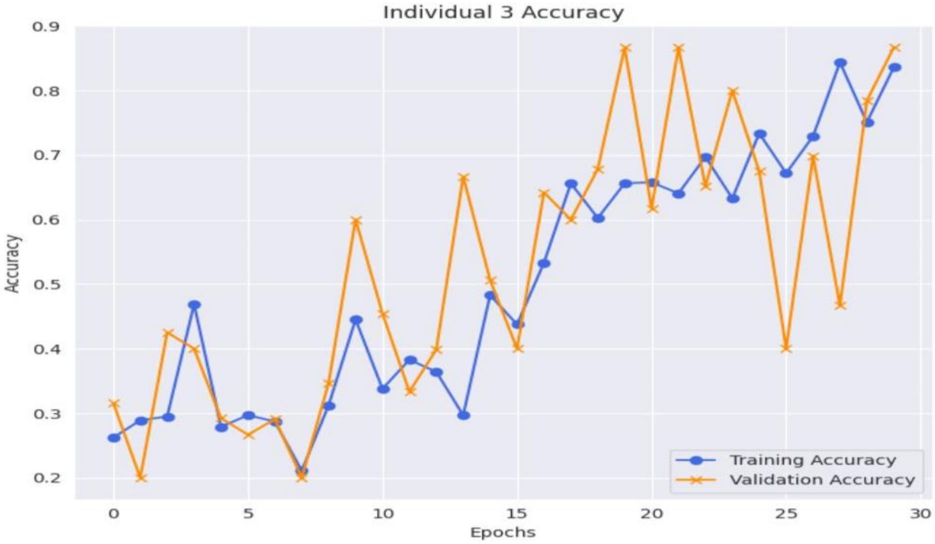


Figure 15 Individual 3 Accuracy Trend

b) Loss Trends

The loss graph shows a steady decrease in training loss, indicating learning progress. Validation loss also drops initially but may level off, suggesting potential overfitting and limited generalization to new data.

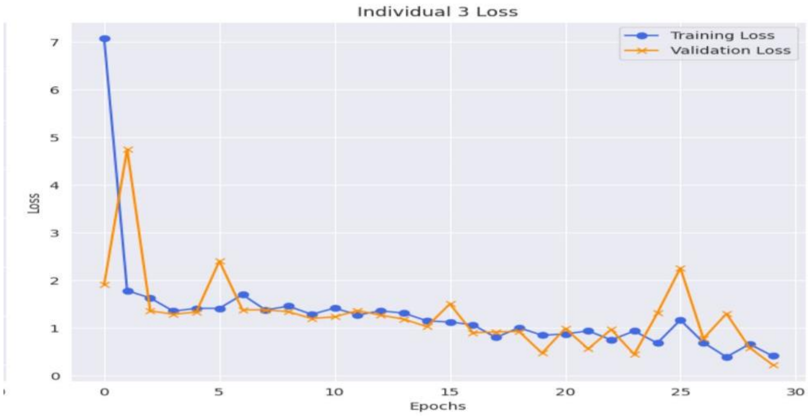


Figure 16 Individual 3 Loss Trend

c) Confusion Matrix Analysis

The confusion matrix shows the model's performance across tumor types. It correctly identified 32 gliomas but misclassified 6, while for meningiomas, 100 were correctly classified, with 60 misclassified. All 200 notumor cases were accurately detected, but 2 pituitary tumors were misclassified.

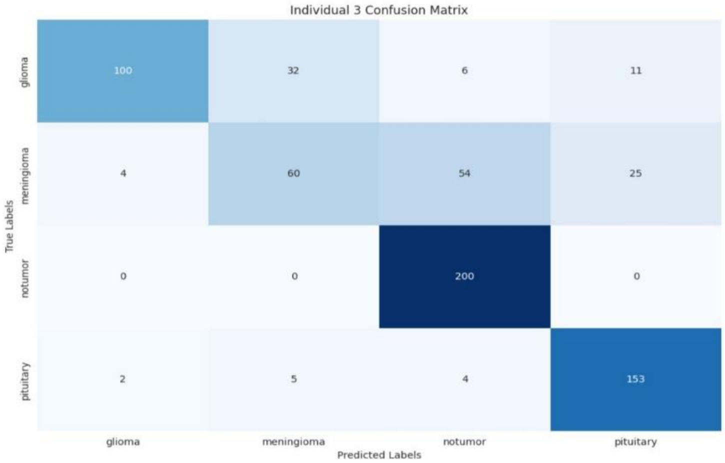
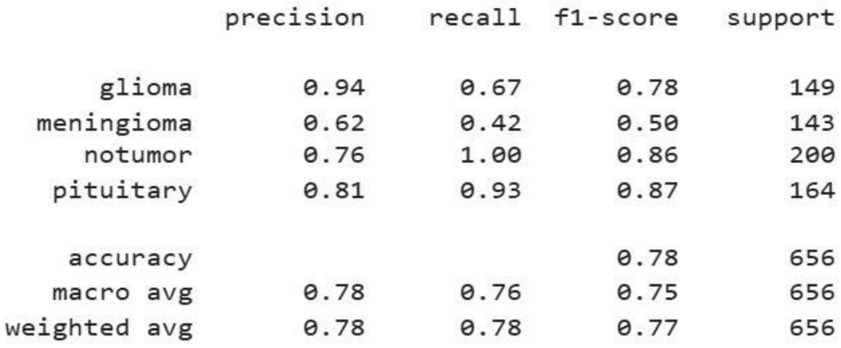


Figure 17 Individual 3 Confusion Matrix

d) Performance Metrics Table

The classification metrics show that the model performs well overall, with 78% accuracy. Gliomas have a high precision of 0.94, meaning most predicted gliomas were correct, but a lower recall of 0.67, indicating some were missed. While notumors were classified well, there is room for improvement in detecting meningiomas and pituitary tumors.



```
              precision    recall  f1-score   support

      glioma       0.94      0.67      0.78       149
  meningioma       0.62      0.42      0.50       143
     notumor       0.76      1.00      0.86       200
   pituitary       0.81      0.93      0.87       164

    accuracy                           0.78       656
   macro avg       0.78      0.76      0.75       656
weighted avg       0.78      0.78      0.77       656
```

Figure 18 Individual 3 Performance Metrics

4.1.4 Individual 4

Individual 4 is a model configured with a batch size of 64, the Adam optimizer, a learning rate of 0.01, and it trains for 30 epochs.

a) Accuracy Trends

The accuracy graph shows excellent model performance, with training accuracy reaching 100% and validation accuracy peaking at 97%. This indicates strong learning from training data and effective generalization to new cases.

Figure 19 Individual 4 Accuracy Trend

b) Loss Trends

The loss graph shows a steady decrease in training loss, indicating efficient learning. The validation loss also remains low, confirming that the model performs well on both training and validation data without signs of overfitting.

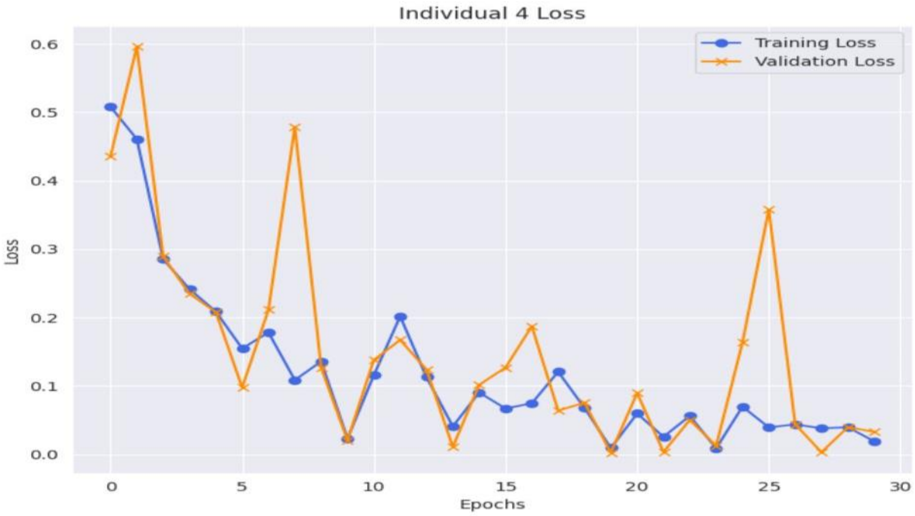


Figure 20 Individual 4 Loss Trend

c) Confusion Matrix Analysis

The confusion matrix shows the model's performance across tumor types. It correctly identified 2 glioma cases but misclassified 5. For meningiomas, it achieved 146 correct classifications with only 1 error. The model perfectly classified all 200 notumor cases and performed well with pituitary tumors, misclassifying just 1 case.

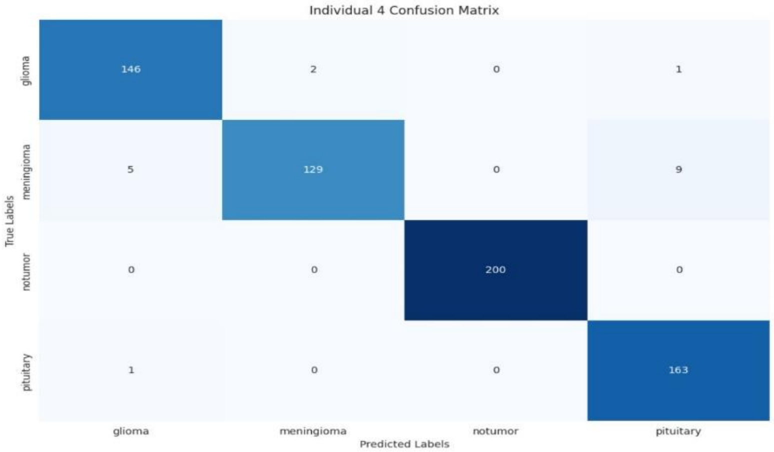
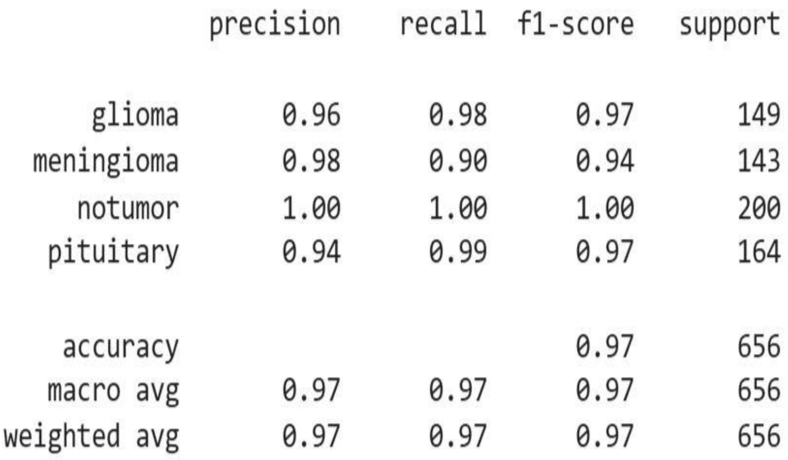


Figure 21 Individual 4 Confusion Matrix

d) Performance Metrics Table

The classification metrics highlight the model’s strong performance across tumor types. For gliomas, it achieved a precision of 0.96 and a recall of 0.98, indicating high accuracy in identifying actual cases. With an overall accuracy of 97%, the model demonstrates excellent reliability, showing high precision, recall, and F1scores for all tumor types.



```
              precision    recall  f1-score   support

      glioma       0.96      0.98      0.97       149
  meningioma       0.98      0.90      0.94       143
     notumor       1.00      1.00      1.00       200
   pituitary       0.94      0.99      0.97       164

    accuracy                           0.97       656
   macro avg       0.97      0.97      0.97       656
weighted avg       0.97      0.97      0.97       656
```

Figure 22 Individual 4 Performance Metrics

4.2 Child Hyperparameter Set

The Child model is configured with a batch size of 64, the Adam optimizer, a learning rate of 0.0001, and it trains for 30 epochs. This model achieves an impressive accuracy of 99%, indicating that it performs exceptionally well on both the training and validation datasets.

a) Accuracy Trends

The accuracy graph shows the model learns effectively, achieving 100% training accuracy and 99% validation accuracy, indicating strong generalization to new data.

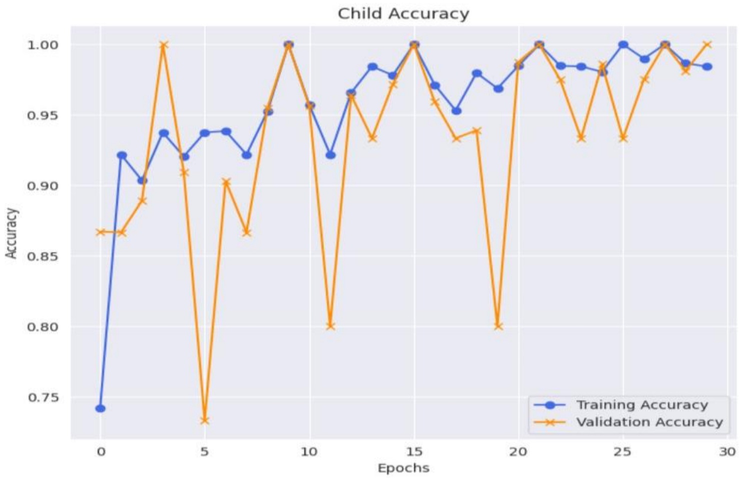


Figure 23 Child Accuracy Trend

b) Loss Trends

The loss graph shows a steady decrease in both training and validation loss, indicating efficient learning and no signs of overfitting.

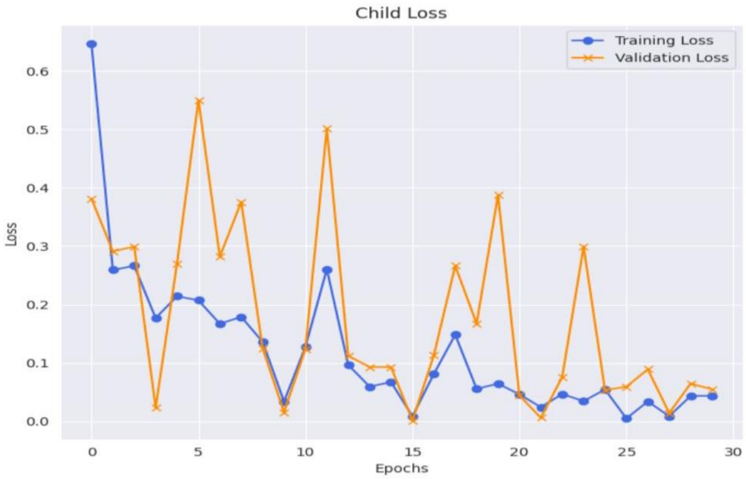


Figure 24 Child 4 Loss Trend

c) Confusion Matrix Analysis

The confusion matrix provides a detailed view of how the model predicts different types of brain tumors. For gliomas, the model correctly identified 3 cases but misclassified none. For meningiomas, it accurately identified 146 cases with only 1 misclassification. The model performed perfectly with notumors, correctly identifying all 200 cases, and it also performed well with pituitary tumors, misclassifying only 1 case.

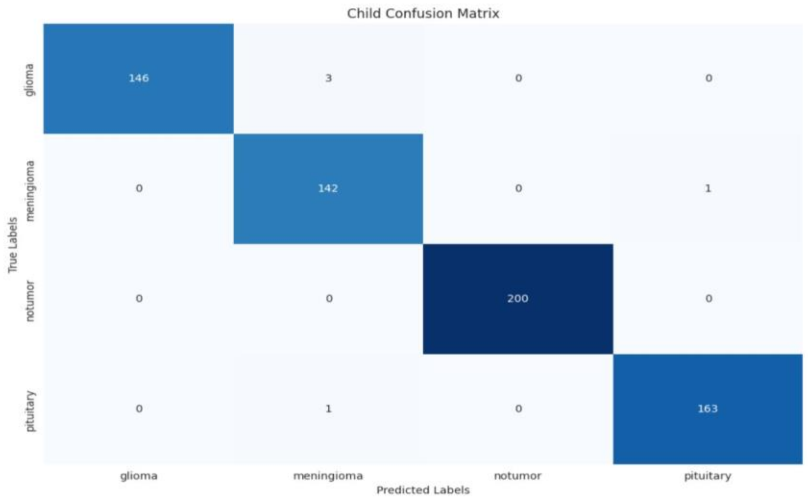
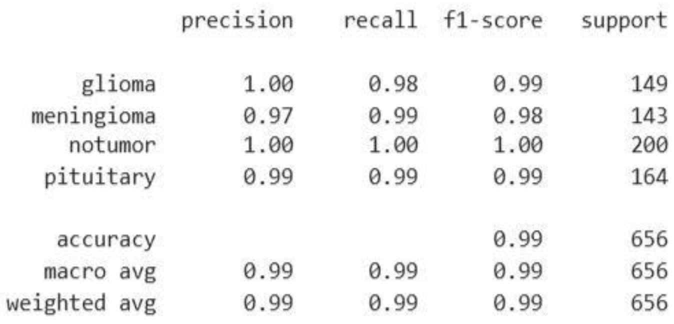


Figure 25 Child 4 Confusion Matrix

d) Performance Metrics Table

The classification metrics highlight the model's exceptional performance, achieving 99% overall accuracy with perfect precision for gliomas and high recall across all tumor types.



```
              precision    recall  f1-score   support

      glioma       1.00      0.98      0.99       149
  meningioma       0.97      0.99      0.98       143
     notumor       1.00      1.00      1.00       200
   pituitary       0.99      0.99      0.99       164

    accuracy                           0.99       656
   macro avg       0.99      0.99      0.99       656
weighted avg       0.99      0.99      0.99       656
```

Figure 26 Child Performance Metrics

Accuracy of CNN + Genetic Algorithm (GA)

The accuracy of the model was evaluated on the test set after training for 30 epochs. The results indicate in table [7] that the model achieved a test accuracy of 99%. The accuracy is presented in the table below for each of the four classes.

Table 4 VGG16 Models with GA Results

Phase	Accuracy (%)
Training Accuracy	100
Validation Accuracy	99
Test Accuracy	99

4.3.1 Performance Metrics

The model demonstrates outstanding performance in brain tumor classification, achieving 99% overall accuracy with balanced precision, recall, and F1scores across all classes.

- **Glioma:** Precision 1.00, Recall 0.98, F1score 0.99 (149 cases). The model correctly classified nearly all glioma cases with minimal misclassification.
- **Meningioma:** Precision 0.97, Recall 1.00, F1score 0.99 (143 cases). It identified all meningioma cases, with very few false positives.
- **No Tumor:** Precision 1.00, Recall 1.00, F1score 1.00 (200 cases). Perfect classification with no errors.
- **Pituitary:** Precision 0.99, Recall 0.99, F1score 0.99 (164 cases). Excellent detection with rare misclassifications.

The macro and weighted averages for precision, recall, and F1score are 0.99, indicating the model’s reliability and ability to generalize well across different tumor types.

Table 5 Performance Metrics of VGG16 Model with GA

Class	Precision	Recall	F1Score	Support
Glioma	1	0.98	0.99	149
Meningioma	0.97	1	0.99	143
No Tumor	1	1	1	200
Pituitary	0.99	0.99	0.99	164
Accuracy			0.99	
Macro Avg	0.99	0.99	0.99	656
Weighted Avg	0.99	0.99	0.99	656

The model demonstrates strong performance across most classes, with particularly high recall for the 'No Tumor' and 'Pituitary' classes, which is crucial in medical applications where identifying the presence of a tumor is important. However, the recall for 'Glioma' and 'Meningioma' could be improved, as the model misses some instances of these classes.

4.4 Model Validation with GA

In the context of model validation, a Genetic Algorithm (GA) was employed to optimize the hyperparameters. The GA was used to explore various combinations of hyperparameters such as learning rate, batch size, and optimizer type. By selecting the best performing hyperparameter combinations based on training performance, the model's efficiency was enhanced.

4.4.1 VGG16 Model Validation

The VGG16 model was validated on a brain tumor MRI dataset over 30 epochs, achieving a 99% test accuracy. Training accuracy steadily increased to 100%, while validation accuracy remained consistently high, indicating good generalization.

Loss decreased throughout training, stabilizing below 0.1, with a final loss of 0.045, suggesting minimal overfitting. The small gap between training and validation accuracy confirms the model’s strong learning and generalization ability.

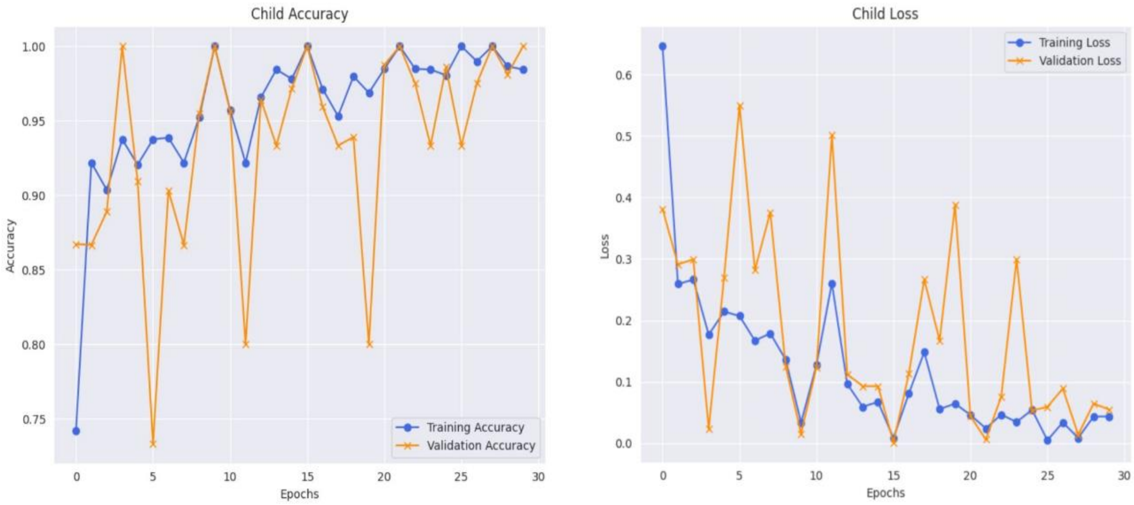
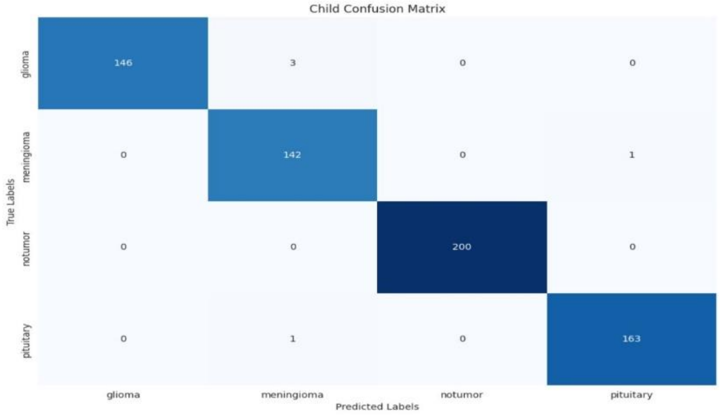


Figure 1 VGG-16 Model Accuracy and Loss

The brain tumor MRI classification task demonstrated outstanding performance using the VGG16 model because it maintained a strong test accuracy rate together with stable training and validation metrics. Proof of accuracy indicates that this model presents valid capability in identifying brain tumors within MRI images.



	glioma	meningioma	notumor	pituitary
glioma	146	3	0	0
meningioma	0	142	0	1
notumor	0	0	200	0
pituitary	0	1	0	163

Figure 28 VGG16 model's predictions

The confusion matrix of VGG16 indicates 99% success in MRI brain tumor image classification. Most glioma (146/149) along with meningioma (142/143) cases were properly classified by the VGG16 model though there was some erroneous grouping of these tissue types. The model achieved complete accuracy for "No Tumor" (200/200) together with 163/164 correct pituitary tumor predictions. The brilliant all-around results of VGG16 exist alongside an area for improvement where it overlaps glioma and meningioma predictions.

5. Conclusion

The research work introduces an optimal system that employs Brain Data Augmentation (BDA) and combined Convolutional Neural Networks (CNNs) with Genetic Algorithms (GA) for brain tumor detection and classification. With 7,023 MRI images as input our approach enables better model generalization to prevent overfitting and maintains effective tumor classifications between Glioma, Meningioma, Pituitary and No Tumor categories.

The VGG16 model processed by Genetic Algorithms reached 99% test accuracy during testing. The selection and optimization of training parameters including optimizer type and batch size along with learning rate and training epochs numbers produced this excellent result. The modern parameter exploration capability of GA outperforms traditional techniques such as random search and grid search because it automatically selects optimal parameter sets for effective learning. Through its selection mechanism combined with crossover and mutation the model trains quicker while it prevents overfitting and achieves strong performance with unknown data.

Our study demonstrated how the model successfully diagnosed No Tumor and Pituitary tumors but had minor errors between differentiating Glioma and Meningioma. The ability to extract better features represents a key area for advancement to make the model distinguish between similar tumor types with higher precision.

The research provides critical medical benefits by enabling early tumor identification along with mistake reduction and accelerating therapeutic choices. Our model shows rapid accurate performance which enables its potential application as a computer aided diagnosis tool to support medical staff in clinical assessments. The implementation of AI brain tumor detection automation results in both reduced medical staff workload along with superior diagnostic inspection performance.

The future development should integrate MRI with CT or PET imaging techniques to achieve better classification outcomes. Better deep learning models including transformers or hybrid CNNRNN architectures have potential to boost feature extraction along with classification precision. Under federated learning models doctors could train their medical information jointly with other hospitals keeping each hospital's patient details confidential.

This research proves that applying Genetic Algorithm hyperparameter optimization techniques on CNN structures produces an effective method that achieves precise brain tumor identification. The designed clinical AI diagnosis system combines high precision with low processing demands to establish itself as an effective medical tool for improving AI driven healthcare practices.

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