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**Research Article**

# An Optimized Genetic Neural Network for Brain Tumour Detection

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**ABSTRACT**

Brain tumour classification is an important function of medical research, contributing to timely and accurate treatment decisions. This research uses a convolutional neural network (CNN) optimized by genetic algorithms to classify MRI scanned images of brain tumors into four groups. The CNN algorithm uses hierarchical feature extraction layers, capturing complex tumor-specific patterns greater than traditional methods. By programmatically adjusting genetic algorithm learning rates and dropout rates, the models are normalized and enhanced in real-time to ensure efficient training, reduction of redundancy for the model work well, ensure high levels of input, dealing with changes in brightness and contrast. A grayscale MRI scans dataset was used to train and validate the system, demonstrating the ability to generalize to unseen data obtaining significant classification accuracy Visualization methods including confusion matrices and class-wise accuracy analysis for insights a delve into the predictive capabilities of the genetic algorithm Integration Therapy - highlights a new approach to improve the performance of CNNs in image analysis. The results highspot the capability of such machine learning methods to improve brain tumor diagnostic tools, providing a foundation for future developments in automated healthcare systems.

**Keywords:** Hierarchical Feature Extraction, Genetic Algorithms (GAs), Optimization Techniques, Grayscale MRI Scans, Tumor-Specific Pattern Recognition

## 1. INTRODUCTION:

Although convolutional neural networks show great promise in classifying brain tumors, there are several limitations in their application. The limited accessibility of large datasets raise a significant challenges, potentially limiting model ability to generalize to patient populations and imaging settings[11]. Furthermore, CNNs are often overfitting, especially in situations with small data or within an imbalanced class distribution It is, because the "blackbox" nature of deep learning makes it tough for clinicians to understand the approach or the actual deductions behind the predictions. This lack of insight can reduce confidence on the results of the model in important clinical measures. In addition, CNNs require significant computational resources to train and test, are difficult to implement in clinical settings with limited resources[12]. Finally, differences in image acquisition techniques, including differences in MRI equipment or protocols, can affect model performance when applied to external datasets. It requires collaboration, transfer-learning, and collaborative efforts to generate standardized annotated datasets representing imaging conditions and tumor characteristics[13].

Tuning a CNN is necessary to maximize its performance and assure accurate predictions in a various applications, including image segmentation, object recognition, and gender segmentation Tune hyperparameters with number of classes, batch size, epochs , and network design are included to improve convergence and reduce overfitting . Using normalization, a well-converged CNN guarantees model performance in the face of missing data. Continuous, stop learning, and data enhancement include techniques that help improvise the model and decrease the risk of memorizing training data and also, adapting a pre-trained model to a set of data sets which, can accelerate learning using prior knowledge By searching for the optimal combination, parameter optimization techniques include web search, Bayesian optimization to further improve the speed control performance parameters and iteratively changing settings based on validation set comments are part of the tuning This approach enhances the ability of CNNs to extract generally suitable attributes is greater, thus providing more accurate and reliable results in practical applications.

**Table 1: Tuning Parameters of CNN**

| Parameter | Description | Recommended Range or Value | Effect |
|---|---|---|---|
| **Learning Rate** | Controls the step size for updating weights during backpropagation. | 0.0001 to 0.01 | High values speed up training but risk divergence; low values ensure stability but may slow convergence. |
| **Dropout Rate** | Fraction of neurons randomly deactivated to prevent overfitting during training. | 0.1 to 0.5 | Higher values improve generalization but may slow learning; lower values reduce regularization. |
| **Batch Size** | Number of samples processed simultaneously during one forward and backward pass. | 16 to 256 | Larger sizes improve stability but require more memory; smaller sizes enhance training speed. |
| **Number of Filters** | Number of kernels in a convolutional layer to capture features. | 16 to 512 | Larger numbers extract finer details but increase computational cost. |
| **Kernel Size** | Dimensions of the filter applied during convolution. | 3×3, 5×5 | The sizes that are small focus on local features; sizes that are large capture broader patterns. |

1.1. Impact of Learning Rate and Dropout Rate on CNN

The learning rate and dropout rate are crucial hyperparameters that significantly affect the performance and stability of a Convolutional Neural Network (CNN). Learning rate determines the amount of parameter change during back propagation, and thus directly affects convergence speed and the probability of reaching a global minimum in the loss function Higher learning rate speeds up convergence but can make the optimization process more than ideal parameter values However, it risks long training times and potential traps in local minima. It is important to balance this hyperparameter to achieve optimal performance without overextending computational resources.

Strategies to control overfitting work by randomizing a proportion of neurons during dropout training. This controlled decomposition forces the network to generalize better by preventing the co-optimization of neurons, increasing the ability to work efficiently on unseen data. If you set the dropout rate too high it can hindering the learning ability of the network, because the model can lose a lot of information with each internal iteration. On the other hand, stopping the learning rate too low can make the network prone to overfitting, especially when trained on a complex dataset of small size. The optimal value of these all parameters depends on the type of dataset and on complex CNN structures. Combining well-estimated learning rates with appropriate dropout rates creates a synergistic effect, allowing for efficient learning while preserving generalization ability, which is a strong model to perform in real-world applications the cornerstone.

1.2. Need of genetic algorithm for tuning learning rate and dropout rate

In order to optimize the CNN model’s performance to classify brain tumor, genetic algorithm (GA) is used to tune key over-parameters, ie. learning rate and dropout rate These over-parameters dramatically impact the capability of the model to predict never seen data and converge across training. The number of learnings will be used to control the speed of the model and update its parameters, while the dropout rate helps to deal with overfitting by randomly turning off neurons in dense layers. Manually choosing optimal values for these parameters can be time-intensive and imprecise, especially for complex models. The GA implemented with DEAP in the code simulates evolutionary processes such as selection, crossover, and mutation to efficiently evaluate multiple parameter combinations Over several generations, the algorithm evaluates each parameter set based on the accuracy of the model to the optimal configuration. This approach provides the model with high accuracy and robustness without full manual tuning, and ensures that it can generalize well across unobserved data.

## 2. LITERATURE SURVEY:

Monika Agarwal et al [1] has developed a two-phase methodology for the prediction of brain tumor in early stage. The data was retrieved from Figshare which hold improper images and quality images. ODTWCHE approach utilized for the lower image quality to improve its pixels with some limited techniques. This process includes images with lower contrast then build the histogram these images are segmented with some threshold values. The probability was modified according to the requirement then PSO was applied. Histogram, gamma, filtering process was done and finally a new quality image was obtained. Later phase includes pre-processing the images with proposed technique while extraction of features utilizing GLCM then detection of tumour images with modified InceptionV3. This process was simple initial process includes Conv 2D, pooling data this was repeated up to 93 time. Filtered data was transmitted to flattern layers and finally FC layers are connected to predict Benign or Malignant.

Muhammad Faheem Khan et al [2] has implemented a CNN and LSTM for the detection of Brain tumor with couple of datasets. The data was collected from glioma & BVH-RDL. The images are pre-processed with 2D gaussian smoothing filter was utilized. This was mainly utilized for the reducing the noise in images. It includes sharpening, stripping which focus on the shapes and tissues. The classification process was included with optimized hybrid DNN. Two techniques are included CNN and LSTM. CNN was well known for prediction of images with simple layers like conv, pooling, dense, and FC. These are mapped using some features to LSTM. This includes a ARO approach with transfers data as weights to approach and transfers the optimal features. Hence the predicted images are transmitted to hybrid approach and detection. This method was evaluated with 10-folds where the CNN has achieved high performances than LSTM.

Loveleena Gaur et al [3] has introduced a CNN methodology through LIME & SHAP for identify tumour in brain via MRI Scans. The dataset was collected from publicly accessible MRI images from Bhuvaji, categorized in four tumours. The dataset contained two thousand images, with some images used for model training and the rest to test the model. In data pre-processing the image rearrangement was performed to improve convergence and stop the CNN framework from figuring out the training sequence. Gaussian noise was introduced for better classification results, with a mean value of zero(0) and a standard deviation of 100.5. Comprising including frameworks for explanation the extraction process, a CNN framework, quantitative performance measurements, and feature extraction. The CNN model receives two copies of the dataset to enhance accuracy, comprising six layers that are hidden & a result layer that is 1 * 4 in size. ReLU and softmax are used as ac with Adam optimizer. The For the statistical precision evaluation, LIME, & SHAP clarifications, CNN model is employed. Disturbance is used in LIME explanations whereas a gradient explainer is used in SHAP.

Omar Kouli et al [4] has focused on survey on ML and DL techniques for identify tumour in brain via MRI Scans. The search was conducted in databases like PubMed, Web of Science, and Scopus within a specific timeframe. Including those developing or validating aged brain tumour identification or segmentation methods utilizing MRI. In exlcusion phase encompassed tumour classification studies, pediatric tumours, studies using only MRI spectroscopy, abstracts, and studies without performance metrics. Quality was evaluated using CLAIM, while Bias and relevance risks were assessed with the QUADAS-2 guideline, incorporating some CLAIM items. DL or TML based on the algorithms used. A meta-analysis compared DL and TML methods for automated detection.

Sohaib Asif et al [5] has introduced Xception, NasNet Large, DenseNet121, CNN for identify tumour in brain via MRI Scans. Two publicly available brain MRI datasets, contains low and high MRI's, were employed for experiments. MRI-large consists of 1500 tumour pictures and 1k general images, while low MRI's contains 155 tumour & 98 general images. The workflow involves four stages: pre-processing, data augmentation, exploration of DL models with TL, and classification using a softmax layer. In data pre-process cropping utilized extreme points and contour finding for removing unnecessary part & noise from MRI images. Augmentation generated new training images, mitigating overfitting risks and enhancing classification accuracy. By utilising pre-trained CNN methodologies for feature extraction. TL aided in using previously trained values on dataset related to imagenet, as the MRI dataset was relatively small. Models were trained for 50 epochs with different optimizers.

Naeem Ullah et al [6] has proposed a Inception and Resnetv2 for identify tumour in brain via MRI Scans. The process begins with acquiring a Kaggle dataset includes four kind of tumours. Augmented images are used for training only. Images are resized to match previously-trained CNN methodology inputs the requirement. Different pre-trained DNN are employed to BT identification & classifications. Transfer learning is applied to modify these models for the new task to classify brain tumor. The final layer of every method are modified for involving in brain tumor classification domain. Limited training data and computational resources make TL a practical choice. TL involves transferring knowledge from pre-trained models to new domains. Nine pre-trained TL algorithms are chosen based on their popularity and performance.

Zahraa H. Ali et al [7] has intend a CNN, SVM, MLP, BPNN methodologies for identify tumour in brain via MRI Scans. The process for detecting brain tumors comprises multiple steps, including as picture taking, prior processing, segmentation of images, extraction of features, & classifications. Various techniques like grayscale conversion, median filtering, edge detection, and watershed segmentation are used to preprocess MRI images. The GLCM is applied for texture analysis. Feature extraction is a process that transforms input data into a manageable set of operations. The classification of brain tumors involves pattern recognition methods. By utilizing proposed methodologies sfor brain tumor classification. BPNN input layer's neuron count corresponds to the number of extracted features. Different numbers of hidden neurons are evaluated for optimization, and the network is trained with a certain portion of the dataset for classification. SVM is a hyperplane that optimally devides classes in multic-dimensional space. CNN model with 19 layers is employed for classification. The entire procedure consists of pre-processing, image segmentation, morphological image processing, brain tumor feature extraction and various classification methods for accurate tumor identification.

Hasnain Ali Shah et al [8] has developed a CNN with EfficientNet-B0 for identify tumour in brain via MRI Scans. The dataset contained 3k MR images, divided into tumour 1 and non-tumour 0 classes. An automated resizing script was used to standardize image dimensions. The EfficientNet-B0 CNN model, pre-trained on ImageNet, was chosen as a baseline due to its scaling methods. It extracts features using convolutional layers and mobile inverted bottleneck convolution. For extraction of features, additional layers are added. The sigmoid classifier assigns 0 or 1 to predict non-tumour or tumour images. Transfer learning involved using the previously-trained methodology as a base model and freezing its layers. Fine-tuning was performed by training the added layers with the BT MRI dataset while preserving the base model's feature extraction. A cross-entropy loss function was selected for binary classification. Adam was chosen for its memory efficiency and quick convergence. The efficiency of the suggested model was contrasted with different CNN. The evaluation showed the model's cpability to identify images with tumor and no tumor effectively.

Ramy A. Zeineldin et al [9] has introduced a NeuroXAI for identify tumour in brain via MRI Scans. The NeuroXAI framework includes a deep neural network and an explanation generator. It processes brain MRI images through a CNN. NeuroXAI adapts XAI methods for medical image segmentation. It converts segmentation into multi-label classification by pooling each class on the output prediction layer. VG is a basic method to visualize image regions contributing most to neural network classification output. GBP calculates the gradient of the result relative to the data provided by a deconvolution approach. IG computes the gradient along a path from a baseline black image to the input image, producing a sensitivity map. GIG is an extension of IG, determining the path at each step. It identifies a subset of less important features by calculating gradients on the baseline-to-input path. SmoothGrad sharpens sensitivity maps by averaging gradients over multiple samples around the input image, reducing noise and enhancing visualization. GCAM extends class activation mapping to various CNNs. GGCAM combines GBP and GCAM through element-wise multiplication. MRI data from BraTS 2019 and 2021 are used for classification and segmentation tasks. Pre-processing includes values of z-score & crop of images. Models like ResNet50 and 3D DeepSeg were utilized, trained using TensorFlow with Adam optimizer.

Asaf Raza et al [10] has proposed a CNN with GOOGLENET for identify tumour in brain via MRI Scans. a CE-MRI dataset containing 3062 images from 233 patients with BT. DeepTumorNet is a hybrid model based on GoogLeNet, a pretrained classifier with 22 learning and 44 layers. The exit five layers of GoogLeNet were re-arranged to fifteen fresh layers to enhance the model. The model used Leaky ReLU activation functions and a global average for a pooling layer. The feature maps were generated using convolution operations. Leaky ReLU activation functions were used in mapping the features to overcome the dying ReLU problem, enhancing model expressiveness. Batch normalization normalized the outputs of convolutional layers, improving training efficiency. Pooling layers downscaled feature maps, simplifying information. Global average pooling was used in the last layers. The final fully connected layer had an output size of 3 for the 3 classes. The Softmax activation function normalized outputs and created a probability distribution for each class. The classification layer produced final output probabilities based on the learned features and Softmax activation.

**Table 2: Comparative Analysis on the Existing Approaches**

| Author | Algorithm | Merits | Demerits | Accuracy |
|---|---|---|---|---|
| Monika Agarwal et al | Modified InceptionV3, ODTWCHE | It's a two-phase methodology which has separated the process and predicted the outcome efficiently. | Training data was not predicted efficiently. | 98.89% |
| Muhammad Faheem Khan et al | CNN, LSTM, ML | Simple process which can be applied for many medical applications. | Comparison methods does not show much differences in accuracy. | 84.5% |
| Omar Kouli et al | DL, TML | Multiple methods are analyzed. | The transparent validation was not accurate. | |
| Sohaib Asif et al | Xception, NasNet Large, DenseNet121, CNN | The model was very efficient. | No much difference among approaches. | 99.6% |
| Naeem Ullah et al | Inception Resnetv2 | Using tl prediction was efficient. | By utilizing image segmentation the performances can be increased. | 98.9% |
| Zahraa H. Ali et al | CNN | Customized layer can be used. | For initial steps the additional techniques can be used. | 99.26% |
| Hasnain Ali Shah et al | CNN EfficientNet-B0 | The image classification was accurate. | Takes long time until the last layer prediction. | 98.8% |
| Ramy A. Zeineldin et al | NeuroXAI | It was derived with seven methods. | The maps should contains high quality. | 98,6% |
| Asaf Raza et al | CNN, GoogleNet | By adding 15 layers of GoogleNet the prediction of images was efficient. | It only works on proposed dataset. | 99.6% |

## 3. PROPOSED METHODOLOGY:

Brain tumor classification analysis shows a new development in combining genetic algorithms to optimize convolutional neural network (CNN) hyperparameters. Although CNN is a well-established method for image segmentation, this research demonstrates a robust approach to improve performance by combining genetic algorithms with hyperparameter tuning. Emulating evolutionary principles such as selection, crossover, mutation, etc., the genetic algorithm analyzes various configurations, eventually identifying very nearly optimal solutions Furthermore, the analysis includes preprocessing steps for MRI grayscale images are normalized to ensure uniform input data That enhance feature extraction The use of real-time data development and class classification visualization further helps the model to handle inherent variation in medical image datasets Four different tumor types each focus also contributes to innovation Thereby, the research demonstrates the ability to combine advanced machine learning techniques with biologically inspired algorithms to overcome important limitations in medicine in the analysis of the solution. The suggested architecture is displayed in figure 1

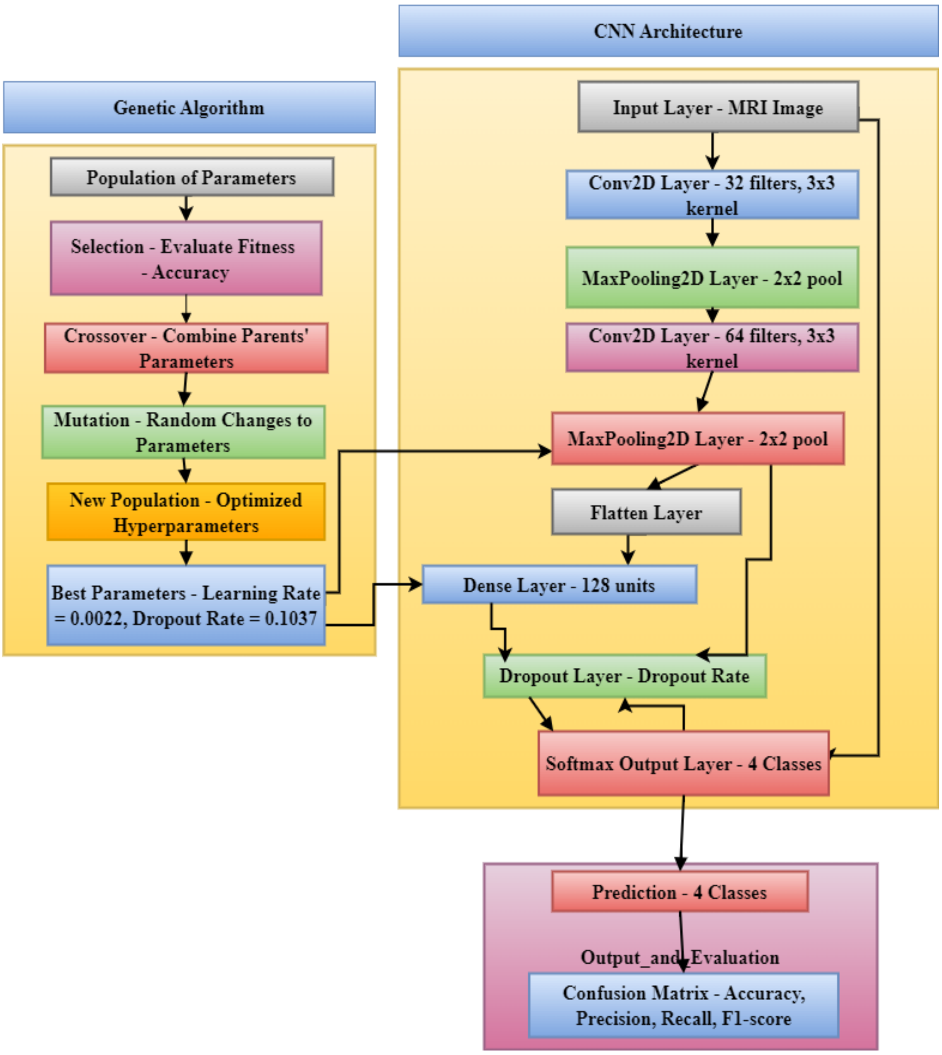


**Figure 1: Block Structure of Proposed Genetic CNN**

3.1. Data Generation using Augmentation Techniques: Data preparation is fundamental in machine learning pipelines, particularly for complex tasks such as MRI brain tumor classification. Using Keras' ImageDataGenerator class, data is augmented in real-time, ensuring a diverse range of input variations to increase the understanding of the model to adapt to never seen data. Augmentation techniques containing random rotations, shifts, and zoom flips, which mimic variations that can occur in an MRI scan, reduce overfitting, and increase robustness Each image is reshaped to the standard dimension of 128x128 pixels and in grayscale , are modified, so that important space features By retaining, the computational requirements are reduced and then pixel entries is standardized to a range frm 0 to 1, using transformations as shown in equation (1).

$$Rescaled\ Pixel\ Value = \frac{Original\ Pixel\ Value}{255} - (1)$$

This normalization ensures consistency in pixel intensity, improving model convergence and training consistency. In addition, the class distribution of the dataset is examined visually, usually with a bar chart, to ensure a stable depiction of the classes. Imbalanced groups can lead to biased predictions, which makes this research important. The dataset is then devided into learning and validation sets, typically following a split ratio of 4:1, which allows the model to generalize well. Balanced dataset classification is verified after splitting, avoiding the risk of data drift or biased learning.

Normalization is an important preprocessing step in this project to improve the efficiency and robustness of the convolutional neural network (CNN) used to label brain tumor. When normalization is used, especially scaling the pixel values in ranging from 0 to 1, lets the model to handle images efficiently. Normalized pixel values prevent large changes that can cause gradients to oscillate or disappear during surface propagation, improving the convergence rate of the learning process. During model building, the ImageDataGenerator from Keras handles this normalization automatically by setting the rescaling parameter to 1.0/255.0, dividing each pixel by 255. This has the images used fill in all over Ensure equal scaling, provide comparability, and minimize the effect of brightness or contrast occurring across the dataset. This step is especially important for grayscale MRI images where pixel intensity directly affects feature detection. The normalization therefore brings the dataset into line with CNN requirements, enabling the model to focus on understanding important aspects of brain tumors without changes in exposure or exposure in the 19th century is not affected.

3.2. Working of Customized CNN: In this model, the CNN algorithm is outlined for the classification of MRI images of brain tumors by sequentially collecting hierarchical features through successive layers. The mesh starts with two convolutional layers, each of which will reduce spatial dimensions and increase pooling to highlight important features. The main convolutional layer are having thirty-two filters and the second layer are having 64 filters, letting the model to indentify more complex patterns, such as edges and textures indicative of tumors In the learning process, neurons are activated arbitrarily with variable amounts of unlearning followed by hyperadaptive inhibition. Finally, a softmax layer displays the input image in one of four possible groups, representing tumor types. This design using the Keras API series uses both convolutional layers and layers that are fully connected, making it ideal for image classification tasks where microtumor features differentiation is important.

The CNN algorithm is carefully designed to efficiently extract spatial structure from MRI images, which contributes to accurate tumor classification. The architecture begins with a Conv2D layer with thirty two filters of 3x3 matrix size, which detects basic shapes, such as edges and textures, in a 128x128 grayscale image Each convolutional layer uses a ReLU activation, a leads to nonlinearity as shown in equation (2).

$$ReLU(x) = \max(0, x) \text{- } (2)$$

This activation function contains only positive values, speeds up training and avoids missing mounts. Each convolutional block is succeeded by a Max-Pooling layer, that decreases the geometric proportions by taking the maximum value from each 2×2 field, effectively preserving key features and minimizing the risk of overlap and then it flattens the feature maps as one-dimensional vectors before entering a complete network of complex connectivity. The final cubic layer consists of four neurons with softmax activation as shown in equation (3).

$$Softmax(z_i) = \frac{e^{z_i}}{\Sigma_j e^{z_i}} - (3)$$

where $z_i$ represents the raw score for each class. The softmax activation converts these scores into probabilities for each class, assisting in multi-class classification. During model compilation, the Adam optimizer is used to dynamically adjust learning rates based on gradient changes, optimizing faster than traditional methods. The loss function which is ideal to classify data with multi labels is categorical cross-entropy loss and is given by equation (4)

$$L = -\sum_i y_i log(\hat{y}_i) - (4)$$

where $y_i$ is the actual label, and $\hat{y}_i$ is the predicted probability. These architectural and training choices collectively enhance the model's capability to classify brain tumors effectively.

3.3. Working of Genetic Algorithm: The genetic algorithm (GA) optimizes hyperparameters, like learning rate, by simulating the procedure of natural selection. Each individual in the population represents a unique configuration of hyperparameters, with each combination evaluated based on validation accuracy. The fitness score F for each individual, measured as validation accuracy, determines its selection probability

The GA begins with a randomly generated population of hyperparameter settings, and individuals are selected for reproduction using tournament selection, where a subset of the population competes, and the best-performing individual is chosen. The selected parents undergo crossover using cxBlend, producing offspring with blended hyperparameter values:

$$Child\,Value = \alpha \times Parent\ 1 + (1 - \alpha) \times Parent\ 2 - (5)$$

where αis a blending factor between 0 and 1. Mutation introduces variation by randomly altering genes (i.e., hyperparameter values) within individuals, using a Gaussian distribution to control the extent of mutation:

$$Mutated\,Value = Original\,Value + \sigma \cdot N(0,1) - (6)$$

where σ is the mutation strength, and N(0,1) is a standard normal distribution. Elitism is applied by directly carrying forward the best-performing individuals to the next generation, ensuring that optimal traits are preserved. Over multiple generations, the population evolves, converging towards an optimal hyperparameter set that maximizes model performance. This iterative process of selection, crossover, and mutation culminates in a final solution that enhances model accuracy by fine-tuning learning rate, dropout, and other hyperparameters crucial to CNN performance and is shown in figure 2

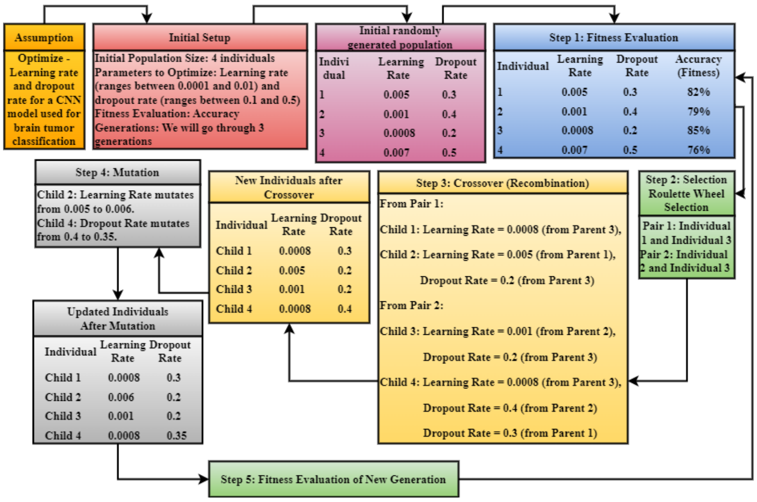


**Figure 2: Tuning the Learning Rate and Dropout Rate using Genetic Approach**

## 4. RESULTS & DISCUSSION:

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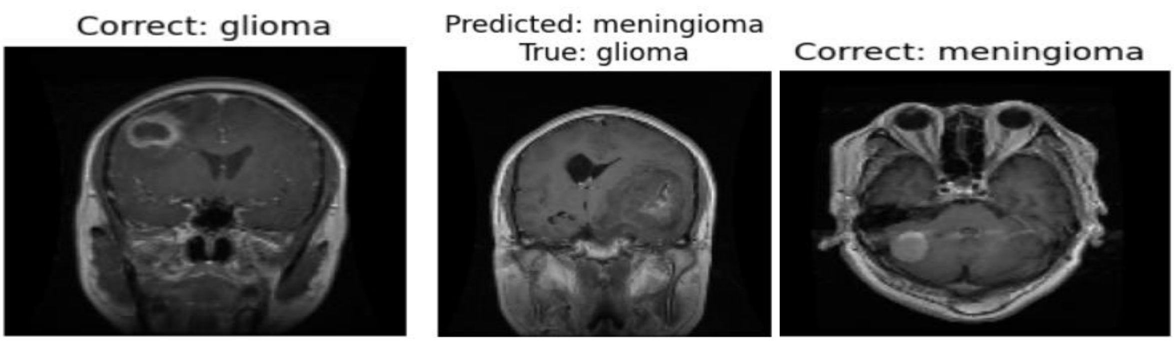
Best parameters found: 0.0021805203444177916 0.10368381437132414
Epoch 1/10
179/179 ━━━━━━━━━━━━━━━━━━━━ 17s 74ms/step - accuracy: 0.5594 - loss: 1.0602
Epoch 2/10
179/179 ━━━━━━━━━━━━━━━━━━━━ 0s 35us/step - accuracy: 0.0000e+00 - loss: 0.0000e+00
Epoch 3/10
179/179 ━━━━━━━━━━━━━━━━━━━━ 11s 60ms/step - accuracy: 0.8654 - loss: 0.3361
Epoch 4/10
179/179 ━━━━━━━━━━━━━━━━━━━━ 0s 24us/step - accuracy: 0.0000e+00 - loss: 0.0000e+00
Epoch 5/10
179/179 ━━━━━━━━━━━━━━━━━━━━ 12s 62ms/step - accuracy: 0.9391 - loss: 0.1798
Epoch 6/10
179/179 ━━━━━━━━━━━━━━━━━━━━ 0s 26us/step - accuracy: 0.0000e+00 - loss: 0.0000e+00
Epoch 7/10
179/179 ━━━━━━━━━━━━━━━━━━━━ 11s 59ms/step - accuracy: 0.9688 - loss: 0.0936
Epoch 8/10
179/179 ━━━━━━━━━━━━━━━━━━━━ 0s 25us/step - accuracy: 0.0000e+00 - loss: 0.0000e+00
Epoch 9/10
179/179 ━━━━━━━━━━━━━━━━━━━━ 10s 55ms/step - accuracy: 0.9731 - loss: 0.0746
```

**Figure 3: Identification of Best Values for Learning Rate & Dropout Rate**

Figure 3 presents the epochs that are trained using the genetic approach. The model tries to find the best parameters by calculating the maximum accuracy and minimum loss. It finds the learning rate and drop-out rate.



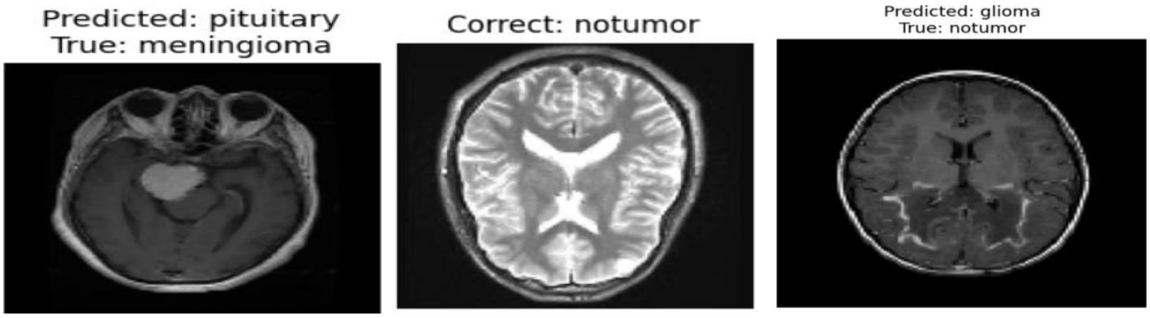



**Figure 4: Prediction of Tumour Cells using Genetic Neural Network**

Once optimized hyperparameters are obtained, the model undergoes full training across ten epochs, learning complex patterns necessary for accurate tumor classification. Model evaluation is conducted using several key metrics, including accuracy, which measures the correctness ratio of predictions which were correct to the overall predicitons. A high accuracy score indicates the model's effectiveness to real-world suitability on unseen test data. However, to warrant thorough testing, the model's efficiency is also calculated in terms of precision, recall, and F1-score. The precision determines the ratio of actual positives from all positive predictions, while recall evaluates the model's capability to detect all real positives. The F1-score, harmonic mean prior to two metrics precision and recall, is specifically important for classes that are not balanced and balancing the trade-off between sensitivity and specificity Confusion matrices for further classification of prediction performance for each class, showing distribution areas incorrect and facilitating new model refinement. Nevertheless, these metrics together deptect the consistency of the model in identifying brain tumor images prove that efficacy, containing glioma, meningioma, pituitary, and tumor per tumor, is shown in Fig. 4 .

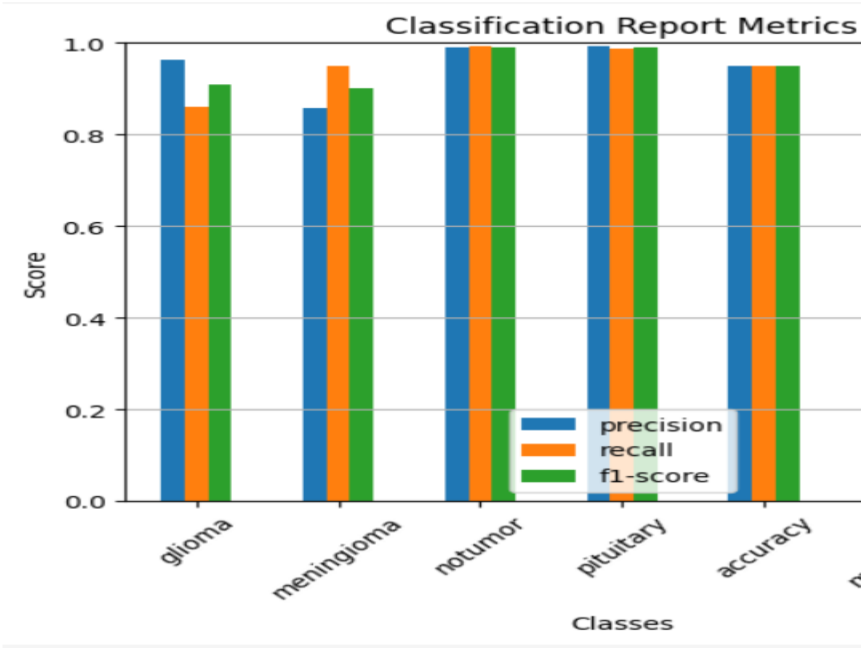



**Figure 5: Classification Report**

Figure 5 shows the Visualization reports. Imaging is important in evaluating the classification performance of CNN in MRI brain tumor images. The bar chart representation of class-specific accuracy highlights the robustness and possibility for example of bias towards specific tumor types. For example, some groups may have high accuracy, indicating that the model adequately recognizes the heterogeneity of these tumor types. Conversely, less accurate studies can highlight areas where data enhancement or additional training data can improve performance. Model predictions of test images, including correct and incorrect classification, provide additional thoughts and feedbacks into the how model make decsions to help identify possible misclassification patterns. Mixed matrix visualization deepens this analysis, it shows positive positives, positive positives, negatives, and negative predicted negatives The statistics helps identify pairs that are frequently misclassified such as glioma confusing meningioma, due to shared features between MRI scans. Overall, this visual support highlights the readiness of the model for practical use, ensuring that it is against standards of accuracy and reliability required for clinical or research use meet.

## 5. CONCLUSION

The research successfully uses a convolutional neural network (CNN) optimized combined with genetic algorithms to classify brain tumors from MRI images through systematic hyperparameter optimization, the genetic algorithm obtained a better learning rate each of 0.00218 and the dropout rate of 0.1037, which contributed to the model's strong performance training for dataset a it has 5712 images and was validated on 1311 images, the model achieved 97.31% accuracy in learning and 95% accuracy in validation, as reflected by weighted average accuracy, recall, and F1 scores Further validated Visual analysis of model output including feature maps and predictive classification for each tumor group day and the ability to find micropatterns characterizing the tumor but fall sometimes a poor distribution in a validation set can highlight the need for extensive adjustment through large heterogeneous data sets Evolutionary algorithm streamlined hyperparameter tuning and reduced manual intervention to achieve consistent results This strategy demonstrates the power of to combine deep learning and bio-inspired algorithms in medical image analysis, provides a reliable tumor classification tool. Future work could extend these findings by investigating transfer learning, domain adaptation, and incorporating multiple modal images

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