A hybrid approach using convolutional neural networks and genetic algorithm to improve of sensing brain tumor prediction

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Article Info	ABSTRACT
	Brain tumor is the most constantly diagnosed cancer, and the opinion of the brain is veritably sensitive and complex, which is the subject of numerous studies and inquiries. In computer vision, deep literacy ways, similar as the convolutional neural network (CNN), are employed due to their bracket capabilities using learned point styles and their capability to work with complex images. still, their performance is largely dependent on the network structure and the named optimization system for tuning the network parameters. In this paper, we present new yet effective styles for training convolutional neural networks. The maturity of current state-of-the-art literacy styles for convolutional neural networks are grounded on grade descent. In discrepancy to traditional convolutional neural network training styles, we propose an enhancement by incorporating the inheritable algorithm for brain tumor prediction. Our work involves designing a convolutional neural network model to grease the bracket process, training the model using different optimizers (Adam and the inheritable algorithm), and assessing the model through colorful trials on the brain magnetic resonance imaging (MRI) dataset. We demonstrate that the convolutional neural network model trained using the inheritable algorithm performs as well as the Adam optimizer, achieving a bracket delicacy of 99.5.

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1. INTRODUCTION

Many different types of brain tumors exist. Some brain tumors are cancerous (malignant), and some are noncancerous (benign) [1]. With the development of medical technology, brain tumor images can display the excrescence's position. Still, this raises advanced conditions for croakers' image recognition capacities. Croakers need to reuse a great quantum of brain excrescence images every day, which consumes a lot of time and energy [2]. Thus, it is of significant significance in computer-backed opinion of brain tumor to discover and treat them as beforehand as possible. Brain excrescence images are an important consideration in the opinion of tumor, as they can increase the effectiveness and delicacy of computer-backed opinion systems, which have come essential in the brain cancer bracket problem to grease the opinion process and increase survival chances. As a subset of machine literacy ways, the convolutional neural network (CNN) has surfaced as a precious volition in brain cancer opinion [3].

CNN is a particular type of deep, feed-forward neural network that learns features directly from the image. The dataset undergoes a training process. Despite advancements in computer-aided diagnosis (CAD) systems, brain cancer diagnosis remains a crucial health concern, prompting ongoing efforts to enhance the sensitivity of CAD systems. This research specifically investigates the utilization of CNNs in analyzing brain

cancer histology images. The CNN draws inspiration from the neural networks found in the human brain, operating on the premise that the system can acquire knowledge from past data. It comprises various layers, such as convolutional, pooling, and fully connected layers, positioned between the input and output layers, as illustrated in Figure 1. The perfection of the uprooted features in CNN is largely dependent on the weights of the network, including the weights of all complication pollutants and the weights of connecting edges in the completely connected subcaste. Accordingly, these weights play a pivotal part in bracket delicacy. During the training phase of the model, the weights are continuously streamlined to achieve a minimal bracket error rate.
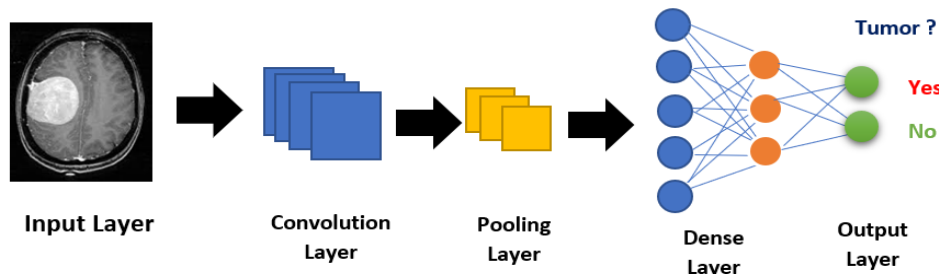

Figure 1. General architecture of a convolutional neural network

This is a feasibility study of hybridizing an evolutionary algorithm with machine learning (ML) models for the brain cancer bracket problem. To the stylish of our knowledge, in this work, we apply the inheritable algorithm (GA) [4] rather of backpropagation to classify brain excrescence images. We compare the performance of the GA-grounded convolutional neural network with mini-batch grade descent and Adam optimizers. The models are estimated using criteria similar as bracket delicacy, recall, perfection, F1-score, and prosecution time. We use the brain MRI images dataset, which contains brain cancer images, to train and test our proposed fashion. This work makes the following benefactions: i) Optimization of convolutional neural network weights for the brain image bracket problem using the inheritable algorithm (GA) hunt heuristic, ii) Design and development of a GA-CNN model for double bracket (non-cancerous and cancerous) of brain excrescence images, and iii) Training the model using different optimizers, videlicet mini-batch grade descent, Adam, and the inheritable algorithm (GA) [5]. Evaluation of the model through colorful trials conducted on the brain MRI dataset.

2. BACKGROUND

2.1. Brain tumors and magnetic resonance imaging

Brain tumor can be intracranial (similar as gliomas) or extracranial (similar as meningiomas or pituitary adenomas). Intracranial brain tumor, especially in late stages, pose significant challenges for treatment, frequently performing from mass effect on the supplemental brain [6] Treatment failure can be attributed to colorful factors, including the limited capability of current imaging modalities in directly delineating intraparenchymal lesions [7]. Thus, the application of advanced imaging ways to assess brain tumor and girding structures is pivotal for perfecting overall operation [8]. It is important to note that extracranial brain tumor, similar as pituitary adenomas and meningiomas, can also lead to complications and long- term damage [9], [10]. In clinical practice, MRI serves as the primary imaging modality for brain excrescence evaluation, furnishing structural, microstructural, functional, and metabolic information [11]. also, evolving imaging technologies in Rome are enabling the identification, characterization, and assessment of brain excrescence responses [12]. As a result, numerous operations of artificial intelligence (AI) in brain tumor imaging are grounded on MRI. For farther details on brain tumor, please relate to [6].

2.2. Deep learning

Deep learning (DL) is a branch of machine learning that utilizes ways inspired by neuroscience [13]. Goodfellow *et al.* [14] emphasize that while neuroscience was once the primary source of alleviation for deep literacy, it is no longer the case. DL algorithms have now established themselves as an integral part of medical image analysis tasks, including object discovery, bracket, and segmentation. Among these algorithms, convolutional neural networks are generally employed for developing brain excrescence bracket and segmentation ways [15]. A CNN has the capability to learn the spatial relationship between voxels in an MRI checkup. In CNNs, multiple pollutants are applied to an input image with the ideal of learning colorful

image characteristics. A typical CNN model consists of several layers an input subcaste, a convolutional subcaste, an activation function, a pooling subcaste, a completely connected subcaste, and an affair subcaste. The input subcaste receives the input image for farther processing by posterior layers. Convolution, pooling, and activation functions are used to prize high- position features from the image [15]. The completely connected subcaste is responsible for tasks similar as image bracket, object segmentation, or object identification. The affair subcaste generates the final prognostications or results of the network. The overall structure of a CNN is depicted in the figure.

2.3. Convolutional neural network

A typical artificial neural network (ANN) model consists of a single input and affair subcaste, as well as multiple retired layers [16]. Each neuron in the network takes an input vector X and produces an affair Y by applying a function F to it, frequently represented by (1) as given by [17].

$$F(X, W) = Y \tag{1}$$

Then, W represents a weight vector that represents the strength of connections between neurons in conterminous layers. Image bracket can now be achieved using the attained weight vector. There's a significant quantum of being literature on pixel-grounded image bracket, where contextual information, similar as shape, has been shown to yield better results [18]. Convolutional neural networks have gained attention for their bracket capabilities grounded on contextual information. The general structure of a CNN is depicted in Figure 1. It comprises four main corridors i) convolutional subcaste, ii) pooling subcaste, iii) activation functions, and iv) completely connected layers (also known as thick layers). The functionality of each element is described as follows [19].

2.3.1. Convolution layer

The image to be classified is inputted to the input subcaste, and the affair is the prognosticated class marker reckoned using features uprooted from the image [20]. Each neuron in the coming subcaste connects to multiple neurons in the former subcaste, forming original correlations known as open fields [21]. open field birth is employed to capture the original features of the input image [22]. The open fields of neurons associated with specific regions in the former subcaste form a weight vector that remains constant across all points in the position where the neuron is linked to the coming subcaste [23]. Due to neurons in the same aero plane having identical weights, analogous features can be detected in different positions of the input data [24]. This conception is illustrated in Figure 2.
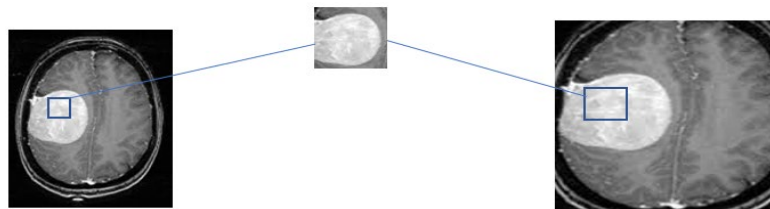

Figure 2. Receptive field of particular neuron in the next layer

A vector of weights, also appertained to as a sludge or kernel, is applied to the input vector through a sliding operation to induce a point chart [25]. This process of moving filters horizontally and vertically is known as a complication operation. In this operation, N features are uprooted from the input image within a single subcaste, representing different characteristics and performing in N filters and N feature charts [1]. The original open field miracle contributes to a significant reduction in the number of trainable parameters [26]. The affair value a_{ij} of the coming subcaste at position (i, j) is reckoned after the complication operation is applied. This calculation can be expressed using (2) [27].

$$a_{ij} = \sigma\big((w * x)_{ij} + b\big) \tag{2}$$

Then, X represents the input transmitted to the subcaste, W represents the sludge or kernel sliding over the input, b represents the bias term, $*$ denotes the complication operation, and σ denotes the nonlinearity introduced in the network.

2.3.2. Pooling layer

Once a feature has been identified, its exact placement becomes less significant [22]. Therefore, the pooling or sub-sampling subcaste follows the complication subcaste [23]. The application of pooling strategy provides significant benefits, including introducing restatement invariance and significantly reducing the number of trainable parameters [24]. Figure 3 illustrates the process of performing a pooling operation. It involves opting a window and passing the input factors within that window through a pooling function.

Another affair vector is generated by the pooling function. There are several pooling approaches, including average pooling and maximum-pooling, with maximum-pooling being the most generally used fashion that effectively reduces the size of the point chart [25]. Due to its part in calculating crimes, the winning unit does not share in the forward inflow and the error is not backpropagated to it.
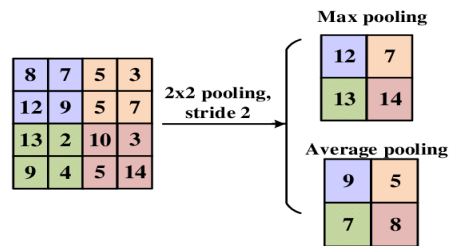
Figure 2. Pooling operation performed by choosing a 2×2 window [28]

2.3.3. Fully connected layer

The completely connected subcaste in traditional models serves an analogous function as the completely connected network. It takes the affair of the former phase, which involves repetitious complication and pooling, and calculates the fleck product between the weight vector and the input vector to induce the final affair [26]. Grade descent, also known as batch mode literacy or the offline approach, minimizes the cost function by assessing the cost over the entire training dataset. It updates the parameters only formerly per time, which corresponds to a complete traversal of the training dataset. While this approach converges to global minima, the size of the training dataset significantly affects the training time. The stochastic gradient method is employed as an alternative to decrease the cost function, addressing the limitations of the traditional gradient descent method.

2.3.4. Activation function

There is extensive literature on the utilization of sigmoid activation functions in traditional machine learning algorithms. To introduce nonlinearities, it has been demonstrated that rectified linear units (ReLU) outperform sigmoid activation functions due to two primary factors. First, computing the partial derivatives of ReLU is straightforward [27]. Second, in terms of training time, saturated nonlinearities like the sigmoid function $(f(x) = (1 + e^{(-x-1)}))$ are slower compared to non-saturated nonlinearities like $(f(x) = \max(0, X))$ Furthermore, in study [28], ReLU does not suffer from the vanishing gradient problem, which can occur when large gradients propagate through the network, leading to the inefficiency of ReLU activation and causing the "Dying ReLU" problem. This issue can be mitigated by employing Leaky ReLU, where if x > 0, the function is activated as $f(x) = x$, and if $x < 0$, the function is activated as $f(x) = \alpha x$, where α is a small constant [29].

2.4. Genetic algorithms

Genetic algorithms (GAs) are a research method based on the principles of natural selection and genetics, as proposed by Fraser (1957), Bremermann (1958), and Holland (1975) [30]. GAs encodes the decision variables of a search problem as finite-length strings using a specific base alphabet. These strings, which represent potential solutions to the research problem, are called chromosomes. The individual elements of the alphabet are referred to as genes, and their specific values are known as alleles. To develop optimal solutions and enforce natural selection, it is essential to assess the quality of solutions. This assessment is typically done using an objective function or mathematical model that evaluates the fitness of candidate solutions. The fitness function determines the relative quality of the candidate solutions, and the GA utilizes this information to guide the generation of improved solutions. Another fundamental concept in GAs is the notion of a population. Unlike traditional research methods, genetic algorithms rely on a large number of candidate solutions [31]. The population evolves over subsequent generations towards the best possible solution [32].

A typical GA consists of four phases:

a. Initial population: The process begins with a population comprising a set of chromosomes, where each chromosome represents a potential solution to the problem at hand. The chromosomes are characterized by a set of variables known as genes.

b. Selection: Two dyads of chromosomes, appertained to as parents, are named grounded on their fitness scores. Chromosomes with advanced fitness have a lesser liability of being chosen for reduplication.

c. Crossover: This phase is pivotal in the GA algorithm. For each brace of parents named for lovemaking, a crossover point is aimlessly determined along the genes. seed are produced by swapping genes between the parents. The crossover driver improves the application of the algorithm by exploring the hunt space girding the chromosomes.

d. Mutations: Some of the newly generated offspring may exhibit mutations in certain genes. Mutation operators are employed to facilitate exploration and improve the search process.

Genetic algorithms are now extensively applied in training deep learning infrastructures, similar as convolutional neural networks (GA-CNN). In these designs, the weights and impulses of the CNN are optimized using GA [33]. The modeling process for this particular problem is described in the following paragraphs, where defining a result in the form of a chromosome is a pivotal step in GA modeling.

3.   USING AG TO IMPLEMENT CNN
3.1. Data description

However, advancements in technology, including microscopes, cameras, and sensors, have led to the creation of databases that are rich in information and applicable to various fields. However, analyzing a large number of images manually poses challenges in terms of time, repetitive tasks, and the level of attention required. In study [34], this is where computer programs come into play, as they can process images represented by digital values and automatically assign classes to them through image classification. Such systems enable the performance of specialized tasks that might be costly or challenging for humans due to physical limitations like concentration, fatigue, or the time required to handle large volumes of image data.

Automatic image classification finds applications in diverse fields, including document analysis, medical research, and military operations. Within the medical domain, it aids in tasks such as cell and tumor recognition, as well as handwritten recognition of checks and postal codes. For our project, we utilized a database obtained from Kaggle, a web platform hosting the largest data science community. This database provides brain X-ray images of both patients and non-patients, as depicted in Figure 4, allowing machine learning experts on Kaggle to contribute their expertise in this domain [35].

Figure 4. brain X-ray images

3.2. Evolving the convolutional neural network through the genetic algorithm

The feedforward neural networks are capable of solving regression and classification problems of any type. However, when it comes to computer vision tasks, they face challenges due to the large number of parameters that need to be optimized in a fully connected layer. In study [36], consequently, artificial neural networks alone are not recommended for object identification in images. In recent years, CNNs have emerged as highly successful in the field of image classification. The automation of CNN design is crucial to assist users with limited domain knowledge in refining architectures to achieve desired performance and accuracy. Evolutionary methods, such as genetic algorithms, have been employed to simplify and automate CNN architectures and improve their performance.

GAs are heuristic search algorithms inspired by biological evolution, where offspring are generated through the selection of the most suitable chromosomes. By applying "random" modifications to the current solution, genetic algorithms create new solutions. The fitness function is employed to evaluate different settings and select the solution with the highest fitness value [37]. The way involved in enforcing an inheritable algorithm are explained in the following illustration. Figure 5 presents a block illustration of our model, and the layers employed by the model are described below.

After creating the CNN blocks, the entire system is trained. Training involves streamlining the weights of the network iteratively until the most accurate affair is achieved. In our network, three different optimization ways are employed and compared grounded on their bracket delicacy mini-batch grade descent, the Adam optimizer, and the inheritable algorithm (GA).
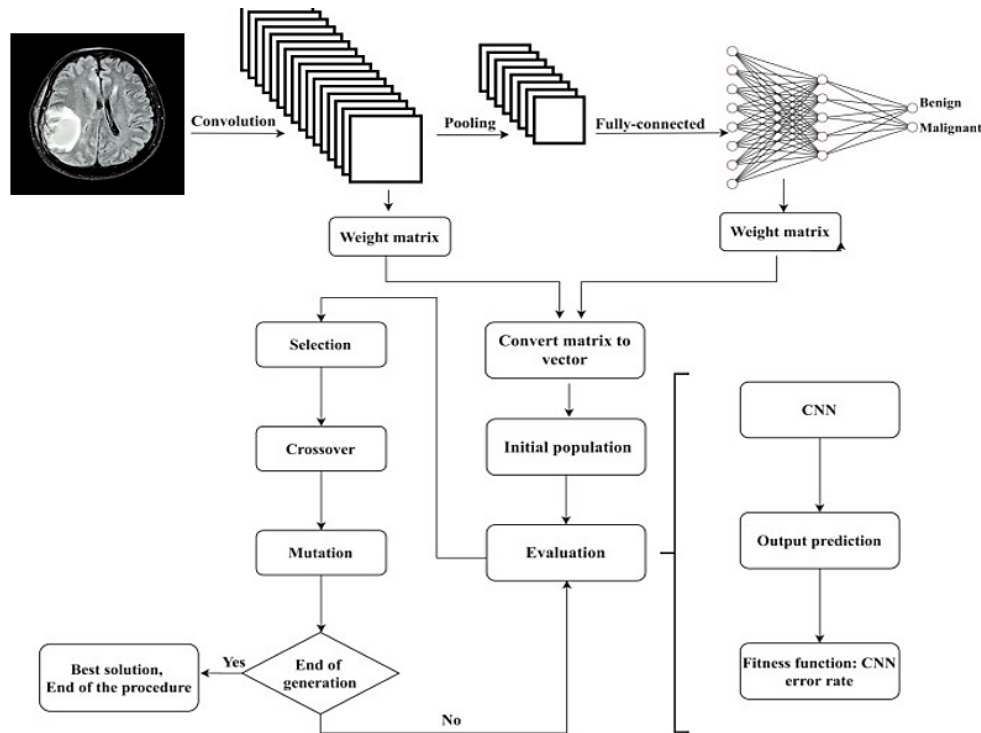

Figure 5. Block illustration of optimizing the parameters of the convolutional neural network using the inheritable algorithm

4.   RESULTS

In this section, we present the results of brain excrescence image bracket using the brain MRI dataset. Our proposed CNN model is trained using the Brain MRI dataset images as input, and three different optimization approaches are employed mini-batch grade descent, the Adam optimizer, and the inheritable algorithm (GA). The thing is to perform double bracket of the input images, distinguishing between benign and nasty cases. To estimate the performance of the model, the prognosticated markers are compared to the factual markers handed by the dataset. This allows us to calculate the bracket delicacy, recall, perfection, and prosecution time for each of the three optimization ways. The evaluation is performed on an identical test set from the Brain MRI dataset.

4.1. Initialization parents CNN architectures

To initiate a genetic algorithm, a population needs to be provided for evolution. For each individual in the initially generated population, we train the CNN using the training data and calculate the accuracy of the CNN architecture using the test dataset. The accuracy is multiplied by 100 and serves as a fitness function to optimize or maximize the performance. Based on these fitness values, parents for the next generation are selected. Following the four convolutional layers, we employ a neural network composed of completely connected layers, as depicted in Table 1. The activation function used in these layers is sigmoid, enabling the calculation of probability distributions for the two classes [38].

Table 1. Initial population parameter CNN

Individu	Number of filters			Size of filter			Fitness (%)
	L1	L2	L3	L1	L2	L3	
1	45	48	65	16	1	19	40.5
2	68	68	10	4	18	15	50.21
3	84	22	37	8	1	2	94.11
4	88	71	89	10	1	11	74.2
5	89	13	59	4	12	19	63.96
6	66	40	88	3	1	1	70.43
7	47	89	82	5	6	7	60.8
8	38	26	78	9	18	16	84.7
9	73	10	21	5	10	11	77.23
10	81	70	80	2	2	8	90.45

4.2. Selected parents CNN architectures

The selection of individuals in the roulette system is inspired by the concept of a lottery roulette. Each person in the population is associated with a sector of the wheel, where the angle of a sector is proportional to the fitness or quality of the individual it represents. When the wheel is spun, one person is selected. Consequently, the attractiveness of individuals is determined by their qualities. It is logical that individuals with better qualities have a higher probability of being selected and contribute to the improvement of our population as depicted in Table 2.

Table 2. Selected parents

Individu	Number of filters			Size of filter			Fitness (%)
	L1	L2	L3	L1	L2	L3	
1	84	22	37	8	1	2	94.11
2	81	70	80	2	2	8	90.45
3	38	26	78	9	18	16	84.7
4	73	10	21	5	10	11	77.23
5	88	71	89	10	1	11	74.2

At each stage, the individual with the highest fitness value in the population is selected as a parent. This selection process persists until the necessary number of parents is acquired for crossover and mutation in subsequent stages. Ensuring that individuals with the most promising fitness characteristics are chosen as parents contributes to the efficiency and effectiveness of the genetic algorithm.

4.3. Crossings parents CNN architectures

Crossovers are used to create new individuals by combining genetic material from existing individuals. Random crossovers are possible, but a commonly used approach is to perform multipoint crossovers. In this method, two parent chromosomes are selected, and a fixed or randomly chosen crossover point is used. Half of the genetic values are taken from the first parent, and the remaining values are taken from the second parent. The number of resulting children is shown in Table 3.

Table 3. Child population

Individu	Number of filters			Size of filter		
	L1	L2	L3	L1	L2	L3
1	84	22	80	8	1	8
2	81	70	78	2	2	16
3	38	26	21	9	18	11
4	73	10	89	5	10	11
5	88	71	37	10	1	2

4.4. Mutation CNN architectures

An alternative to crossing for creating new individuals is to modify existing individuals. Once again, this opportunity can be highly beneficial. Randomly modifying a few individuals in our population by altering one gene or another can be an effective strategy. There is no guarantee that a mutated individual will be better or worse, but it provides additional opportunities that can be valuable in generating good solutions. Similar to crossovers, it is not advisable to mutate all individuals. Any individual can be transformed as desired, with the only limitation being that the mutated individual should still represent a potential solution.

Typically, a single gene is modified to transition from one solution to another of the same form, although it can lead to a completely different evaluation as shown in Table 4.

Table 4. Mutation child population

Individu	Number of filters			Size of filter		
	L1	L2	L3	L1	L2	L3
1	84	**30**	80	8	**11**	8
2	**90**	70	78	**5**	2	16
3	38	**40**	21	**20**	18	11
4	**60**	10	89	**19**	10	11
5	**80**	71	37	10	**11**	2

The entire process repeats iteratively until the population achieves its maximum fitness value. This iterative approach ensures that the algorithm continues to evolve and improve over successive generations. The goal is to achieve stability or convergence, indicating that the algorithm has reached an optimal or near-optimal solution.

4.5. GA parameters

The genetic algorithm is implemented with specific parameters, as outlined in Table 5. These parameters play a crucial role in determining the algorithm's performance and effectiveness. Adjusting the values of these parameters can influence the convergence speed, solution quality, and computational efficiency of the genetic algorithm. Therefore, careful selection and tuning of these parameters are essential for achieving optimal results in genetic algorithm-based optimization tasks.

Table 5. Genetic algorithm parameters

Parameter	Value
Number individuals of population	10
Number generation	15
Maximum number of filters	100
Maximum core size	20
Number parents and children	5

Due to the inherent fluctuations during the training process of the TensorFlow tensor, the maximum accuracy of the test data steadily increased to 99.5%, as depicted in Figure 6. This upward trend in accuracy indicates the progressive improvement of the model's performance over time. The visualization provided in Figure 6 offers valuable insights into the training dynamics and highlights the model's capability to learn and generalize from the training data.
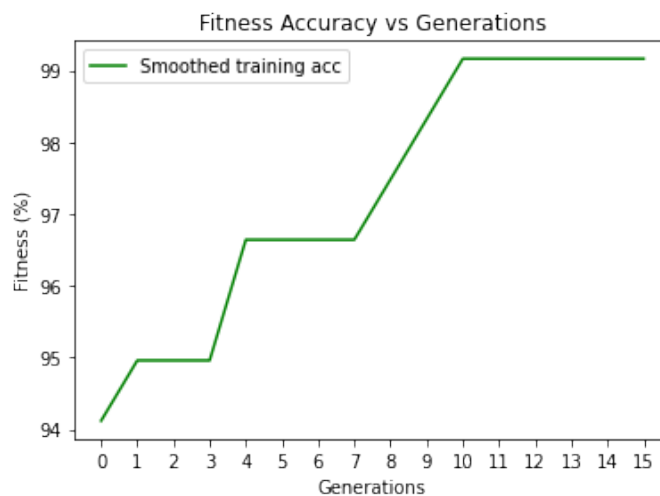

Figure 6. Fitness efficiency graph for AG

After 15 generations, the best architecture obtained is as follows, as detailed in Table 6. It consists of four convolutional layers, each accompanied by a max-pooling layer, facilitating feature extraction from the input data. This multi-layered architecture allows for the progressive abstraction of features, enabling the model to capture complex patterns present in brain tumor images more effectively.

Furthermore, the network incorporates two fully connected layers, serving to integrate the extracted features for final classification. These fully connected layers play a crucial role in synthesizing the hierarchical features learned by the convolutional layers, enhancing the model's discriminative capabilities. The architecture outlined in Table 6 strikes a balance between depth and complexity, optimizing the model's performance while maintaining computational efficiency.

Table 6. Best architecture CNN

Individual	Number of filters			Size of filters			Fitness (%)
	Layer1	Layer2	Layer3	Layer1	Layer2	Layer3	
Best	90	30	80	2	1	1	99.5%

It should be noted that even with a maximum kernel size limit of 20 at the end, we obtained the best kernels with a size of 2.1.1, which is a common size in popular CNN architectures. In conclusion, this paper describes the application of the genetic algorithm for computer vision tasks. This approach greatly benefits individuals who are not very familiar with complex architectures, as it allows for efficient exploration without sacrificing precision and saves time compared to traditional trial and error methods. Genetic algorithm applications can be employed in various domains where parameter search is required to maximize fitness functions.

5. CONCLUSION

The perfection of the uprooted features in the CNN is largely dependent on the network's weights, including the weights of the complication pollutants and the connecting edges in the completely connected subcaste. These weights have a critical impact on the bracket delicacy. In this study, we propose to optimize the CNN weights using an inheritable algorithm (GA) for the brain tumor image bracket problem. The GA is a well-known global optimization fashion that has been extensively applied in colorful real- world operations. still, there's limited exploration on combining nature-inspired computing with machine literacy, and this study aims to address this gap by hybridizing the CNN with the GA for Brain Tumor image bracket.

The proposed algorithm consists of five way the input subcaste, complication subcaste, pooling subcaste, activation subcaste, and completely connected subcaste, along with the training process. The bracket delicacy heavily relies on the weights of these layers, which are evolved using selection, crossover, and mutation drivers. We conducted several trials with different batch sizes and figures of duplications to dissect criteria similar as delicacy, recall, perfection, F1-score, and prosecution time. also, we examined the impact of inheritable parameters on the proposed algorithm.

Our findings indicate that the GA achieved an advanced perfection rate, suggesting that our model's false-positive prognostications are significantly reduced. The total prosecution time for the GA is longer compared to the other two optimizers. Since the GA is an evolutionary process, the stability and delicacy are told by the selection, crossover, and mutation procedures over time. A larger population size yielded better results. Likewise, we observed that using an invariant distribution to induce the original weights slightly bettered the bracket delicacy compared to the normal distribution. In summary, the proposed GA classifier demonstrates viability as a system for evolving network weights. The fusion of machine learning and evolutionary algorithms (evolutionary machine learning) holds promise for practical applications, and further investigation in this direction is encouraged.

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