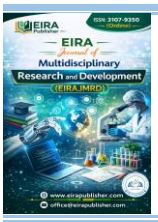

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Adaptive and Diversity Genetic Algorithm-Based Convolutional Neural Network for the Detection of Heart Attack

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Abstract **Original Research Article**

Convolutional Neural Networks (CNNs) have emerged as powerful tools for medical imaging analysis, which is essential for effective clinical interventions. However, standard CNNs often suffer from overfitting and sensitivity to noise in complex medical datasets, compromising diagnostic accuracy. While metaheuristic optimization techniques like Genetic Algorithms (GAs) can address these limitations, but struggles with slow convergence to achieve global optima solution. Over the years, improvement over GA has produced Elitist Genetic Algorithm (EGA) which is known as an efficient metaheuristic for complex structural optimizations, it improves upon GA by preserving the optimal solutions across generations, yet it remains highly susceptible to premature convergence and over-exploitation of restricted regions of the search spaces. Hence, this research developed an Adaptive and Diversity Genetic Algorithm (ADGA) by integrating adaptive parameter control to balance exploration and exploitation, alongside a diversity preservation technique to prevent premature convergence and used to optimize CNN which produces ADGA+CNN for better detection of heart conditions in Cardiac Magnetic Resonance Images (CMRIs). Cardiac Magnetic Resonance Images was acquired from Kaggle and augmented via left-right flipping. Preprocessing was performed using contrast enhancement, followed by segmentation using Fuzzy C-Means segmentation technique. Adaptive and Diversity Genetic Algorithm (ADGA) was formulated using adaptive parameter control and diversity preservation technique. The formulated ADGA was used to optimize CNN to achieve ADGA+CNN and translate to feature extraction. The performance of the ADGA+CNN was evaluated and compared with EGA+CNN and standard CNN based on False Positive Rate, Specificity Sensitivity, Precision, Recognition Accuracy and Computational Time. The empirical results demonstrate that the developed ADGA+CNN model significantly outperforms conventional CNNs and EGA-optimized model. The ADGA+CNN represents a powerful, highly automated, and reliable diagnostic tool that holds great potential to reduce human error, alleviate the workload of clinicians, and ultimately contribute to earlier and more accurate heart attack diagnoses, improving patient survival rates.

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Introduction

The invention of artificial intelligence was a revolutionary breakthrough for humanity and it opened the gateway to a different world. AI has achieved extra ordinary results in the field of speech and facial recognition, natural language processing, intelligent robots, and image recognition. AI was directed to the invention of great machines, these machines has rendered daily human life easier and more convenient. Machine learning is one of the techniques that has made this possible (Sadia *et al*., 2022). Machine learning is the ability of computers to learn without being explicitly programmed. The main objective of machine learning is to enable machines to learn without being thoroughly programmed (Sadia *et al*., 2022). Deep learning is a subset of machine learning that can be thought

of as the automation of predictive analytics (Tucci, 2021). Deep learning is one of those advancements has rendered AI to become smarter. Over the course of the last few years, deep learning has grown exponentially in the domain of computer vision and has become a research interest in image recognition issues. Deep learning has shown state-of-the-art performance on quantitative analysis of multiple cardiac MRI sequences and holds great promise for future use in clinical practice and scientific research (Tao *et al.,* 2020).

Convolutional Neural Networks (CNNs) is an outstanding branch of deep learning applications to visual purposes and it has earned major attention in the last years due to its breakthrough performances in varied computer vision applications, such as in object recognition, detection and segmentation challenges, in which they have achieved astonishing performances. CNNs have been used in medical imaging applications since the 1990s (Bernal *et al.,* 2018).

The healthcare system would be incomplete without radiology. AI is expected to significantly assist the radiologist in improving the diagnosis specificity because they are always on the frontline to adopt digital information related to medical imaging. AI could identify abnormal results at a very first glance, showing a high sensitivity rate in comparison to other conventional technology after performing a wide range of experimental analysis (Iqbal *et al.,* 2021). Magnetic Resonance Imaging is a technique in radiology which uses magnetism, radio waves and a computer to produce images of body structures. Cardiac Magnetic Resonance Imaging (CMRI) is an imaging modality that can accompany the diagnostic algorithms in multiple clinical applications. It includes not only functional, but also anatomical and morphological assessments that allow ventricular and valvular functions at once to be evaluated, as well as characterization of metabolic function and perfusion (Lachezar, 2019). Cardiovascular disorder identifies a number of heart disorders. Heart disease is a common disease. One of the common illnesses is a heart attack, the supply of blood does not act perfectly when a heart attack takes place. Heart attack is one of the primary causes of high death rates throughout the world, due to the lack of human and logistical resources (Mohammad and Abdulkareem, 2023).

Driven by the continuous growth of artificial intelligence and deep learning, Convolutional Neural Networks (CNNs) have made themselves to be recognized as a keystone technology in computer-aided radiology (Matsuzaka, 2025; Papageorgiou *et al*., 2025). Despite their prevalent deployment and high effectiveness in tasks like disease classification, organ segmentation, and anomaly localization, Convolutional Neural Networks (CNNs) suffer from persistent technical limitations that restrict their integration into clinical practice. Among these limitations are a high vulnerability to overfitting on medical datasets and sensitivity to noise in medical images (Jia *et al*., 2024). In cardiac MRI analysis, these limitations hinder the practical application of CNN in critical care settings, where reliable and rapid diagnosis is crucial (Hosssain *et al.,* 2021).

Genetic Algorithm has been in existence and it is known to solve the problem of optimization, genetic algorithm still has certain limitations and one of which is the difficulty to accurately converge to the global optimal solution. (Han and Xiao, 2022). Over the years, improvement over genetic algorithm has produced Elitist Genetic Algorithm (EGA). The Elitist Genetic Algorithm is widely recognized as an efficient metaheuristic for solving complex structural optimizations due to its ability to prevent the loss of optimal solutions across generations (Mustapha *et al*, 2026). However, EGA still suffer from certain limitations, among them are vulnerability to premature convergence and over exploitation of the restricted regions of the search space. (Mustapha *et al*, 2026).

Therefore this research aims to address this critical gap by modifying the crossover and mutation probabilities of EGA by using adaptive parameter control to improve the balance between exploitation and exploration and also to use diversity preservation technique through fitness sharing to solve the limitation of premature convergence during the search process. The improved EGA which is called ADGA will be used to optimize CNN to solve the limitation of overfitting and high sensitivity to noise in medical images for better detection of heart attack in Cardiac Magnetic Resonance Images.

Review Of Related Works

Han & Xiao (2022) proposed an Improved Adaptive Genetic Algorithm (IAGA). In traditional GAs, crossover probability (Pc) and mutation probability (Pm) remain static, which often causes the population to stagnate in local optima. Han and Xiao designed a feedback loop where Pc and Pm adjust dynamically based on individual fitness relative to the population's average and maximum fitness values. It reduced convergence time while improving the likelihood of reaching global optima in complex search spaces.

Snigdha *et al.,* 2022, discovered the specific attributes that are responsible for the heart attack to occur. The dataset was utilized from Researchers which is an open information entry of heart failure clinical record dataset. To improve this, the k-means Clustering were utilized. The

research helped to uncover the relationship between heart attack and the attributes causing it. Among all of those classifier, meta.AdaboostM1 happened to be the best classifier among them, however the model has limitations of overfitting.

Feng *et al*. (2022) proposed a directed crossover operator that uses the current best individuals as an evolutionary target, combined with a multilayer adaptive mutation operator that stratifies the population and applies different mutation strategies per layer. This was shown to reduce premature convergence and improve search accuracy in image-matching tasks compared to standard GA. The directed crossover operator introduces a strong directional bias which leads to greedy convergence.

Anwaar *et al.* (2022) Analyzed modifications in selection and stable crossover operators for global optimization problems. They addressed the "survival of the fittest" selection pressure which frequently discards potentially useful genetic materials prematurely. it Maintained population heterogeneity across successive generations, enabling better exploration in multimodal landscapes. The algorithm experienced slow convergence speed by explicitly lowering selection pressure and preserving sub-optimal ("unfit") genetic material to maintain diversity.

Poohoi *et al*. (2023) introduced a Stable Crossover (Stas Crossover) operator designed to preserve structural genetic information during parent recombination. The method increases the variety of offspring creation while ensuring that high-performing parent traits are transferred directly to offspring without excessive disruption. By prioritizing structural stability during crossover, the algorithm lowers overall exploration pressure, making it prone to slower progress or convergence traps in highly rugged, multi-peak (multimodal) search spaces.

Kaur and Kaur, 2023 predicted the likelihood of coronary heart disorder in patients by implementing a modified machine learning algorithm. The input data passed through various procedures comprising preprocessing, clustering, and selection of effective attributes before classification. To determine the heart illness, four algorithms which include random forest, K-means, genetic algorithm, and logistic regression were assimilated. The irrelevant attributes of heart dataset are discarded to improve the performance and to decrease the training period time. The process was completed by random forest technique. K-means clusters were optimized by genetic algorithm in order to group all the outlier data points. At last, logistic regression was applied to classify the patients based on the heart disease. Performance comparison among various existing techniques has analyzed on the basis of some performance measures. The calculated accuracy increased up to 95%. However, the model has limitations of overfitting and generalization.

Sri *et al*., (2023) addressed the problem of heart disease detection in public health. The performance of Convolutional Neural Networks (CNN) with conventional machine learning algorithms in diagnosing heart disease was compared using a dataset comprising 14 features. The primary objective was to determine whether CNNs can provide more accurate and reliable results than traditional techniques. The dataset was split into an 80-20 training-testing split. The model was trained for 300 epochs with a batch size of 64, and performance evaluation was conducted. The results reveal that the CNN model achieved a remarkable accuracy of 100%, demonstrating its potential to outperform conventional machine learning algorithms. These findings emphasize the significance of deep learning techniques in improving heart disease diagnostics, although further research is needed to optimize CNN models and address interpretability concerns for practical implementation in healthcare settings. The model has the problem of generalization which hinders the model's applicability across diverse patients group.

Wang *et al.* (2023) Proposed a Genetic Algorithm based on Two-Direction Crossover (TDX) and Grouped Mutation. Two-direction crossover adds an additional search vector (at a 45-degree angle to the direction between parents) to discover better search directions in non-linear spaces. Grouped mutation divides the population into two sub-groups and applies distinct mutation operators with different properties to each group to balance local and global exploration. The algorithm struggles to perform tight, fine-grained local refinement where optimal solutions sit precisely on the boundary between feasible and infeasible spaces.

Malonzo *et al*. (2024) added a new crossover process and local search for a tour-planning problem. They further modified it by introducing a new crossover operator to remove redundant nodes, a dynamic mutation rate to increase population diversity, and optimizations to reduce runtime as the number of nodes grows. The Algorithm has difficulty in reaching the global optimum because of premature elimination of candidate paths.

Huang *et al.* (2024) developed an Improved Genetic Algorithm (IGA) tailored for multi-threshold optimization in digital pathology image segmentation. Enhanced both the selection mechanism and crossover operations to maintain population diversity and optimize multi-level threshold searching across complex medical images. It was noted that the calculation and convergence times are relatively high due to complex fitness evaluations

Hidayat *et al.,* 2024 optimized early coronary heart disease (CHD) prediction using a genetic algorithm (GA)-based convolutional neural network (CNN) feature engineering approach. The study sought to overcome the limitations of traditional hyperparameter optimization techniques by leveraging a GA for superior predictive performance in CHD detection. The advanced GA-based CNN model outperformed traditional methods, achieving a substantial increase in accuracy. The optimized model delivered a promising accuracy range, with a peak of 85% in hyperparameter optimization and 100% accuracy when integrated with machine learning algorithms, namely naïve Bayes, support vector machine, decision tree, logistic regression, and random forest, for both binary and multiclass CHD prediction tasks. The model has limitation of computational complexity.

Saba *et al.,* 2024, investigated a hybrid strategy that combines genetic algorithms (GAs) with convolutional neural networks (CNNs). GAs are included into the system to enhance feature selection and boost prediction accuracy, improving CNN performance using evolutionary optimization methods. Standard cardiac disease datasets were used to test the suggested model, and its effectiveness is shown by evaluating measures like accuracy, precision, recall, and computing economy. According to the results, the CNN-GA hybrid strategy performs better than conventional techniques and offers a reliable, scalable solution for the prediction of heart disease. However, the model has limitation of limited dataset size and diversity high computational cost.

Gao *et al.* (2025) developed a hybrid feature-selection method (FNN-GA) that integrates an improved Genetic Algorithm with a Fuzzy Neural Network. They enhanced the GA component with a multi-point crossover mechanism using a diversity-aware adaptive selection strategy**,** and dynamic parameter adjustments to preserve population diversity while searching high-dimensional feature subsets. The performance of the FNN wrapper relies on proper rule initialization; poor initial fuzzy partition parameters can cause slow early-stage convergence.

Srinivasulu *et al.,* 2025 presented an improved Convolutional Neural Network (CNN) model designed to enhance heart attack prediction and detection while addressing the common issues of overfitting and poor generalization found in traditional machine learning methods. The enhanced model utilizes advanced regularization techniques and optimization strategies to improve its performance, capitalizing on CNNs' ability to effectively extract spatial features. The experimental results reveal significant improvements in both accuracy and robustness of the model. The enhanced CNN achieved a maximum accuracy of 100% and a validation accuracy of up to 75% after 50 training epochs. The model has limitation of generalization and scalability.

Yilmas and Kus (2026) addressed the challenge of hyperparameter selection, a key factor affecting convolutional neural networks (CNNs) performance in biomedical image classification. A genetic algorithm (GA) was employed to optimize activation function, padding, number of filters, kernel size, dropout rate, pooling size, and batch size. The optimized CNN was trained on brain Magnetic Resonance Imaging (MRI) images of Multiple Sclerosis (MS) and validated on Alzheimer's MRI and COVID-19 chest X-ray datasets. Results show substantial improvements across all datasets. On MS, the proposed model achieves up to 37.6 % F1-score and 33.7 % accuracy gains compared to other models. On Alzheimer's, improvements reach 32.8 % in F1-score and 32.5 % in accuracy. For COVID-19, gains are smaller but consistent, ranging from 0.8% to 12.1%. Overall, the GA-optimized CNN consistently outperforms widely used architectures such as Xception, InceptionV3, VGG16, VGG19, AlexNet, ResNet50, and GoogleNet, demonstrating both enhanced classification performance and strong generalizability across biomedical imaging tasks. There is limitation of generalization across datasets.

Mustapha *et al*., (2026) introduced a competitive element in genetic algorithm which both parents and offspring compete for survival, and only fit individuals will be part of the next generation. While selecting fit individuals helps the algorithm to produce better results. The findings from the study demonstrate that integrating the parenting fitness parameter leads to better results in comparison with a typical elitist genetic Algorithm. The algorithm has limitation of population diversity.

Methodology

1. Data acquisition, Preprocessing and Segmentation

Cardiac magnetic resonance images was acquired from *Kaggle* which is a publicly available repository https://www.kaggle.com/datasets/samdazel/automated-cardiac-diagnosis-challenge-miccai17. Kaggle reported that the dataset comprises 150 patients evenly distributed across five distinct classes, each characterized by specific physiological parameters. Ambiguous cases based on clinical indices were excluded. The patients made several visits to the hospital over six years period in which their images were captured during each visitation. The patient classes were:

NOR (Normal): Normal cardiac anatomy and function with an ejection fraction > 50%, diastolic wall thickness < 12 mm, and specific volume criteria.

MINF (Systolic Heart Failure with Infarction): Ejection fraction < 40%, abnormal myocardial contractions, and potential LV remodeling.

DCM (Dilated Cardiomyopathy): Ejection fraction < 40%, LV volume > 100 mL/m2, and diastolic wall thickness < 12 mm.

HCM (Hypertrophic Cardiomyopathy): Normal cardiac function (ejection fraction > 55%) with myocardial segments thicker than 15 mm in diastole.

ARV (Abnormal Right Ventricle): Abnormal RV parameters with or without normal LV function.

Originally, two thousand, eight hundred and seventy-six (2,876) images were acquired. The acquired datasets undergo data augmentation where the data were flipped left and right and eventually make a total of five thousand, seven hundred and fifty-two (5,752) images. K-fold cross validation method was used for data division. The datasets were divided into ten (10) folds Where K=10, and all trained datasets were used for testing. The acquired datasets was preprocessed using Contrast Enhancement because the datasets are already in gradescale. The preprocessed images was segmented using Fuzzy C-Means segmentation technique which produces smooth boundaries.

2. Formulation of Adaptive and Diversity Genetic Algorithm (ADGA)

Elitist Genetic Algorithm (EGA) was enhanced by using Adaptive parameter control and Diversity preservation technique, the improved EGA is called Adaptive and Diversity Genetic Algorithm (ADGA). Adaptive parameter control adjusts parameters dynamically during evolution and increase mutation when diversity drops. It also reduce crossover when convergence stabilizes and improves balance between exploration and exploitation. Diversity preservation techniques maintain population diversity to avoid premature convergence using fitness sharing method.

The algorithm begins with the initialization of a population represented as

$$P^{(0)} = \{X_1, X_2, \dots, X_P\}, \quad 1$$

where each chromosome is randomly generated within the predefined search boundaries using the uniform distribution

$$x_j \sim U\left(x_j^{\min}, x_j^{\max}\right). \quad 2$$

This initialization ensures that the candidate solutions are well distributed across the search space to encourage broad exploration during the early stages of optimization. Similar to the Elitist Genetic Algorithm, the objective function $F(X)$ is used to evaluate the quality of each chromosome. The initialized population serves as the starting point for iterative evolutionary operations aimed at obtaining the optimal solution.

In the fitness evaluation stage, each chromosome X_i is assessed using the fitness function

$$(X_i) = f(X_i) \quad 3$$

where the algorithm determines the maximum fitness value $F_{\max}$ and the average fitness value F_{avg}. These statistical measures are essential because they provide the basis for the adaptive control of crossover and mutation probabilities in the modified algorithm. The computation of $F_{\max}$ identifies the best-performing chromosome in the population, while F_{avg} reflects the general performance level of the population. Unlike the Elitist Genetic Algorithm, where crossover and mutation probabilities remain constant throughout the optimization process, the modified approach dynamically adjusts these probabilities according to the fitness distribution. This adaptive strategy enables the algorithm to balance exploration and exploitation more effectively during the search process.

A major enhancement introduced in the Adaptive and Diversity Genetic Algorithm is the diversity preservation mechanism implemented through fitness sharing. The Euclidean distance between individuals is calculated using

$$d_{ij} = \|X_i - X_j\|, \quad 4$$

which measures the similarity between chromosomes in the population. A sharing function is then defined as

$$\text{sh}(d_{ij}) = 1 - \left(\frac{d_{ij}}{\sigma_{\text{share}}}\right)^{\alpha_s} \text{ when } d_{ij} < \sigma_{\text{share}}, \quad 5$$

otherwise the sharing value becomes zero. The shared fitness of each chromosome is computed using

$$F_i' = \frac{F(X_i)}{\sum_{j=1}^{P} \text{sh}(d_{jj})}, \quad 6$$

thereby penalizing individuals located in densely populated regions of the search space. This mechanism reduces the dominance of highly similar chromosomes and maintains genetic diversity across generations. Consequently, the algorithm avoids premature convergence and enhances its ability to explore multiple promising regions simultaneously.

The adaptive crossover probability is another important improvement integrated into the modified algorithm. Instead of assigning a fixed crossover probability as in the Standard Genetic Algorithm, the Adaptive and Diversity Genetic Algorithm computes an individual crossover probability for each chromosome using the expression

$$p_c^{(i)} = p_c^{\max} \times \frac{F_{\max} - F(X_i)}{F_{\max} - F_{\text{avg}}} \quad 7$$

for chromosomes with fitness values greater than or equal to the population average. For chromosomes with lower fitness values, the minimum crossover probability $p_c^{\min}$ is applied. This adaptive mechanism allows weaker chromosomes to undergo more extensive recombination, thereby improving population exploration. Strong chromosomes are protected from excessive disruption, which preserves high-quality genetic information across generations. The adaptive crossover strategy therefore increases the convergence efficiency of the optimization process.

Similarly, the Adaptive and Diversity Genetic Algorithm introduces an adaptive mutation probability to strengthen the search capability of the population. The mutation probability is dynamically adjusted according to chromosome fitness using

$$p_m^{(i)} = p_m^{\max} \times \frac{F_{\max} - F(X_i)}{F_{\max} - F_{\text{avg}}} \quad 8$$

for chromosomes with fitness above the average, while $p_m^{\min}$ is assigned to chromosomes with lower fitness. This adaptive mutation mechanism increases the mutation rate for poorly performing individuals, thereby introducing new genetic patterns into the population. By doing so, the algorithm enhances exploration and minimizes the possibility of stagnation in local optima. The Gaussian mutation operation

$$x_j' = x_j + \delta, \quad 9$$

where $\delta \sim N(0, \sigma^2)$, further improves solution refinement by introducing controlled random perturbations. Consequently, the modified algorithm achieves a more robust global search performance compared to the Elitist Genetic Algorithm.

Parent selection in the Adaptive and Diversity Genetic Algorithm is performed using tournament selection, where a subset of chromosomes competes and the fittest individual is selected as a parent according to

$$X_{\text{parent}} = \arg\max\{F(X_{i_1}), F(X_{i_2}), \dots, F(X_{i_k})\}. \quad 10$$

Tournament selection provides a stronger selection pressure than roulette wheel selection and improves the probability of selecting high-quality chromosomes for reproduction. This approach also reduces the likelihood of weaker individuals dominating the population. The selected parents then undergo arithmetic crossover represented by

$$X_{\text{child}} = \lambda X^{(1)} + (1 - \lambda) X^{(2)}, \quad 11$$

where $\lambda \in [0,1]$ is the crossover coefficient. Arithmetic crossover generates offspring that inherit characteristics from both parents in a balanced manner. As a result, the offspring population contains more diverse and potentially superior candidate solutions.

The mutation operation in the modified algorithm further strengthens the search efficiency of the optimization process. After crossover, offspring chromosomes are mutated using Gaussian mutation

$$x_j' = x_j + \delta, \quad 12$$

where $\delta \sim N(0, \sigma^2)$. This operation introduces random variations into chromosome genes, enabling the population to escape local optima and maintain diversity throughout the evolutionary process. The adaptive mutation probability ensures that the mutation intensity is controlled according to the quality of each chromosome. High-quality individuals experience minimal mutation to preserve valuable genetic information, while low-quality individuals undergo stronger mutation for exploration purposes. Therefore, the combination of adaptive mutation and diversity preservation significantly improves the robustness and convergence reliability of the algorithm.

The elitism ensures that the best chromosome obtained in the current generation is preserved into the next generation using

$$X_{\text{best}}^{(t+1)} = X_{\text{best.}}^{(t)}. \quad 13$$

This mechanism guarantees that the optimal solution found so far is not lost during crossover or mutation operations. The population update stage then replaces the old population with the newly generated offspring population according to

$$P^{(t+1)} = P_{\text{offspring}}^{(t)}. \quad 14$$

Through repeated iterations of selection, crossover, mutation, and elitism, the algorithm progressively improves the overall population fitness. The iterative process continues until the maximum generation limit

$$t = t_{\max} \quad 15$$

is reached or the convergence condition $\left|F_{\text{best}}^{(t)} - F_{\text{best}}^{(t-1)}\right| < \epsilon$ is satisfied. The final optimal solution is then obtained using

$$X^* = \arg\max F(X_i). \quad 16$$

The primary difference between the Elitist Genetic Algorithm and the Adaptive and Diversity Genetic Algorithm lies in the adaptive parameter control and diversity preservation equations. In the Elitist Genetic Algorithm, the crossover and mutation probabilities remain constant and are represented simply as p_c and p_m. However, the modified algorithm dynamically adjusts these parameters using the adaptive equations

$$p_c^{(i)} = p_c^{\max} \times \frac{F_{\max} - F(X_i)}{F_{\max} - F_{\text{avg}}} \quad 17$$

And

$$p_m^{(i)} = p_m^{\max} \times \frac{F_{\max} - F(X_i)}{F_{\max} - F_{\text{avg}}}. \quad 18$$

Furthermore, the Elitist Genetic Algorithm lacks a diversity preservation mechanism, whereas the modified algorithm introduces fitness sharing using

$$F_i' = \frac{F(X_i)}{\sum_{j-1}^{P} \text{sh}(d_{ij})}. \quad 19$$

The Elitist Genetic Algorithm mainly relies on roulette wheel selection, while the modified algorithm employs tournament selection for stronger selective pressure. These mathematical modifications improve exploration capability, convergence speed, and solution quality in the Adaptive and Diversity Genetic Algorithm. The step-by-step algorithm follows:

Algorithm 1: Formulation of Adaptive and Diversity Genetic Algorithm

Input

- **Objective function: $F(X)$**
- **Population size: P**
- **Maximum number of generations: $t_{\max}$**
- **Maximum crossover probability: $p_c^{\max}$**
- **Minimum crossover probability: $p_c^{\min}$**
- **Maximum mutation probability: $p_m^{\max}$**
- **Minimum mutation probability: $p_m^{\min}$**
- **Sharing radius: σ_{share}**

Step 1: Population Initialization

Generate an initial population randomly:

$$\mathcal{P}^{(0)} = \{X_1, X_2, \ldots, X_P\}$$

Each chromosome is initialized within the search bounds:

$$x_j \sim \mathcal{U}(x_j^{\min}, x_j^{\max})$$

Where:

- **x_j is the j^{th} variable of a chromosome.**

Step 2: Fitness Evaluation

Evaluate the fitness of each individual:

$$F(X_i) = f(X_i)$$

Determine:

- **Maximum fitness:**

$$F_{\max} = \max(F(X_i))$$

- **Average fitness:**

$$F_{\text{avg}} = \frac{1}{P}\sum_{i=1}^{P} F(X_i)$$

Step 3: Diversity Preservation Using Fitness Sharing

Compute the Euclidean distance between individuals:

$$d_{ij} = \|X_i - X_j\|$$

Define the sharing function:

$$sh(d_{ij}) = \begin{cases} 1 - \left(\frac{d_{ij}}{\sigma_{\text{sharc}}}\right)^{\alpha_s}, & d_{ij} < \sigma_{share} \\ 0, & \text{otherwise} \end{cases}$$

Compute shared fitness:

$$F_i' = \frac{F(X_i)}{\sum_{j=1}^{P} \text{sh}(d_{ij})}$$

This reduces dominance of similar individuals and maintains population diversity.

Step 4: Adaptive Crossover Probability

Adapt crossover probability dynamically as:

$$p_c^{(i)} = \begin{cases} p_c^{\max} \times \dfrac{F_{\max} - F(X_i)}{F_{\max} - F_{\text{avg}}}, & F(X_i) \geq F_{\text{avg}} \\ p_c^{\min}, & F(X_i) < F_{\text{avg}} \end{cases}$$

This increases exploration for weak individuals while preserving strong individuals.

Step 5: Adaptive Mutation Probability

Adapt mutation probability as:

$$p_m^{(i)} = \begin{cases} p_m^{\max} \times \dfrac{F_{\max} - F(X_i)}{F_{\max} - F_{\text{avg}}}, & F(X_i) \geq F_{\text{avg}} \\ p_m^{\min}, & F(X_i) < F_{\text{avg}} \end{cases}$$

This enhances diversity and avoids local optima trapping.

Step 6: Parent Selection

Select parents using tournament selection:

$$X_{\text{parent}} = \arg\max\{F(X_{i_1}), F(X_{i_2}), \dots, F(X_{i_k})\}$$

Where:

- k **is the tournament size.**

Step 7: Crossover Operation

Generate offspring using arithmetic crossover:

$$X_{\text{child}} = \lambda X^{(1)} + (1 - \lambda) X^{(2)}$$

Where:

- $\lambda \in [0, 1]$ **is the crossover coefficient.**

Step 8: Mutation Operation

Mutate offspring as:

$$x_j' = x_j + \delta$$

Where:

$$\delta \sim \mathcal{N}(0, \sigma^2)$$

and:

- $\mathcal{N}(0, \sigma^2)$ **is Gaussian mutation noise.**

Step 9: Elitism Strategy

Preserve the best solution:

$$X_{\text{best}}^{(t+1)} = X_{\text{best}}^{(t)}$$

This ensures that the best chromosome survives to the next generation.

Step 10: Population Update

Replace the old population with offspring:

$$\mathcal{P}^{(t+1)} = \mathcal{P}_{\text{offspring}}^{(t)}$$

Step 11: Termination Criterion

Repeat Steps 2-10 until:

$$t = t_{\max}$$

or

$$\left| F_{\text{best}}^{(t)} - F_{\text{best}}^{(t-1)} \right| < \epsilon$$

Where:

- ϵ **is the convergence threshold.**

Output: Optimal solution:

$$X^* = \arg\max F(X_i)$$

3. ADGA+CNN for heart attack detection in cardiac magnetic resonance images.

Convolution Neural Network (VGG 19) was optimized by the formulated Adaptive and Diversity Genetic Algorithm (ADGA), assigning optimal weight parameters for CNN, and translate to feature extraction.

i. Problem formulation and optimization objective.

The primary objective is to automate the discovery of the most effective CNN hyper parameter configuration, denoted as θ. The hyper parameters targeted for optimization include:

W: The filter weights or sizes within the convolutional layers.

N: The number of filters or hidden units.

η: The learning rate for the training optimizer.

D: The dropout rates utilized to prevent overfitting.

The optimization goal is mathematically expressed as finding the optimal parameters θ^* that maximize a predefined fitness function F(θ), which is θ^*=arg max F(θ)

ii. Inputs and outputs

The algorithm processes a CMR dataset D, which is divided into a training set (D_{train}) for model fitting and a validation set (D_{val}) for evaluating hyper parameter fitness. Additionally, ADGA relies on a set of initialization parameters, including the population size P, maximum generations t_{max}, and boundaries for adaptive crossover (P_c^{min} , P_c^{max}) and mutation rates (p_m^{min}, P_m^{max}).

The execution yields two primary outputs: the optimal hyperparameters $\theta^* = (W^*,N^*,\eta^*,D^*)$ and a fully trained, highly accurate CNN classifier capable of heart attack detection.

iii. Chromosome Encoding and Constraints

To apply genetic operations, the hyper parameters of the network are mapped into a data structure known as a chromosome, represented as a vector X, which is $X_i = (w_1,\ldots,w_k, n_1,\ldots,n_L, \eta, d_1,\ldots,d_L)$. Each element (gene) in the chromosome represents a specific architectural choice or training setting. To ensure the generated networks are physically viable and training remains stable, the search space is confined by strict mathematical boundaries:

The filter sizes W_j must remain within a functional window (w_{min},w_{max}).

The number of filters N_i must scale between a minimum and maximum allocation (n_{min},n_{max}).

The learning rate η is bounded by stabilizing operational thresholds (η_{min},η_{max}).

The dropout rate D_i is bound as a probability constraint between 0 and 1.

iv. Structural CNN equations

The underlying model evaluated by the genetic algorithm is a standard feedforward CNN utilizing spatial abstractions and regularizations. The forward and backward propagation steps follow a structured series of algebraic operations:

Convolution and Activation: The core feature extraction is driven by the convolution operation, where the input $X^{(1)}$ is convolved with weights $W^{(1)}$ and adjusted by a bias $b^{(1)}$ to produce net inputs $Z^{(1)}$, which is $Z^{(1)} = W^{(1)} * X^{(1)} + b^{(1)}$. To introduce non-linearity, allowing the network to learn intricate patterns in cardiac tissues, the Rectified Linear Unit (ReLU) activation function is applied as A = max (0, $z^{(1)}$).

Subsampling, Classification, and Loss: Following activation, a Pooling layer reduces the spatial dimensions of the feature maps to ensure translation invariance and reduce computational load. The extracted features are then flattened and fed into a Fully Connected Layer to compute raw class logits which is Z=WA+b. These logits are normalized into probabilities using the Softmax function. The discrepancy between the predicted probabilities and true clinical labels is computed via a cross-entropy Loss Function (L) which is

$$L = -\sum_{i=1}^{C} yi \log(\hat{y}i) \qquad 3.20$$

Weight Optimization and Dropout: During the backpropagation phase, network weights are updated using gradient descent. The Weight Update formula systematically adjusts parameters opposite to the direction of the error gradient, scaled by the genetically optimized learning rate η, which is

$$W^{(t+1)} = W^{(t)} - \eta \frac{\partial L}{\partial W}. \qquad 3.21$$

To reinforce structural robustness, Dropout is introduced. It randomly deactivates neurons during training using a Bernoulli distribution based on the optimized dropout probability ($1 - d_l$).

v. The fitness function

The fitness function $F(X_i)$ serves as the evolutionary bridge connecting the genetic algorithm to the CNN's objective performance. It assesses how well a specific chromosome's hyperparameters perform on the validation dataset: $F(X_i) = \alpha$. Accuracy $(X_i) - \beta$. $L(X_i)$. Here, α and β act as weight coefficients to balance model accuracy against its validation loss. Accuracy measures the ratio of correctly identified cardiac cases over total samples:

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \qquad 3.22$$

By penalizing high loss (L) and rewarding high classification accuracy, the function guides the population toward configurations that are both accurate and highly confident in their predictions.

vi. Adaptive parameter control (ADGA)

Standard genetic algorithms often stall when using static crossover and mutation rates. ADGA circumvents this by calculating dynamic probabilities (P_c and P_m) at every generation based on population fitness variance. If the population begins to homogenize, mutation rates increase to introduce fresh genetic sequences, maintaining an optimal exploratory equilibrium throughout execution.

i. Adaptive Crossover

$$P_m^{(i)} = \begin{cases} P_c^{\max,} \frac{F_{\max} - F(X_1)}{F_{\max} - Fang} \\ P_c^{\min}, \end{cases} \begin{cases} F(X_i) \geq Favg \\ F(X_i) < Favg \end{cases} \quad 3.23$$

ii. Adaptive Mutation

$$P_m^{(i)} = \begin{cases} P_c^{\max,} \frac{F_{\max} - F(X_1)}{F_{\max} - Fang} \\ P_c^{\min}, \end{cases} \begin{cases} F(X_i) \geq Favg \\ F(X_i) < Favg \end{cases} \quad 3.24$$

vii. Tournament selection

To determine which hyperparameter configurations get to pass on their traits, a Tournament Selection mechanism is deployed. A subset of k chromosomes is chosen at random, and their fitness values are compared: X_{parent} {$F(X_{i1})$, …, $F(X_{ik})$}. The chromosome with the highest fitness wins the tournament and is selected as a parent for the next generation.

viii. Crossover (Recombination)

Once parents are selected, they undergo Crossover to produce offspring. The framework employs a linear combination crossover strategy, which blends the numerical hyperparameter vectors of two parents ($X^{(1)}$ and $X^{(2)}$) using a random scaling factor $\lambda \varepsilon[0,1]$: $X_{child} = \lambda X^{(1)} + (1 - \lambda)X^{(2)}$, $\lambda \varepsilon[0,1]$. This allows child networks to inherit interpolated, intermediate structural properties from both high-performing parents.

ix. Mutation

To prevent the algorithm from getting trapped in local optima, random Mutations are applied to the offspring. Numerical values like learning rates receive minor stochastic adjustments within controlled boundaries: $\eta^1 = \eta + \varepsilon$, $\varepsilon \sim \mu$ (- 0.01, 0.01). Similarly, dropout rates are perturbed to test adjacent structural behaviors: $d_1^i = d_1 + \delta \sim \mu(-0.1, 0.1)$.

x. Diversity preservation via fitness sharing

A common pitfall in genetic optimization is "crowding," where the population clusters around a single sub-optimal design. ADGA prevents this using Fitness Sharing. First, the Euclidean distance (d_{ij}) between any two chromosomes is measured: $d_{ij} = ||X_i - X_j||$. A Sharing Function $Sh(d_{ij})$ evaluates how crowded an individual's neighborhood is. If an individual is surrounded by many similar configurations, its fitness is penalized, producing a Shared Fitness value (F_{shared}). This forces the algorithm to explore diverse architectural niches across the search landscape.

Shared Fitness

$$F_i^i = \frac{F(X_i)}{\sum_{j=1}^{P} sh(d_{ij})} \quad 3.25$$

xi. Elitism

To ensure that top-tier discoveries are never lost due to the randomness of crossover or mutation, Elitism clones the absolute best-performing chromosomes (X_{elite}) directly into the next generation without modification: $X_{best}^{(t+1)} \; X_{best}^{(t)} X$

xii. Termination Condition

The process iterates continuously until it meets a Termination Condition. The loop breaks either when the generation counter t reaches its maximum cap tmax, or when the change in population fitness drops below a critical convergence threshold ϵthreshold:

$$t = t_{max} \text{ or } |F_{best}^{(t)} - F_{best}^{(t-1)}| < \varepsilon \quad 3.26$$

iii. Upon termination, the system outputs a mathematically refined, robustly generalized CNN ready for deployment in clinical environments.

The Step-by-step algorithm follows:

Algorithm 2: ADGA+CNN

(i) Input CMR dataset *D*
Preprocess images (resize, normalize)
(ii) Split into d_{train}, D_{val}
(iii) Initialize population $P^{(0)}$
(iv) Evaluate fitness $F(X_i)$
(v) Apply fitness sharing → compute F_i
(vi) For each generation $t = 1$ to t_{max}:

- Compute F_{max}, F_{avg}

- Adapt $P_c^{(i)}, P_m^{(i)}$
- Select parents (tournament)
- Apply crossover using $P_c^{(i)}$
- Apply mutation using $P_m^{(i)}$
- Train CNN for offspring
- Evaluate fitness
- Apply fitness sharing
- Apply elitism
- Update population

(vii) Output:
X' = arg max F (X_i)

Definition of Parameters

(A) Genetic Algorithm

Symbol	Description
P	Population size
t_{max}	Maximum generations
X_i	Chromosome
$F(X_i)$	Fitness
F_{max}	Maximum fitness
F_{avg}	Average fitness
P_c^{max}, P_c^{min}	Crossover bounds
P_m^{max}, P_m^{min}	Mutation bounds
λ	Crossover factor
σ	Mutation variance

(B) (CNN)

Symbol	Description
W	Weights
b	Bias
N	Number of neurons
η	Learning rate
D	Dropout rate
L	Number of layers
C	Number of classes

(C) Diversity Parameters

Symbol	Description
d_{ij}	Distance between individuals
σ_{share}	Sharing radius

α_g	Sharing exponent
F_i	Shared fitness

(D) Dataset and Metrics

Symbol	Description
x_i	CMR image
y_i	Label
TP, TN, FP, FN	Confusion matrix terms
L	Loss

The optimized CNN (ADGA+CNN) was implemented using the pre-processed and segmented cardiac MRI image data. K-fold cross validation method (Standard K-Fold to be precise) was used for data division. The ADGA+CNN was used for classification for the detection and prediction of heart attack.

Results And Discussion

The results show there is improvement on the performance of ADGA+CNN compared to EGA+CNN and standard CNN. A total of five thousand, seven hundred and fifty-two (5,752) images was used for training and testing. There are five patient classes: one thousand, one hundred and seventy (1,170) Dilated Cardiomyopathy (DCM) images, one thousand, one hundred and twenty eight (1,128) Hypertrophic Cardiomyopathy (HCM) images, one thousand, four hundred and ninety six (1,496) Abnormal Right Ventricle (ARV) images, eight hundred and eighty eight (888) Systolic Heart failure with infarction (MINF) images and one thousand seventy (1,070) Normal (NOR) images making a total of five thousand, seven hundred and fifty two (5,752) images.

Table 1. shows the result for ADGA+CNN, Elitist Genetic Algorithm was improved using Adaptivity and Diversity and was used to optimize CNN for the detection of heart attack in cardiac magnetic resonance images. The system was tested at different threshold; 0.25, 0.35, 0.5, and 0.75 respectively. The model has the same rate of false positivity at threshold 0.25 and 0.35, the level of accuracy was higher at 0.35 than when it was at 0.25 and the computational time was reduced at 0.35. As the threshold increased to 0.5, the rate of false positivity was reduced, though the model maintains the same level of accuracy and computational time as when it was at 0.5. As the threshold increased to 0.75, the rate of positivity was reduced, the same level of accuracy was maintained but the computational time was reduced. These analysis shows that ADGA+CNN has its best performance at threshold 0.75.

Table 1. Results for ADGA+CNN model

Threshold	False Positive Rate (FPR)	Specificity	Sensitivity	Precision	Accuracy	Time
0.25	0.6%	99.4%	97.9%	97.1%	99.1%	50secs
0.35	0.6%	99.5%	97.8%	97.4%	99.2%	46.8secs
0.5	0.49%	99.5%	97.7%	97.7%	99.2%	46.8secs
0.75	0.44%	99.6%	97.6%	97.9%	99.2%	46.6secs

Table 2. Results for EGA+CNN model

Threshold	False Positive Rate (FPR)	Specificity	Sensitivity	Precision	Accuracy	Time
0.25	1.2%	98.8%	95%	94.2%	98.1%	75.5secs
0.35	1.2%	98.8%	95%	95%	98.2%	75.3secs
0.5	1.1%	98.9%	95%	95.1%	98%	75.2secs
0.75	1.1%	99%	95.1%	95.1%	98.2%	75secs

Table 3. Results for CNN model

Threshold	False Positive Rate (FPR)	Specificity	Sensitivity	Precision	Accuracy	Time
0.25	1.7%	98.1%	92.6%	91.9%	97.3%	106.4secs
0.35	1.7%	98.3%	92.5%	92.1%	97.3%	106.5secs
0.5	1.6%	98.4%	92.4%	92.3%	97.4%	106.4secs
0.75	1.6%	98.4%	92.3%	92.5%	97.4%	107secs

Comparison of ADGA+CNN, EGA-CNN and CNN

Comparing the results in Table 4.1, 4.2 and 4.3, it implies that the developed system worked better in terms of False Positive Rate (FPR), Specificity, Sensitivity, Precision, and Accuracy.

Also, the developed system (ADGA+CNN) compute with a lower computational time compared to EGA-CNN and CNN. ADGA+CNN has the lowest False Positive Rate, highest Accuracy and lowest Computational Time compared to EGA-CNN and CNN which is preferred because it provides reliable results while using fewer computational resources.

Table 4. Comparison of ADGA+CNN, EGA+CNN and CNN model

Metrics	ADGA+CNN	EGA+CNN	Standard CNN
False Positive Rate	0.5%	1.2%	1.7%
Specificity	97.4%	96.9%	93.3%
Sensitivity	98%	95%	92.5%
Precision	97.5%	95%	92.1%
Accuracy	99.2%	98%	97.3%
Computational time	59.1secs	75.3secs	106.6secs

Table 5. Comparison Summary

Evaluation	ADGA+CNN	EGA-CNN	CNN
False Positive Rate	Extremely low	Very low	Low
Accuracy	Extremely high	Very high	High
Sensitivity	Extremely high	Very high	High
Precision	Extremely high	Very high	High
Specificity	Extremely high	Very high	High
Time	Extremely low	Very low	High

Conclusion

The Adaptive and Diversity Genetic Algorithm provides a significant improvement over the Elitist This research successfully developed and evaluated an Adaptive and Diversity Genetic Algorithm-Based Convolutional Neural Network (ADGA+CNN) for the automated detection of myocardial infarction (heart attack) using Cardiac Magnetic Resonance (CMR) images. The formulated Adaptive and Diversity Genetic Algorithm (ADGA) effectively mitigated premature convergence, maintaining a robust balance between exploration and exploitation. The developed model (ADGA+CNN) significantly outperforms conventional CNN and EGA-optimized models.

The empirical results demonstrate that the developed ADGA+CNN achieved superior accuracy, sensitivity, and

specificity in identifying occurrence of heart attack from CMR slices. Furthermore, the adaptive nature of the algorithm drastically reduced the computational overhead typically associated with exhaustive architectural searches, proving that high-accuracy medical image analysis can be achieved efficiently. In conclusion, the ADGA+CNN represents a powerful, highly automated, and reliable diagnostic tool. It holds great potential to reduce human error, alleviate the workload of clinicians, and ultimately contribute to earlier and more accurate heart attack diagnoses, improving patient survival rates.

To advance the development and clinical adoption of the Adaptive and Diversity Genetic Algorithm-Based Convolutional Neural Network (ADGA+CNN) framework, the developed ADGA+CNN model could be validated using larger, multi-center Cardiac Magnetic Resonance (CMR) datasets from different hospitals and patients populations to improve its generalizability and clinical reliability. Future research could compare the developed ADGA+CNN with newer architectures Vision Transformer (ViTs), hybrid CNN-Transformer models, and foundation models for medical imaging.

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