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An Optimized Convolutional Neural Network for Detection of Heart Attack in Cardiac Magnetic Resonance Images

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Abstract

Convolutional Neural Networks (CNNs) are 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 application. However, CNNs often suffer from overfitting and sensitivity to noise in complex medical images despite their exceptional capabilities. While metaheuristic optimization techniques like Genetic Algorithms (GAs) can mitigate these limitations, but struggle with slow convergence to achieve global optima solution. Over the years, improvement over Genetic Algorithm has produced Elitist Genetic Algorithm (EGA) which is known as an efficient algorithm to solve complex optimization problems. Hence, this research developed an optimized CNN using EGA to fine tune the hyper parameters of the CNN to solve the limitation of overfitting and sensitivity to noise in medical images. Cardiac Magnetic Resonance Images (CMRI was acquired from Kaggle which is an online repository. The images were preprocessed and segmented using contrast enhancement and fuzzy c-means respectively. The features were classified using the optimized CNN (EGA+CNN). The performance evaluation was performed based on False Positive Rate which is 1.2%, Specificity rate of 95%, Precision value of 95%, Accuracy of 98% and computational time of 73.3seconds. The developed EGA+CNN outperforms the conventional CNN in detecting heart attack in MRI, this makes it a reliable diagnostic tool to reduce human error and contribute to earlier and more accurate heart attack diagnoses, improving patient survival rates.

Keywords: *Artificial Intelligence, Machine learning, Convolutional Neural Network, Genetic Algorithm, Elitist Genetic Algorithm, Cardiac Magnetic Resonance Images, Heart attack.*

Introduction

AI combines wisdom and process for complex decision making, and AI-enabled support is present in many forms of modern computer-aided learning. We know that artificial intelligence (AI) has developed incredible machines created to make human workings easier, comfortable and effective. One of the factors that keep making this advancement is machine learning (Sadia et al., 2022). The main goal of machine learning is to allow machines to learn from data and get better at tasks without specifically programming their every move (Sadia et al., 2022). Deep learning is a branch of machine learning, which could potentially be viewed as automation of predictive analytics (Tucci, 2021). This has been a major step forward that powered machines to learn complicated patterns via enormous datasets. Deep learning draws inspiration from the structure of and algorithms of human brains in particular, a network of interconnected nodes (neurons). Deep learning has grown exponentially in the field of computer vision over the last few years, becoming an important part of research within image recognition. High-quality images and accurately labelled datasets for training, testing and validating algorithms are the principal foundations behind creating efficient computer vision models (Sadia et al., 2022). Convolutional Neural

Networks, or CNNs are an important class of deep learning that is suitable for visual application tasks. Convolutional neural networks (CNNs) have gained a lot of attention due to their great success on challenging computer vision tasks such as object recognition, detection and segmentation. They have also been used in medical imaging since the 1990s, proving their capability to support clinical diagnosis and image analysis (Bernal et al., 2018).

Radiology is essential to the health care system; it plays a pivotal role in receiving diagnosis and treatment for many medical conditions. Considering the high level of use of digital technologies in medical imaging, radiology is one of the first fields that will greatly utilize Artificial Intelligence to assist with diagnostic accuracy and specificity (Iqbal et al., 2021) [5]. Radiology is the most vital imaging tool which encompasses MRI (Magnetic Resonance Imaging), a medical imaging procedure that utilizes magnetic fields, radio waves and computer-based processing approach to construct detailed images of internal structures in an object. CMRI is a unique and invaluable imaging modality that can augment important components of all current cardiovascular diagnostic algorithms across multiple clinical applications (Lachezar, 2019). Cardiovascular disorders can be defined as a group of diseases which includes the diseases of heart and blood vessels. A heart attack is one of the most serious and common long-term cardiovascular diseases, occurring when blood flow to the heart is substantially reduced or obstructed (Mohammad & Abdulkareem, 2023). Thus, due to the importance of AI and deep learning methods in medicine, especially CNN-based models for cardiac imaging; The application of such technologies may have a great impact on early identification, diagnosis and treatment of some types of CVD.

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, demonstrating exceptional capabilities in automated biomarker recognition, pathology classification, and targeted disease detection (Matsuzaka, 2025; Papageorgiou *et al*., 2025). Despite their high effectiveness in tasks like disease classification, organ segmentation, and anomaly localization, Convolutional Neural Networks (CNNs) suffer from 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 them is 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). This research addresses the critical gap of CNN by optimizing its hyper parameters using EGA, the elitism mechanism in EGA prevents the loss of optimal solutions across generation helps to produce a robust optimization model. Therefore this research developed an optimized Convolutional Neural Network which is called EGA+CNN for a better detection of heart attack in cardiac magnetic resonance images.

Review of related works

Machine learning has become an important tool in heart-disease prediction, particularly because of its ability to identify complex patterns in clinical data. Gokulnath and Shantharajah (2018) proposed an optimization-based support vector machine (SVM) approach for heart-disease detection, in which a genetic algorithm (GA) was employed to select the most significant features. Using the Cleveland Heart Disease Database, the proposed system achieved an accuracy of 88.34% in cardiac disease classification. However, the study reported poor generalization ability, indicating that the model's performance may not extend effectively to other datasets or patient populations. Khourdif and Baha (2019) investigated the application of machine-learning algorithms for heart-disease prediction and classification by developing a hybrid approach that combined fast correlation-based feature selection (FCBF), particle swarm optimization (PSO), ant colony optimization (ACO), and different classification algorithms. Using the UCI heart-disease dataset containing 14 attributes, including age, gender, chest pain type, blood pressure, and cholesterol, the study demonstrated the potential of combining feature-selection and optimization techniques to improve prediction. However, the study was constrained by an imbalanced distribution of positive and negative cases.

Shah *et al.* (2020) developed a supervised machine-learning system for predicting the likelihood of heart disease using the UCI repository dataset. The dataset contained 303 instances and 76 attributes, although only 14 attributes were selected for the analysis, comprising 13 predictor variables and one class attribute. Following data preprocessing, the researchers compared several classification algorithms, including naïve Bayes (NB), decision tree (DT), random forest (RF), and K-nearest neighbor (KNN). The results showed that KNN achieved the highest classification accuracy of 90.789% at $k = 7$. Despite this promising result, the study was limited by the relatively small dataset, which increases the possibility of overfitting and may restrict the generalizability of the findings. Shen *et al.* (2021) reviewed the application of deep-learning techniques in medical image analysis and emphasized the transformative role of deep neural networks, particularly Convolutional Neural Networks (CNNs), in disease diagnosis, image segmentation, classification, detection, and image registration. Their review covered several medical imaging modalities, including MRI, CT, X-ray, PET, and histopathological imaging, and discussed supervised, unsupervised, semi-supervised, and transfer-learning approaches for improving diagnostic performance.

Overall, the reviewed studies demonstrate that machine learning and deep learning techniques have considerable potential for improving heart-disease prediction and medical-image analysis. Traditional machine-learning approaches, such as SVM, KNN, decision trees, random forests, and naïve Bayes, have produced encouraging classification accuracies, while deep-learning models, particularly CNNs, offer greater potential for extracting complex features directly from medical images. Nevertheless, important limitations remain, including small and imbalanced datasets, overfitting, computational inefficiency, limited generalization, and sensitivity to variations in medical images. These limitations highlight the need for robust datasets, effective preprocessing and feature-selection techniques, and optimized deep-learning architectures to develop reliable and generalizable heart-disease prediction systems.

Snigdha et al. (2022) examined the neurological characteristics correlated with heart-attack instances through a clinical record set of data on open heart failure. It used k-means clustering to find associations between heart attacks and underlying features. Among the classifiers evaluated, Meta. AdaBoostM1 demonstrated the best performance. The results showed that machine learning techniques are useful in identifying key patterns and risk factors for heart attacks. The proposed model was also not exempted from the overfitting curse that might reduce its validity on unseen datasets.

A modified machine-learning approach was developed by Kaur and Kaur (2023) for predicting risk of coronary heart disease in patients. Each of these components—preprocessing, clustering, feature selection, and classification with random forest, k-means, genetic algorithm and logistic regression respectively–was wrapped up into a framework for prediction. Random forest was used to eliminate irrelevant attributes from the data set in order to position the model for greater performance and less training time, while a genetic algorithm optimized k-means clustering that grouped outlier data points. Then, logistic regression was utilized for grouping patients according to their bet for heart disease. On comparison, the proposed approach had an accuracy of 95% in best case. However, the model suffered from overfitting and generalization issues that could limit its performance in the application of independent datasets.

Hidayat et al. (2024) proposed a genetic algorithm (GA)-based Convolutional Neural Network (CNN) feature-engineering framework to detect optimized performances for early coronary heart disease (CHD) prediction. The research focused on overcoming the drawbacks that conventional hyperparameter optimization suffers using GA, in order to find better configurations of models. Once hyperparameter tuning was performed, the GA-based CNN showed better performance compared to more established methods, with about 85% top-1 accuracy and 100% accuracy when combined using approaches in machine-learning classifiers such as naïve Bayes, support vector machine, decision tree, logistic regression, random forest for binary and multiclass CHD prediction. The results show good performance when using GA and CNN techniques, but the method has an important limitation regarding its computational complexity; thus, in a resource-limited environment, these approaches could be difficult to implement.

Srinivasulu et al. An improved Convolutional Neural Network (CNN) model for heart-attack prediction and detection was presented in (2025), which also overcomes prevalent challenges of overfitting and weak generalization encountered with classical machine-learning models. The new CNN model used optimized regularization techniques and optimization strategies, taken advance of the fact neural networks can innovate between statistical analysis to perform classification tasks well at robust extraction of spatial features from the data. Experimental results indicate that the proposed model reached a maximum accuracy of 100%, with validation accuracy up to 75% in 50 epochs. These results may indicate that the performance of heart-disease prediction can be achieved by an optimized CNN, but this also could increase the robustness of the model. But the research was still constrained by worries of generalizability and scalability, especially when applying the model to more extensive and comprehensive datasets.

In their study of hyperparameter selection problem in CNN-based biomedical image classification, Yilmaz and Kuş (2026) optimized essential parameters, such as activation functions, padding, filter count, kernel size, dropout rate, pooling size and batch size using a genetic algorithm. Brain Images of Multiple Sclerosis (MS) were trained with a highly optimized CNN, using Alzheimer's MRI and

COVID-19 chest X-ray images as validation. Results showed significant increases in classification performance on the tested datasets. For MS, the proposed method outperformed other approaches with improvements up to 37.6% in F1-score and 33.7% in accuracy, while for Alzheimer disease it achieved improvements of up to 32.8% in F1-score and 32.5% in accuracy over previous methods. The improvements for COVID-19 ranged from 0.8% to 12.1%. In summary, the near-optimization achieved through GA-based architectures highlighted how evolutionary optimization can enhance CNN performance and the architecture outperformed previously established architectures such as Exception, InceptionV3, VGG16, VGG19, Alex Net, ResNet50 and GoogLeNet. The study, however, had limitations such as generalizability across datasets therefore needing additional validation on larger, more diverse and clinically representative datasets.

Methodology

Cardiac magnetic resonance images was acquired from *Kaggle* which is a publicly available repository. 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) 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.

EGA+CNN for heart attack detection in magnetic resonance images.

Elitism Genetic Algorithm (EGA) was used to optimize CNN (VGG19) assigning optimal weight parameters for CNN, and translate to feature extraction. The features extracted are the relevant and informative characteristics that best represent the underlying patterns in the data.

1. Problem Formulation

Given CMR images, the goal is to optimize CNN hyperparameters using a Genetic Algorithm to improve classification of heart attack conditions

$$\theta = \{W, N, \eta, D\} \tag{1}$$

Where:

- W: CNN weights (or initialization/scaling factors)
- N: number of neurons/filters
- η: learning rate
- D: dropout rate

Objective:

$$\theta^* = \arg\max_{\theta} F(\theta) \tag{2}$$

2. Input and Output

Input

- CMR dataset: $\mathcal{D} = \{(\chi_i, y_i)\}_{i=1}^{M}$ (3)
- Training set: $\mathcal{D}_{train}$, validation set: $\mathcal{D}_{val}$
- GA parameters: P, t_{max}, P_c, p_m

Output

- Optimal CNN parameters: θ^*
- Trained CNN model for heart attack detection

3.Chromosome Encoding

$$X_i = (w_1, \ldots, w_k, n_1, \ldots, n_L, \eta, d_1, \ldots, d_L) \tag{4}$$

Constraints:

- $W_j \varepsilon [w_{min}, w_{max}]$
- $n_i \varepsilon [n_{min}, n_{max}]$
- $\eta \varepsilon [\eta_{min}, \eta_{max}]$
- $d_i \varepsilon (0,1)$

4. CNN Model Equations

(a) Convolution Layer

$Z^{(l)} = W^{(l)} * X^{(l)} + b^{(l)}$ (5)

(b) Activation Function (ReLU)

$A = \max(0, Z^{(l)})$ (6)

(c) Pooling Layer

$A^{(l)}_{pool} = Pool(A^{(l)})$ (7)

(d) Fully connected Layer

$Z = WA + b$ (8)

(e) Softmax Output $\hat{yi} = \frac{e^{z_i}}{\sum_{j=1}^{C} e^{zj}}$ (9)

(f) Loss Function (Cross-Entropy)

$L = -\sum_{i=1}^{C} yi \log(\hat{y}i)$ (8)

(g) Gradient Descent Update

$W^{(t+1)} = W^{(t)} - \eta \frac{\partial L}{\partial W}$ (9)

(h) Dropout Regularization

$A^{(l)}_{drop} = A^{(l)}.r, \quad r \sim$ Bornoulli $(1 - d_l)$ (10)

5. Fitness Function

$F(X_i) = \alpha$. Accuracy $(X_i) - \beta \,.\, L(X_i)$ (11)

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \quad (12)$$

6. Genetic Algorithm Equations

(a) Population Initialization

$P^{(0)} = \{X_1, X_2,,,,, X_p\}$ (13)

(b) Selection (Roulette Wheel)

$$P_i = \frac{F(X_i)}{\sum_{j=1}^{P} F(X_j)} \quad (14)$$

(c) Crossover

$X_{child} = \lambda x^{(1)} + (1 - \lambda)X^{(2)}, \lambda\varepsilon|0,1|$ (15)

(d) Mutation

$x^1 = x\ \delta, \delta \sim N(0,\sigma^2)$ (16)

Learning rate mutation

$\eta^1 = \eta + \varepsilon, \qquad \varepsilon \sim U(-0.01, 0.01)$ (17)

(e) Elitism

$X^{(t+1)}_{best} = X^{(t)}_{best}$ (18)

(f) Termination Condition

$t = t_{max}$ or $|F^{(t)}_{best} - F^{(t-1)}_{best}| < \varepsilon$ (19)

The step by step Algorithm follows:

Algorithm: EGA+CNN

(i) Input CMR dataset D

(ii) Preprocess images (normalization, resize)

(iii) Splits dataset into D_{train}, D_{val}

(iv) Initialize population $P^{(0)}$ randomly

(v) For each individual X_i

- Decode Xi $\rightarrow \theta_i$
- Build CNN model
- Train CNN using gradient descent
- Evaluate fitness $F(X_I)$:

(vi) For generation $t = 1$ to t_{max}:

- Compute selection probabilities P_i
- Select parents
- Apply crossover (P_c)
- Apply mutation (P_m)
- Train offspring CNN models
- Evaluate new fitness
- Apply elitism
- Update population

(vii) **Select best solution:**

$$X' = \arg\max_{X_i} F(X_i)$$

(viii) Output optimized CNN model for heart attack detection

The optimized CNN (EGA+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 datasets were divided into ten (10) folds Where K=10. One fold was selected as the test set and the remaining 9 folds was selected as the training set. The model was trained on the training folds and evaluated on the test fold, the performance metrics: False Positive Rate, Specificity, Sensitivity, Precision, Recognition Accuracy and Computational Time was recorded. The process was repeated 10 times, each time using a different fold as the test set. The EGA+CNN was used for classification for the detection and prediction of heart attack.

The performance of EGA+CNN was evaluated based on False Positive Rate (FPR), Specificity, Sensitivity, Precision, Recognition Accuracy, and Computational time. The confusion matrix was used to determine the value of the performance metrics. It contains "True Positive (TP), False Positive (FP), False Negative (FN) and True Negative (TN)."

$$\text{False Positive Rate} = \frac{\text{FP}}{\text{TN} + \text{FP}}\ x\ 100\%$$

$$\text{Specificity} = \frac{\text{TN}}{\text{TN} + \text{FP}} \times 100\%$$

$$\text{Sensitivity} = \frac{\text{TP}}{\text{TP} + \text{FN}} \times 100\%$$

$$\text{Precision} = \frac{\text{TP}}{\text{TP} + \text{FP}} \times 100\%$$

$$\text{Accuracy} = \frac{\text{TP} + \text{TN}}{\text{TP} + \text{TN} + \text{FP} + \text{FN}} \times 100\%$$

$$\text{Computational time} = \frac{\text{Total Recognition Time}}{\text{Number of recognized foods}}$$

The model was validated by comparing the performance of EGA+CNN for heart attack detection system with the standard CNN based on the highlighted performance metrics.

Results and Discursions

The results shows there is improvement on the performance of EGA+CNN compared to the 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, and seventy (1,070) Normal (NOR) images making a total of five thousand, seven hundred and fifty two (5,752) images.

CNN model was used 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. Table 1. shows the summary of results for CNN model. The model has a stable rate of false positivity and stable accuracy at threshold 0.25 and 0.35, though the computational time was much higher at 0.35 than when it was at 0.25. As the threshold increased to 0.5, the False Positive Rate dropped but the accuracy increased and the computational time was reduced, at threshold 0.75, it maintains the same rate of false positivity and the same level of accuracy but has a higher computational time. These analysis shows that the CNN model has its best performance at threshold 0.5.

Table 1. Summary of the 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

The CNN was optimized by Elitist Genetic Algorithm (EGA) and used to detect cardiovascular disease (heart attack) in cardiac magnetic resonance images. The system was tested at different threshold; 0.25, 0.35, 0.5, and 0.75 respectively.

Table 2. shows the summary of EGA+CNN model. The model has a stable rate of false positivity at threshold 0.25 and 0.35, though the level of accuracy was much higher at 0.35, also, the computational time was lesser at 0.35 than when it was at 0.25. As the threshold increased to 0.5, the rate of false positivity dropped and the level of accuracy also reduced, though the computational time also reduced by 0.1. At threshold 0.75, the model maintains the same rate of positivity at 0.5, it has a higher accuracy and a reduced computational time. These analysis shows that the EGA+CNN has its best performance at threshold 0.75.

Table 2. Summary of the 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. Comparison of ADGA+CNN, EGA+CNN and CNN model

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

Table 4. Comparison Summary

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

Conclusions

The empirical results demonstrate that the developed ADGA+CNN achieved superior accuracy, sensitivity, and specificity in identifying occurrence of heart attack from CMR slices. The elitism mechanism in EGA successfully prevent the loss of optimal solutions across generations, making the optimization to significantly outperform conventional CNN model. In conclusion, the EGA+CNN represents a reliable diagnostic tool. It holds great potential to alleviate the workload of clinicians, and contribute to more accurate heart attack diagnoses, improving patient survival rates.

Recommendations

Future studies should train and evaluate datasets collected from multiple hospitals and different patient populations, this would improve the generalizability of the model and reduce dependence on a single dataset. Future research can investigate other optimization approaches to determine whether CNN architecture and hyperparameters can be optimized more effectively.

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