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Research paper

Diagnosis of Cardiac Arrhythmia using an Optimized Two-stage Deep Learning Model

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Abstract

Background and Objectives: Cardiovascular diseases, particularly cardiac arrhythmias, are among the leading causes of mortality worldwide. Early and accurate diagnosis is essential for improving patient outcomes. Although electrocardiogram (ECG) signals are widely used for arrhythmia detection, manual interpretation remains time-consuming and error-prone. Therefore, this study proposes an innovative, optimized two-stage deep learning framework for the reliable diagnosis of cardiac arrhythmias from ECG signals, aiming to enhance both accuracy and robustness.

Methods: The key innovation lies in the first stage, where the autoencoder's reconstruction error threshold is optimized using a Genetic Algorithm (GA) to maximize the separation between normal and abnormal signals. Only signals identified as abnormal proceed to the second stage, a Convolutional Neural Network (CNN) that classifies them into four arrhythmia types (Supraventricular, Ventricular, Fusion, and Unknown beats). All experiments were conducted on the MIT-BIH Arrhythmia Database using a stratified split, with SMOTE applied exclusively to the CNN training set to address class imbalance. Performance was evaluated through 5-fold cross-validation.

Results: The proposed AE-GA-CNN+SMOTE framework achieved an average accuracy of 97.89 ± 0.25%, precision of 97.90 ± 0.24%, recall of 97.68 ± 0.29%, and an F1-score of 97.69 ± 0.28%. It outperformed the single-stage CNN+SMOTE baseline by +6.28% in accuracy ($p < 0.001$) and showed statistically significant improvements over all other two-stage variants ($p < 0.05$).

Conclusion: The two-stage architecture, enhanced by GA-driven threshold optimization and SMOTE balancing, demonstrates high accuracy and robustness for automated arrhythmia screening. The statistically validated performance gains support its potential as a decision-support tool for clinical and real-time ECG analysis.

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Introduction

Cardiovascular diseases (CVDs) remain a global public health crisis, standing as one of the principal causes of death worldwide. Early and precise detection of these conditions is paramount to administering timely, life-saving treatments and improving long-term patient outcomes. Cardiovascular diseases (CVDs) can be broadly categorized into several major groups, each posing unique diagnostic and management challenges. These categories include: (1) Coronary Artery and Vascular Diseases, characterized by the hardening and narrowing of cardiac arteries, which often lead to heart attacks or angina [1]. (2) Heart Rhythm Disorders (Arrhythmias) [2], [3], involving abnormal heartbeat patterns (too fast, too slow, or irregular) that disrupt blood flow and affect millions worldwide. (3) Structural Heart Diseases, encompassing congenital or acquired abnormalities of the heart valves, walls, or muscles [4]. (4) Heart Failure, a serious condition typically resulting from a weakened heart, often due to a prior heart attack or chronic high blood pressure [5]. (5) Other Cardiac Conditions, including infections and hereditary disorders [6]. Recognizing these conditions early is crucial, as it has been shown to substantially reduce treatment costs and extend patient longevity [7].

Studies investigating the automated diagnosis and classification of cardiac arrhythmias have generally employed two distinct approaches: conventional machine learning (ML) models and deep learning (DL) models. Machine learning is an interdisciplinary field dedicated to replicating human learning processes. It is broadly categorized into supervised, unsupervised, and semi-supervised paradigms. In the supervised setting, models are trained exclusively on labeled datasets to predict outcomes for new, unseen samples. However, a major limitation of these traditional ML techniques is their heavy reliance on the manual feature extraction stage. This manual process necessitates domain expertise, and if features are poorly selected, the model's overall diagnostic performance can be severely compromised [8].

Deep learning (DL), a powerful sub-field of machine learning, has been widely applied to numerous complex analytical tasks. The primary advantage of DL architectures, in contrast to their conventional counterparts, lies in their ability to automatically derive robust, high-level features directly from the raw input data. This inherent capability eliminates the need for labor-intensive, manual feature engineering , as it automatically acquires meaningful data representations. However, a significant consideration when utilizing DL models is the persistent challenge of overfitting. Successfully mitigating this challenge requires both extensive datasets and considerable computational resources during the training phase [9]-[13]. The following section provides a critical review of several key studies that have employed these AI methodologies specifically for cardiac arrhythmia diagnosis.

Despite the significant advances in automated arrhythmia diagnosis, a key challenge remains: the lack of robust and optimally tuned mechanisms to reliably separate normal from abnormal signals before classification. While many previous studies have relied on single-stage classifiers (e.g., CNN or LSTM) or have utilized autoencoders without optimal threshold tuning, this research introduces an integrated two-stage framework that optimizes the detection threshold with a Genetic Algorithm (GA), aiming to simultaneously improve diagnostic accuracy and computational efficiency.

The remainder of this paper is organized as follows. Section 2 presents a critical review of the related literature. Section 3 describes the proposed two-stage deep learning framework and the genetic algorithm (GA)-based optimization method. Section 4 outlines the dataset and experimental setup. Section 5 presents and discusses the experimental results. Finally, Section 6 concludes the paper and highlights potential directions for future research.

Related Work

Sraitih et al. [14] conducted research focused on the detection and prediction of cardiac arrhythmias from ECG signals, deploying a range of machine learning techniques. Their methodology involved training models specifically a Deep Neural Network (DNN), Support Vector Machine (SVM), and K-Nearest Neighbor (KNN) on the UCI dataset, which features seventeen distinct classes of heartbeats. The authors emphasized the need to minimize human diagnostic error by introducing automated, real-time machine learning tools. While noting the high accuracy achieved and the innovative approach as strengths, the paper also pointed out limitations such as algorithmic complexity and the requirement for robust data preprocessing, including the imputation of missing values and cleaning procedures.

Acharya et al. [15] introduced an innovative technique designed for the automated detection of Myocardial Infarction (MI) via ECG signals, aiming to circumvent the difficulties associated with visual interpretation. They implemented an eleven-layer Deep Convolutional Neural Network (DCNN), which yielded notable average accuracies of 93.53% (for noisy data) and 95.22% (for clean data). A key achievement of their work was the successful operation without any requirement for manual feature engineering. The strengths of the proposed model, particularly its ability to analyze previously unseen and noisy signals, highlight the potential of computer-aided diagnosis systems in

clinical settings to improve early detection of myocardial infarction (MI).

Tan et al. [16] explored an unsupervised learning framework to identify various arrhythmia subtypes within ECG data. Utilizing the ICENTIA11K dataset, which encompasses records from more than 11,000 patients, their method employed techniques such as Autoencoders, Principal Component Analysis (PCA), and Fast Fourier Transform (FFT) for model training. The core objective of their research was to effectively capture the latent representations and uncover hidden structural patterns within the cardiac signals. Ultimately, their findings validated the efficacy of unsupervised learning as a powerful mechanism for pattern discovery and the fine-grained classification of arrhythmia subtypes in large-scale ECG data.

Kuznetsov et al. [17] proposed a Variational Autoencoder (VAE) network for the dual purpose of generating synthetic ECG signals and learning representative latent features. By training the VAE on a raw ECG database to reconstruct the cardiac cycle, they successfully derived novel and interpretable features that often corresponded directly to clinical markers like the T wave and ST segment. The high fidelity of the synthetic data was confirmed by a Maximum Mean Discrepancy (MMD) criterion value of 3.83×10^{-3}, demonstrating the generation quality. This research highlights how VAE-extracted features can significantly boost heart disease diagnostic performance, especially in scenarios constrained by the limited availability of labeled data.

Bikova et al. [18] undertook a comparative study by evaluating six distinct machine learning models for cardiac arrhythmia classification using the widely-referenced MIT-BIH dataset. Among the models assessed, the Convolutional Neural Network (CNN) exhibited superior performance, achieving a notable 95% accuracy alongside an F1-score of 84.75%. Other models, including the Support Vector Classifier (SVC) and Long Short-Term Memory (LSTM) networks, also performed strongly, with accuracies of 94% and 93%, respectively. Furthermore, their research addressed critical diagnostic difficulties such as data imbalance, noise interference, and class similarity, proposing methodological remedies like resampling techniques and the integration of expert clinical knowledge.

Sahoo et al. [19] performed advanced analysis of cardiac arrhythmias in ECG signals, focusing specifically on noise reduction using adaptive filters and mathematical morphology techniques. While the strength of their approach lies in achieving high accuracy for arrhythmia detection, the authors noted the necessity for further optimization of the proposed methods to enhance robustness.

Li et al. [20] addressed the classification of seven cardiac arrhythmia types from a large-scale database of 51,579 ECG records by employing Deep Convolutional Neural Networks (DCNNs) integrated with the concept of Transfer Learning (TL). Despite the method's efficacy, the authors highlighted key limitations, including the substantial requirement for extensive training data and the inherent complexity of the final DCNN model.

Sattar et al. [21] concentrated on cardiac arrhythmia classification, combining Convolutional Neural Network (CNN) and Long Short-Term Memory (LSTM) architectures to achieve an accuracy of 92%. The primary benefits of their methodology included a significant improvement in prediction accuracy and a reduction in manual analysis time. However, a key challenge identified was the necessity for acquiring a diverse range of training data.

Raza et al. [22] introduced a 9-layer CNN model specifically designed for classifying ECG signals within the MIT-BIH dataset, reaching an accuracy of 94.03%. Their model demonstrated superior accuracy and sensitivity compared to prior models. Nevertheless, a major constraint noted in the study was the high demand for computational hardware resources necessary to effectively train and deploy the model.

In a systematic approach, Bi et al. [23] focused on the prediction of heart disease using Graph Neural Networks (GNNs). Their study aimed to classify patient data into two categories: cardiac disease and non-cardiac disease, following a structured process including model definition, training, and optimization. Notably, this research utilized Feed Forward Neural Networks (FNNs) alongside GNNs for the core prediction tasks, establishing a foundational reference for the development and enhancement of subsequent cardiac diagnostic models.

Based on the critical review of the literature, two principal limitations are identified in existing arrhythmia diagnosis models: (1) single-stage classification architectures often struggle to maintain robust performance when dealing with highly imbalanced datasets; and (2) multi-stage approaches, while promising, frequently employ sub-optimal, manually-tuned, or statistically-derived thresholds in their detection phase. Our proposed framework directly addresses these two gaps: by utilizing the Genetic Algorithm (GA) for threshold optimization, we establish a scientifically robust and superior boundary, and by decoupling the anomaly detection (Autoencoder) from the fine-grained classification (CNN) through a dedicated two-stage pipeline, we significantly enhance the overall system's accuracy and reliability over prior art.

Method

In this study, the objective is to identify cardiac arrhythmia using a two-stage model consisting of an

autoencoder and a convolutional neural network (CNN), with an integrated Genetic Algorithm (GA) for threshold optimization. As shown in Fig. 1, the proposed method implements anomaly detection with GA-optimized thresholding followed by multi-class classification. In the following sections, the utilized database is first introduced, and then the details of each component of the proposed methodology are described.

MIT-BIH Database

The availability of a suitable and extensive database is a critical component of any research in this field. For cardiac arrhythmia research, a well-known database is the MIT-BIH Arrhythmia Database, which was compiled in 1980 by Beth Israel Hospital and MIT.

This database consists of 48 half-hour, two-channel ECG recordings.

It contains 87554 samples categorized into 5 classes: one normal class (N) and four types of cardiac events, Supraventricular (S), Ventricular (V), Fusion (F), and Unknown (Q) beats.

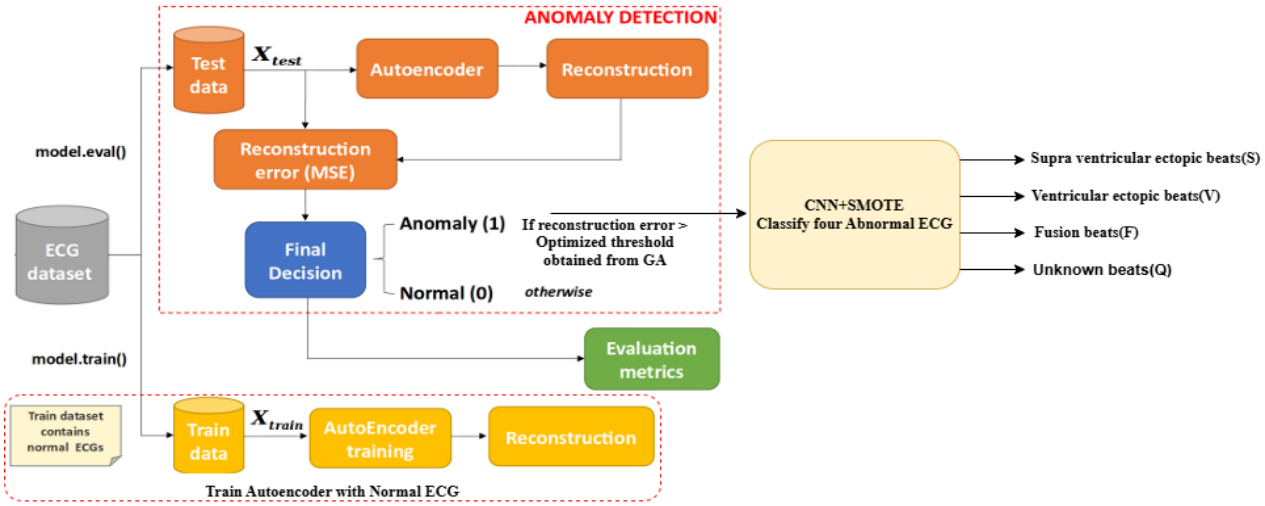

Fig. 1: Overall workflow of the proposed two-stage arrhythmia detection framework.

Fig. 2 illustrates representative ECG signal samples for each of these five classes. The signals were sampled at a frequency of 360 Hz. Table 1, which shows the number of samples in each class, clearly indicates the significant problem of dataset imbalance [24].

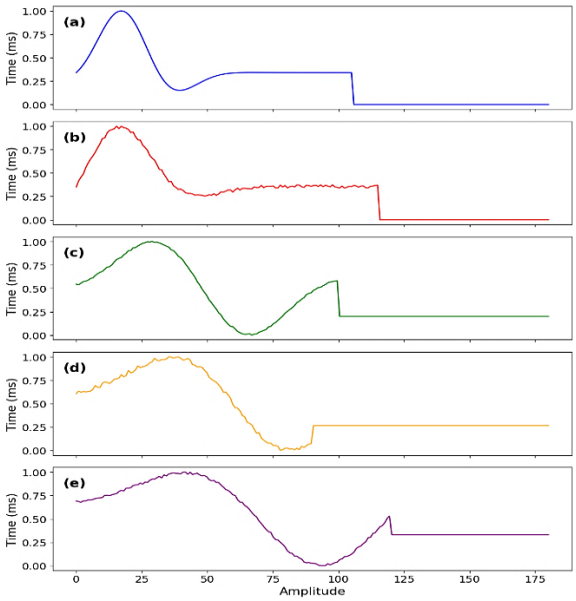

Fig. 2: Sample ECG signals from different classes (a) Normal beat, (b) Supraventricular ectopic beat, (c) Ventricular ectopic beat, (d) Fusion beat, (e) Unknown beat.

Table 1: Classes of MIT-BIH database

Class	Number of each class
Normal beats(N)	72471
Supra ventricular ectopic beats(S)	2223
Ventricular ectopic beats(V)	5788
Fusion beats(F)	641
Unknown beats(Q)	6431

Preprocessing Step

The first stage of the proposed method is data preprocessing, which consists of three key steps:

Data Normalization: This step ensures that all features are scaled to a common range, thereby giving them equal importance during the learning process. In this research, the Standard Scaler normalization method was used. The specific normalization formula is presented in (1).

$$x_{\text{Scaled}} = \frac{(x - \text{median}(x))}{\sigma} \quad (1)$$

Handling Missing Data: To address the issue of missing values, features with a high percentage of empty entries were first removed. The remaining missing values in each feature were then imputed based on the mode value of that feature, considering only samples from the same class.

Addressing Class Imbalance: As evidenced in Table 1, the MIT-BIH database suffers from a significant class imbalance. A major challenge with imbalanced datasets is the classifier's bias toward the majority class. To mitigate this issue, two complementary approaches were employed: SMOTE (Synthetic Minority Over-sampling Technique) and Weighted Loss Function. SMOTE balances the data by generating new synthetic samples in the vicinity of existing samples within the minority class, leveraging the k-nearest neighbors algorithm to measure distances and create artificial samples. Concurrently, the weighted loss function assigns higher penalties to misclassifications of minority classes during CNN training [25]. To eliminate any risk of data leakage, a strict cross-validation protocol was followed. Within each fold of the 5-fold cross-validation, the data were first split into training (80%) and test (20%) subsets. After this split, SMOTE was applied solely to the training subset to generate synthetic samples for the minority classes. The test subset remained completely untouched and contained only original (non-synthetic) samples. This ensures that no information from the test set influences the creation of synthetic data, thereby preserving the integrity of the evaluation.

ECG Beat Segmentation and Signal Representation The ECG recordings in the MIT-BIH database are provided as continuous multi-channel signals. For this study, we used a pre-segmented version of the database where each heartbeat is extracted as a fixed-length window of 187 samples, centered on the R-peak annotation. This segment length corresponds to approximately 0.52 seconds at the original sampling rate of 360 Hz and fully captures the P-wave, QRS complex, and T-wave morphology of a single cardiac cycle. Each 187-point beat was normalized using StandardScaler (subtracting the median and dividing by the standard deviation). The normalized beats were fed directly as raw 1D sequences to the models: as vectors of shape (187,) for the autoencoder, and reshaped to (1, 187) for the 1D CNN.

Data Classification Step

For the classification stage, a two-stage deep learning model is presented for the detection and classification of cardiac arrhythmias, as illustrated in Fig. 1. This model utilizes a combination of an autoencoder and a convolutional neural network (CNN). In the first stage, the autoencoder is exclusively trained to reconstruct normal ECG signals, enabling it to distinguish between normal and abnormal data.

First stage(AE+GA)

An Autoencoder (AE) [26] is an unsupervised neural network designed to learn an optimal data compression and decompression scheme. It is generally composed of an input layer, an output layer, an encoder neural network, a decoder neural network, and a latent space. The encoder compresses the input data into a compact representation within the latent space, while the decoder subsequently reconstructs this compressed representation back to the output layer. The reconstructed output is then compared to the original input, and the reconstruction error is backpropagated through the network to update the weights [27], [28]. The training process of the autoencoder aims to minimize this reconstruction error, L, as defined in (2):

$$L = \frac{1}{n}\sum_{i=1}^{n} (Y_i - Y_i')^2 \tag{2}$$

where Y_i is the original input signal, Y_i' is the reconstructed output, and n is the total number of samples. An ideal autoencoder's goal is to simply replicate the input at the output, but with a hidden space that has a smaller dimension than the input. This process allows the autoencoder to learn the most salient features of the training data, effectively reducing the data's dimensionality while preserving its most crucial information.

The autoencoder was exclusively trained on normal ECG beats (Class N, 72,471 samples) using Mean Squared Error loss, Adam optimizer (lr=0.001), batch size of 256, for 200 epochs. Reconstruction errors were computed per sample as the maximum absolute difference between input and reconstructed signals. The autoencoder specifications are summarized in Table 2. Subsequently, a Genetic Algorithm was employed to optimize the detection threshold for distinguishing normal from abnormal beats based on reconstruction errors.

The genetic algorithm was introduced in 1971 by John Holland. This algorithm belongs to the class of stochastic optimization algorithms and is particularly suitable for solving complex problems with an unknown search space. The implementation steps of the genetic algorithm are summarized as follows:

1- Given the problem of finding an optimal threshold to distinguish between normal and abnormal signals, an initial population of candidate solutions is generated. Each solution, or chromosome, represents a single threshold value (a single gene), randomly generated within a specified range.

2- The fitness of each candidate solution (threshold) is evaluated using a fitness function defined as the sum of normal accuracy and abnormal accuracy
3- New offspring are produced from the current population using genetic operators, namely crossover and mutation. In each iteration, the best-performing solutions are selected from both the current population and the newly produced offspring to form the population for the next iteration. These steps are repeated until a suitable solution is found [29], [30].

Table 2: Autoencoder model specifications

Category	Specification	Details
Architecture	Encoder	Dense(187 → 128) + ReLU + BatchNorm → Dense(128 → 64) + ReLU + BatchNorm → Dense(64 → 32) + ReLU
	Latent Space	32-dimensional compressed representation
	Decoder	Dense(32 → 64) + ReLU + BatchNorm → Dense(64 → 128) + ReLU + BatchNorm → Dense(128 → 187)
Training parameters	Dataset	72,471 normal beats (Class N) 80% training, 20% validation split
	Loss Function	Mean Squared Error (MSE)
	Optimizer	Adam (lr=0.001, β_1=0.9, β_2=0.999, ε=1e-8)
	Batch Size	256
	Epochs	200
Reconstruction Error	Computation Method	Maximum Absolute Error (MAE)
Input/Output	Input Dimension	187 time points (raw ECG length)
	Output Dimension	187 (reconstructed signal)

For full reproducibility, the key operational parameters of the Genetic Algorithm used in this study are presented in Table 3. The selection process employs a hybrid strategy combining Tournament Selection with Elitism, where the top 50% of the population (based on fitness) are directly transferred to the next generation. The remaining 50% of the population are generated via recombination, where a Simple Averaging Crossover operator is applied to selected parents from the elite pool. The mutation operator involves adding a small random value to the chromosome (threshold value) with the specified mutation rate, ensuring a local search around promising solutions.

Table 3: Genetic algorithm parameters for threshold optimization

Parameter	Value
Population Size	50
Number of Generations	100
Initialization Range	[0.008, 0.5] (min_err, max_err)
Fitness Function	acc_normal + acc_abnormal
Selection Strategy	Tournament Selection(size=3) + Elitism (Top 50%)
Crossover Type	Simple Averaging child = α × $parent_1$ + (1-α) × $parent_2$ where α ~ U(0,1)
Crossover Rate	90%
Mutation Mechanism	Adding a small random value (Gaussian noise) threshold_new = threshold + δ where δ ~ N(0, 0.02 × range) range = max_error − min_error
Mutation Rate	0.1
Replacement Strategy	Generational (Entire population replaced each generation (except elites))

Second stage(CNN)

In the second stage, the abnormal signals detected by the autoencoder are passed to a CNN, which serves as a supervised classifier.

The CNN architecture includes three convolutional blocks with batch normalization and max-pooling, followed by fully connected layers with dropout regularization to prevent overfitting. This CNN is tasked with diagnosing the specific type of arrhythmia among four predefined classes. The detailed architecture of the CNN model and its training parameters are presented in Table 4.

In summary, the proposed model leverages the anomaly detection capability of the autoencoder and the high classification power of the CNN. This two-stage strategy first separates abnormal from normal signals, then performs precise multi-class arrhythmia classification, enhancing both diagnostic accuracy and computational efficiency. The complete procedure is summarized in the pseudocode presented in Algorithm 1.

Table 4: CNN model specifications

Category	Specification	Details
Input Specification	Signal Length	187 samples
	Channels	1 (univariate ECG)
	Input Shape	(batch_size, 1, 187)
Architecture	Layer1	Conv1d(1, 32, kernel_size=5, padding='same')→ReLU→BatchNorm(32, momentum=0.1)→MaxPool1d(2, stride=2)
	Layer2	Conv1D(32, 64, kernel_size=5, padding='same')→ReLU→BatchNorm(64, momentum=0.1)→MaxPool1d(2, stride=2)
	Layer3	Conv1D(64, 128, kernel_size=5, padding='same')→ReLU→BatchNorm(128, momentum=0.1)→MaxPool1d(2, stride=2)→Flatten→Dense(128)→Dropout(0.5)→Dense(64)→Dense(4)
	Flatten	Output size: 128 * 23 = 2944
	Fully Connected 1	Dense(2944, 128) → ReLU → Dropout(0.5)
	Fully Connected 2	Dense(128, 64) → ReLU
	Output Layer	Dense(64, 4) (Softmax)
Training parameters	Dataset	4 classes (S, V, F, Q)
	Loss Function	Categorical Cross Entropy
	Optimizer	Adam(lr=0.0005, weight_decay=1e-4)
	Learning Rate Scheduler	CosineAnnealingLR(T_max=50)
	Batch Size	128
	Epochs	50
	Regularization	Batch Normalization(Momentum,0.1), Dropout (0.5), Label Smoothing (0.1), Weight Decay (1e-4)

Algorithm 1 Exact Implementation

Input: MIT-BIH train/test, $Y \in \{0, 1, 2, 3, 4\}$
Output: $\hat{Y}$, θ_{opt}, metrics
1. Data Prep: Keep test separate, extract normal beats from train
2. Autoencoder: 187→128→64→32→64→128→187
  Train on normals (MSE loss, 100 epochs, lr=0.001)
3. Genetic Algorithm (EXACT):
  $e_{\text{norm}} = \max(|X_{\text{norm}} - AE(X_{\text{norm}})|)$
  $e_{\text{abnorm}} = \max(|X_{\text{abnorm}} - AE(X_{\text{abnorm}})|)$
  Pop=50, Gens=100, Tournament=3, Mutation=0.1
  Fitness: $F(\theta) = \text{mean}(e_{\text{norm}} < \theta) + \text{mean}(e_{\text{abnorm}} \geq \theta)$
  Selection → Blend Crossover → Gaussian Mutation → Elitism
4. CNN (EXACT): Input(1,187) → Conv32 → Conv64 → Conv128 → FC128 → FC64 → 4
  Method A: SMOTE on training folds only
  Method B: Weighted Loss: $w_c = \frac{N_{\text{total}}}{4 \cdot N_c}$
5. 5-Fold CV: Stratified, 12,066 train / 3,017 val per fold
  Compare: RandomForest, XGBoost, AdaBoost (all n_estimators=100)
  Generate: 4-class CM

Evaluation metrics

The proposed method was evaluated using common classification metrics: accuracy, precision, recall, and F1-score.

All metrics are derived from the confusion matrix components:

True Positives (TP), True Negatives (TN), False Positives (FP), and False Negatives (FN).

The definitions and formulas are summarized in Table 5.

Table 5: Evaluation metrics

Metric	Formula	Definition
Accuracy	$\text{ACC} = \frac{TP + TN}{TP + TN + FP + FN}$	Proportion of correctly classified samples
Precision	$\text{P} = \frac{TP}{TP + FP}$	Proportion of true positives among predicted positives
Recall	$\text{R} = \frac{TP}{TP + FN}$	Proportion of actual positives correctly identified
F1-Score	$F1 = \frac{2 \times R \times P}{R + P}$	Harmonic mean of precision and recall

Results

In this research, a two-stage hybrid deep learning model was designed and implemented to classify ECG signals and identify cardiac arrhythmias. The model's first stage uses an Autoencoder (AE) network as a screening tool to separate normal signals from abnormal ones.

The autoencoder, with the architecture detailed in Table 2, was trained for 200 epochs exclusively on normal ECG beats, achieving stable convergence as demonstrated by the training loss curve in Fig. 3. The reconstruction error between the original and reconstructed signals was calculated and used as an indicator for anomaly detection.

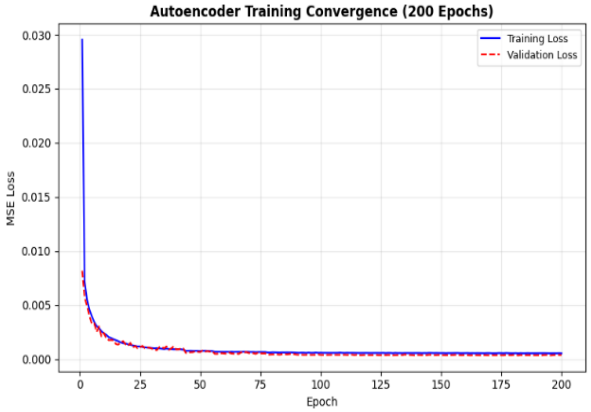

Fig. 3: Training and validation loss curve of the autoencoder.

To determine the optimal threshold for binary classification, a genetic algorithm was applied to the reconstruction error distribution. The GA searched the threshold space to maximize the fitness function defined as the sum of normal and abnormal classification accuracies.

This optimization identified an optimal threshold of 0.1277. The discriminative capability of the reconstruction errors, along with the GA-optimized threshold, was evaluated via ROC analysis, yielding an AUC of 0.8128 (Fig. 4).

The ROC curve clearly shows the selected threshold point, which maximizes the separation between normal and abnormal ECG signals.

Signals with reconstruction errors exceeding this threshold were classified as abnormal and proceeded to the second stage, while normal signals were discarded, significantly reducing computational load and improving processing efficiency.

The second stage utilizes a CNN classifier to accurately diagnose the specific type of arrhythmia among four predefined classes. The performance of the proposed model was examined through 5-fold cross-validation using both SMOTE and weighted class approaches for handling class imbalance.

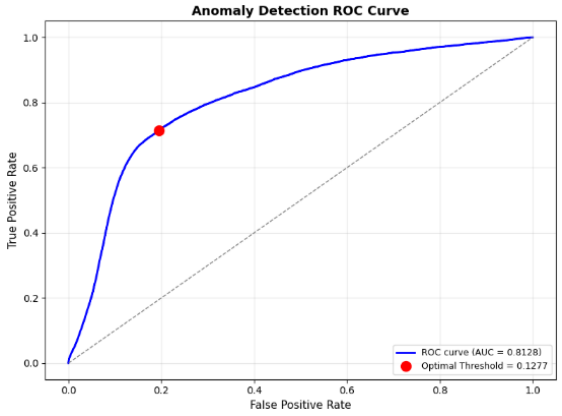

Fig. 4: Receiver Operating Characteristic (ROC) curve for anomaly detection with GA-optimized threshold (θ = 0.1277) marked.

As shown in Table 6, the SMOTE-based method achieved an average accuracy of 97.88%, precision of 97.90%, recall of 97.68%, and F1-score of 97.69%, with low standard deviations across folds (0.25–0.29%).

Table 6: 5-fold results of the proposed model

Method	Fold	Accuracy	Precision	Recall	F1-score
SMOTE	1	98.08	98.07	98.08	98.07
	2	97.88	97.89	97.87	97.88
	3	97.65	97.64	97.66	97.65
	4	98.24	98.27	97.21	97.23
	5	97.58	97.65	97.59	97.61
Average		97.88	97.90	97.68	97.69
Variance		0.062	0.059	0.085	0.080
Standard Deviation		0.25	0.24	0.29	0.28
Weighted class	1	97.78	97.81	97.78	97.79
	2	97.91	98	97.91	97.95
	3	97.38	97.62	97.37	97.45
	4	97.98	98.10	97.98	98.04
	5	96.98	97.35	96.97	97.10
Average		97.61	97.78	97.60	97.67
Variance		0.14	0.072	0.14	0.12
Standard Deviation		0.37	0.27	0.38	0.35

Training convergence was consistent across all folds, with loss and accuracy curves (Fig. 5) showing stable learning without overfitting.

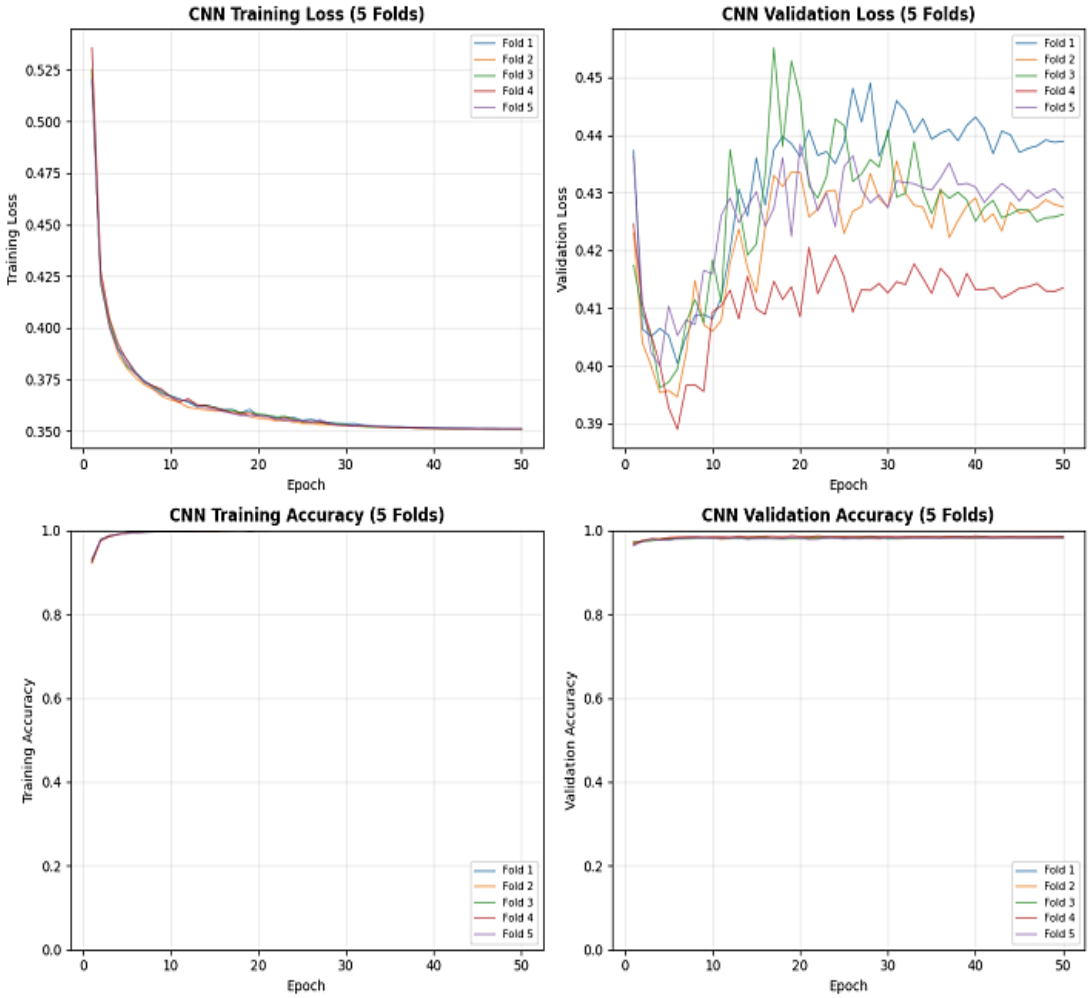

Fig. 5: CNN training loss and accuracy convergences across 5-fold cross-validation.

Detailed Classification Performance Analysis

Per-Class ROC Curves: To evaluate the discriminative power of the CNN classifier for each arrhythmia type, one-vs-rest ROC curves were generated. Fig. 7 presents these curves, with AUC values of 99.8 % for Unknown (Q), 98.6 % for Ventricular (V), 98.4 % for Supraventricular (S), and 95.1 % for Fusion (F). All AUC scores exceed 0.95, confirming the model's strong ability to distinguish each arrhythmia class from the others. The highest AUC (99.8 %) for class Q indicates near-perfect separability, while the lowest (95.1 %) for class F, the smallest and most challenging class, suggests its potential utility as a decision-support aid in clinical settings.

Precision-Recall (PR) Curves: Given the class imbalance, PR curves provide a more informative view of performance on minority classes. Fig. 7 shows the PR curves for each class.

The Fusion (F) class, the smallest class, maintains an average precision (AP) of 79.8 %, demonstrating that the model retains reasonable precision even at high recall levels for this challenging minority. The higher AP values for S, V and Q reflect their stronger separability, consistent with the ROC analysis.

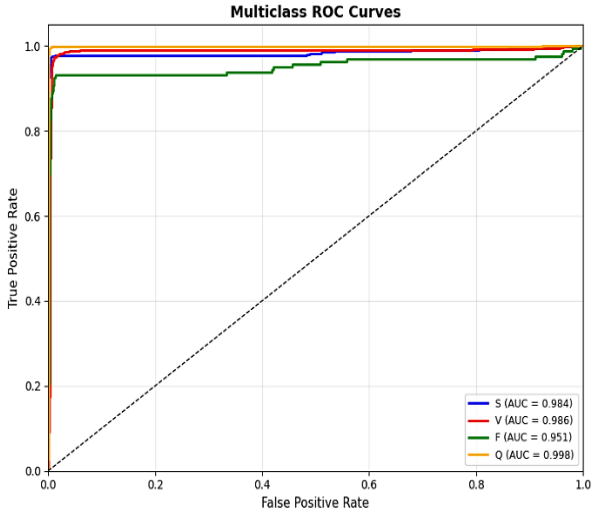

Fig. 6: One-vs-rest ROC curves for the four arrhythmia classes.

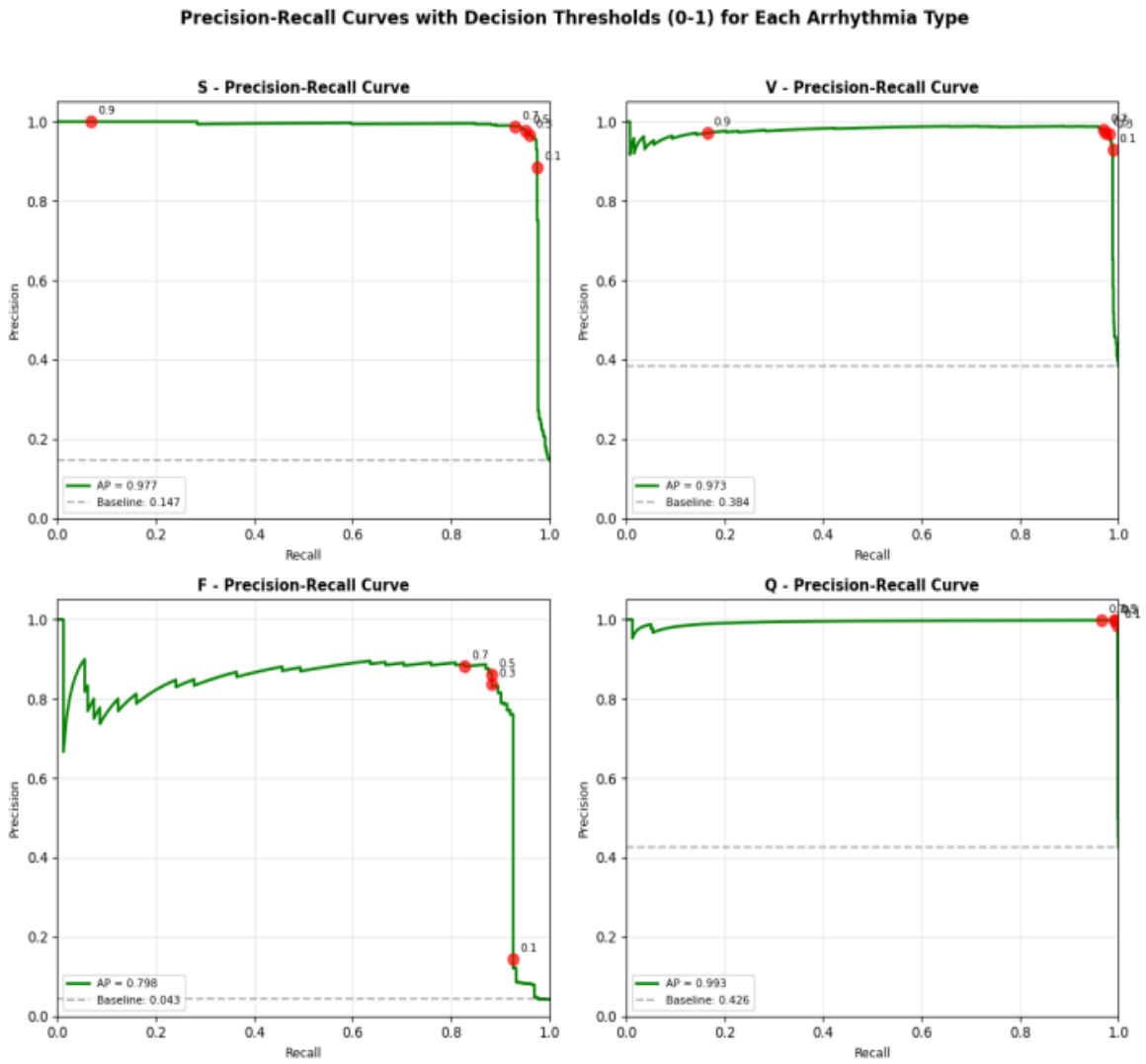

Fig. 7: Precision-Recall curves for each arrhythmia class.

Gradient-Weighted Class Activation Mapping (Grad-CAM): To interpret the CNN's decision-making process, Grad-CAM was applied to sample ECG signals from each class.

Fig. 8 displays the original ECG along with the Grad-CAM heatmap, highlighting the regions most influential for classification. For example, in Ventricular beats, the network focuses on the widened QRS complex, while for Supraventricular beats, it emphasizes the P-wave morphology. This visual explanation aligns with clinical features used by cardiologists, offering a transparent insight into the model's reasoning process and supporting its potential utility as an interpretable decision-support aid.

Confusion Matrix Analysis: The normalized confusion matrix (Fig. 9) provides a detailed view of per-class performance.

The model achieves high diagonal values: 99.32 % for Unknown (Q), 97.79 % for Ventricular (V), 95.68 % for Supraventricular (S), and 88.27 % for Fusion (F).

These values indicate accurate classification, with the highest accuracy for class Q and the lowest though still acceptable for the minority class F. The most common misclassification occurs between Fusion (F) and Ventricular (V) beats, which is clinically understandable given their morphological similarity. No significant misclassification between normal and abnormal beats is observed, supporting the practical utility of the first-stage anomaly detector in a clinical decision-support context.

It should be noted that all models, including the Autoencoder, the Genetic Algorithm (GA) optimization process, and the Convolutional Neural Network (CNN), were implemented using Python 3 within the Google Colab environment.

The deep learning models were constructed using the TensorFlow/Keras framework.

Training and evaluation were accelerated using an NVIDIA Tesla T4 GPU.

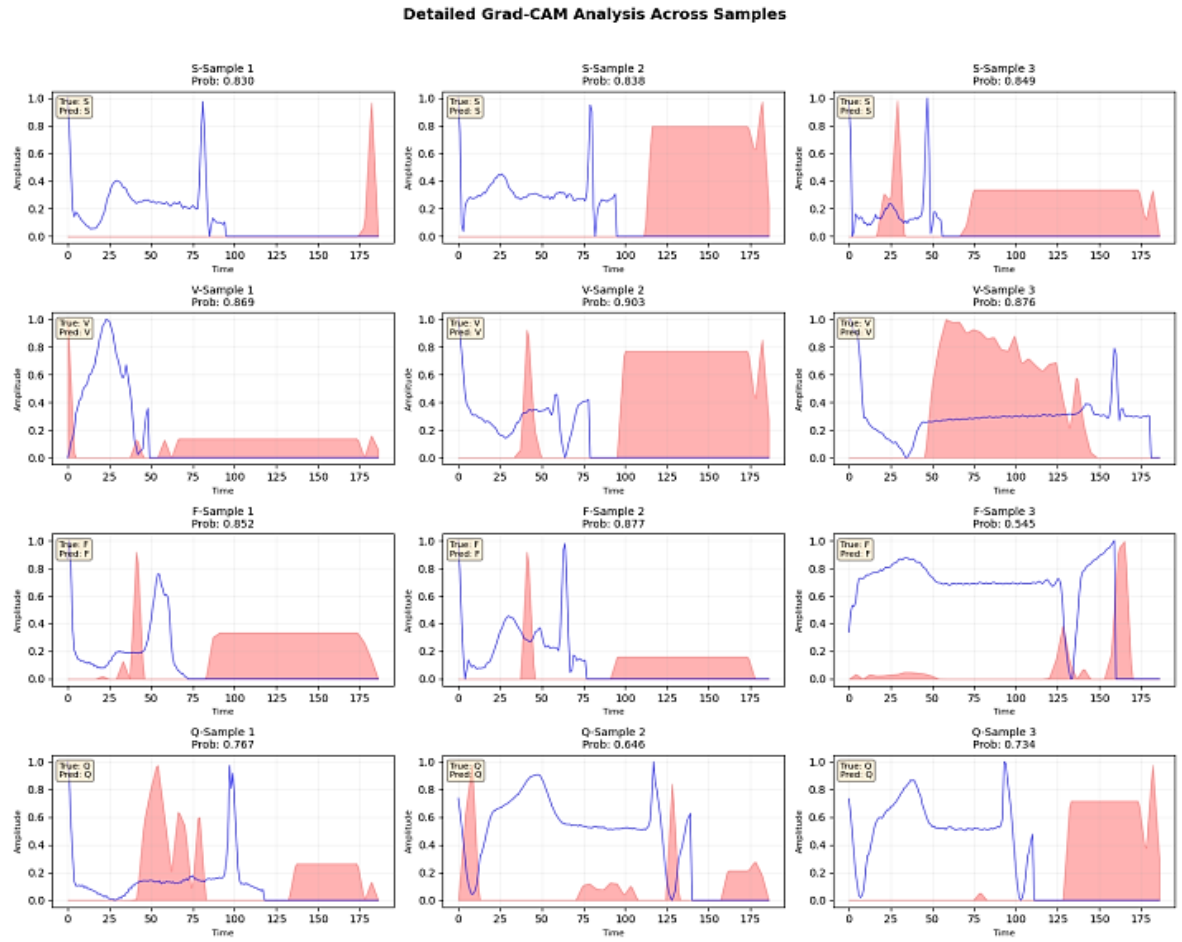

Fig. 8: Grad-CAM visualizations for sample ECG beats. The heatmap indicates regions with high activation for the predicted class.

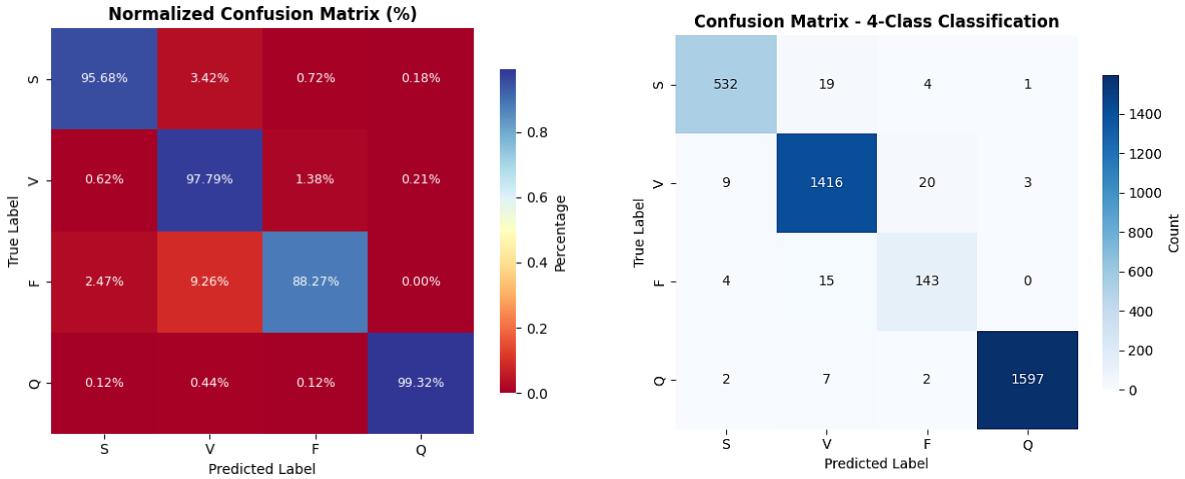

Fig. 9: Normalized confusion matrix and confusion matrix for the four arrhythmia classes (S, V, F, Q).

Discussion

The integrity and comparability of analytical outcomes are paramount in cardiac arrhythmia detection research. Our study employed the well-established MIT-BIH arrhythmia database under strictly controlled experimental conditions to ensure valid comparisons. Table 7 presents a performance comparison of various classification approaches under identical experimental setups. Our proposed AE-GA-CNN+SMOTE framework achieves the highest accuracy (97.89 %) and F1-score (97.69 %). The two-stage architecture demonstrates clear advantages, showing an absolute improvement of +6.28 % in accuracy over the single-stage CNN+SMOTE baseline and a further +3.04 % improvement over the AE+CNN+SMOTE variant with a fixed (median-based) threshold. This enhancement is statistically validated in Table 8, which confirms that all performance differences are significant ($p < 0.05$).

Table 7: Performance comparison of classification methods

Method	Accuracy	Precision	Recall	F1-Score	95% CI Accuracy
AE-GA-CNN+SMOTE	**97.89±0.25**	**97.90±0.24**	**97.68±0.29**	**97.69±0.28**	**[97.54, 98.23]**
AE-GA-CNN+Weighted	97.61±0.38	97.78±0.27	97.60±0.38	97.67±0.35	[97.08, 98.13]
AE-GA-XGBoost+SMOTE	97.57±0.13	97.60±0.13	97.57±0.13	97.58±0.13	[97.40, 97.75]
AE-GA-RandomForest+SMOTE	97.36±0.29	97.38±0.28	97.36±0.29	97.37±0.28	[96.96, 97.76]
AE-GA-AdaBoost+SMOTE	86.72±1.11	88.05±1.08	86.72±1.11	87.05±1.10	[85.18, 88.26]
CNN+SMOTE (single-stage)	91.61±3.28	96.39±0.47	91.61±3.28	93.34±2.19	[88.33, 94.89]
AE + CNN + SMOTE (fixed threshold = median error)	94.85±0.35	95.10±0.32	94.80±0.38	95.20±0.30	[94.35, 95.35]

Table 8: Statistical Significance Analysis (Paired t-test Results)

Comparison	p-value	Mean Difference (%)	95% CI of Difference	Significant (α=0.05)
AE-GA-CNN+SMOTE vs CNN+SMOTE	<0.001	+6.28	[+3.65, +8.91]	Yes (p<0.001)
AE-GA-CNN+SMOTE vs AE+CNN+SMOTE (fixed threshold)	<0.001	+3.04	[+2.15, +3.93]	Yes (p<0.001)
AE-GA-CNN+SMOTE vs AE-GA-CNN+Weighted	0.0486	+0.28	[+0.003, +0.557]	Yes (p<0.05)
AE-GA-CNN+SMOTE vs AE-GA-XGBoost+SMOTE	0.0222	+0.32	[+0.073, +0.551]	Yes (p<0.05)
AE-GA-CNN+SMOTE vs AE-GA-RandomForest+SMOTE	0.0171	+0.53	[+0.154, +0.894]	Yes (p<0.05)
AE-GA-CNN+SMOTE vs AE-GA-AdaBoost+SMOTE	0.000015	+11.17	[+9.928, +12.404]	Yes (p<0.001)

The consistent superiority across all metrics, combined with narrow confidence intervals and low standard deviations, indicates robust performance. As presented in Table 9, our approach achieves competitive performance relative to recent studies on the same MIT-BIH dataset, encompassing various architectures and classification tasks (binary and multi-class). The superior and balanced performance of our model evidenced by the highest F1-score (97.69 %) stems from two key innovations: (1) the two-stage design, which isolates abnormal signals before fine-grained classification, and (2) the Genetic Algorithm, which optimizes the detection threshold globally, avoiding local optima that limit gradient based or heuristic methods. This combination yields not only higher accuracy but also greater reliability, as reflected in the tight confidence intervals across all evaluation folds.

Table 9: Performance comparison with recent studies on the MIT-BIH database

Model type	Accuracy	Precision	Recall	F1-Score
CNN [31]	97.6%	94.4%	93%	93.6%
Machine Learning [32]	89%	88.5%	89.9%	89.3%
Graph Convolutional Network (GCN) [33]	92.68%	68.24%	95.5%	95.24%
Autoencoder [34]	97.19%	90.75%	99.14%	94.84%
Transformer-Based Anomaly Detection [34]	89.5%	98.2%	87.1%	92.3%
1DCNN+BERT [36]	95.1%	94.92%	94.69%	94.81%
Bidirectional Transformer [37]	95.88%	95.47%	93.15%	94.26%
Proposed method	97.88%	97.90%	97.68%	97.69%

Computational Efficiency and Runtime Analysis

The proposed framework demonstrates favorable computational characteristics. The autoencoder trained in approximately 10 minutes (200 epochs, batch size = 256). The Genetic Algorithm, optimized for a single threshold variable with a population of 50 over 100 generations, converged in only 0.79 seconds a negligible overhead given its one-time execution during the configuration phase. The complete CNN stage, including 5-fold cross-validation with SMOTE balancing, required about 40 minutes. Despite its minimal runtime cost, the GA contributed a +3.04 % improvement in accuracy over a fixed-threshold baseline, underscoring its cost-effectiveness. The low per-component runtime indicates that the computational load is sufficiently light to support interactive use in clinical decision-support systems.

Conclusion

Identifying cardiac abnormalities through ECG signals represents a vital diagnostic procedure in cardiology. The accurate and rapid automated interpretation of these signals holds significant potential to enable early intervention, reduce healthcare costs, assist clinicians in decision-making, and ultimately improve patient outcomes. To address this need, this study proposed a novel two-stage hybrid deep learning model for ECG-based arrhythmia detection. The core innovation of this work is an optimized architecture that strategically combines an autoencoder for efficient anomaly screening with a convolutional neural network (CNN) for precise multi-class classification. A pivotal component is the integration of a Genetic Algorithm (GA) to automatically determine the optimal reconstruction error threshold, thereby significantly enhancing the separation between normal and abnormal beats.

This methodological approach yielded superior performance, with the model achieving an average F1-score of 97.69% and an accuracy of 97.88%. The strength of the proposed framework stems from its two-stage design: the first stage effectively filters out the majority of normal cases, reducing the computational burden, while the second stage focuses classification resources only on the remaining abnormal signals, establishing a robust foundation for accurate diagnosis. This synergy between efficient screening and targeted classification is the primary reason for its performance advantage over conventional single-stage methods.

Despite these promising results, the study acknowledges certain limitations. The evaluation was conducted exclusively on the MIT-BIH database, which may affect the model's generalizability to more diverse, real-world clinical datasets. Furthermore, the clinical impact of critical misclassifications, such as mislabeling a dangerous arrhythmia as normal, was not explicitly assessed—a vital consideration for ensuring patient safety in practical deployments. Additionally, while the two-stage design improves processing efficiency, direct implementation on resource-constrained wearable devices would require further optimization.

For future work, several directions are suggested to further advance this research. First, evaluating the model on larger multi-center datasets is expected to enhance its generalizability. Second, incorporating clinical risk-aware loss functions during training can minimize dangerous misclassifications. Additionally, applying model compression techniques, such as pruning and quantization, will facilitate real-time implementation on wearable hardware. Finally, exploring advanced architectures like variational autoencoders or transformer-based networks could enhance both accuracy and robustness. With these refinements, the proposed framework could serve as a foundation for future decision-support tools and wearable cardiac monitoring systems, potentially contributing to more efficient and accessible cardiac care.

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Author Contributions

M. Akbari Poodineh conceptualized the study, developed the methodology, and conducted software development, validation, and formal analysis. F. Zare Mehrjardi contributed to the investigation, data curation, writing, review and editing. M. Sardari Zarchi supervised the project, provided manuscript review and feedback, and handled project administration.

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Conflict of Interest

The authors declare no potential conflict of interest regarding the publication of this work. In addition, the ethical issues, including plagiarism, informed consent, misconduct, data fabrication and/or falsification, double publication and/or submission, and redundancy, have been completely witnessed by the authors.

Abbreviations

ECG	Electrocardiogram
CNN	Convolutional Neural Network
PCA	Principal Component Analysis
FFT	Fast Fourier Transform
VAE	Variational Autoencoder
MMD	Maximum Mean Discrepancy
GA	Genetic Algorithm
MSE	Mean Squared Error
FNN	Feedforward Neural Network
GNN	Graph Neural Network
ReLU	Rectified Linear Unit
DL	Deep Learning
GCN	Graph Convolutional Network
LSTM	Long Short-Term Memory
ML	Machine Learning
SVM	Support Vector Machine
KNN	K-Nearest Neighbor
TL	Transfer Learning
SMOTE	Synthetic Minority Over-sampling Technique
TP	True Positives
TN	True Negatives
FP	False Positives
FN	False Negatives

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