

# A Novel Feature Vector for ECG Classification using Deep Learning

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## Abstract

In the past decade, deep learning techniques have been widely used in the healthcare industry to detect heartbeats and diagnose heart conditions. However, these tools have been criticized for being a “black box” and lacking transparency. Therefore, in this paper, we propose a new approach to making the classification results obtained by deep learning more comprehensible. We suggest forming a vector of features based on ECG signals that correspond to specific heart conditions. This vector includes measurable characteristics of the cardiac cycle, such as wave durations and amplitudes, which are typical and understandable to healthcare professionals. This feature vector serves as input data for a deep neural network that acts as a feature encoder and classifier. Our computational experiments with the handcrafted feature vector achieved an average accuracy of 98.69%, comparable to other deep learning tools based on the complete cardiac cycle. The results of this study suggest that future research should focus on developing interpretable deep learning tools that are transparent and comprehensible to healthcare professionals.

## Keywords <sup>1</sup>

Electrocardiogram signals, MIT-BIH arrhythmia database, feature extraction, deep learning, explainable artificial intelligence

## 1. Introduction

Electrocardiography is a commonly used method in diagnosing heart disease because it is a straightforward and dependable way to monitor heart muscle activity. This process produces a visual record of changes in electrical potentials caused by heart muscle excitation, known as an electrocardiogram (ECG) [1]. In medical practice, ECG is an effective tool for identifying heart issues like an irregular heartbeat or arrhythmia, which can lead to life-threatening heart diseases like myocarditis or atherosclerosis [2]. Prompt detection of arrhythmia is essential for successful treatment, but manually analyzing ECG signals to identify arrhythmia under different conditions can be both time-consuming and prone to errors [3].

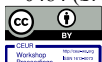
Recently, artificial intelligence (AI) methods and tools, particularly machine learning (ML) [4] and deep learning (DL) [5] have been actively used to automate the diagnosis of arrhythmia based on ECG signals. However, DL-based arrhythmia detection methods typically require much training data to achieve satisfactory results. There is a shortage of well-annotated ECG data available in the public domain for training multi-layer DL models [6]. Therefore, it is essential to develop new approaches to prepare input data and form sets of target features for an automated image classifier. To evaluate the

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effectiveness of arrhythmia detection based on ECG signals, the Association for the Advancement of Medical Instruments (AAMI) has designed a novel standard [7] (ANSI/AAMI EC57:2012). However, not all DL-based approaches to arrhythmia detection meet the AAMI standard. Some approaches report near-perfect classification accuracy (>99%) [5], [8] but provide misleading and unreliable results when evaluated with the MIT-BIH database [9]. Further experiments have shown that classification accuracy significantly decreases when evaluated according to AAMI guidelines.

Detecting heart pathologies is a critical task in the healthcare field, and it is essential not only to obtain accurate results but also to explain how these results were obtained [10]. Thus, the scientific community has emphasized the importance of developing AI-based systems for healthcare that are based on principles of trust [11], which have been formalized into the concept of FATE (Fairness, Accountability, Transparency, Ethics) in AI [12]. In other words, healthcare professionals should be able to understand how AI results for medical issues were generated and have the tools to trust these results. This issue is a significant challenge that needs to be considered carefully when developing AI methods for healthcare [13].

In this work, the authors consider the interpretability of AI decision-making for ECG signal classification that can be defined as follows: the system's user must understand, based on which features of the ECG signal the AI method reached one or another decision regarding the possible presence of heart pathologies. The proposed approach involves inputting a vector of features into the neural network, which represents the signal in a manner similar to how healthcare professionals interpret it. This approach differs from previous ones, where the entire cardiac cycle signal was used as input data. The feature vector is formalized so that the results of the deep neural network are no worse by the classification metrics than using the full ECG signal.

The study presented here offers several important scientific contributions:

- We proposed a novel approach for representing ECG signals as a feature vector that uses characteristics commonly used by healthcare professionals.
- We created a new subset of data from the MIT-BIH database using the inter-patient paradigm.
- We showed that our approach, which uses ECG fragments, achieves classification accuracy similar to other methods that use the complete cardiac cycle signal.

The article's structure is as follows: Section 2 provides an analytical overview of deep learning methods and techniques for processing ECG signals. Section 3 explains the data preprocessing and the proposed approach for identifying heart pathologies from ECG signals. Section 4 presents the experimental results on a benchmark dataset, including implementation details, and compares the proposed approach with state-of-the-art methods. Finally, Section 5 summarizes the research findings.

## 2. Related works

The process of using AI to analyze ECG signals generally involves several stages, as outlined in [8]: 1) preprocessing and noise reduction of the ECG signal, 2) segmenting heart contractions, 3) extracting features, 4) training a model, and 5) classifying ECG signals using the trained model. Recently, researchers have focused on identifying features from isolated fragments of the ECG signal (such as pre-selected cardiac cycles) and building a DL model based on these features. Such an approach can result in higher accuracy due to the detection of hidden features by the DL model. However, the resulting model may be perceived as a "black box," which may not provide the end user with an understanding of the criteria used to make decisions about the classification of ECG signals.

In recent years, researchers have focused on developing methods for processing ECG signals. For instance, one study proposed a modified and extended Kalman filter structure [14], which can be used to reduce ECG signal noise and compress it. Another study [15] presented a method for segmenting heart contractions using wavelet transforms (WTs), which can detect the QRS complex behind high P or T waves even in the presence of solid noise or drift. In addition, a new fractional WT technique was proposed in another study [16] to extract features from ECG signals, which were then used with traditional ML algorithms to detect peaks and segments.

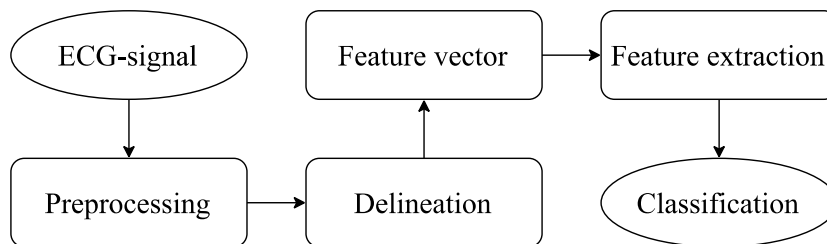
In the past few years, researchers have proposed various methods to detect heart pathologies from ECG signals. For example, in [17], a system is suggested to use a combination of RR intervals, signal morphology, and higher-order statistics. In [18], a system is presented that classifies arrhythmias based

on normalized RR intervals and morphological features using VP and regression modeling. Additionally, [19] utilized a support vector machine classifier with reduced features derived from linear discriminant analysis. In [20], the authors used a hidden Markov model to simulate continuous signals for arrhythmia detection, which combines temporal information and statistical knowledge of the ECG signal. In [21], an end-to-end convolutional neural network (CNN) is proposed to directly accept raw ECG signals as input data without prior feature selection. The construction of CNN architecture to analyze medical images and signals is described in [22]. Furthermore, [23] suggests a CNN autoencoder-decoder to classify heartbeats based on ECG signals using temporal and statistical characteristics. In [24], a new approach based on DenseNet architecture achieved over 95% accuracy in classifying ECG signals with heart pathology signs, with class activation gradient maps visualizing specific ECG leads and parts of ECG waves significantly impacting predictive decisions.

In this study, we have taken a different approach to process ECG signals than previous studies, such as [16], [21], and [23]. We created a feature vector based on pre-selected fragments of the ECG signal using the “human-in-a-loop” principle. An autoencoder CNN was then applied to this vector to detect hidden dependencies in the original ECG signal. By doing so, the accuracy of the built model is comparable to that of a model which accepts a full ECG signal as input. As a result, this approach is able to provide both high accuracy in classification inherent in DL methods and an understandable mechanism for healthcare professionals to identify heart disease pathologies.

### 3. Methodology of research

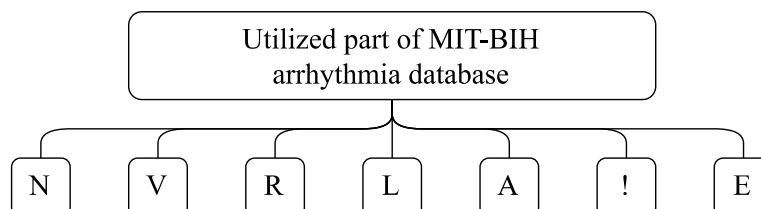
Our research consists of the following steps: data preprocessing, feature extraction, and signal classification. The stages of the utilized methodology are shown in Fig. 1.



**Figure 1:** The scheme of the methodology that performs the proposed approach.

#### 3.1. Dataset and data preprocessing

For experimental research, this work utilized the MIT-BIH arrhythmia database [9], which contains 48 half-hour segments of two-channel ambulatory ECG recordings taken from 47 patients at a frequency of 360 Hz. Two or more cardiologists independently annotated each sample in the dataset at the heart rate level. According to the AAMI guidelines, the fourteen original heartbeat types are classified into seven categories, as depicted in Fig. 2.



**Figure 2:** A scheme of the subset of the MIT-BIH database based on the inter-patient paradigm.

The derivative set from the MIT-BIH database (Fig. 2) comprises seven types of heartbeats: 1) N – normal beat; 2) V – premature ventricular contraction; 3) R – right bundle branch block beat; 4) L – left

bundle branch block beat; 5) A– atrial premature beat; 6) ! – ventricular flutter wave; 7) E – ventricular escape beat.

The MIT-BIH database was initially divided into training and test subsets based on different paradigms, such as intra-patient and inter-patient. Table 1 presents a comprehensive breakdown of the data from the MIT-BIH database and the data used in this study.

**Table 1**

Heart rate distribution by classes of raw data in the MIT-BIH dataset.

Data	N	V	R	L	A	!	E	Total
Full MIT-BIH set	163,037	12,293	24,954	2,817	4,569	793	1,258	209,721
Intra-patient split	72,471	5,789	14,445	173	2,223	155	642	95,898
Training (80 % split)								
Testing (20 % split)	18,118	1,447	2,889	346	556	310	161	23,827
Inter-patient split	45,866	3,788	4,756	394	944	317	415	56,480
Training (DS1)								
Testing (DS2)	26,582	1,269	2,864	1,904	846	11	40	33,516

Using ECG signals from the same patient for both the training and test sets is known as the intra-patient paradigm while using ECG signals from different patients is called the inter-patient paradigm. The inter-patient paradigm has the advantage of avoiding the issue of overlapping information, where the patient’s personal characteristics may affect the training and testing of the model, leading to inaccurate classification results.

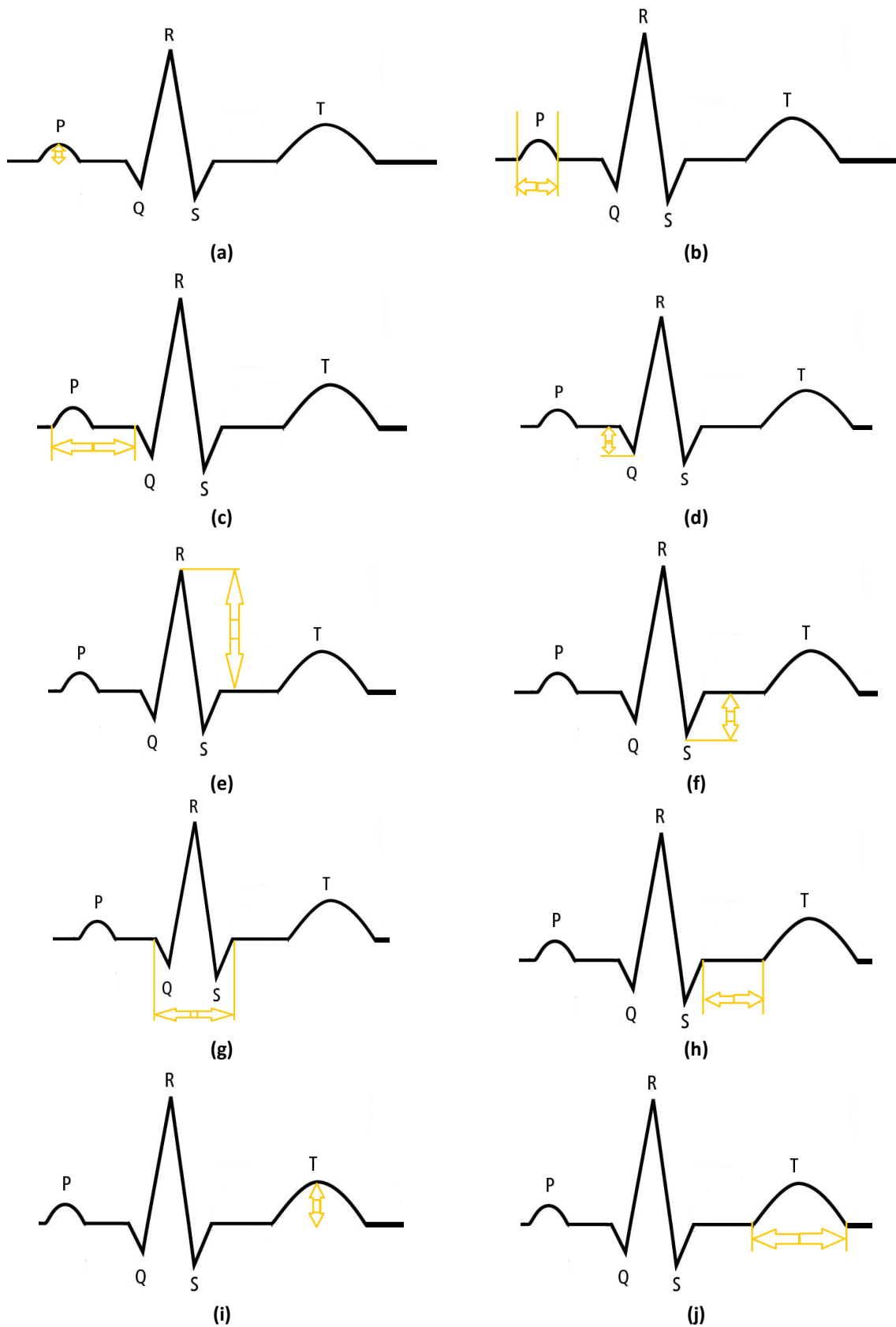
In this study, only the derivative set of the MIT-BIH database was used according to the inter-patient paradigm. The MIT-BIH subset was split into two groups, DS1 and DS2, based on patient identification numbers. DS1 included patients 102, 107, 109, 110, 115, 116, 117, 120, 123, 125, 202, 204, 206, 208, 209, 216, 224, and 231, while DS2 included patients 101, 104, 106, 112, 114, 118, 124, 126, 201, 203, 207, 213, 214, 215, 219, 222, 225, 229, and 232 [17]. DS1 was used as the training dataset, while DS2 was used as the testing dataset to evaluate the model.

Raw ECG signals obtained from the MIT-BIH database typically had noise, including myoelectric artifacts and signal baseline drift. Therefore, we processed all ECG signals using Daubechies 6 wavelet (db6) and decomposed them into six levels to eliminate noise. The wavelet coefficients from the 3rd to the 6th level were saved and used for signal reconstruction, as recommended in [15]. After denoising, the ECG signals were segmented into heart contractions based on the R-peak location coordinates provided in the MIT-BIH arrhythmia database.

### 3.2. Feature vector

The research provides a novel approach to feature extraction that employs the “human-in-the-loop” principle. The proposed technique involves feeding a classifier with a feature vector consisting of quantitative properties of the ECG signal that are relevant to healthcare professionals in diagnosing heart diseases and are easily understood by them. Performing our contribution includes the following stages:

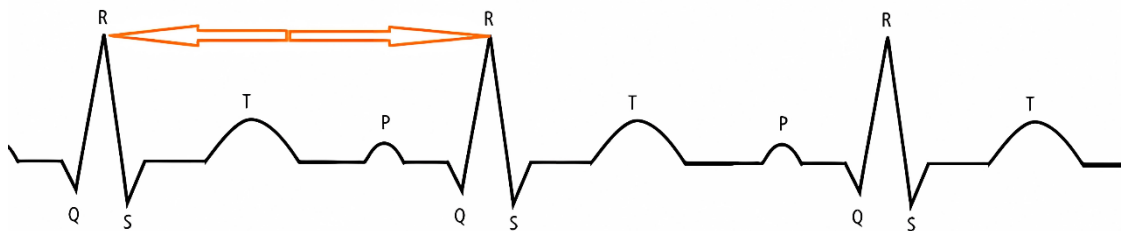
- Identifying the primary characteristics of the ECG signal, such as peaks and wave boundaries, using the neurokit2 library [25].
- Using the coordinates of the detected peaks and boundaries to create a list of cardiac cycles. Excluding those cardiac cycles with incorrectly defined peaks and boundaries was essential for constructing a valid feature vector.
- Formation of a vectorized representation of each cardiac cycle. The feature extraction approach involves creating a vector representation for each derivative cardiac cycle of 10 ms. This vector includes several amplitudes and durations of cardiac cycle waves that are schematically illustrated in Fig. 3.



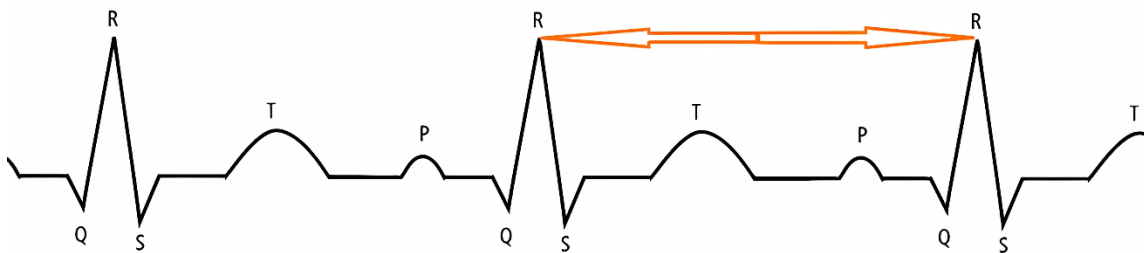
**Figure 3:** Amplitudes and durations of cardiac cycle waves included in the proposed feature vector: (a) P-wave amplitude; (b) P-wave duration, ms; (c) PQ-interval duration, ms; (d) Q-wave amplitude; (e) R-wave amplitude; (f) S-wave amplitude; (g) QRS-complex duration, ms; (h) ST-segment duration; (i) T-wave amplitude; (j) T-wave duration, ms

Below is a short description of each vector's element.

1. P-wave amplitude.
2. P-wave duration in milliseconds (ms).
3. PQ-interval duration, ms.
4. Q-wave amplitude.
5. R-wave amplitude.
6. S-wave amplitude.
7. QRS-complex duration, ms.
8. ST-segment duration.
9. T-wave amplitude.
10. T-wave duration, ms.
11. A fragment that represents the duration of the interval between the current and previous R peaks in ms (Fig. 4a).
12. A fragment that represents the duration of the interval between the current and the following R peaks in ms (Fig 4b).



(a)



(b)

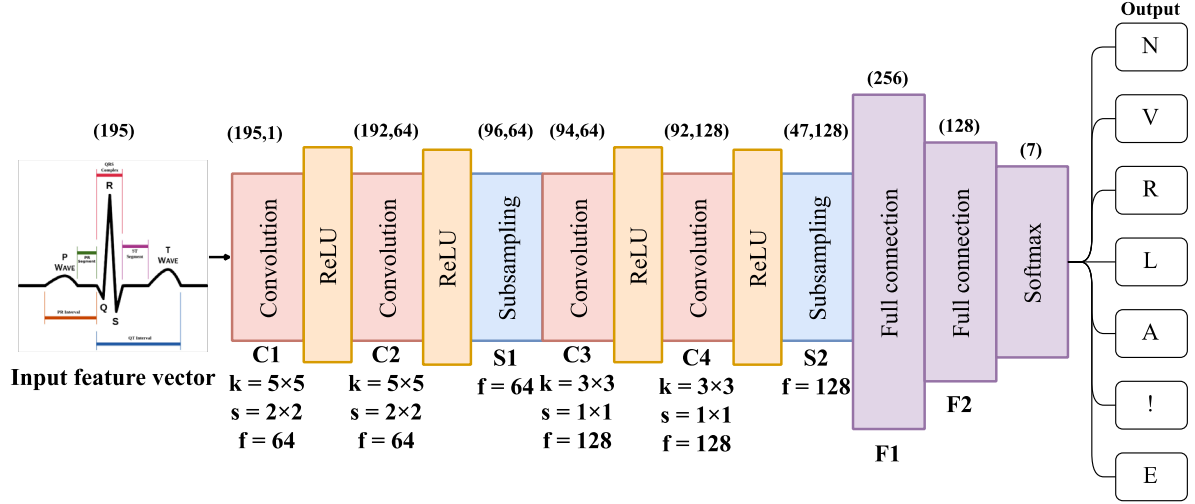
**Figure 4:** (a) duration between the current and previous R peaks, ms; (b) duration between the current and the following R peaks, ms.

13. P-wave fragment, which lasts 80 ms and corresponds to 30 elements of the input signal of the cardiac cycle. These 30 elements are added to the feature vector.
14. QRS complex fragment, which lasts up to 100 milliseconds and corresponds to 37 elements of the input signal of the cardiac cycle. These 37 elements are added to the feature vector.
15. ST segment – this fragment lasts up to 150 ms, corresponding to 56 elements of the input signal of the cardiac cycle. These 56 elements are added to the feature vector.
16. T-wave fragment, which lasts 160 ms and corresponds to 60 elements of the input signal of the cardiac cycle. These 60 elements are added to the feature vector.

As a result of the above steps, the feature vector should contain 195 quantitative elements.

### 3.3. Feature extraction and classification

The extraction of hidden features from the constructed feature vector and subsequent classification of heartbeats is performed by the autoencoder-type CNN [22]. The scheme of it is shown in Fig. 5.



**Figure 5:** The scheme of the utilized CNN.

The CNN used in this study comprises nine layers: four convolutional layers, two subsampling layers, two fully connected layers, and one SoftMax classification layer. The convolutional layers, namely C1, C2, C3, and C4, consist of convolutional cores of sizes 5, 5, 3, and 3, respectively. The convolution operation is expressed mathematically as follows.

$$x_k^l = \text{ReLU} \left( \sum_{i=1}^{M_k} x_i^{l-1} * w_{ik} + b_k \right), \quad (1)$$

where  $x_k^l$  is the output value of the  $k$ -th neuron in the  $l$ -th layer,  $M_k$  is the effective range of the convolution kernel,  $x_i^{l-1}$  is the output value of the  $k$ -th neuron in the  $l$ -th convolutional layer,  $b_k$  is the displacement of  $k$ -th neuron in the  $l$ -th layer,  $w_{ik}$  is the kernel weight value between the  $i$ -th neuron in the  $l$ -1-st layer and the  $k$ -th neuron in the  $l$ -th layer, ReLU is the activation function.

In this study, the CNN architecture's sub-sampling layers S1 and S2 use the MaxPool function. The role of these layers is to reduce the input size for the next layer and decrease the dimensionality of the ECG signals to lessen the computational load. The MaxPool function in the subsampling layer is formalized as follows.

$$x_k^l = \text{subsample}(x_{k_{cluster}}^{l-1}), \quad (2)$$

where  $x_k^l$  is the output value of the  $k$ -th neuron in the  $l$ -th layer,  $\text{subsample}$  is a subsampling operation,  $x_{k_{cluster}}^{l-1}$  is the output value of the  $k$ -th cluster in the  $l$ -1-st layer.

The purpose of fully connected layers F1 and F2 in the CNN architecture is to increase the number of nonlinear operations. The mathematical expression of the full connectivity operation is given below.

$$x_k^l = f \left( \sum_{i=1}^N x_i^{l-1} * w_{ik} + b_k \right), \quad (3)$$

where  $x_k^l$  is the output value of the  $k$ -th neuron in the  $l$ -th layer,  $x_i^{l-1}$  is the output value of the  $k$ -th neuron in the  $l$ -th convolutional layer,  $b_k$  is the offset of the  $k$ -th neuron in the  $l$ -th layer,  $w_{ik}$  is the kernel weight value between the  $i$ -th neuron in the  $l$ -1-st layer and the  $k$ -th neuron in the  $l$ -th layer,  $N$  is the total number of neurons in the  $l$ -1-st layer.

The output layer of the CNN architecture implies the SoftMax activation function with an output of seven types of heartbeats.

$$P(y = i|X) = \frac{e^{X^T w_i}}{\sum_{j=1}^7 e^{X^T w_j}}, i = \overline{1,7}, \quad (4)$$

where  $X^T$  is the output value vector of the final fully connected layer,  $w_i$  is the kernel weight value between the  $i$ -th neuron in the final fully connected layer.

More details about the utilized CNN architecture are presented in our previous work [26].

### 3.4. Evaluation criteria and experiment setup

We shall denote the number of positive and negative cases in the initial dataset as P and N, respectively. When a classifier is applied to the dataset, the objects are sorted into true positive (TP), true negative (TN), false positive (FP), and false negative (FN) categories. This study assessed the proposed approach using several statistical metrics, which are defined as follows.

$$\text{Accuracy} = \frac{TP + TN}{TP + TN + FP + FN} \quad (5)$$

$$\text{Precision} = \frac{TP}{TP + FP} \quad (6)$$

$$\text{Recall} = \frac{TP}{TP + FN} \quad (7)$$

$$F_1 = \frac{2TP}{2TP + FP + FN} \quad (8)$$

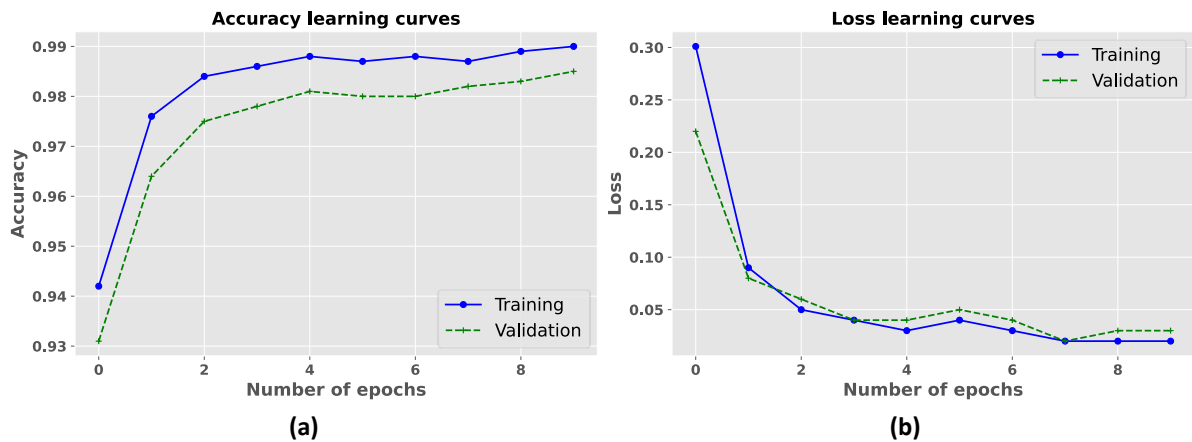
To train the network, we employed Adam optimization with a total of 10 epochs. We set the training parameters based on our previous research [22], [26]: the learning rate was set between 0.0001 and 0.001, weight decay was 0.0005, momentum was 0.85, and batch size was 64. On a single GPU, the training process lasted about 155 minutes.

The computational experiments were performed based on the software setup of Python v3.9, neurolink2 [25], Scikit-learn [27], and TensorFlow [28]. The experiments were run on a system with an eight-core Ryzen 2700, 32GB RAM, and a single NVIDIA GeForce GTX1080 CPU with 8 GB video memory.

## 4. Results and discussion

The proposed approach was tested using a stratified approach to create training and testing datasets that are mutually exclusive. The training dataset was divided into 90% for direct training data and 10% for validation data, which are also mutually exclusive. The results of the training and validation are shown in Fig. 6.

In Fig. 6, the blue curve indicates the classification accuracy for the training set, while the green curve represents the validation set.

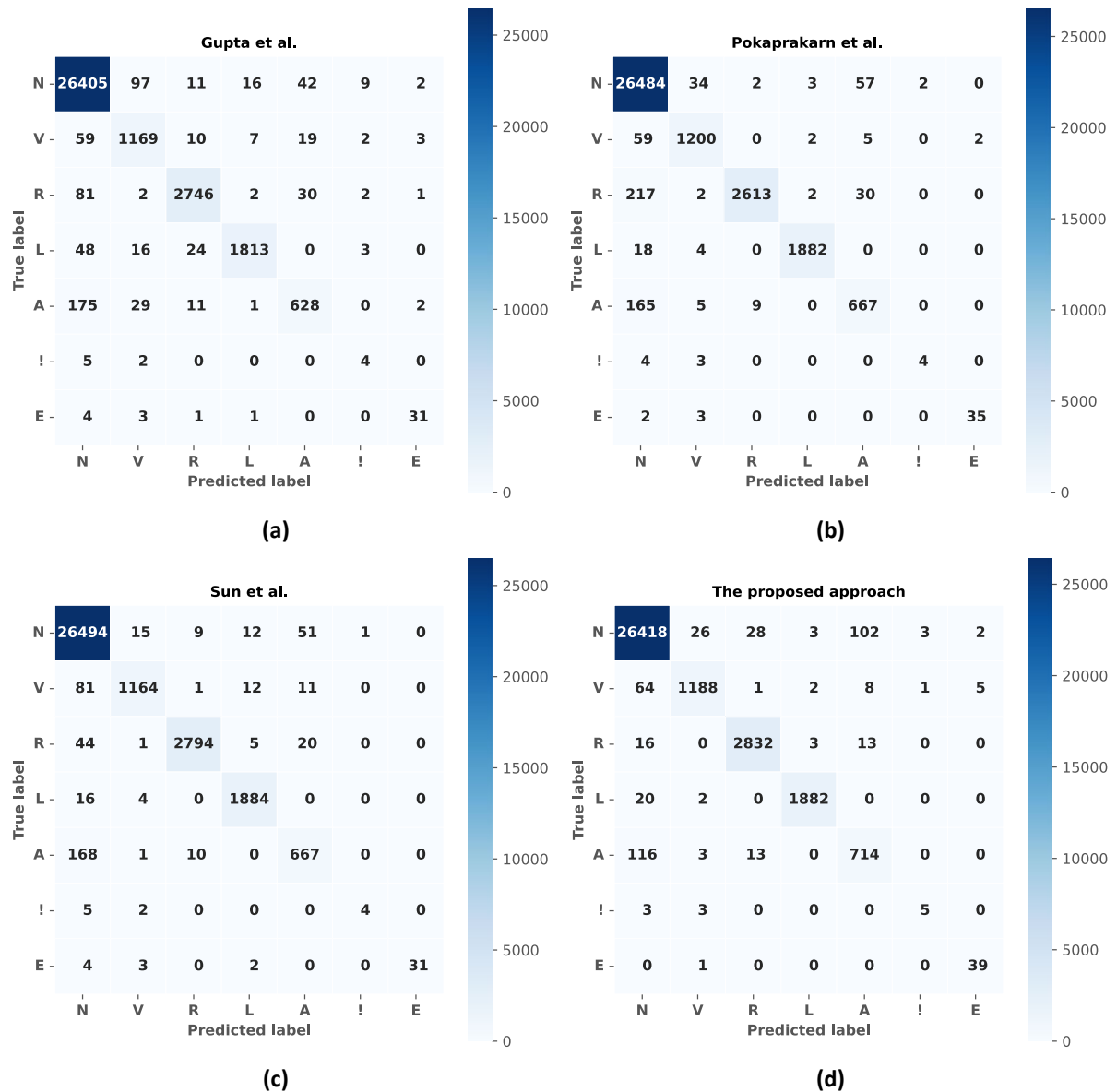


**Figure 6:** Learning curves obtained by the CNN model built based on the proposed approach: (a) accuracy and (b) loss.



As we can observe, both curves nearly overlap, indicating that the CNN model developed was trained effectively without overfitting.

The proposed approach's classification results were compared to those of Gupta et al. [16], Pokaparakarn et al. [21], and Sun et al. [23]. All three analogs were initially introduced and examined based on an entire cardiac cycle as input data. The confusion matrices of the four testing approaches are shown in Fig. 7.



**Figure 7:** Confusion matrices of heart rate by ECG signals on the test dataset obtained by approaches: (a) Gupta et al., (b) Pokaparakarn et al., (c) Sun et al., and (d) the proposed approach.

Ten experiments were conducted to confirm the built CNN model's stability and practical significance. Table 2 shows the statistical indicators obtained by the testing approaches on the test dataset.

The proposed approach achieved an overall classification accuracy of 98.69%, while Gupta et al. achieved 97.96%, Pokaparakarn et al. – 98.12%, and Sun et al. – 98.57%. The relative classification accuracy values indicate that the proposed model is stable and competitive. Notably, high accuracy was achieved when using both the entire cardiac cycle and its individual fragments, demonstrating the practical significance of the selected amplitudes and durations of cardiac cycle waves in the constructed feature vector.

Meanwhile, examining related works revealed opportunities to enhance the classification accuracy of ECG signals and improve the transparency of the results obtained by using additional techniques. One of the techniques is normalizing the ECG signal, which could assist the model in determining the significance of individual signal fragments, ultimately increasing the model’s capability to detect hidden patterns.

**Table 2**

Statistical indicators obtained by the testing approaches on the test dataset.

Class	Approach	Precision	Recall	$F_1$	Number of samples
N	Gupta et al. [16]	0.96	0.98	0.97	26582
	Pokaprakarn et al. [21]	0.98	1.0	0.99	
	Sun et al. [23]	0.99	1.0	0.99	
	Ours	0.99	0.99	0.99	
V	Gupta et al. [16]	0.96	0.93	0.94	1269
	Pokaprakarn et al. [21]	0.96	0.95	0.95	
	Sun et al. [23]	0.98	0.92	0.95	
	Ours	0.97	0.94	0.95	
R	Gupta et al. [16]	0.97	0.93	0.95	2864
	Pokaprakarn et al. [21]	1.0	0.91	0.95	
	Sun et al. [23]	0.99	0.98	0.98	
	Ours	0.99	<b>0.99</b>	0.98	
L	Gupta et al. [16]	0.97	0.97	0.97	1904
	Pokaprakarn et al. [21]	1.0	0.99	0.99	
	Sun et al. [23]	0.98	0.99	0.99	
	Ours	1.0	0.99	0.99	
A	Gupta et al. [16]	0.86	0.77	0.82	846
	Pokaprakarn et al. [21]	0.88	0.79	0.83	
	Sun et al. [23]	0.89	0.79	0.84	
	Ours	0.85	<b>0.84</b>	0.85	
!	Gupta et al. [16]	0.62	0.33	0.49	11
	Pokaprakarn et al. [21]	0.67	0.36	0.47	
	Sun et al. [23]	0.80	0.36	0.50	
	Ours	0.56	<b>0.45</b>	0.50	
E	Gupta et al. [16]	0.88	0.92	0.90	40
	Pokaprakarn et al. [21]	0.95	0.88	0.91	
	Sun et al. [23]	1.0	0.78	0.87	
	Ours	0.85	0.97	0.91	

Furthermore, the model’s transparency could be enhanced by incorporating into the constructed feature vector individual characteristics of a person, such as age, gender, weight, and height, which are typically known to healthcare professionals during diagnosis but are usually omitted in DL tools. By doing so, these modifications could improve both classification accuracy and the mechanisms that healthcare professionals use to detect heart disease pathologies.

## 5. Conclusion

This study focuses on developing a novel approach to create a feature vector that can detect heart diseases through ECG signals. This new approach aims to enhance the interpretability of the results obtained. Unlike previous approaches that utilized the entire signal of the cardiac cycle as the input data for neural networks, this approach inputs information about the signal in terms that doctors use. The feature vector comprises discrete fragments of the cardiac cycle, along with the amplitude and duration of the waves, which are crucial in diagnosing heart diseases. To test this approach, a derivative subset of the MIT-BIH database was utilized under the inter-patient paradigm. The proposed approach achieved an average accuracy of 98.69%, comparable to other methods based on a complete cardiac cycle. High accuracy was achieved when using both the entire cardiac cycle and its individual

fragments, demonstrating the practical significance of the selected amplitudes and durations of cardiac cycle waves in the constructed feature vector.

Furthermore, the information system based on this approach can be directly implemented on wearable devices for long-term ECG monitoring. Future research will aim to develop transparent and understandable solutions for healthcare professionals using AI tools.

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