# Benefits of Machine learning models within electrocardiograms for arrhythmias detection

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## Abstract

The electrocardiograms are the primary source of diagnosing cardiac arrhythmia. Health information that are delicate to detect and, in some cases, potentially fatal. Manual analyzing of electrocardiogram signals is a complex process that can be subject to errors particularly in a high-pressure environment. the difficulty is amplified by the variance of co-occurring arrhythmia types. Therefore, this work presents a multi-input deep learning architecture that combines signal analysis on lead II with domain-specific features extracted from all 12 leads. This dual- pathway is designed to leverage both signal intra-lead dynamics and inter-lead dependencies enhancing model performance. Evaluated on the Chapman-Shaoxing 12 lead dataset, by the use of Convenlutional Neural Networks based architectures, the proposed approach achieved an encouraging F1 score of 91,10.

Keywords: Cardiac Arrythmia, Convolutional neural network, Signal processing.

# 1 Introduction

Cardiac arrhythmia is defined as any irregularity in the cardiac rhythm, indicating abnormal heart activity such as an irregular heart rate or irregular waveform [1]. Sudden Cardiac Death (SCD) is the leading cause of mortality [2] with arrhythmia being a major underlying cause [3]. Different types of arrhythmia require varying degree of urgency and intervention. For instance, while benign episodes of atrial fibrillation (AFib) may occasionally happen to healthy individuals, conditions like ventricular tachycardia (VT) and ventricular flutter (VFL) can be instantly fatal [4]. Clinically, the presentation of arrhythmia differs widely, ranging from asymptomatic cases to severe symptoms such as palpitations, breathing difficulties, and dizziness [2]. Therefore, patients undergo electrocardiogram (ECG) recordings to monitor their cardiac cycle over a period of time that may span 10 seconds for a standard 12-lead ECG or extend to several days for continuous ambulatory ECG monitoring [5]. Diagnosing arrhythmia from ECG signals is an intricate process involving the analysis of signal deformation [6]. This task is a time-consuming and is performed by specialized physicians with broad specific knowledge [7]. Manual analysis is prone to errors, particularly in high-pressure emergency scenarios, considering the large morphological variances in the signals [8]. Hence, the crucial need for an accurate and automated system for arrhythmia detection and classification.

With the availability of large and annotated accessible datasets such as MIT-BIH [9], Chapman-Shiaoxing dataset, CPSC2018 dataset [10, 11], PTB-XL [12], a lot of research in the ECG classification and arrhythmia detection has been done. Most of them use Deep learning techniques, which have demonstrated superior efficiency and accuracy to experts' manual detection [13].

However, ECG records are generally affected by various noises and artifacts which can be caused by the patient breathing or movements. This adds an extra layer of complexity to the task. Additionally, most publically available datasets suffer from a certain degree of class imbalance, where certain labels are underrepresented [14]. This issue, may bias deep learning models prediction and limits their ability to generalize. Addressing these additional challenges, is crucial to accurately classify ECGs.

In real-word scenarios, patient often have multiple overlapping arrhythmia [15] and with the proliferation of pathologies, the number of possible label combinations grows which increases the difficulty of the task. Therefore, most existing studies have focused on detecting a single abnormality from ECG signals, while multi-label ECG classification has received comparatively limited attention in the literature [16].

# 2 Related works

This section is a review of single label classification approaches to lay the foundational methods and then transition to a discussion of emerging multi-label techniques that more accurately reflects the complexity of real diagnoses.

## 2.1 Single label Approaches

Due to the nature of the problem, most studies use convolutional neural networks (CNN) and long short-term memory network (LSTM) based models [17]. The approaches differ in the model architecture and data processing techniques.
Generally, existing studies can be categorized into CNN-based methods and CNN-LSTM approaches.

### 2.1.1 CNN-based models

Convolutional networks are widely used for their ability to extract relevant features and capture complex dependencies. They have proven their effectiveness in ECG analysis and arrhythmia classification. Zhang et al [18], implemented a uni-dimensional CNN on de-noised single-lead ECG signals, using a wavelet transform for preprocessing. Similarly, Wu et al [19] designed a 12-layer uni-dimensional CNN, utilizing wavelet-based preprocessing and oversampling algorithms on under-represented classes, to help the classifier to generalize.
To improve CNN performance, Sadeghi et al. [20] introduced SE-Residual blocks and a self-attention mechanism for detecting left bundle branch block (LBBB). Their approach improved the accuracy and ensured robustness, by : appling Z-score normalization, addressing amplitude scaling issues, and standardizing all signals to a fixed duration.

While the ECG signal is a uni-dimensional input some studies treats it as an image rather than a signal. Huang et al. [21], transformed TF spectrograms extracted from ECG beats into spectrogram images using short-time Fourier transform (STFT). These images where presented as inputs to 2D CNN. Degirmencia et al [1] converted segmented ECG signals into 2-dimensional grayscale images by plotting the time-amplitude waveform of each beat, the image in result is used as an input for CNN model.

### 2.1.2 CNN-LSTM-Based models

To capture both spatial and temporal dependencies in ECG signals, several studies have combined CNNs with recurrent networks, particularly LSTM and bidirectional LSTM (BiLSTM). Hybrid models aim to combine the strength of CNN feature extraction ability with LSTM's temporal pattern modeling.

Yao et al. [22], also proposed an attention-based time-incremental CNN, designed to handle varied-length records. Their model preserves spatial and temporal characteristics of ECG signals with the integration of a CNN and recurrent cells.

Petmezas et al. [23] proposed a CNN-LSTM model, where the convolution output is fed into the LSTM network. To minimize the class imbalance impact on the model's learning, they employed Focal Loss (FL) which reduces the impact of dominant classes. Chopannejad et al. [24] introduced a CNN-BiLSTM-BiGRU model with a multi-head self-attention mechanism. Their approach also incorporated sequential denoising (Butterworth filtering, LOESS, and Non-Local Means) and SMOTE Tomek resampling to improve performance on imbalanced data.

## 2.2 Multi label approaches

Cheng et al. [25] proposed a classification algorithm named Encoder-Decoder Dynamic Graph Convolutional Network (ED-DGCN). In their approach, a CNN serves as an encoder for feature extraction, while an LSTM functions as a decoder to identify important regions in the signal and capture class relationships. It incorporates a dynamic graph convolutional network that constructs a dynamic adjacency matrix providing a representation of label dependencies. This method was evaluated on the China Physiological Signal Challenge 2018 (CPSC2018) dataset which contains 8 pathologies. Additionally, to improve accuracy, the authors used transfer learning by pre-training their network on a large dataset. Eventually reporting an F1 score of 0.843.

Zheng et al. [26] used a two stages deep learning model combining CNN, BiLSTM, and attention mechanisms. The first stage performs abnormality detection while the second stage is designed for multi-label classification. Their model is tested on proprietary dataset provided by wearable ECG monitoring devices and the authors also provided result on the benchmark MIT-BIH database. They achieved F1 score of 0.736.

Cheng et al. [27], focused on feature representation through a Lead Feature Guide Network (LFG-Net), designed to enhance classifier performance by emphasizing the most informative features. Their network selected each feature and identify their contribution with the shapely Additive explanations (SHAP) method. They obtained F1 score of 0.842 using the CPSC2018 dataset.

Cai et al. [28], proposed Multi-ECGNet, a model that utilize all 12 ECG leads and integrates a ResNet-based backbone with depthwise separable convolutions from the Xception model and Squeeze-and-Excitation (SE) modules to enhance feature fusion. Their approach was evaluated on the the 2019 Tianchi Hefei High-Tech Cup ECG Human-Machine Intelligence Competition dataset, achieving a micro-F1-score of 0.863.

In this study, a multi-input deep learning architecture is proposed to treat the multi-label ECG arrhythmia classification. The model is composed of two sub-networks, each targeting distinct but important aspects of the ECG. The first sub-network is a CNN-based model that processes domain-specific features: morphological features, temporal features and Heart Rate Variability (HRV) descriptors extracted individually from all 12 pre-processed leads. This branch captures inter-lead relationships that are important for accurate diagnosis.

The second sub-network operates directly on the raw signal of lead II. The model architecture is formed of uni-dimensional CNNs and bidirectional LSTM, enhanced with an attention mechanism to dynamically focus on the most informative regions. This stream aims to preserve fine-grained waveform dependencies and dynamics that might be neglected in high-level feature extraction.

The outputs from both sub-networks are used to perform multi-label classification across 11 co-occurring arrhythmias.

The used approach combines both engineered features across all leads with raw signal information from a clinically relevant lead, the proposed architecture jointly exploits structured inter-lead features and unprocessed waveform data, offering a certain degree of interpretability and high precision.

# 3 Materials and methods

## 3.1 Dataset description

The Chapman-Shaoxing dataset [11] is a collection of 10 seconds 12-lead ECG recordings sampled at 500hz from 45,152 patients. The signals were recorded over multiple days and sessions under the supervision of Chapman University, Shaoxing People's Hospital and Ningbo First Hospital. A sample of the 12 lead recording is displayed in figure 1.

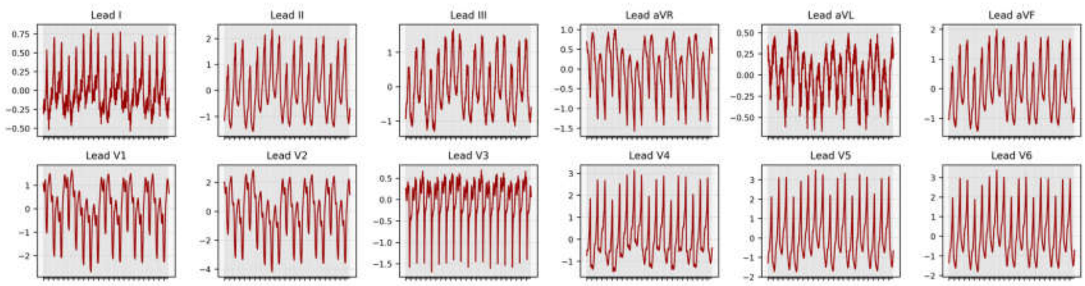


*FIG. 1 : Illustration of a raw 12-lead ECG signal from the Chapman–Shaoxing dataset.*

The dataset follows a multi-label structure that can have up to 11 simultaneous diagnostic labels with the following distribution as shown in figure 2.

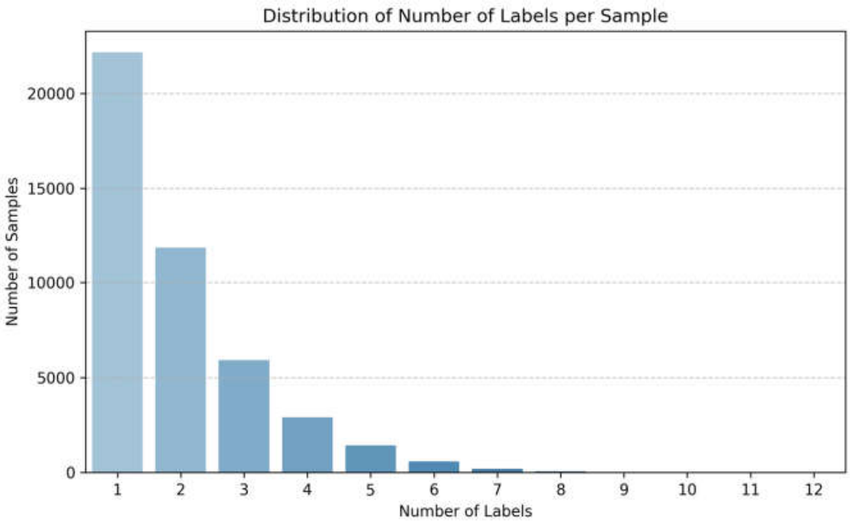


*Fig 2: Distribution of simultaneous arrhythmia labels.*

## 3.2 Pre-processing

During ECG acquisition, the signal is often impacted by multiple types of noise, which can result from several sources, including patient movements, breathing, and the instability of electrode-skin interaction. These external noises deteriorate the signal quality which complicate the detection of key intervals and important waveform regions. As a result, the overall diagnostic process becomes more complex and less reliable. To reduce these interferences, the raw ECG signals were passed through a series of processing steps to improve their quality and increase their reliability of subsequent analysis.

**High-pass filter**

In ECG signal processing, a Butterworth High-pass filter given by Eq. 1, is often used to remove unnecessary frequency components [29]. It primarily helps by eliminating low-frequency baseline wander and reducing high-frequency noise. Baseline wander usually comes from patient movement or breathing which appears as a slow drifting in the signal's baseline [30]. To address this, high-pass filters are typically used with a cutoff frequency set around 0.5 Hz.

$$H_{\mathrm{HP}}(s) = \frac{s^n}{s^n + \omega_c^n} \tag{1}$$

- $H_{\mathrm{HP}}(s)$: Transfer function of the high-pass filter.
- $s$: Complex frequency variable, defined as $s = j\omega$, where $\omega$ is the angular frequency in radians per second.
- $n$: Order of the filter.
- $\omega_c$: Cutoff angular frequency (in radians per second), calculated as $\omega_c = 2\pi f_c$, where $f_c$ is the cutoff frequency in hertz (Hz).

**Notch filters**

Notch filters as defined in Eq. 2, are typically employed to reduce narrow band interference, such as power line noise at 50 or 60 Hz and its harmonics. These disturbances usually originate from nearby electrical devices or power supplies and can significantly overlay with essential components of the ECG signal, such as the QRS complex [30]. Notch filters improve signal quality by attenuating these specific frequencies while maintaining the nearby signal content.

$$H_{\text{Notch}}(s) = \frac{s^2+\omega_0^2}{s^2+\frac{\omega_0}{Q}s+\omega_0^2} \tag{2}$$

- $\omega_0$: Notch frequency (rad/s), e.g., $2\pi \times 50\,\text{Hz}$.
- $Q$: Quality factor (higher $Q$ = narrower stop band).

**Low pass filter** In signal processing, Low-pass filters expressed with Eq. 3 are widely used to attenuate high-frequency noise which can be caused by muscle activity, motion artifacts, electromagnetic interference, poor electrode contact, and human voice disturbances. [30].

$$H_{\text{LP}}(s) = \frac{\omega_c^n}{s^n+\omega_c^n} \tag{3}$$

- $s = j\omega$: Complex frequency variable ($\omega$ is the angular frequency in rad/s).
- $n$: Filter order.
- $\omega_c = 2\pi f_c$: Cutoff frequency (rad/s), where $f_c$ is the cutoff frequency in Hz.

Finally, the resulting signal was normalized to reduce its complexity.
Figure 3 illustrates the signal at each stage of the filtering process.

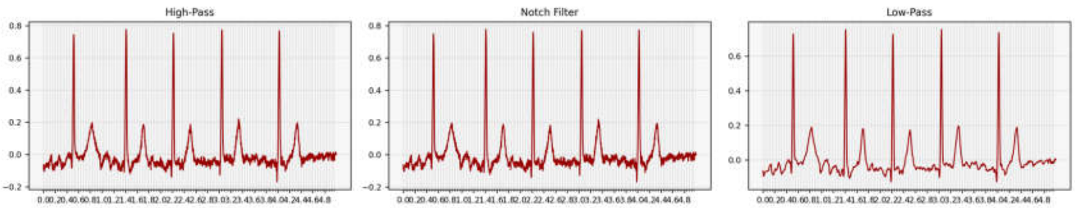


*Figure 3: Ten second segment of Lead II illustrating the main pre-processing steps.*

The figure shows the impact of the high-pass, notch filter and low-pass

## 3.3 Feature extraction

In this work, features were extracted following a logic inspired by the clinical analysis of ECG signals. Features were synthesized into three main groups: morphological features, temporal features and heart rate variability (HRV) features.
These categories were derived based on key components of the cardiac cycle presented in figure 4.

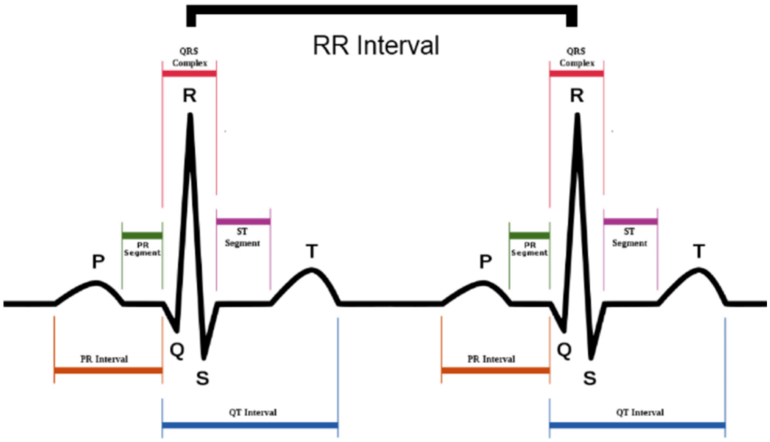


*Figure 4 : Annotated cardiac cycle showing the main ECG waveform components : the P wave, QRS complex, and T wave.(Jatmiko et al. 2019).*

**Morphological features**

These features describe the shape of P, R, and T picks and QRS complex. Each is essential in identifying specific cardiac abnormalities.

- P-Wave Amplitude: This wave reflects atrial contraction. An abnormal amplitude is a direct indicator of atrial enlargement, which associates with atrial fibrillation (AF) [32].
- R-Wave Amplitude: The R-wave is crucial for assessing ventricular depolarization. Variations in its amplitude may suggest conditions like ventricular hypertrophy [32].
- T-Wave Amplitude: T-wave abnormalities, including inversion, tall peaks, and flattening, can signal various arrhythmia, notably ventricular arrhythmia [32].
- QRS Fragmentation: This refers to abnormal notching in the QRS complex, representing the depolarization of the ventricles, this feature is the key marker of potential structural abnormalities [32].

**Temporal features**

This set of features describes the general rhythm and regularity, which physicians closely monitor since any deviations in these patterns can indicate a potential arrhythmia.

- QRS Duration : This measurement refers to the duration of the QRS complex. Prolonged QRS duration is usually a sign of conduction delays or heterogeneous ventricular activation, which in turn may provide a basis for arrhythmia detection [32].
- QT Interval : This interval measures the time from the start of the Q wave to the end of the T wave, corresponding to the complete electrical depolarization and re-polarization of the ventricles. It is often associated with a high risk of ventricular arrhythmia [32].
- Heart Rate : This is derived from the timing of R-peaks and often serves as often as a first indicator of arrhythmic events.

**HRV features**

HRV features are a measure of variability in heartbeat intervals that provides insights into cardiac regulations. Any compromise in this regulations will manifest with a reduced variability serving as a warning for heart conditions especially arrhythmia.

- RR Interval Statistics : These are statistical measures of the intervals between successive R-peaks. They capture both the central tendency with median and variability with standard deviation, inter-quartile range giving insights into the rhythmic stability of the heart. Given that many arrhythmia manifest with irregular RR intervals, these statistics are crucial for detecting rhythm abnormalities.

- Standard Deviation of Normal-to-Normal (NN) intervals (SDNN): The square root of the mean squared differences between successive NN intervals, providing insight into parasympathetic nervous system activity [33].

- pNN50: This feature represents the percentage of successive NN intervals that differ by more than 50 ms. Lower pNN50 values are linked with diminished parasympathetic activity and increased cardiovascular risk [33].

Frequency power is a crucial metric of abnormal HRV. For this reason, frequency power was computed at various band intensity.

- High-Frequency Power (HFP), computed within the high-frequency band, stand as a measure of vagal activity [33]. A substantial drop in HFP can be associated with multiple cardiovascular diseases, including arrhythmia.

- Low-Frequency Power (LFP), is the measure of the low-frequency band and reflects the influence of sympathetic and parasympathetic activity [33]. A low or an imbalanced LFP potentially signaling an increased risk of arrhythmia.

- Very Low Frequency Power (VLFP) measuring the power within the very low frequency band of the HRV spectrum, it offers insights into variation in long-term regulatory mechanisms.

To reinforce the feature set and have a better understanding of the signal variability, wavelet coefficients were added. These coefficients are obtained through wavelet decomposition by analyzing the ECG signal in RR intervals. They capture premature beats or sudden changes that are common in arrhythmia episodes.
Spectral metrics were also used to enhance the signal description.

- Spectral Entropy: Entropy will measure the disorder in signal, which indicates irregularities reflecting an arrhythmic state.

- Spectral Centroid and Bandwidth: Their value helps indicating change in the dominant frequencies of cardiac electrical activity, which are altered during arrhythmic events.

To portray, the complex and the non-linearity behavior of the cardiovascular activity. Several features based on non-linear dynamics were extracted.

- Detrended Fluctuation Analysis (DFA): DFA is used to quantify the fractal scaling identifies properties in a cardiovascular cycle that appear due to the underlying dynamics of the system. Changes in these patterns may indicate physiological pathology [34].

- Approximate Entropy(ApEn) : It measures the regularity and complexity of the signal and is insensible to noise. It assesses the conditional probability of repetitive patterns. It is a broadly used feature in ECG analysis to detect arrhythmia, due to its ability to reflect the complexity of the signal [35].
- Sample Entropy: It is calculated by assessing the estimating complexity across different data lengths. It helps assess autonomic nervous system regulation. A low SampEn is an indicator of a reduced signal complexity, a characteristic observed in patients with cardiac arrhythmias.

## 3.4 Model architecture

**Convolution in feature extraction** Convolutionnal networks, fundamental of deep learning, have shown their strength in the extraction of relevant features from raw data. Originally intended for 2-dimensional data particularly images as it is visualized in figure 5, they paved the way for one-dimensional CNNs designed for uni-dimensional (1D CNN) inputs [36].

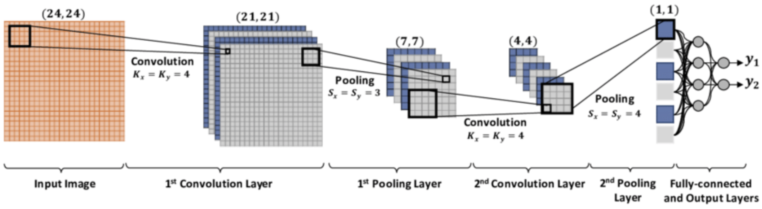


*Figure 5: CNN architecture use in image classification [36].*

Features extracted from all 12 pre-processed leads are reshaped into a matrix and then processed by CNNs to detect inter-lead dependencies. In parallel, the raw signal from the second lead is treated using 1D CNN. This specific lead was selected for its clear view of the important waves [37] and its elevated variance.
Batch normalization is applied at the end of each convolutional layer to help stabilize and speed up training.

**Bidirectional Long Short-Term Memory (Bi-LSTM)** The extracted feature vector, obtained through convolutional extraction, is fed into a Bidirectional Long Short-Term Memory (Bi-LSTM) network whose architecture is presented in figure 6, which has proved his strong effectiveness in analyzing sequential features in ECG signals [38]. While standard LSTM networks are well adapted for diverse time-series problems due to their ability to capture long-term dependencies, the Bi-LSTM extends this capability by processing the sequence in both forward and backward directions. The model feeds the input into two separate LSTM layers, each responsible for a direction. Resulting in a better sequence modeling and often out-performing the classical LSTM [39].

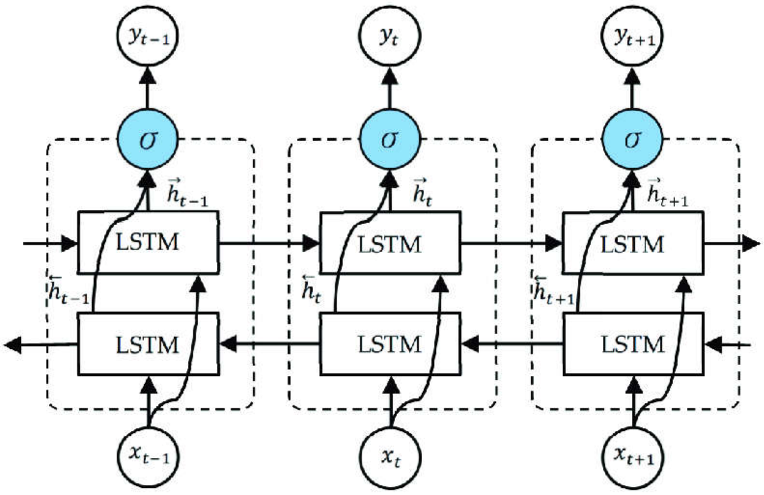


*Figure 6: Illustration of the Bidirectional LSTM (Bi-LSTM) architecture [40].*

**Additive Attention (AA)**

Additive attention is a technique that compute a weighted combination of a given input. It is formed of a one-hidden layer feed-forward network to calculate the attention score [41]. Mathematically, additive attention is expressed with Eq. 4:

$$c_i = \sum_{j=1}^{T_x} \alpha_{ij} h_j \tag{4}$$

Where $c_i$ is the context vector for the $i$-th output element, $h_j$ is the hidden state of the $j$-the input element, and $\alpha_{ij}$ are attention weights calculated following Eq. 5:

$$\alpha_{ij} = \frac{\exp(e_{ij})}{\sum_{k=1}^{T_x} \exp(e_{ik})} \tag{5}$$

with $e_{ij}$ computed using a small neural network using a sigmoid function as presented in Eq. 6:

$$e_{ij} = v_a^T \tanh(W_a s_{i-1} + U_a h_j) \tag{6}$$

$s_{i-1}$ here, represents the previous hidden state, and $W_a$, $U_a$, and $v_a$ are learnable parameters.

**Fully connected layers** The outputs from each processing branch are combined and fed into a fully connected neural network for multi-label classification. Dropout layer is used to minimize the risk of overfitting. By periodically deactivate a subset of neurons, it prevents the model from relying on the interdependence between neuron [42], which improves the model's generalization. The complete architecture is summered up by figure 7 bellow:

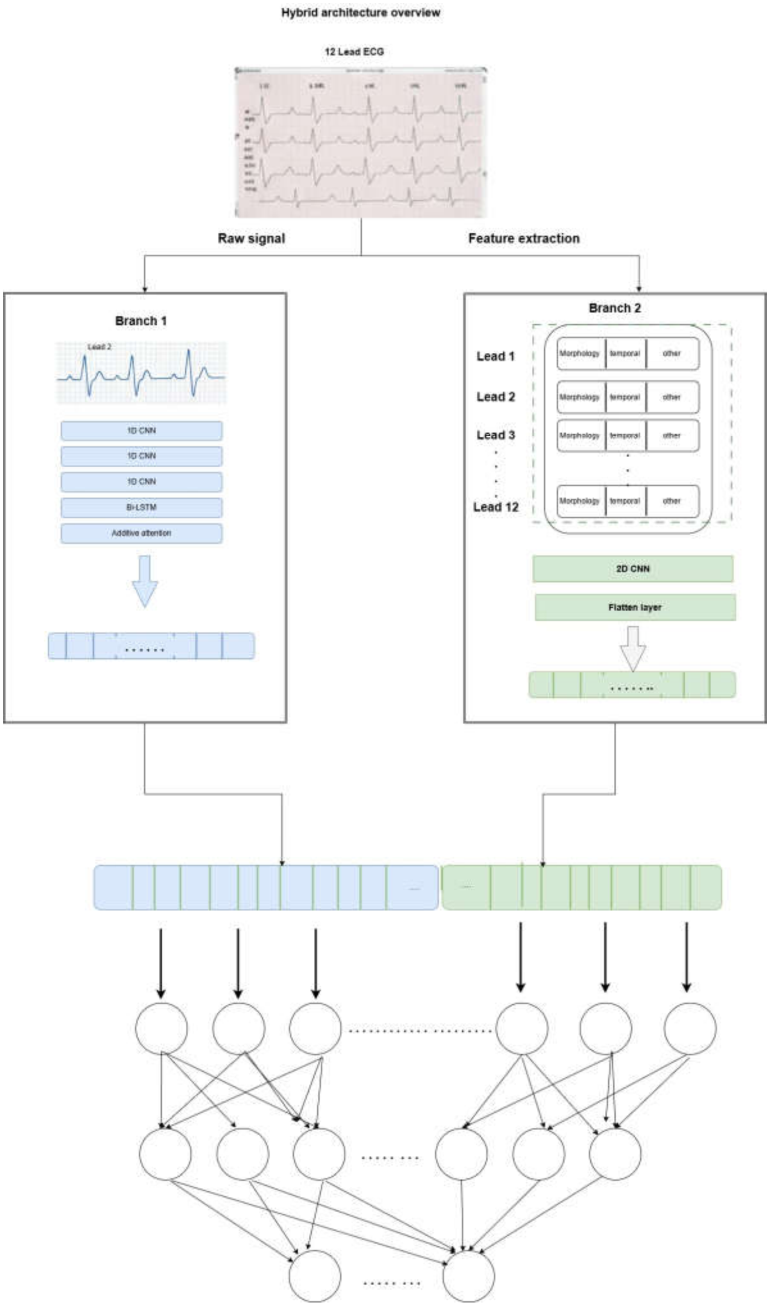


*Figure 7: Overview of the complete processing pipeline on pre-processed waveforms.*

## 3.5 Training setup

The model was trained using the Adam optimizer [43] with default learning rate settings. For this multi-label classification task, binary cross-entropy was used as the loss function. Training was performed for 30 epochs with a batch size of 128, and early stopping was applied to prevent overfitting. Since each sample originates from a unique individual, no patient-level data leakage occurs, making a randomized 80/20 split for training and validation safe to use.

## 3.6 Evaluation and performance

**Evaluation metric**

In this study, the F1 score is adopted as the primary evaluation metric. Although accuracy has been considered the standard measure when judging a model performance in classical single-label classification tasks [44], its relevance in the multi-label context is limited because it evaluates whether the predicted label set exactly matches the desired label set, which is inherently difficult to achieve. The difficulty increases when dealing with imbalanced datasets which is often the case for multi label dataset. F1 score gives a more nuanced view by balancing precision and recall, which makes it more adapted for multi-label classification, where partially correct prediction is meaningful. The F1 score for a single label is defined as:

$$\mathrm{F1} = 2 \cdot \frac{\mathrm{Precision} \cdot \mathrm{Recall}}{\mathrm{Precision} + \mathrm{Recall}}$$

where:

$$\mathrm{Precision} = \frac{TP}{TP + FP} \quad \text{and} \quad \mathrm{Recall} = \frac{TP}{TP + FN}$$

$TP$ represents true positives, $FP$ false positives, and $FN$ false negatives.

Macro-F1 score computes the F1 score for each label and then averages them. This treats all labels equally and guarantees that the model's performance remains balanced for both frequent and rare labels [45].

Wu et al. [45] linked this metric to margin maximization equation 7:

$$\gamma_{\mathrm{inst}}^{j} = \min_{a \in Y_{\cdot j}^{+},\, b \in Y_{\cdot j}^{-}} \left[ f_j(x_a) - f_j(x_b) \right] \tag{7}$$

It measures separation between positive ($Y_{\cdot j}^{+}$) and negative ($Y_{\cdot j}^{-}$) instances for a label. Maximizing this margin optimizes macro-F1, which reflects the model's ability to generalize across the entire label space.

**Performance**

Different architectures were evaluated after splitting the dataset, and the results are displayed in Table 1.

*Table 1: Comparison with Existing Methods.*

| **Architecture** | ***F1 Score*** |
|---|---|
| + 2 × 1D CNN + LSTM | 85.6% |
| + 2 × 1D CNN + BLSTM | 88% |
| + 2 × 1D CNN + BLSTM<br>+ SqueezeExtraction Attention | 89.7% |
| **Proposed Model** | **91.10%** |

The obtained results from the proposed approach are compared to those of recent state of art work as presented in Table 2:

*Table 2: Comparison with Existing Methods.*

| **Method** | ***F1 Score*** |
|---|---|
| Zheng et al. (Zheng et al. 2024) | 73.6 |
| Cheng et al. (Cheng, Li, et al. 2024) | 84.2 |
| Cheng et al. (Cheng, Zhu, et al. 2024) | 84.3 |
| Cai et al. (Cai et al. 2020) | 86.3 |
| The proposed approach | **91.10** |

From table 2, the proposed approach proposes a F1-score greater than the other ones, which confirms that the approach is confident.

# 4 Conclusion

In this work, a novel approach for multi-label arrhythmia classification based on 12-lead ECG signals is proposed. Combining both signal analysis on lead II and domain-specific features extracted from all 12 leads, enables the model to leverage inter-lead and intra-lead dependencies increasing its interpretability and performance. To this end, a multi-input deep learning architecture is developed, consisting of two parallel sub networks: one for raw signal processing and the other dedicated to simultaneous 12 lead analysis.

The model was trained and evaluated on the Chapman-Shaoxing ECG dataset. A dual-branch convolutional neural network (CNN) and 1D CNN-BiLSTM-AA outperformed the other models, with an F1-score of 91.10.

These results are particularly encouraging given the complexity of the task caused primarily by the imbalanced data and the wide variability of arrhythmic conditions, mirroring the complexity encountered in real-world clinical scenarios. These results prove that the model can serve as a valuable decision aided system for supporting both specialists and non-specialists in making quick and accurate clinical decisions.

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