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AI-Enhanced ECG Diagnosis System for Myocardial Infarction with RBBB: Constant-Q Transform and ResNet50 Integration

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Abstract Myocardial infarction, more commonly referred to as heart attack, is a significant cause of mortality related to cardiovascular diseases. Conduction disorders are commonly associated with this condition, the most prominent being RBBB. RBBB refers to an anomaly in electrical conduction of the heart, which can cause distortions to standard ECG patterns. Both of these can mask and mimic the classical ECG signs of MI and therefore result in misdiagnosis or delayed diagnosis. Moreover, early and accurate diagnosis is very important in saving patients from MI with a good prognosis; hence, it becomes a prime concern for the clinician. In this work, a novel approach to the accurate classification of ECG signals has been proposed with a Q-transform deep learning model of horizontal data concatenation. This study focuses essentially on the differentiation of myocardial infarction from RBBB-associated myocardial infarction. Further, the proposed model uses collective information from various ECG leads, drastically improving its capability to capture intricate cardiac patterns. In addition, the proposed model harnesses the unique electrical signatures of MI and MI with RBBB, which may manifest differently between leads. By merging multi-lead data and spectral-temporal features, the proposed model gains a comprehensive understanding of these conditions and leads thus to a substantial improvement in diagnostic accuracy. However, publicly available digital PTB-XL datasets are also used for the evaluation of the suggested architecture, where the ECGs are categorized into two classes: MI and MI associated with RBBB. In this regard, this system demonstrates exceptional performance, achieving an impressive 97. 82% precision and an exceptionally low 0.0032% training loss after 100 trained epochs. Stringent 10-fold cross-validation reinforces and strengthens these results. This groundbreaking approach simplifies diagnostic complexities by consolidating 12-lead ECG data and using CQT for precise analysis in the time-frequency domain.

Keywords ECG signals, myocardial infarction, right bundle branch block, ResNet50, 2D ECG representation, Constant-Q Transform.

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1. Introduction

Cardiovascular diseases are an important contributor to global mortality, accounting for a substantial number of annual deaths [1]. Projections signal a troubling surge in these fatalities, potentially reaching alarming numbers by 2030 [2]. Within this spectrum of diseases, Acute Myocardial Infarction (AMI) holds particular severity. Similar to other triggers of irregular depolarization, right Bundle Branch Block (RBBB) induces repolarization anomalies that might obscure or imitate ischemic changes, especially noticeable in right-sided precordial leads displaying RSR patterns. However, the concept of appropriate discordance can serve as a guiding principle to navigate through these complexities. The key feature lies in the discordance between the main part of the QRS complex and the initial section of the ST segment/T wave, positioning them on opposing sides of the isoelectric baseline. Consequently, in right to mid-precordial leads, a predominantly positive QRS complex will correspond with ST-segment depression and an inverted T wave. Any deviation from this norm would reveal ST-segment elevation,

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aligning with the main part of the QRS complex; changes in T-wave patterns can vary, either sustaining inversion or becoming indistinguishable within the larger ST segment. Identifying an anterior wall ST-elevation myocardial infarction (STEMI) becomes more evident when the healthcare provider is comfortable discerning the appropriate appearance of the ST segment in the context of the right bundle branch block (RBBB) [3]. Diagnosing RBBB poses challenges in detecting important ECG markers, potentially obscuring vital indicators. Consequently, healthcare practitioners employ supplementary tools such as evaluating symptoms, reviewing medical history, and utilizing imaging techniques like echocardiography. However, manual interpretation of ECGs can be intricate and prone to variability, particularly in remote locations or emergency situations [4]. Recent studies have delved into the realm of artificial intelligence (AI) and deep learning methodologies to enhance the diagnosis of myocardial infarction (MI) by leveraging 12-lead electrocardiograms (ECGs). In [5], researchers initiated noise reduction in ECG data and implemented the ML-ResNet network for MI detection. However, the intricacies of this method presented significant challenges. Conversely, [6] employed ResNet-50, a deep learning model, for medical image analysis. They transformed 12-lead ECG data from Chapman University and Shaoxing People's Hospital into scalogram and grayscale images. Their innovative approach involved a stacking ensemble technique incorporating logistic regression, support vector machine, random forest, and XGBoost as the meta learner. They introduced a "multi-modal stacking ensemble" by combining predictions from scalogram and ECG grayscale images. Meanwhile, [7] developed a specialized MI detection model emphasizing feature fusion.

Our research addresses these challenges by integrating data from all 12 ECG leads, streamlining the diagnostic process and providing a more comprehensive representation. A key novelty of this work lies in the preprocessing step, where we horizontally concatenate the leads before applying the Q transform. This approach generates a new time-frequency representation, allowing us to retain a greater number of samples compared to using individual leads. By doing so, we provide the pre-trained model with a more detailed and enriched representation of the signal. This enhanced representation captures critical spectral characteristics, improving the accuracy of myocardial infarction (MI) diagnosis. As we will discuss in the related work, this method addresses the limitations of single-lead analysis and contributes to better patient outcomes by reducing the risk of misdiagnosis.

The motivation for this study stems from the persistent difficulty of accurately detecting myocardial infarction (MI) in the presence of conduction abnormalities such as right bundle branch block (RBBB), a problem frequently encountered in clinical practice but inadequately addressed by conventional deep learning methods. The main contributions of our paper are as follows: (1) We propose a novel horizontal concatenation strategy for 12-lead ECG signals, enabling the preservation and integration of temporal and spatial information across all leads; (2) We employ the Constant-Q Transform (CQT) to generate rich time-frequency representations, enhancing the detection of subtle pathological changes; (3) We design and train a ResNet-50-based deep learning model tailored to multi-lead ECG data, achieving robust performance on the large-scale PTB-XL dataset; (4) We provide a thorough evaluation using rigorous cross-validation and clinical metrics; and (5) We curate and make transparent a well-annotated, clinically relevant ECG dataset, encouraging reproducibility and future research. Collectively, these innovations advance the state of the art in automated ECG-based MI detection, especially in complex diagnostic scenarios involving RBBB.

Our key contributions can be summarized as follows:

- Addressing complexity through data concatenation from all 12 leads.
- Following the removal of noise from the 12-Leads signals, the 1D ECG signals undergo a process of horizontal concentration.
- We adopt the CQT algorithm to convert the 1D ECG signal into a 2D time-frequency representation, which is then input into the pre-trained ResNet50 CNN model.

The article will be organized as follows: Section 2 reviews related work on the detection of ECG-based myocardial infarction. Section 3 describes the proposed methodology, including database selection, preprocessing, and data transformation. Section 4 details the mathematical evaluation of time-frequency representations and the model architecture. Section 5 presents the performance evaluation and experimental results. Finally, Section 6 concludes the paper and discusses.

2. A brief review of existing methods

AI technology has played an important role in ECG analysis methods recommended for heart disease diagnosis. These investigations focused on the electrocardiogram signal processing , starting with signal processing, feature detection, and classification. The ECG analysis has regarded the employment of machine learning and deep learning algorithms in terms of both accuracy and efficiency[8][9][10]. The researchers have also targeted artificial intelligence adoption in image analysis for the ECGs, which has shown very positive results in screening and identifying cardiac anomalies[15]. Improvements like AI-based ECG analysis may be the mother of new remote ECG monitoring systems or revamped telemedicine solutions which will also provide an accurate and fast identification of cardiovascular illnesses[8][11]. In particular, some studies use a multi-lead residual neural network model, a multi-branch fusion network, and a convolutional neural network with a multiple-feature branch in contrast to the MI from normal ECG signals. The authors applied an initial noise reduction to the ECG data. The ML-ResNet network has been harnessed to detect and pinpoint myocardial infarction (MI). This network architecture encompasses a total of 13 layers, integrating a distinctive lead feature branch within its structure. Specifically, this single feature branch is composed of three residual blocks, each containing three convolutional layers. However, it's important to note that this approach encounters a challenge in terms of complexity, as it involves a substantial number of parameters that need to be carefully managed and optimized. Similarly, [14] adopts a 1D-ECG signal within a deep learning framework for MI diagnosis. The MFB-CNN approach involves 12 independent feature branches, each operating on a single lead from the 12-lead ECG. This study introduces an innovative method for the detection and localization of automated myocardial infarction (MI) using 12-lead electrocardiogram (ECG) data. The Multiple-Feature-Branch Convolutional Neural Network (MFB-CNN) capitalizes on the integrity and diversity of ECG signals, as each feature branch captures distinct lead-related data. The integration of these features through a global softmax layer obviates the necessity for manual feature crafting. However, a notable challenge arises due to the high complexity when dealing with the separate analysis of 12 leads. In contrast, the study [13] introduces a model tailored for myocardial infarction detection using 12-lead electrocardiogram (ECG) images. Their proposed methodology encompasses a multi-branch network, feature fusion, and a classification network. Following thorough experimentation, they opted for a shallow CNN as the multi-branch network to extract features from individual leads. The fusion of feature maps was accomplished through depth fusion, and these integrated features were subsequently channeled into a classification network founded on the DenseNet architecture. The resultant model exhibited exceptional sensitivity and specificity in the realm of myocardial infarction screening. Nonetheless, a notable drawback of this approach lies in its complexity, and there's a lack of data preprocessing incorporated within the method. Further advances include [14], which introduces an innovative approach to medical diagnosis using ResNet-50 for the automatic classification of 12-lead ECG data encompassing multiple cardiovascular diseases, They presented an efficient DL model designed for the automatic diagnosis of 12-lead electrocardiogram (ECG) signals categorized into 27 classes. These classes include 26 different types of CVD and a normal sinus rhythm. The proposed model is built on the Residual Neural Network (ResNet-50) architecture and is evaluated through experimentation using combined public databases from the USA, China, and Germany as a proof of concept. In [22], the authors applied the ECG data to undergo an initial noise reduction. The ML-ResNet network has been harnessed to detect and pinpoint myocardial infarction (MI). This network architecture encompasses a total of 13 layers, integrating a distinctive lead feature branch within its structure. Specifically, this single feature branch is composed of three residual blocks, each containing three convolutional layers. However, it's important to note that this approach encounters a challenge in terms of complexity, as it involves a substantial number of parameters that need to be carefully managed and optimized. Similarly, [23] adopts a 1D-ECG signal within a deep learning framework for MI diagnosis. 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The application of deep learning in medical image analysis, particularly ResNet-50, is shown in [27], where the study conducted experiments utilizing 12-lead electrocardiogram (ECG) databases sourced from Chapman University and Shaoxing People's Hospital. To fine-tune the pre-trained ResNet-50 model for each lead, the ECG signals were transformed into scalogram images and grayscale images of the ECG. The ResNet-50 model served as the base learner for a stacking ensemble method. The meta learner, used for combining predictions from the base learner, employed logistic regression, support vector machine, random forest, and XGBoost. This study introduced a novel approach termed "multi-modal stacking ensemble," which integrates predictions from two modalities: scalogram images and ECG grayscale images.

In this work, we introduce a novel preprocessing method by horizontally concatenating the 12 ECG leads before applying the Constant Q Transform (CQT). This approach generates a comprehensive time-frequency representation that retains more samples compared to using individual leads. The enriched representation enhances the ability of our ResNet-50 model to detect myocardial infarction (MI), especially in cases involving left bundle branch block (RBBB), which primarily affects the lower frequency spectrum. CQT is particularly effective in capturing critical spectral characteristics in these low-frequency ranges, outperforming linear methods. Additionally, CQT's flexibility in adjusting its frequency resolution allows for higher resolution in detecting pathological events like MI and lower resolution for normal beats. This multi-resolution capability is especially important for handling non-stationary ECG signals, offering a significant advantage over the Short-Time Fourier Transform (STFT) in detecting subtle changes in conditions such as MI and right bundle branch block (RBBB).

3. Contributions

We present a novel ECG diagnostic system that integrates a pre-trained model with the Constant-Q Transform (CQT), offering enhanced accuracy and efficiency in analyzing ECG signals. Illustrated in Fig. 1, our model's stages encompass signal preprocessing, concatenation of data from 12 leads in a horizontal format, CQT transformation, and the utilization of the ResNet50 model. This pioneering approach merges signal processing techniques with deep learning models to elevate ECG analysis, thereby fostering improved healthcare outcomes. Furthermore, the incorporation of k-fold cross-validation bolsters the credibility and reliability of our experimental findings, facilitating a comprehensive evaluation of the integrated ECG diagnostic system.

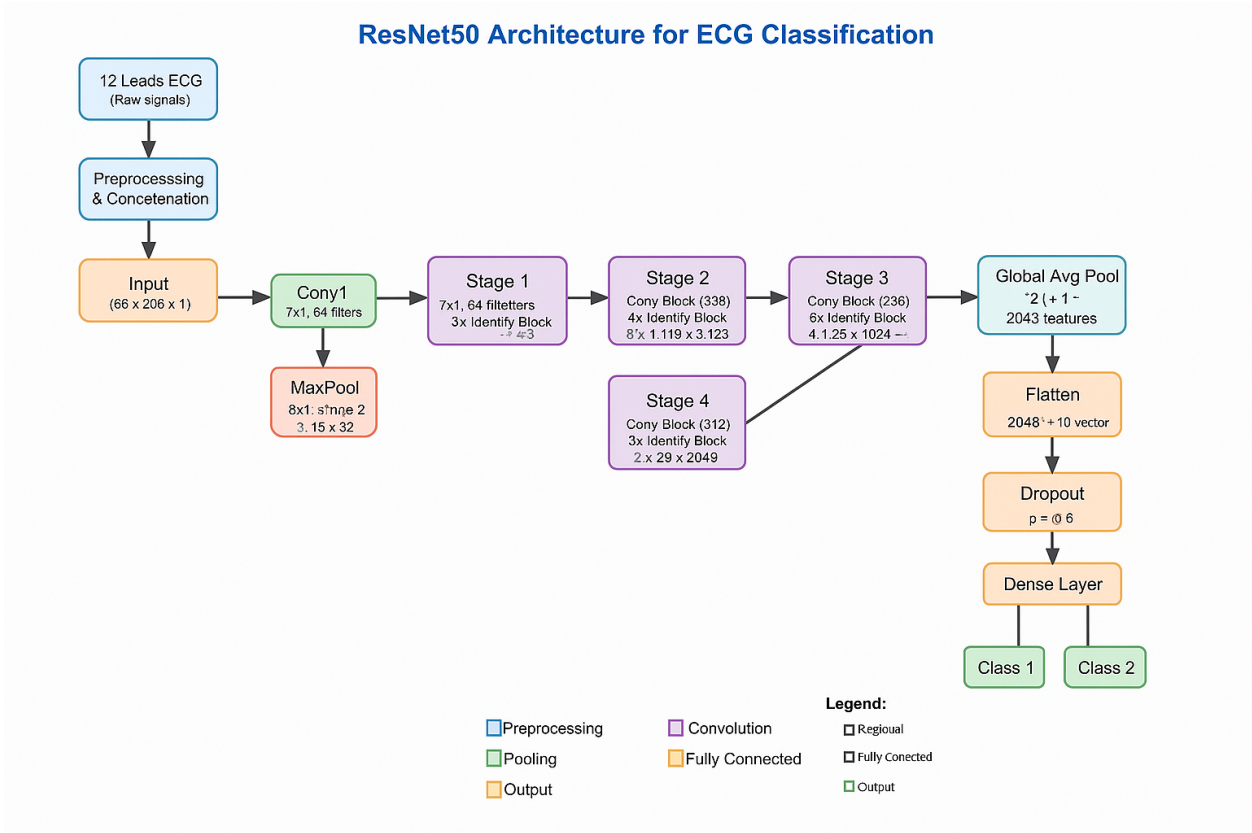


Figure 1. Our Model Architecture.

3.1. Database and preprocessing:

For this research, we obtained electrocardiograms (ECGs) from the publicly available PTB-XL database, which consists of 21799 clinical 12-lead ECG data from 18869 individuals, each lasting 10 seconds. from 18869 patients, 52% percent of whom are men and 48% percent of whom are women, ranging in age from 0 to 95 years. However, we only took ECG data from the MI categories. Our dataset includes simultaneous 12-lead ECG recordings from 445 individuals with MI who fell into one of two categories: MI without RBBB and MI with RBBB, which comprises ECG signals from 191 participants in both AMI and AMI associated with RBBB categories. The records last 10 seconds, are labeled by cardiologists. Most records may have multiple annotations, and the signal is sampled at 500Hz.[19] Table 1 summarizes all relevant information about the dataset used in this study However, ECG signals often suffer from various types of noise that can adversely affect the accuracy of the diagnostic results. These noise types include power line interference, baseline wander, and electrode contact noise, which

Table 1. Class distribution of MI categories in the study dataset.

Class	Description	Number of Samples
MI	Myocardial Infarction (without RBBB)	254
MI+RBBB	Myocardial Infarction with RBBB	191

must be adequately addressed before applying machine learning algorithms to diagnose MI. Thus, ECG signal denoising and preprocessing become a discriminative need [20]. In our study, we applies several filters to an electrocardiogram (ECG) signal to improve its quality.

- Firstly, a bandpass filter is applied to remove static noise and high-frequency noise. This filter uses a Butterworth filter of order 5 with a lowcut frequency of 0.5 Hz and a highcut frequency of 100 Hz.
- Next, a median filter with kernel size of 3 is applied to remove burst noise. The signal is then processed to remove baseline drift by subtracting the moving average of the signal using a window size of 0.2 seconds.
- Finally, any obvious outliers in the signal are detected and removed using Z-score thresholding. The resulting signal is then ready for further analysis or interpretation.Figure 1 visually depicts the difference between the Electrocardiogram (ECG) signal before and after preprocessing.

The original ECG signal is represented in blue, while the preprocessed ECG signal is shown in red (see Fig. 2). The outlier removal thresholds for ECG amplitudes ($> 2.0mV or < -2.0mV$) were selected based on clinical standards. According to the American Heart Association (AHA), the normal amplitude for the QRS complex typically does not exceed 2.5–3.0 mV in the limb leads. Values outside the ±2.0 mV range are considered physiologically uncommon and may represent noise or artifacts rather than true cardiac events [28]. Thus, these thresholds were used to filter out non-physiological values in accordance with established guidelines.

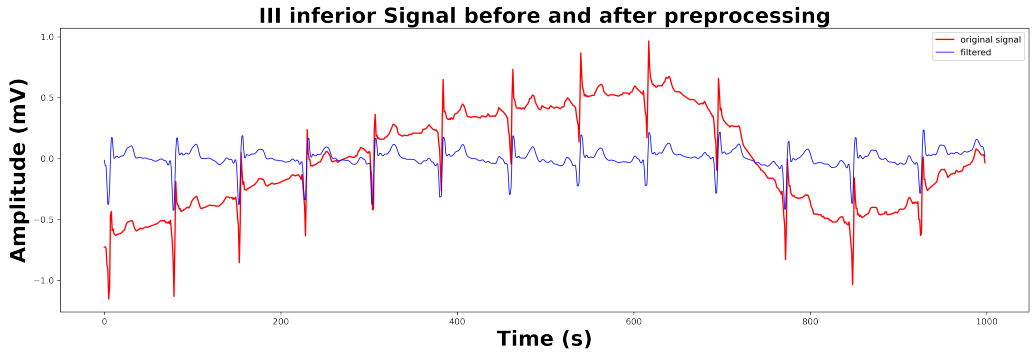


Figure 2. One lead ECG signal before and after preprocessing

3.2. 12-Lead Data Concatenation and 2D Transformation:

Horizontally concatenating the 12 ECG leads provides a consolidated representation of multiple leads within a single waveform, which proves valuable for both visualization and analysis. This approach allows for a more comprehensive assessment of interactions between leads, improving diagnostic accuracy. Let $X \in \mathbb{R}^{N\times 12}$ represent the raw multi-lead ECG signal matrix, where N is the number of time samples, and each column corresponds to one of the 12 leads. Horizontal concatenation across leads forms a unified signal:

$$X_{\text{concat}} = [x_1; x_2; \ldots; x_{12}] \in \mathbb{R}^{12N}$$

This operation ensures time-aligned integration of cardiac activity from multiple perspectives see fig 3.

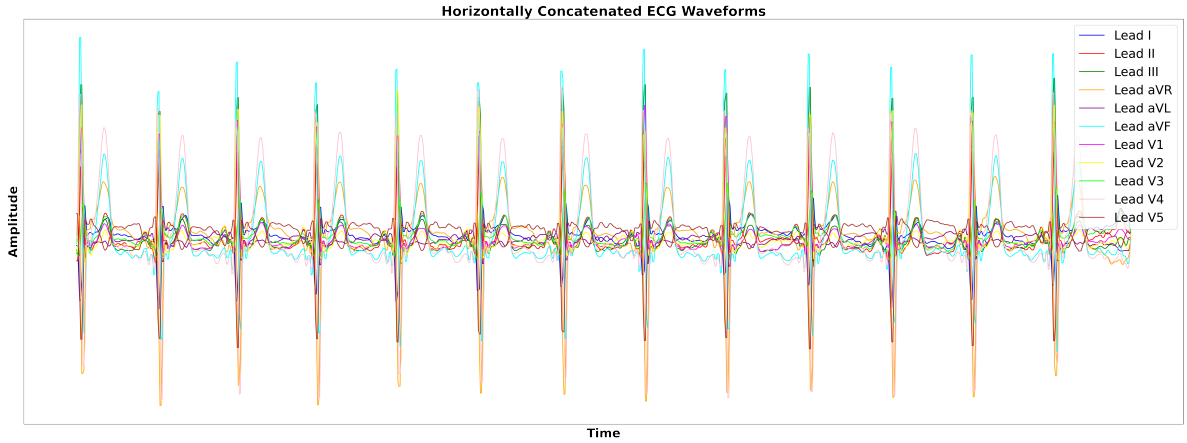


Figure 3. 12 lead ECG signal concatenation

By applying the Constant Q Transform (CQT) to ECG data, we can extract critical features with high precision, significantly enhancing the detection of cardiac conditions. CQT offers adjustable frequency resolution, making it particularly well-suited for analyzing non-stationary signals like ECGs. Lower-frequency components, often associated with pathological events such as myocardial infarction (MI), require higher frequency resolution, while higher-frequency components, associated with normal heartbeats, can tolerate lower resolution. This adaptability gives CQT a major advantage over the Short-Time Fourier Transform (STFT), which maintains a fixed resolution across all frequencies. Moreover, CQT's multi-resolution capabilities allow it to capture time-varying changes in ECG signals without sacrificing either time or frequency detail, which is critical for detecting subtle abnormalities related to conditions like MI and right bundle branch block (RBBB). as input, the model takes an ECG signal $X \in \mathbb{R}^{N*12}$ after the horizontal concatenation the new format of ower data is a matrix of N samples and 12 columns each column represent a lead. The perceptually motivated CQT [8] [9] approach to the spectro-temporal analysis of a discrete signal x(n) is defined by:

$$X_{CQ}(k,n) = \sum_{l=n-\lfloor \frac{Nk}{2} \rfloor}^{n+\lfloor \frac{Nk}{2} \rfloor} x(j) \cdot a_k^* \left(l - n + \frac{Nk}{2} \right) \tag{1}$$

This equation represents the computation of $X_{CQ}(k,n)$, which signifies the CQT coefficients for a given frequency scale k and time index n. The summation involves the signal $x(l)$ multiplied by the scale-related factor a_k and k within a specific range determined by N and k.

- n represents the sample index within the signal.
- k ranges from 1 to K and stands for the frequency bin index.
- $a_k(n)$ denotes the basis functions, which are functions of both n (sample index) and k (frequency bin index).
- The symbol $*$ denotes the complex conjugate operation.
- N_k refers to the frame length specific to the frequency bin k.

Within the framework of Continuous Wavelet Transform (CQT), the basis functions $a_k(n)$ are precisely outlined as complex-valued functions reliant on both the sample index n and the frequency bin index k. These functions hold significant importance in the decomposition of a signal into its constituent frequency components across varying time intervals. This decomposition proves instrumental in conducting analyses within the time-frequency domain, enabling a detailed examination of signal characteristics across both time and frequency axes. In the CQT context, the basis functions $a_k(n)$ are defined as complex-valued functions that depend on both the sample index n, and the frequency bin index k. These functions play the role of decomposing a signal into its frequency components across

different time intervals, facilitating analysis in the time-frequency domain. The basis functions $a_k(n)$ in the CQT are defined as Hann-windowed complex exponentials:

$$a_k(n) = w_k(n) \cdot e^{2\pi i f_k n / f_s} \tag{2}$$

where:

- $w_k(n)$ is the Hann window function for the k-th frequency bin,
- f_k is the center frequency of the k-th bin,
- f_s is the signal sampling rate,
- n is the sample index, $0 \leq n < N_k$,
- N_k is the window length for the k-th bin.

The Hann window is given by:

$$w_k(n) = 0.5 \left[1 - \cos\left(\frac{2\pi n}{N_k - 1}\right)\right] \tag{3}$$

for $0 \leq n < N_k$.

Table 2. CQT Parameters for ECG signal

Parameters	Value
Sampling rate (Hz)	500
$f_{\text{min}}(Hz)$	0.05
$f_{\text{max}}(Hz)$	100
Hop Length	64 samples
Bins per Octave	6

Formulae and Concepts:

1. **Frequency Range:** The CQT operates in a logarithmic frequency range from f_{min} to f_{max}. To calculate the number of frequency bins across this range, we use the formula:

$$N_{\text{bins}} = \text{Bins per Octave} \times \log_2\left(\frac{f_{\text{max}}}{f_{\text{min}}}\right)$$

Substituting the values:

$$N_{\text{bins}} = 6 \times \log_2\left(\frac{100}{0.05}\right) = 6 \times \log_2(2000) \approx 6 \times 10.96 = 65.76$$

Rounding this, we obtain approximately **66 frequency bins**.

2. **Time (Number of Frames):** The number of time frames depends on the length of the signal and the hop length. If the signal has a length of T samples, the number of frames N_{frames} is calculated as:

$$N_{\text{frames}} = \frac{T - 64}{64} + 1$$

For an input signal length of $T = 5000$ samples (10 seconds at 500 Hz), the number of time frames would be:

$$N_{\text{frames}} = \frac{5000 - 64}{64} + 1 = 78$$

3. **CQT Output Dimensions:**

- The **number of frequency bins** is 66 (as calculated above).
- The **number of time frames** is 78 (from the time frame formula).

- However, since we are stacking 12 ECG signals (one for each lead), the total number of time frames will increase by a factor of 12.

Final Dimensions: The resulting CQT spectrogram for the stacked 12 ECG signals will have:

- **66 frequency bins** (unchanged from the individual signal CQT output).
- **78 $\times$ 12 = 936 time frames** (since we are stacking the time frames of each of the 12 signals).
- **1 channel** (since the signals are concatenated along the time axis, forming a single spectrogram).

Thus, the **CQT output dimensions** for the stacked signals will be **66 x 936**.

Discrepancies in lead quality often result in variations in the extracted features and subsequent analyses. To mitigate this challenge, we adopted an innovative approach involving the horizontal concatenation of data from multiple leads prior to employing the CQT transform. This method aims to capitalize on the complementary information across leads, enhancing the overall signal quality. By merging the leads horizontally, the resultant signal gains an improved signal-to-noise ratio while reducing artifacts and noise present in individual leads. Consequently, upon applying the CQT transform to the concatenated signal, the extracted features demonstrate heightened consistency and reliability compared to those derived from individual leads. This methodology has shown promise across diverse signal analysis tasks, including classification or anomaly detection, where concatenating leads before the CQT transform has notably improved performance and accuracy. Fig. 4 visually depicts the distinctions between applying the Constant-Q Transform (CQT) to the horizontally concatenated 12-lead ECG signals, and shows the difference between MI and MI associated to RBBB.

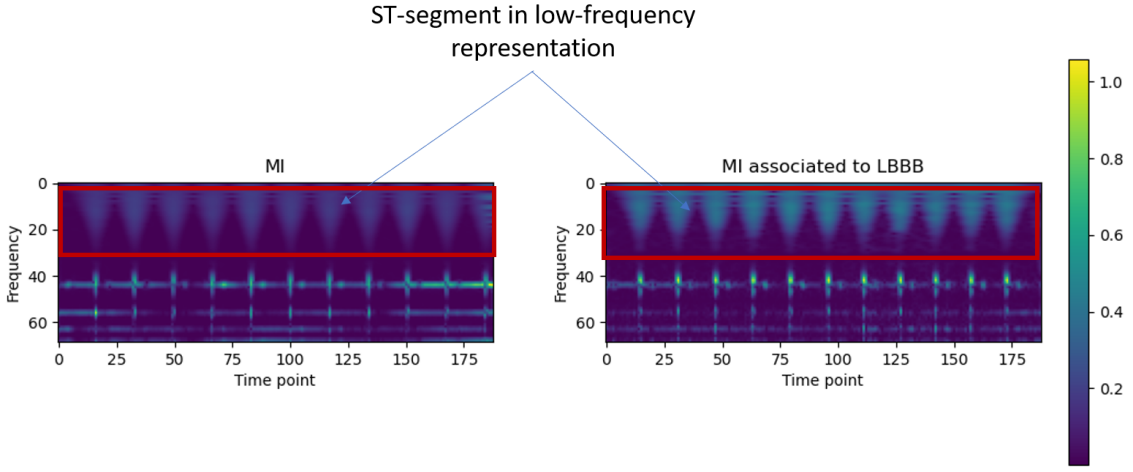


Figure 4. The difference between MI and MI associated to RBBB in time frequency domaine.

Mathematical Evaluation of Time-Frequency Representations

To quantify the spectral richness and complexity of our ECG representations, we employ two complementary metrics based on the Constant Q Transform (CQT), which provides superior time-frequency resolution compared to traditional Fourier-based methods, particularly for biomedical signals with non-stationary characteristics.

1. Mean Spectral Energy. The total energy is computed as:

$$E = \frac{1}{T} \int_0^T \int_0^F |\text{CQT}(x(t))|^2 \, df \, dt$$

This metric quantifies the average spectral power density across the entire time-frequency domain, where T represents the signal duration and F the frequency bandwidth. We compare the energy for:

- E_{single}: one lead ECG,
- E_{concat}: horizontally concatenated 12-lead ECG.

If $E_{\text{concat}} > E_{\text{single}}$, the representation is spectrally richer, indicating that the multi-lead concatenation preserves and potentially enhances the spectral content compared to single-lead analysis. This comparison provides insight into whether our concatenation strategy maintains the diagnostic information distributed across multiple leads.

2. Spectral Entropy (Shannon).

$$H = -\sum_i p_i \log(p_i), \quad p_i = \frac{|\text{CQT}(x_i)|^2}{\sum_j |\text{CQT}(x_j)|^2} \tag{4}$$

The spectral entropy measures the randomness and complexity of the frequency distribution, where p_i represents the normalized spectral power at each frequency bin. Higher entropy indicates higher complexity and variability in the spectrum, suggesting a more diverse frequency content. This metric is particularly valuable for assessing the information content of different ECG representations, as pathological conditions often manifest as increased spectral complexity due to irregular cardiac rhythms and morphological variations. The comparison between single-lead and concatenated representations using spectral entropy helps validate whether our multi-lead approach captures the inherent complexity of cardiac electrical activity more effectively than conventional single-lead analysis.

Table 3. Quantitative evaluation methods for comparing time-frequency representations.

Method	**Objective**	**Expected Outcome**
Spectral Energy E	Global intensity	$E_{\text{concat}} > E_{\text{single}}$
Entropy H	Spectral diversity	$H_{\text{concat}} > H_{\text{single}}$

3.3. ResNet50:

ResNet-50, a variation within the ResNet architecture, represents a deep convolutional neural network extensively utilized in computer vision assignments. Renowned for its depth and exceptional performance in tasks related to image recognition, the ResNet structure comprises convolutional layers, batch normalization, and activation functions in its fundamental building blocks. These blocks also integrate shortcut connections, enabling the network to learn residuals or variations between the output of the current layer and the desired output. In the context of a 2D convolutional neural network (CNN), similar operations to those in the 1D scenario are performed, but considering two-dimensional data. our model architecture is defined in this table

3.4. k cross-validation:

K-fold cross-validation stands as a prevalent technique in machine learning, specifically employed to evaluate classification algorithms. Its methodology entails partitioning the data into k subsets, where k-1 subsets are utilized for training and the remaining subset for testing, thereby generating k distinct accuracy scores for evaluation purposes. This technique serves as a critical tool for estimating model performance, guarding against overfitting, and maximizing data exploitation. Additionally, it assists in tasks such as model selection, fine-tuning hyperparameters, and facilitating algorithm comparisons. [10]

Table 4. ResNet-50 architecture summary

Stage	Output Size	Block Type	Configuration
Conv1	112×112×64	Convolution	7×7, 64 filters, stride 2
MaxPool	56×56×64	Max Pooling	3×3, stride 2
Conv2_x	56×56×256	Bottleneck Block ×3	1×1, 64 filters 3×3, 64 filters 1×1, 256 filters
Conv3_x	28×28×512	Bottleneck Block ×4	1×1, 128 filters 3×3, 128 filters 1×1, 512 filters
Conv4_x	14×14×1024	Bottleneck Block ×6	1×1, 256 filters 3×3, 256 filters 1×1, 1024 filters
Conv5_x	7×7×2048	Bottleneck Block ×3	1×1, 512 filters 3×3, 512 filters 1×1, 2048 filters
AvgPool	1×1×2048	Global Average Pooling	-
FC	1000	Fully Connected Layer	Softmax activation

4. Performance evaluation :

We employed the Sensitivity, Specificity, and accuracy metrics—all widely used in the field of pattern recognition, to assess the performance of each class. In order to calculate these metrics, the values of true positive (TP), true negative (TN), false positive (FP), and false negative (FN) were used, which were stated in the appropriate way in the equations. (2), (3), and (4). These are their definitions:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \times 100, \tag{5}$$

$$Sensitivity\,(Se) = \frac{TP}{TP + FN}, \tag{6}$$

$$Specificity\,(Sp) = \frac{TN}{TN + FP}. \tag{7}$$

$$F1\text{-}score = \frac{2 \cdot Precision \cdot Sensitivity}{Precision + Sensitivity}, \tag{8}$$

Where TP and TN represent, respectively, the quantity of true positive and true negative patients. The terms FN and FP stand for false negative and false positive rates, respectively.

5. Result and discussion:

Experiments were conducted using Python software on a personal system equipped with an Intel i7-series processor @ 3.12 GHz and 16 GB of RAM, utilizing the Kaggle platform for data handling and computational resources, alongside Weights and Biases (wandb) for experiment tracking and visualization. The ResNeXt-50 model was trained and tested using a 10-fold cross-validation method, with parameters set to a batch size of 100, an Adam optimizer, and an initial learning rate of 0.01 to ensure consistency and reliability of results. To quantitatively demonstrate the improved signal quality from horizontal concatenation, we compare the spectral energy and entropy of the 1-lead versus 12-lead CQT representations in Table 5. To objectively assess the enhancement in

Table 5. TIME-FREQUENCY COMPARISON

Metric	**1-lead**	**12-leads concat**
Spectral Energy	36042.05	84173.22
Spectral Entropy	11.46	12.31

signal representation quality resulting from the horizontal concatenation of the 12 ECG leads, we calculated and compared two quantitative metrics: spectral energy and spectral entropy. As shown in Table 5, the concatenated 12-lead representation exhibits significantly higher spectral energy (84,173.22 vs. 36,042.05) and greater spectral entropy (12.31 vs. 11.46) compared to the single-lead representation. This indicates not only a stronger signal presence but also richer and more diverse frequency content, which is essential to capture the complex spatio-temporal dynamics of cardiac activity. These results confirm that the concatenated representation retains more diagnostic information, making it a more robust input for deep learning models.

In contrast to traditional methods that rely on hand-crafted features, which struggle with individual patient differences, our method leverages advanced techniques. We utilized the constant-Q transform (CQT), which provides superior frequency resolution compared to the Short-Time Fourier Transform (STFT). This adaptability preserves the temporal resolution and richness of the original signals, thus enhancing the analysis of cardiac dynamics in the time-frequency domain.

Several studies in the literature emphasize the use of artificial intelligence (AI) in ECG analysis. For instance, some studies, like those employing multi-lead residual neural networks and convolutional neural networks, have demonstrated varying success in MI detection, but often grapple with complexities due to high parameter counts. For example, the multi-lead residual neural network (ML-ResNet) in one study utilized 13 layers and multiple residual blocks, which, while effective, poses challenges related to managing and optimizing such a complex architecture.

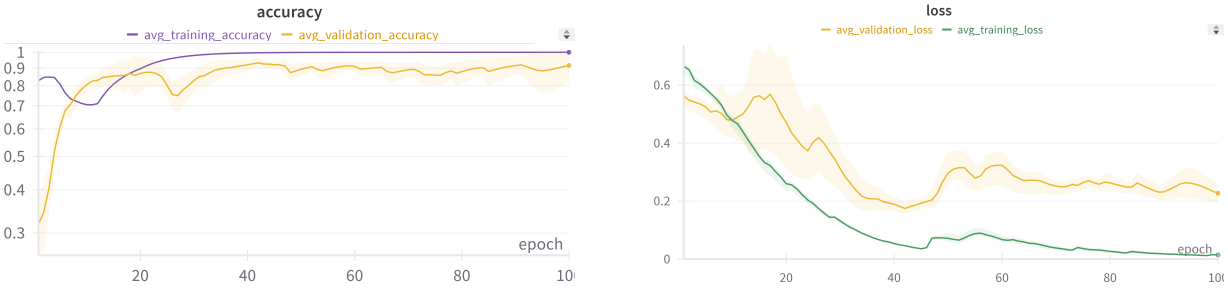
Table 6. Comparison of Methods

Method	Dataset	Performances			
		Accuracy	Sensitivity	Specificity	F-score
ML-ResNet [22]	PTB	95.49%	94.85%	97.37%	–
Improved ResNet-18 [23]	MIT-BIH	96.50%	93.83%	–	–
Multi-branch fusion network [24]	ECG images	94.73%	96.41%	95.94%	–
Multiple-feature-branch CNN [25]	PTB	99.95%	99.97%	99.90%	–
ResNet-50 [26]	MITBIH, PTB, CPSC, Fantasia, BIDMC	97.63%	–	–	–
Multi-Modal Stacking Ensemble + ResNet-50 [27]	PTB-XL	93.97%	94.0%	–	–
Proposed method	PTB-XL	**97.82%**	**98.03%**	**97.38%**	**98.03%**

Our approach contrasts with these methods by utilizing a single ResNet-50 model instead of processing 12 individual leads. This streamlining reduces the model's complexity and dimensionality while maintaining high performance. While the referenced ML-ResNet achieved 95.49% accuracy and 94.85% sensitivity, our model achieves an impressive training accuracy of 97.82% with a training loss score of only 0.0032% after 100 epochs. Furthermore, our method efficiently classifies MI associated with RBBB, addressing a gap in existing databases that lack combined patient data for these specific conditions.

Similarly, other studies in Table 6, such as those adopting MFB-CNN architectures, face challenges of high complexity due to separate analysis of 12 leads. Our method effectively mitigates these issues by concatenating leads to form a comprehensive representation that captures complementary information. This process not only improves the signal-to-noise ratio (SNR) of the ECG signal representation but also enhances visualization and feature extraction related to cardiac dynamics. only clean PTB-XL used; plan noisy-ECG stress tests and missing-lead simulation. Further advancements have been made by researchers using ResNet-50 models to classify various cardiovascular diseases based on 12-lead ECG data. While these models exhibit exceptional sensitivity and specificity, they often encounter issues related to gradient vanishing during training, impeding their ability to learn complex patterns effectively. Our approach, leveraging ResNet-50, not only addresses these limitations but also enhances classification accuracy without inflating model size excessively.

As depicted in Fig. 5a and Fig. 5b. These exceptional performances validate the effectiveness and reliability of our model in accurately classifying ECG signals. The high accuracy and low training loss score highlight the robustness and precision of our approach in addressing the given task.



(a) Mean Accuracy Scores for 10-Fold Cross-Validation

(b) Mean Loss Scores for 10-Fold Cross-Validation

Figure 5. Our model's mean accuracy and loss scores across 10-fold cross-validation.

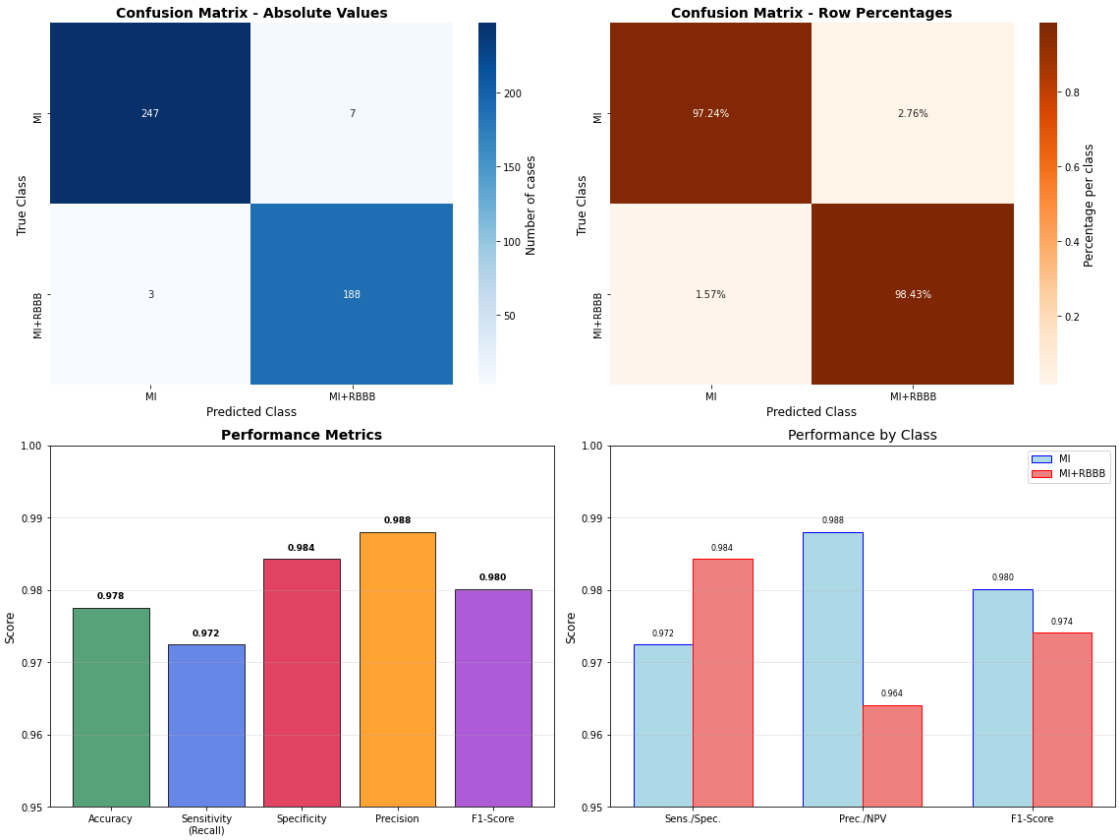


Figure 6. Our Model performance.

The classification performance of the proposed model is illustrated in Figure 6, demonstrating robust discrimination between myocardial infarction (MI) and MI associated with right bundle branch block (MI+RBBB). The confusion matrices reveal very low misclassification rates: 97.24% of MI cases and 98.43% of MI+RBBB

cases were correctly identified. Only 7 MI cases were misclassified as MI+RBBB, and 3 MI+RBBB cases were misclassified as MI, indicating high sensitivity and specificity for both categories.

The summary metrics further underscore the effectiveness of the approach, with overall accuracy, precision, and F1-score exceeding 97%. Notably, the precision (0.988) and specificity (0.984) values suggest a low rate of false positives, which is especially important in clinical settings to avoid unnecessary interventions. The sensitivity (recall) of 0.972 and F1-score of 0.980 indicate that the model is highly capable of detecting true positive cases, minimizing the risk of missed diagnoses. Class-wise analysis shows that the model maintains balanced performance across both categories, further supporting its potential utility in differentiating these clinically challenging conditions.

These results validate the model's ability to generalize across the dataset and suggest that the combination of horizontal concatenation, CQT transformation, and deep learning architecture provides a robust framework for ECG-based MI and MI+RBBB classification. The low misclassification rates and high metric values indicate strong reliability, although further external validation on independent cohorts is warranted to confirm generalizability in broader clinical contexts.

6. Conclusion

Our research presents a novel ECG diagnosis system that integrates advanced signal processing with deep learning to improve the detection and characterization of acute myocardial infarction (MI) and MI associated with right bundle branch block (RBBB). By leveraging the Constant-Q Transform (CQT) for time-frequency feature extraction and a pre-trained deep neural network, our approach achieves high diagnostic performance, with an accuracy of 97.82% and a minimal training loss of 0.0032% after 100 epochs. This innovative framework has the potential to enhance patient care and advance ECG-based cardiac diagnostics. The application of rigorous 10-fold cross-validation further reinforces the credibility and reliability of our findings, providing robust performance estimates and valuable insights for future development.

7. Limitation

This study is limited by its reliance on a relatively small, clinically specific cohort from the PTB-XL dataset, comprising only MI and MI+RBBB cases. The exclusive use of complete 12-lead ECG recordings and the absence of external validation restrict the assessment of model generalizability and robustness, particularly under real-world conditions such as missing leads or noisy data. Additionally, the PTB-XL population may not represent broader demographic diversity. Future work will focus on validating the model with larger, multi-center datasets and under varied clinical scenarios to ensure broader applicability.

Code-availability statement

Code available on request

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