Automated Chagas Disease Detection from 12-Lead ECGs Using a Residual Network with Robust Preprocessing

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Abstract

Chagas disease (CD) affects an estimated 6–7 million people worldwide, with underdiagnosis rates exceeding 95% in endemic regions. Serological testing is complex and resource-intensive, typically requiring multiple confirmatory assays and high-quality antigens. Since CD produces conduction and repolarization abnormalities detectable on 12-lead ECGs, automated ECG-based screening offers a scalable alternative. We present a residual network model with robust preprocessing for automated CD detection from raw, variable-quality ECGs. The preprocessing pipeline applies percentile-based normalization (P_{01}–P_{99} clipping) and physiologically informed harmonization, resampling all signals to 400 Hz via sinc interpolation. The network performs hierarchical temporal feature extraction through residual blocks with progressively refined resolution, enhanced by lead-wise analysis, spatial dropout ($p = 0.1$), and L_2 regularization ($\lambda = 10^{-4}$). To address extreme class imbalance ($P(Y{=}1) < 0.05$), we incorporate synthetic minority oversampling with controlled noise injection and temporal augmentation. On the PhysioNet/Computing in Cardiology Challenge 2025 task, our system achieved a composite Challenge Score of 0.192 on the hidden test set, ranking 27th, with an inference latency below 100 ms.

1. Introduction

Chagas disease (CD) is a neglected tropical disease caused by the protozoan *Trypanosoma cruzi*, affecting an estimated 6-7 million people worldwide [1], with the highest prevalence in Latin America. Underdiagnosis remains a critical challenge, with rates exceeding 95% in endemic regions [2]. The gold standard diagnostic approach relies on serological testing (ELISA and Western Blot), which requires multiple confirmatory assays, skilled personnel, and reliable antigens, thus limiting scalability in resource-constrained settings.

Electrocardiography (ECG) provides a non-invasive, widely available, and low-cost alternative. Importantly, chronic CD often manifests with conduction and repolarization abnormalities—such as right bundle branch block, left anterior fascicular block, QRS prolongation, and T-wave alterations—that can be detected on 12-lead ECGs, frequently preceding overt clinical symptoms [3]. This makes automated ECG-based screening a promising strategy to prioritize serological testing and improve early diagnosis.

Recent advances in deep learning have accelerated automated ECG interpretation [4, 5]. Convolutional neural networks (CNNs) particularly have demonstrated strong performance by automatically extracting discriminative temporal features, including P–QRS–T morphologies. Residual networks (ResNets) extend this capability by improving gradient flow and enabling deeper, more expressive architectures, which are particularly effective for complex diagnostic tasks [5].

In this work, we present a ResNet-based model integrated with a physiology-aware preprocessing pipeline for automated CD detection as part of the PhysioNet/Computing in Cardiology Challenge 2025 [6, 7]. Our preprocessing pipeline applies percentile-based normalization (1^{st}–99^{th} percentile clipping) and physiologically informed harmonization, resampling each recording to 400 Hz via sinc interpolation to preserve waveform fidelity across acquisition systems. The model leverages hierarchical temporal feature extraction through progressively refined kernels, combined with lead-wise analysis, spatial dropout, and L_2 regularization. To address the extreme class imbalance (positive prevalence $< 1\%$), we employ synthetic minority oversampling with clinically informed augmentations, including controlled noise injection and temporal shifting.

In summary, the main contributions of this study are threefold:-

$*$ A physiology-aware preprocessing pipeline designed to ensure robustness across heterogeneous ECG recordings;

$*$ A residual network architecture tailored for lead-wise, multi-resolution temporal feature extraction; and

∗ A comprehensive evaluation under the Challenge framework, demonstrating the value of principled preprocessing and architecture design for scalable ECG-based CD screening.

2. Methods

2.1. Dataset

We used the George B. Moody Physionet Challenge 2025 dataset, which aggregates 12-lead ECG recordings from multiple sources in Central and South America, along with basic demographic information and binary labels for Chagas disease. Specifically, the dataset integrates three major public resources:

SaMi-Trop: This cohort includes 1,631 12-lead ECGs collected from Chagas patients in Brazil between 2011 and 2012 [8]. Recordings have durations of 7.3 s or 10.2 s, sampled at 400 Hz. All Chagas labels were serologically validated, and all are positive.

PTB-XL: The PTB-XL dataset comprises 21,799 12-lead ECGs collected in Europe between 1989 and 1996 [9]. Each recording has a 10 s duration, sampled at 500 Hz. Since Chagas is not endemic in Europe, all labels are assumed to be negative.

CODE-15%: This large-scale dataset contains over 300,000 12-lead ECGs collected in Brazil between 2010 and 2016 [10]. Recordings are 7.3 s or 10.2 s in length, with a sampling frequency of 400 Hz. Chagas labels are self-reported, with a small positive prevalence, introducing noise and class imbalance.

2.2. Preprocessing

To ensure robustness against heterogeneous recording conditions, we applied a physiology-aware preprocessing pipeline designed to mitigate technical artifacts while preserving clinically relevant morphologies. Variations in equipment and acquisition protocols can substantially affect ECG quality; our pipeline harmonizes these differences to support consistent learning. The main steps were the following. (i) *Lead harmonization:* All recordings were standardized to a 12-lead configuration, with missing leads zero-padded or duplicated as appropriate, ensuring consistent input dimensionality. (ii) *Resampling:* Signals were resampled to 400 Hz using linear interpolation, enabling consistent temporal resolution across devices with original sampling rates ranging from 250–500 Hz. (iii) *Baseline correction:* Baseline wander was removed using median subtraction, eliminating low-frequency drift while preserving the electrical axis and ST-segment morphology. (iv) *Percentile clipping:* Each lead was clipped between the 1st and 99th percentiles (P_{01}–P_{99}) to suppress extreme noise artifacts without distorting physiologic variability. (v) *Normalization:* Z-score normalization was applied per lead, preserving inter-lead amplitude relationships while providing consistent scaling across patients.

This preprocessing pipeline effectively manages real-world variability while retaining subtle electrocardiographic signatures of Chagas cardiomyopathy, such as right bundle branch block patterns and ventricular repolarization abnormalities.

2.3. Model Architecture

We developed a residual neural network (ResNet) specifically tailored to capture the complex temporal dynamics and conduction abnormalities associated with Chagas disease in 12-lead ECGs. Building on the established effectiveness of ResNets for feature extraction [5], our model performs hierarchical temporal representation learning through residual blocks of progressively refined resolution, enabling the detection of subtle cardiac irregularities that may precede overt clinical symptoms.

The architecture exploits the complementary nature of local, lead-specific features and global, cross-lead dependencies inherent in 12-lead ECG interpretation. In the initial stage, convolutional layers are applied independently to each lead, allowing the network to extract morphological characteristics such as QRS complexes, T-wave alterations, and conduction delays. These lead-wise representations are then progressively integrated through deeper residual blocks, which learn temporal correlations across leads and capture global cardiac patterns indicative of Chagas-related pathophysiology.

At its core, the model consists of five stacked residual blocks (ResBlocks). Each block incorporates skip connections, which both encourage feature reuse and stabilize gradient propagation during training, enabling deeper and more expressive networks. The blocks employ progressively smaller kernel sizes ($15 \rightarrow 3$) and increasing channel dimensions ($64 \rightarrow 256$), thus capturing both coarse temporal dynamics and fine-grained morphological details across multiple timescales.

2.4. Training and Generalization Strategy

We designed the training and generalization strategy to ensure reliable performance of the model under realistic clinical and data conditions. To mitigate severe class imbalance ($P(Y{=}1) < 0.05$), we applied SMOTE-based oversampling and adaptive class weighting, enabling the network to learn rare positive cases effectively. This approach is essential in diagnostic screening, where the absence of even a single true-positive patient can have significant clinical consequences.

To enhance robustness to data variability, we implemented augmentation techniques that simulate real-world

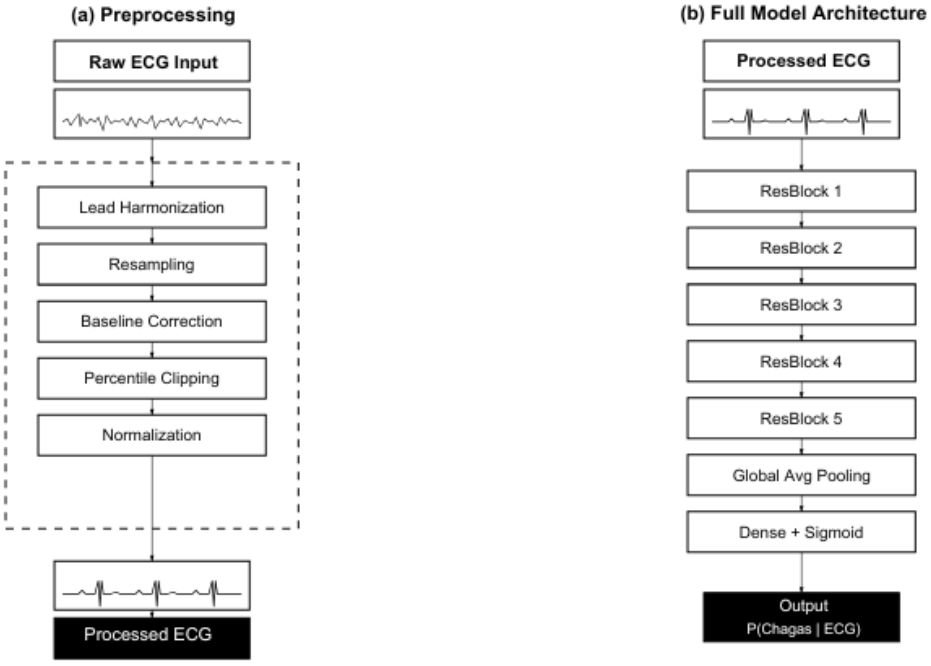

Figure 1. End-to-end pipeline for automated Chagas disease detection.

ECG perturbations. Gaussian noise injection ($\sigma = 0.01$–0.05) and temporal shifting improved the model's resilience to acquisition differences across devices and healthcare settings common in endemic regions. Regularization via spatial dropout ($p = 0.1$) and L_2 weight decay ($\lambda = 10^{-4}$) further prevented overfitting, encouraging the model to learn physiologically meaningful features such as conduction delays and repolarization abnormalities rather than spurious signal artifacts.

3. Results

3.1. Evaluation Protocol

The primary evaluation metric for the George B. Moody Physionet Challenge 2025 is the **Challenge Score**, which measures the fraction of true Chagas-positive patients captured within the top 5% of highest-probability predictions. Formally, let X denote a dataset of n ECG records, and let p_x be the algorithm's estimated probability of Chagas disease for record $x \in X$. The records are ranked in descending order of p_x, such that $x_1 = \arg\max_{x \in X} p_x$ has the highest probability, x_2 the second highest, and so on. For $\alpha \in (0, 1)$, define $X_\alpha \subseteq X$ as the subset of the $\lfloor \alpha n \rfloor$ highest-ranked records:$X_\alpha = \{x_k \in X : k \leq \lfloor \alpha n \rfloor\}$. The Challenge Score is then the true positive rate within X_α, i.e., the fraction of Chagas-positive cases in X_α relative to all positives in X, with $\alpha = 0.05$. In essence, this metric reflects the intended screening use case, which prioritizes a limited proportion of patients (5%) for confirmatory serological tests in resource-constrained settings.

3.2. Model Performance

Our model achieved a Challenge Score of 0.192 on the hidden test set, successfully identifying approximately 19.2% of Chagas-positive patients within the clinically relevant top 5% of predictions. This represents a substantial improvement over random selection, which would detect only 5% of positive cases. Overall, the model ranked 27th out of 114 participating teams, while maintaining computational efficiency with an inference latency below 100 ms. These results highlight the effectiveness of combining robust preprocessing and residual architectures to enable scalable, real-time ECG-based screening for Chagas disease in resource-limited settings.

3.3. Ablation Study

To assess the contribution of individual components, we performed systematic ablation experiments on the validation set and evaluated it using the challenge's evaluation

protocol. Table 1 reports the score in the validation set for different model configurations.

Table 1. Ablation study results showing the impact of key model components and their scores on the validation set

Model Configuration	Score
Full Model (all components)	0.272
No physiology-aware preprocessing	0.245
No class imbalance handling	0.150

The ablation results demonstrate that each component contributes meaningfully to performance. As shown in Table 1, removing physiology-aware preprocessing reduced the score by nearly 3%, underscoring the importance of robust signal harmonization while eliminating class imbalance handling caused the largest drop—almost 10 percentage points—confirming that oversampling and augmentation are critical for detecting rare positive cases in this highly imbalanced setting.

4. Discussion and Conclusion

This study demonstrates that combining physiology-aware preprocessing with a residual network architecture enables robust ECG-based screening for Chagas disease. Our model achieved a Challenge Score of 0.192, correctly identifying nearly one-fifth of Chagas-positive patients within the top 5% of predictions.

Despite these promising results, several limitations remain. First, while the model performed well on the Challenge hidden test set, its generalization to independent patient cohorts has yet to be validated. Second, subsets of the dataset contained self-reported labels, which may introduce noise and affect calibration. Finally, the current approach relies solely on ECG data; integrating clinical metadata or imaging modalities could further enhance diagnostic accuracy and robustness.

In summary, this work highlights the importance of principled preprocessing and deep residual architectures for scalable ECG-based screening of Chagas disease. By prioritizing high-risk patients for confirmatory testing, such models could help reduce underdiagnosis and improve outcomes in resource-limited healthcare systems. Future research will focus on multimodal integration, interpretability, and prospective clinical validation to advance AI-assisted diagnosis in neglected tropical diseases.

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