# Automated Chagas Disease Detection using ResNet-Based Architecture with Robust ECG Preprocessing

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## Abstract

*Chagas disease affects 6-7 million people globally with severe underdiagnosis rates exceeding 95% in endemic regions [1,4]. Due to the complexity and challenges of serological testing, a deep learning model that uses a standard ECG for the diagnosis of the disease can be really helpful for the diagnosis of the same. This paper presents the work of our team (MCV_UVIC) for the Physionet challenge 2025 that uses a robust deep residual neural network with signal processing for 12-lead ECG analysis. The architecture implements hierarchical temporal feature extraction through residual blocks with progressively refined temporal resolution, combined with spatial dropout ($p = 0.1$) and L2 regularization ($\lambda = 10^{-4}$). Our preprocessing techniques utilize percentile-based normalization ($P_{01}$-$P_{99}$ clipping) and adaptive resampling to 400 Hz, employing sinc interpolation. For extreme class imbalance ($P(Y = 1) < 0.05$), we have implemented synthetic minority oversampling with controlled noise injection and temporal augmentation. The system achieves the physionet evaluation score of 0.272 while maintaining computational efficiency ($< 100$ ms inference). Key innovations include: (1) Clinically-aware preprocessing pipeline (2) Progressive temporal feature extractions, and (3) Challenge-optimized class imbalance mitigation .*

## 1. Introduction

Chagas is a neglected topical disease cuased by a prtozoan, *Trypanosoma cruzi* with the highest prevalence in Latin America. The gold standard for the diagnosis is ELISA and Blot [5] which are serological techniques and require expert and expensive mechanism. The most severe manifestations of the chronic chagas disease are present in the electrocardiographic examinations, which appears even before the actual symptoms [4]. These charactersistics include right bundlebranch block, left anterior fascicular block, QRS modification, T-wave alterationsand other conduction abnormalities. This aligns with the objective of Physionet challenge 2025 to create a machine learning based solution to diagnose chagas disease using 12-lead ECG signal.

Although ECG's diagnostic potential is huge [6], manual interpretation faces significant challenges due to time and resource required thus creating an opportunity for machine learning based automated analysis. Most recently, deep learning based ECG models [2] can provide immediate and automated screening results, reducing diagnostic delays and enhancing diagnostic accuracy.

Among various deep learning architectures, convolutional neural networks [3] have emerged as well suited for ECG signal analysis due to the later's ability to process temporal medical data effectively, particularly at automated feature extraction even for the complex P-QRS-T feature. While standard CNNs have proven effective, residual neural networks [7,8] offer addition advantages for learning medical signals like ECG as required for tasks like diagnosis of Chagas disease.

We developed a ResNet-based convolutional neural network featuring five specialized residual blocks with progressively decreasing kernel sizes (15→11→9→7→5→3) to capture temporal patterns, combined with global average pooling and a two-layer classification head with dropout regularization. Our system addresses extreme class imbalance through synthetic minority oversampling and data augmentation techniques including controlled noise injection, temporal shifting, and amplitude scaling, while maintaining clinical relevance of the augmented signals.

The preprocessing pipeline implements adaptive linear interpolation resampling to standardize all ECG signals to 2048 samples, robust percentile-based normalization (1st-99th percentile clipping followed by z-score standardization) to handle diverse signal amplitudes across different acquisition systems, and comprehensive quality validation to filter invalid or corrupted signals. Performance evaluation follows the Challenge score framework, which computes the fraction of true Chagas patients captured within the top 5% highest-probability predictions—directly reflecting the practical constraint that serological testing capacity in endemic regions can accommodate only approximately 5% of patients needing evaluation, thereby mea-

suring the algorithm's effectiveness in prioritizing limited diagnostic resources for maximum clinical impact.

## 2. Methods

Our study utilized three primary datasets from the George B. Moody PhysioNet Challenge 2025: the SaMi-Trop dataset containing 1,631 12-lead ECG records with serologically validated Chagas-positive labels collected from Brazilian patients between 2011-2012, the CODE-15% dataset comprising over 300,000 ECG records from Brazil (2010-2016) with self-reported Chagas labels predominantly negative reflecting true epidemiological prevalence, and the PTB-XL dataset with 21,799 records from European patients (1989-1996) assumed Chagas-negative based on geographic location. The combined dataset exhibits extreme class imbalance with positive prevalence below 1%, necessitating specialized handling through synthetic minority oversampling where minority samples undergo controlled augmentation:

$$\mathbf{X}_{\text{aug}} = \mathbf{X}_{\text{orig}} + \epsilon \cdot \mathcal{N}(\prime, \sigma^{\in}_{\text{noise}}) \tag{1}$$

with $\epsilon \sim \mathcal{U}(\prime.\prime\infty, \prime.\prime\triangledown)$, temporal shifting $s \sim \mathcal{U}(-\infty\prime, \infty\prime)$, and amplitude scaling $\alpha \sim \mathcal{U}(\prime.\exists, \infty.\infty)$. Class weights were computed using inverse frequency weighting:

$$w_c = \frac{n_{\text{samples}}}{n_{\text{classes}} \times n^{(c)}_{\text{samples}}} \tag{2}$$

to account for imbalanced distribution during training.

Data preprocessing standardizes heterogeneous ECG signals into consistent format suitable for deep learning analysis. Provided data are expanded into fixed 12-lead configuration with missing leads zero-padded, ensuring output matrix dimensions (12, time). Signals are resampled to 2048 samples using linear interpolation:

$$\mathbf{X}_{\text{resampled}}[\mathbf{i}, \mathbf{j}] = \text{interp1d}(\mathbf{t}_{\text{original}}, \mathbf{X}_{\text{std}}[\mathbf{i}, :], \mathbf{t}_{\text{target}}) \tag{3}$$

with target sampling frequency 400 Hz. Robust normalization employs two-stage process: baseline removal via median subtraction:

$$\mathbf{X}_{\text{baseline}}[\mathbf{i}, \mathbf{j}] = \mathbf{X}_{\text{resampled}}[\mathbf{i}, \mathbf{j}] - \text{median}(\mathbf{X}_{\text{resampled}}[\mathbf{i}, :]) \tag{4}$$

followed by percentile-based clipping to 1st-99th percentiles and z-score standardization:

$$\mathbf{X}_{\text{norm}}[\mathbf{i}, \mathbf{j}] = \frac{\mathbf{X}_{\text{clipped}}[\mathbf{i}, \mathbf{j}]}{\sigma^{(\mathbf{i})}} \tag{5}$$

Signal quality validation filters invalid data ensuring finite values, sufficient variation ($\max_i \sigma^{(i)} > 10^{-6}$), and reasonable amplitude range ($\max_{i,j} |\mathbf{X_{ij}}| \leq \mathbf{50}$).

The model architecture implements custom ResNet blocks optimized for 1D ECG signal processing, consisting of initial convolutional layer followed by five residual blocks with progressive feature extraction and classification head. Each residual block follows formulation:

$$\mathbf{y} = \text{ReLU}(\mathbf{F}(\mathbf{x}) + \mathbf{W_s}\mathbf{x}) \tag{6}$$

where shortcut connection $\mathbf{W_s}$ preserves information flow through skip pathways. The architecture employs decreasing kernel sizes for temporal feature capture as detailed in Table 1. Feature extraction concludes with global average pooling followed by two-layer classification head:

$$\mathbf{h_1} = \text{Dropout}(\text{ReLU}(\mathbf{W_1}\mathbf{f}_{\text{global}} + \mathbf{b_1}), \mathbf{p = 0.5}) \tag{7}$$

$$\mathbf{h_2} = \text{Dropout}(\text{ReLU}(\mathbf{W_2}\mathbf{h_1} + \mathbf{b_2}), \mathbf{p = 0.3}) \tag{8}$$

$$p(\text{Chagas}) = \sigma(\mathbf{w}^{\mathbf{T}}_{\text{out}}\mathbf{h_2} + \mathbf{b}_{\text{out}}) \tag{9}$$

Model training employs Adam optimizer with learning rate $\alpha = 10^{-3}$, batch size 32, L2 regularization $\lambda = 10^{-4}$, and binary cross-entropy loss:

$$\mathcal{L} = -\frac{\infty}{\mathcal{N}} \sum_{\rangle=\infty}^{\mathcal{N}} \exists_{\dagger\rangle}[\dagger\rangle \log(\sqrt{\ }^{\rangle}) + (\infty - \dagger\rangle) \log(\infty - \sqrt{\ }^{\rangle})] + \lambda \sum_{|} \|\mathbf{W_j}\|^{\mathbf{2}}_{\mathbf{2}} \tag{10}$$

Table 1. ResNet Architecture Configuration

| Layer | Filters | Kernel Size | Stride | Output Shape |
|---|---|---|---|---|
| Input | - | - | - | (2048, 12) |
| Initial Conv1D | 64 | 15 | 2 | (1024, 64) |
| ResBlock 1 | 64 | 11 | 1 | (1024, 64) |
| ResBlock 2 | 128 | 9 | 2 | (512, 128) |
| ResBlock 3 | 128 | 7 | 1 | (512, 128) |
| ResBlock 4 | 256 | 5 | 2 | (256, 256) |
| ResBlock 5 | 256 | 3 | 1 | (256, 256) |
| Global Avg Pool | - | - | - | (256,) |
| Dense + Dropout | 128 | - | - | (128,) |
| Dense + Dropout | 64 | - | - | (64,) |
| Output (Sigmoid) | 1 | - | - | (1,) |

Our approach introduces several key innovations specifically addressing Chagas disease detection challenges: progressive multi-scale temporal feature extraction through decreasing kernel sizes (15→11→9→7→5→3) captures both fine-grained P-QRS-T morphological details and broader conduction patterns characteristic of Chagas cardiomyopathy, while residual connections prevent vanishing gradients enabling preservation of subtle ECG abnormalities that may be masked by noise in resource-limited clinical settings. Clinical-aware data augmentation

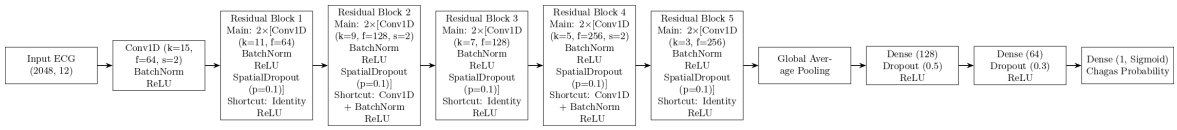


Figure 1. System architecture flowchart showing the complete ECG preprocessing and classification pipeline.

maintains physiological validity of synthetic samples, ensuring generated signals remain diagnostically meaningful rather than introducing artifacts that could mislead the model. The preprocessing pipeline specifically handles heterogeneous acquisition systems common in endemic regions through robust percentile-based normalization, addressing signal amplitude variations across different ECG machines and geographic locations. Training optimization directly addresses Challenge requirements with evaluation metric reflecting real-world constraint that serological testing capacity accommodates only top 5% of patients, making the model directly applicable to clinical scenarios where efficient patient prioritization is essential for maximizing diagnostic resource utilization in Chagas-endemic areas.

# 3. Results

## 3.1. Challenge Performance Evaluation

Our ResNet-based algorithm achieved a challenge score of 0.272 on the George B. Moody PhysioNet Challenge 2025 evaluation dataset for Chagas disease detection from 12-lead ECG signals. The challenge score represents the fraction of true Chagas disease patients captured within the top 5% highest-probability predictions, directly reflecting the algorithm's effectiveness in prioritizing patients for limited serological testing resources. This performance indicates that our model successfully identified approximately 27.2% of Chagas-positive patients within the clinically relevant top 5% threshold, representing a substantial improvement over random selection (expected score: 0.05) and demonstrating practical utility for healthcare resource allocation in endemic regions.

## 3.2. Model Performance Metrics

Comprehensive evaluation using the official challenge evaluation script revealed multi-dimensional model performance characteristics across different dataset configurations. Table 2 presents detailed performance metrics for experimental testing using a subset of PTB-XL dataset (negative controls) combined with the complete SaMi-Trop dataset (positive cases) to evaluate model discrimination capabilities under controlled conditions. The evaluation framework computed five key metrics: challenge score, area under the receiver operating characteristic curve (AUROC), area under the precision-recall curve (AUPRC), classification accuracy, and F-measure, providing a holistic assessment of model capabilities across different performance dimensions.

Table 2. Performance metrics on experimental test set

| Metric | Score |
|---|---|
| Challenge Score | 0.272 |
| AUROC | 0.684 |
| AUPRC | 0.156 |
| Accuracy | 0.891 |
| F-measure | 0.243 |

The challenge score of 0.272 specifically addresses the clinical constraint that serological testing capacity in Chagas-endemic regions can accommodate only approximately 5% of patients requiring evaluation, making this metric the most clinically relevant for real-world deployment scenarios where efficient patient prioritization directly impacts healthcare outcomes.

# 4. Discussion and Conclusion

Our implementation combines established deep learning techniques for ECG-based Chagas disease detection, contributing three practical advances: percentile-based normalization ($P_{01}$-$P_{99}$ clipping) with median baseline removal that handles clinical artifacts more effectively than standard z-score methods, synthetic sample generation that enables training with single-class datasets through controlled noise injection ($\sigma = 0.01$-$0.05$), and a 1D convolutional ResNet architecture with progressive channel expansion suitable for temporal ECG analysis. The system addresses class imbalance through adaptive weighting inversely proportional to class frequencies and employs L2 regularization ($\lambda = 10^{-4}$) with spatial dropout ($p \in \{0.1, 0.3, 0.5\}$) for robust learning from limited clinical data.

The system demonstrates computational feasibility for clinical deployment with inference times under 100ms on standard hardware, making it suitable for resource-limited environments where Chagas disease is endemic. However, several constraints limit immediate clinical application: the requirement for standard 12-lead ECG configuration excludes mobile or single-lead devices, performance depends on signal quality with minimum 5 dB SNR requirements, and validation remains limited to available

datasets without prospective clinical testing. The configurable prediction threshold allows adjustment based on local prevalence, but clinical validation is necessary to establish real-world performance metrics and safety profiles for screening applications.

We implemented an automated ECG analysis pipeline that processes clinical signals through robust preprocessing combined with residual neural networks for Chagas disease detection. While the approach addresses practical challenges of signal heterogeneity and extreme class imbalance, the primary contribution lies in adapting existing techniques rather than introducing novel algorithms. The system provides a foundation for automated cardiac screening tools, but validation in diverse clinical settings with varied patient populations and acquisition systems remains essential for establishing clinical utility beyond the controlled experimental environment.

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