

Article

Correlation Based Dynamic Time Warping for ECG Waveform

Ruri Lee , Byungmun Kang , DongHyeon Kim  and DaeEun Kim * 

School of Electrical and Electronic Engineering, Yonsei University, Seoul 03722, Republic of Korea; leeruri@yonsei.ac.kr (R.L.); kbmang@yonsei.ac.kr (B.K.); donghyeonkim@yonsei.ac.kr (D.K.)

* Correspondence: daeeun@yonsei.ac.kr

Abstract

Electrocardiogram waveform delineation is a fundamental task for quantitative cardiac analysis, yet accurate and consistent estimation of waveform boundaries remains challenging due to heart rate variability, inter-subject morphological differences, and nonlinear temporal distortions across cardiac cycles. Conventional rule-based methods and pointwise Dynamic Time Warping approaches are sensitive to amplitude variations and baseline fluctuations, while deep learning-based models require large annotated datasets and often suffer from limited interpretability and generalization. In this study, we propose a morphology-oriented ECG waveform alignment framework based on Pearson correlation-based Dynamic Time Warping (PCDTW). By integrating window-level matching with a correlation-driven cost function, the proposed method explicitly emphasizes local morphological similarity rather than absolute amplitude differences. Each ECG record is aligned using a subject-specific reference cycle constructed from normalized RR intervals, enabling stable correspondence of waveform boundaries without any training process. The proposed method was evaluated on two publicly available databases, the QT Database (QTDB) and the Lobachevsky University Electrocardiography Database (LUDB). Experimental results show that PCDTW significantly reduces QT and QTcB estimation errors compared with conventional DTW variants, demonstrating improved temporal consistency and lower bias across cardiac cycles. In particular, the mean QTcB error was reduced to 28.14 ms, compared with 124.54 ms obtained using conventional DTW. In addition, on LUDB, the overall mean delineation error for the P wave, QRS complex, and T wave boundaries was 10.68 ms, showing comparable or superior performance to state-of-the-art deep learning-based methods despite requiring no external training data. These findings indicate that morphology-aware, correlation-based temporal alignment provides a robust and interpretable alternative for ECG waveform boundary detection under realistic physiological variability.

Keywords: ECG; waveform alignment; dynamic time warping; Pearson correlation; fiducial point detection



Academic Editor: Elzbieta Olejarczyk

Received: 27 January 2026

Revised: 19 February 2026

Accepted: 20 February 2026

Published: 28 February 2026

Copyright: © 2026 by the authors.

Licensee MDPI, Basel, Switzerland.

This article is an open access article distributed under the terms and

conditions of the [Creative Commons Attribution \(CC BY\)](https://creativecommons.org/licenses/by/4.0/) license.

1. Introduction

Electrocardiography (ECG) is a representative biomedical signal that noninvasively records the electrical activity of the heart and has long been used as a central tool for clinical diagnosis and follow-up monitoring [1]. In recent years, advances in wearable devices and continuous monitoring technologies have expanded ECG acquisition from hospital-centered environments to daily-life settings [2]. Accordingly, the demand for precise analysis of long-term changes in cardiac status, beyond single time-point interpretations,

has increased. These developments suggest the need to interpret ECG not simply as a recorded signal, but as a dynamic signal that continuously reflects individual physiological conditions and cardiovascular responses over time.

In real-world ECG signals, waveform morphology and temporal structure continuously vary due to inter-individual physiological differences, heart rate variability, and baseline fluctuations [3]. Owing to these characteristics, accurately defining and automatically extracting waveform boundary information—such as onset and offset points—using consistent criteria remains a challenging task, as illustrated in Figure 1. Traditionally, waveform boundary delineation has relied on expert experience and visual interpretation; however, this approach exhibits limited scalability in the context of long-duration recordings or large-scale data analysis. In particular, consistently aligning boundary points corresponding to the same physiological waveform across different cardiac cycles directly affects the accuracy of automated estimation of clinically important indices, such as the QT interval and the ST segment.

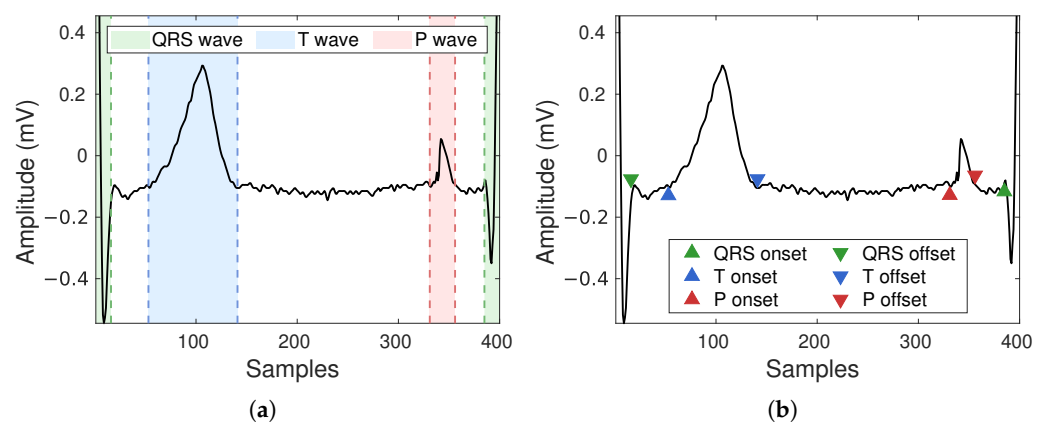


Figure 1. ECG waveform within a single RR interval. (a) QRS complex, T wave, and P wave regions. (b) Onset and offset points of each waveform.

Conventional rule-based ECG waveform analysis methods are designed based on physiological characteristics of the electrocardiogram and offer advantages in terms of implementation simplicity and interpretability [4–7]. However, because these methods rely on a limited set of predefined physiological rules and fixed thresholds, their robustness in real-world ECG environments is substantially reduced. In particular, waveform boundary estimation becomes unstable under conditions involving heart rate variability, inter-individual morphological differences, measurement noise, and baseline fluctuations. Meanwhile, deep learning-based approaches have been actively investigated in recent years and have demonstrated strong performance in classifying individual waveform components, such as T waves or P waves [8–15]. Nevertheless, these methods are relatively less effective in precisely estimating boundary information, including waveform onset and offset points. Moreover, their performance is highly sensitive to factors such as training data composition, annotation criteria, dataset scale, and expert-dependent labeling strategies, leading to considerable variability across studies.

Despite methodological differences, these existing approaches share a fundamental limitation in that they do not explicitly account for nonlinear temporal distortions and morphological variations occurring within and across cardiac cycles. As a result, they face intrinsic difficulties in consistently aligning ECG waveforms from different heartbeats using a unified reference framework, which in turn constrains the stable correspondence of waveform boundaries. In practical ECG signals, even identical physiological waveforms undergo continuous changes in temporal location and duration due to heart rate variability,

and such nonlinear temporal distortions represent a major source of error in waveform boundary estimation. Therefore, instead of alignment strategies based on simple pointwise comparisons, methods that can flexibly align the temporal axis while preserving structural waveform similarity are required.

Dynamic Time Warping (DTW) is a well-established technique that allows nonlinear temporal alignment between time series while preserving morphological similarity, making it suitable for analyzing periodic yet highly variable biosignals such as ECG. However, most conventional DTW-based approaches employ cost functions based on pointwise amplitude differences [16], which are insufficient for capturing local structural similarities of waveforms [17]. Consequently, this limitation often leads to unstable correspondence of waveform boundaries across cardiac cycles.

The aforementioned limitations are attributed not to the alignment mechanism of DTW itself, but rather to the cost function used to evaluate similarity between time series, which fails to adequately capture morphological characteristics of ECG waveforms. In this study, while preserving the structural advantages of the DTW framework, we introduce an alternative alignment strategy that reflects local waveform morphology, rather than relying on conventional DTW schemes based on pointwise amplitude differences. Specifically, we hypothesize that incorporating Pearson correlation [18], a metric that quantifies morphological similarity, into the DTW cost function can improve the stability of waveform boundary correspondence. Based on this hypothesis, this study proposes a correlation-based DTW alignment framework that consistently matches ECG waveforms across different cardiac cycles, thereby enabling more reliable estimation of waveform boundaries, including the onset and offset of the P wave, QRS complex, and T wave.

In this study, a correlation-based DTW alignment method (PCDTW) was proposed and applied to the problem of ECG waveform boundary estimation. Experimental results showed that the proposed method achieved overall competitive performance in terms of waveform alignment stability and boundary estimation accuracy within the datasets and comparison framework considered in this study. In particular, PCDTW demonstrated high clinical reliability in estimating QTcB, a key indicator for cardiac diagnosis. While the conventional pointwise DTW produced a mean error of 124.54 ms, the proposed method reduced the error to 28.14 ms and achieved the lowest standard deviation (37.40 ms), indicating robust performance across subjects. Furthermore, in waveform boundary estimation, PCDTW showed competitive performance compared with state-of-the-art deep learning models. The overall average error was 10.68 ms, which is comparable to that of ECG SegNet (12.23 ms) and 3CNN-2BiLSTM (12.32 ms), demonstrating its capability for precise ECG waveform analysis under diverse conditions.

2. Dataset

In this study, the QT Database (QTDB) and the Lobachevsky University Electrocardiography Database (LUDB), both publicly available through PhysioNet [19], were used.

2.1. QT Database (QTDB)

The QT Database [20] is a publicly available electrocardiogram (ECG) database consisting of a total of 105 records, with all signals sampled at 250 Hz. Each record contains approximately 15 min of two-channel ECG recordings and is composed of segments with relatively high signal quality to minimize the effects of baseline wander and noise. For each record, expert cardiologists manually annotated approximately 30–100 cardiac beats, including the onset and offset of the P wave, QRS complex, and T wave (and the U wave in some records).

QTDB was specifically designed to facilitate the analysis of ECG alternans phenomena, namely beat-to-beat alternation in T-wave amplitude or morphology. To this end, when possible, annotations are provided for 30 consecutive normal cardiac beats corresponding to a representative ECG waveform that is most frequently and consistently observed throughout the entire recording. In records exhibiting pronounced QRS morphological variability, up to 20 additional cardiac beats with morphologies different from the representative pattern were also annotated. All annotations are restricted to normal beats, and expert annotations are provided only for the final 5 min of each 15-min recording. As a result, the annotated segments correspond to approximately 2.8% of the total data per channel.

In addition, QTDB includes automatically detected R-peak location information. In this study, all R-peak locations were manually re-verified to ensure maximum consistency of reference points. The QT interval was defined as the duration from the onset of the Q wave (Q onset) to the end of the T wave (T offset), reflecting the total time required for ventricular depolarization and repolarization. To ensure a direct and unbiased comparison with expert annotations, no additional filtering was applied during QT interval or QTcB calculation, thereby avoiding unnecessary signal distortions.

Within segments where expert annotations were available, the proposed algorithm was applied to newly estimate Q onset and T offset for an average of approximately 27 cardiac beats per channel. These estimates were then compared with expert annotations to quantitatively evaluate the performance of QT interval and QTcB estimation.

2.2. Lobachevsky University Electrocardiography Database (LUDB)

The Lobachevsky University Electrocardiography Database [21] consists of 200 twelve-lead ECG recordings sampled at 500 Hz, with each record containing approximately 10 s of ECG signal. All recordings were independently annotated on a per-lead basis by experienced cardiologists, with the onset, peak, and offset of the P wave, QRS complex, and T wave (and, in some cases, the U wave) manually labeled. The dataset covers a wide age range, from 11 years to over 89 years, thereby reflecting diverse physiological and pathological characteristics. In addition to waveform boundary annotations, each record includes extensive diagnostic information such as sex, age, cardiac rhythm, electrical axis of the heart, conduction abnormalities, extrasystoles, atrial and ventricular hypertrophy, ischemia, and non-specific repolarization abnormalities, making LUDB a comprehensive dataset encompassing a broad spectrum of clinically relevant ECG patterns.

Data acquisition was performed by trained medical personnel using a Schiller Cardiovit AT-101 twelve-lead ECG system (SCHILLER AG, Baar, Switzerland) Response: We have confirmed that this item is equipment. The manufacturer information, including the company name, city, and country, has been added accordingly. , and all participants provided written informed consent prior to recording. The construction of the dataset was approved by the Institutional Review Board of Lobachevsky University (Approval no. #23, 19 October 2017).

Based on these characteristics, all 200 records included in LUDB were used in this study to evaluate ECG waveform boundary detection performance. To ensure consistent algorithm application under identical experimental conditions, the original signals sampled at 500 Hz were resampled to 250 Hz prior to analysis. Waveform delineation algorithms were applied and evaluated using the independent, lead-specific annotations provided in the database. Furthermore, to enable a fair comparison with previous studies, only the Lead I signal from each record was used for analysis.

3. Method

All signal processing procedures were performed using MATLAB (R2024a, MathWorks, Natick, MA, USA). Python (Version 3.10.16, Python Software Foundation, Wilmington, DE, USA) was used only for the deep learning-based comparison experiments. The overall workflow of the proposed PCDTW-based ECG waveform delineation method is illustrated in Figure 2.

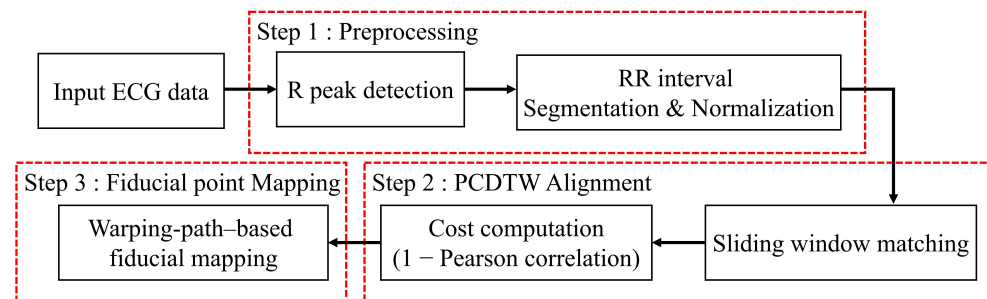


Figure 2. Overall workflow of the proposed PCDTW-based ECG waveform delineation method.

3.1. Data Preprocessing Procedures

The length of the RR interval varies substantially depending on individual physiological characteristics and heart rate conditions. In healthy adults, RR intervals can shorten to approximately 600 ms during elevated heart rates (around 100 bpm) and extend to approximately 1200 ms at lower heart rates (around 50 bpm). In cases of bradycardia, RR intervals may further increase beyond 1500 ms. Such heart rate variability poses a major challenge for direct comparison of ECG waveforms across cardiac cycles.

To robustly accommodate this variability and to ensure that each cardiac cycle contains a complete waveform structure, including the QRS complex, T wave, and P wave, each cardiac cycle was normalized to a fixed duration of 1600 ms [22]. This duration was selected to sufficiently cover a wide range of RR intervals, including slow heart rates, while maintaining a physiologically reasonable window that preserves the full waveform structure throughout the cardiac cycle.

For this purpose, the RR interval between consecutive R peaks was computed for each beat, and the corresponding signal segment was temporally realigned and resampled to a length of $1.6f_s$ (e.g., 400 samples at $f_s = 250$ Hz). Through this normalization and resampling procedure, differences in cycle length across beats were eliminated, enabling direct comparison of waveforms at a uniform temporal resolution and length. Consequently, subsequent waveform matching and alignment procedures were performed under consistent conditions across all cardiac cycles using a DTW-based analysis framework.

3.2. Reference-Based Morphological Alignment for ECG Waveform Boundary Estimation

Electrocardiogram (ECG) signals exhibit repetitive morphological structures across cardiac cycles, and the boundary locations of waveforms within each cycle provide important information for interpreting cardiac functional states. In this study, a matching strategy based on morphological alignment between normalized RR intervals was adopted to achieve stable estimation of waveform boundaries.

First, a reference pattern, denoted as pattern A, was defined. Pattern A was constructed as a representative cycle by averaging multiple cardiac cycles selected from the entire ECG recording after normalization at the RR-interval level. This pattern serves as a subject-specific reference that summarizes the overall morphological characteristics of the ECG waveform. Individual cardiac cycles observed throughout the ECG recording were then defined as pattern B.

Each pattern B was morphologically aligned with pattern A at the level of normalized RR intervals, and the resulting alignment was used to estimate the relative locations of waveform boundaries within each cycle. This approach enables consistent identification of structural correspondences with respect to the reference pattern, even in the presence of variability in cycle length and waveform morphology across beats.

The primary objective of this analysis is to quantitatively estimate ECG waveform boundary locations based on the A–B pattern matching framework and to compare the performance of different alignment and mapping methods for this purpose.

3.2.1. Baseline Method

In this study, Dynamic Time Warping (DTW) was applied to align ECG waveforms between a reference cycle A and a comparison cycle B , enabling the correspondence of fiducial points across cardiac cycles. DTW allows nonlinear temporal distortions between two sequences, thereby effectively aligning structurally similar patterns even when the same features occur at different time instants. Owing to this property, DTW is well suited for reliably matching temporally misaligned peaks and waveform boundaries, even when all cycles have identical lengths. The DTW distance between two sequences is defined as follows. Let $A = (a_1, a_2, \dots, a_n)$ and $B = (b_1, b_2, \dots, b_m)$ be two time series.

The DTW distance between these two sequences can be formally defined as follows:

$$DTW(A, B) = \min_{w \in \mathcal{W}} \left\{ \sum_{(i,j) \in w} cost(a_i, b_j) \right\} \quad (1)$$

Here, $\mathcal{W}$ denotes the set of all admissible warping paths, where each $w \in \mathcal{W}$ is a single warping path defined as an ordered sequence of index pairs (i, j) representing point-wise correspondences between the time series A and B . The local distance between samples a_i and b_j is defined as $cost(a_i, b_j)$.

In order to evaluate the total alignment cost over a warping path w , the DTW algorithm constructs a cumulative cost matrix $D(i, j)$ using the following recursive relation:

$$D(i, j) = cost(a_i, b_j) + \min \begin{cases} D(i-1, j), \\ D(i, j-1), \\ D(i-1, j-1) \end{cases} \quad (2)$$

Once the cumulative cost matrix $D(i, j)$ is computed, the optimal warping path w is obtained by backtracking from the endpoint $D(n, m)$ to the origin $D(1, 1)$, following the path of minimum cumulative cost [16]. This path represents the best alignment between the two sequences, accounting for possible non-linear temporal distortions.

3.2.2. PCDTW (Pearson Correlation–Based Dynamic Time Warping)

Conventional pointwise Dynamic Time Warping (DTW) evaluates the similarity between time series by accumulating sample-wise differences at corresponding time indices, offering simplicity in implementation and a clear computational structure. However, for signals such as ECG waveforms, where morphological structure and local variations are critical, the alignment path can become unstable in the presence of subtle intra-beat morphological changes or nonlinear temporal distortions. As a result, as shown in Figure 3a, clinically meaningful waveform features may not be adequately preserved during alignment.

To address these limitations, various extensions of DTW have been proposed, including correlation-based DTW and local-zone matching approaches [22–24], which compare waveform structures over local segments rather than relying solely on pointwise differences. These methods share the common objective of extending the DTW comparison unit

from the sample level to the local segment level, thereby incorporating relative waveform variations and morphological context more directly into the alignment process.

Following this perspective, the present study introduces a window-based comparison scheme that jointly considers waveform information surrounding each time index. Specifically, the reference pattern (A pattern) and each individual cardiac cycle (B pattern) are normalized to the same RR interval length. For each pair of time indices i and j , local segments $W_A(i)$ and $W_B(j)$ of length $2 \text{ window} + 1$ are constructed, centered at i and j , respectively. This window-based definition enables the alignment process to account not only for individual sample values but also for the surrounding morphological context and local temporal dynamics.

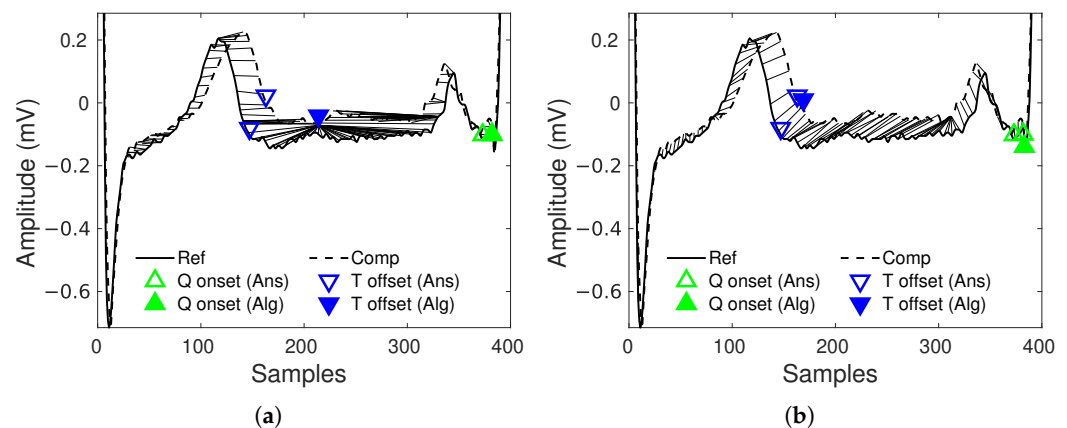


Figure 3. Comparison of DTW-based ECG matching methods. (a) Matching result of conventional DTW using pointwise alignment with Euclidean distance as the cost function. (b) Matching result of correlation-based DTW using window-level alignment with Pearson correlation as the cost function.

Nevertheless, when the cost function in window-based DTW is defined using the conventional Euclidean distance [25], all samples within a window are treated with equal importance. Consequently, clinically significant morphological transition points—such as T-wave onset or offset—may be averaged out and diluted within the window. This limitation indicates that window-based DTW alone may be insufficient to simultaneously achieve both alignment stability and fine-grained morphological preservation.

$$r = \frac{\text{cov}(X, Y)}{\sigma_X \sigma_Y} = \frac{\sum_{i=1}^n (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_{i=1}^n (x_i - \bar{x})^2} \sqrt{\sum_{i=1}^n (y_i - \bar{y})^2}} \quad (3)$$

To overcome this issue, the present study incorporates a Pearson correlation coefficient-based cost function into the window-based DTW framework to more effectively capture ECG morphological characteristics. The Pearson correlation coefficient is defined as shown in Equation (3), and quantifies the strength and direction of the linear relationship between two variables X and Y , with values ranging from -1 to 1 . This coefficient reflects the degree to which deviations from the mean exhibit similar patterns, and is computed based on covariance normalized by the standard deviations of the variables, thereby eliminating dependence on their absolute variance scales.

$$\text{cost}(i, j) = 1 - \text{corr}(W_A(i), W_B(j)) \quad (4)$$

Such a correlation coefficient quantifies the similarity of relative variation patterns with respect to the mean, rather than absolute amplitude differences between two signals, making it suitable for evaluating morphological consistency between waveforms. The cost function defined based on Equation (3), as formulated in Equation (4), is incorporated into

the DTW framework and used to compute the cumulative cost matrix $D(i, j)$ according to the same recursive formulation as conventional DTW, as shown in Equation (2), thereby determining the optimal warping path.

Using the resulting DTW alignment path, the temporal regions in the B pattern corresponding to the waveform boundary points (onsets and offsets) defined in the reference A pattern are estimated. Within each estimated region, extremum detection is applied to identify the actual boundary locations in the B pattern. This DTW-based morphological alignment strategy locally constrains candidate boundary regions, thereby reducing false detections and improving the consistency and reproducibility of boundary estimation.

Furthermore, because the proposed method performs matching based on relative waveform variation patterns rather than absolute amplitude differences, it maintains robust boundary detection performance under conditions such as amplitude scaling and baseline drift, as shown in Figure 3b. In this study, this Pearson correlation-based windowed DTW approach is referred to as PCDTW (Pearson Correlation-based Dynamic Time Warping), and a detailed description is provided in Appendix A.

4. Experimental Results

4.1. ECG Waveform Boundary Detection Performance with QTDB

The purpose of this study is to reduce the manual workload required of experts when analyzing large-scale or long-term ECG signals in clinical environments, and to improve the automation and consistency of ECG waveform analysis. To this end, we introduce a DTW-based approach that aligns structural correspondences between ECG waveforms by explicitly accounting for temporal variability and morphological changes occurring across cardiac cycles, thereby enabling more stable analysis of ECG waveforms that form the basis of disease and stress assessment. In addition, this study aims to evaluate whether the proposed Pearson correlation-based DTW (PCDTW) can be effectively applied in clinically realistic settings and to quantify the extent of performance improvement over conventional DTW methods. To this end, we performed a comparative analysis between the conventional Euclidean distance-based DTW and the proposed DTW framework illustrated in Figure 4.

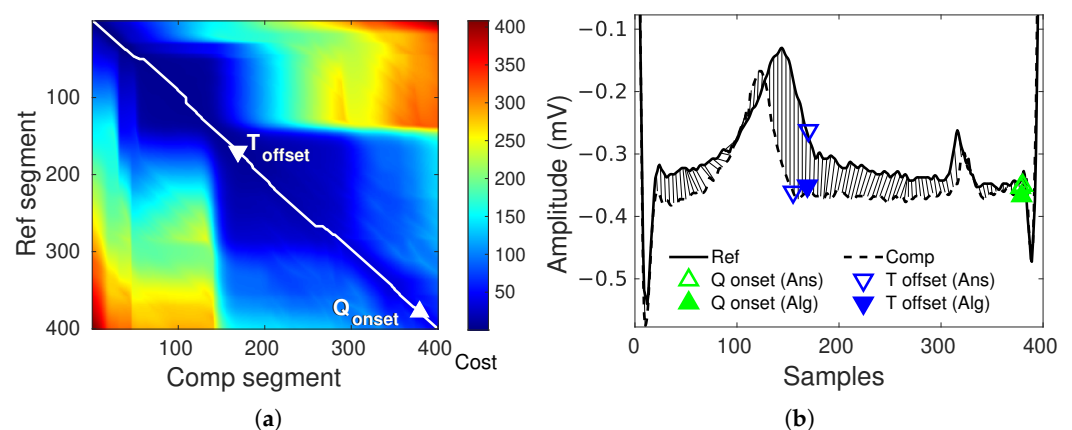


Figure 4. Pearson correlation-based DTW. (a) Window-level Pearson correlation heatmaps and the corresponding DTW warping paths. (b) ECG waveform alignment between the reference pattern and target pattern along the DTW path, where connecting lines indicate matched window pairs.

For this evaluation, the QT Database (QTDB) was employed. The QTDB provides highly precise expert annotations of waveform boundaries, which serve as reliable reference information for quantitatively analyzing temporal variations in the ventricular depolarization–repolarization interval, such as the QT interval and the heart-rate-corrected QT interval (QTcB). Accordingly, QTDB was used in this study for QT interval and QTcB

calculation. Records with missing or discontinuous expert annotations were excluded from the analysis. Specifically, only records in which expert annotations for Q onset and T offset were continuously provided for all target heartbeats from the beginning to the end of the recording were selected. Based on these strict inclusion criteria, a total of 56 records satisfying the continuity and completeness requirements were ultimately included in the final analysis.

The analysis results are summarized in Table 1, which presents the mean and standard deviation of the heart rate–corrected QT interval (QTcB) for each method, calculated according to Equation (5). QTcB is a heart rate–corrected measure that normalizes ventricular repolarization time by adjusting the QT interval—defined as the duration from QRS onset (Q onset) to the end of the T wave (T offset)—with respect to the RR interval. It is widely used as a robust criterion for evaluating the stability of QT interval estimation under conditions of heart rate variability [26].

$$QTcB = \frac{QT}{\sqrt{RR}} \quad (5)$$

Table 1. QTcB errors obtained using DTW-based algorithms.

Method	$ \Delta QTcB $
DTW (norm RR, pointwise)	124.54 ± 164.68
DTW (norm RR, windowed)	33.86 ± 49.63
PCDTW (norm RR, windowed)	28.14 ± 37.40

Values are reported as mean $\pm$ standard deviation (unit: ms). $|\Delta QTcB|$ denotes the absolute difference between algorithm-estimated and reference QTcB values.

The DTW (norm RR, pointwise) method exhibited the largest QTcB error among the compared approaches, with a mean error of 124.54 ± 164.68 ms. This result is not attributable to random variation, but rather reflects an inherent limitation of the pointwise cost function employed by the method. In pointwise DTW, the alignment path is determined by minimizing amplitude differences at individual time points. However, in ECG waveforms, the boundaries of the QT interval, namely the Q onset and T offset, are often located in regions with gradual amplitude changes or locally flat signal characteristics. As a result, the DTW path is prone to being attracted toward segments with coincidentally small amplitude differences rather than true physiological boundaries. Consequently, the QT interval boundaries are systematically misaligned, leading to substantial bias in the estimated QTcB values.

The DTW (normalized RR, windowed) method demonstrated a significant improvement in terms of the mean QTcB error compared to the conventional approaches, indicating that the overall QTcB level was preserved with relatively high accuracy. However, the standard deviation remained comparatively large, suggesting a wide dispersion of QTcB estimation errors across individual cardiac cycles. This indicates that, although average estimation accuracy was achieved, the stability of QTcB estimation may vary substantially depending on specific cycles or subjects.

In contrast, the proposed PCDTW (normalized RR, windowed) method exhibited not only the smallest mean QTcB error but also the lowest standard deviation among the compared approaches, indicating more stable and consistent QTcB estimation performance overall. This improvement can be attributed to the Pearson correlation–based cost function, which emphasizes morphological similarity of ECG waveforms rather than absolute amplitude differences during the matching process. Furthermore, the window-based matching scheme preserves local waveform structures while reducing sensitivity to noise and minor signal distortions, thereby effectively mitigating inter-cycle variability in QTcB estimation.

Nevertheless, it should be noted that mean $\pm$ standard deviation statistics summarize the distribution using only two scalar values and may not fully represent the underlying error characteristics when the distribution is skewed, contains outliers, or exhibits subject-specific clustering. For this reason, complementary analyses based on distribution-level visualization and representative error cases are necessary to enable a more comprehensive comparison of QTcB estimation performance across methods.

As shown in Figure 5, the pointwise DTW exhibits low explanatory power (R^2) and large dispersion in QTcB estimation, with a regression slope greater than unity, indicating a systematic overestimation bias. These characteristics reflect structural limitations in QT boundary alignment, as the pointwise DTW relies primarily on local amplitude differences rather than waveform morphology.

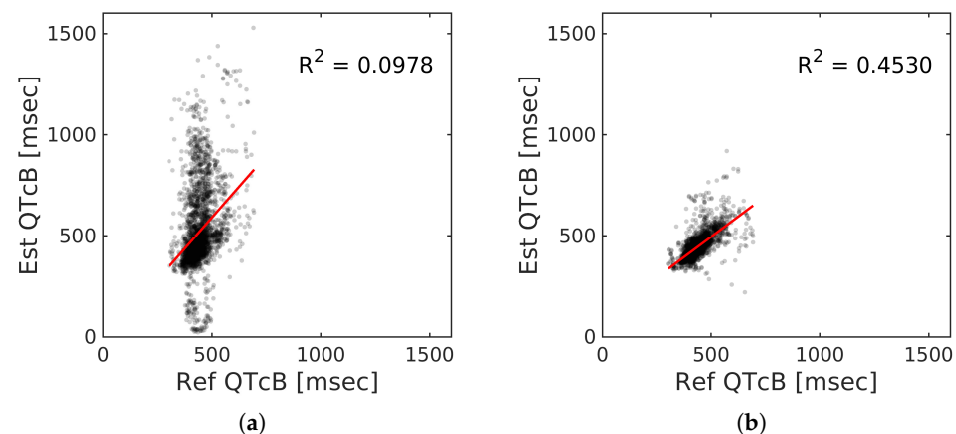


Figure 5. Scatter plots comparing estimated QTcB values with reference annotations ($N = 2912$). (a) DTW (normalized RR, pointwise). (b) PCDTW (normalized RR, windowed).—The red line in the scatter plot denotes the linear regression fitted between the reference QTcB values and the algorithm-estimated QTcB values, providing a visual means to evaluate the algorithm’s overall estimation bias (over- or underestimation) and consistency. Ref QTcB: Bazett corrected QT interval derived from expert annotations (Q onset to T offset). Est QTcB: values automatically obtained using the proposed method.

In contrast, the proposed PCDTW (normalized RR, windowed) demonstrates a substantially higher R^2 and reduced variability, yielding a more consistent estimation trend across the entire QTcB range. Although a slight underestimation tendency is observed, the overall correspondence remains stable and coherent, resulting in markedly improved reliability and robustness of QTcB estimation. These findings strongly support the effectiveness of a window-based alignment strategy that explicitly incorporates morphological similarity.

Next, Figure 6 was used to perform a more detailed comparative analysis of each algorithm. In the Bland–Altman plot, algorithm performance can be evaluated through four key characteristics [27]. The bias (mean difference) is defined as the average difference between the algorithmic estimates and the expert reference across cardiac cycles, indicating the overall tendency toward overestimation or underestimation. A bias close to zero implies good average agreement. The standard deviation (SD) of the differences quantifies the variability of disagreement between the algorithm and the reference, with smaller values indicating more consistent and stable performance. The limits of agreement (LoA), calculated as Bias $\pm$ 1.96 $\times$ SD, represent the range containing 95% of the differences. Narrow LoA indicate high reproducibility and stability, whereas wide LoA suggest increased variability. In addition, the Bland–Altman plot allows assessment of whether estimation errors systematically depend on the mean QT interval, revealing length-dependent error characteristics that are not captured by global summary metrics alone.

Based on these criteria, the three algorithms can be compared as follows. (a) The DTW (normalized RR, pointwise) method exhibited a positive bias, indicating a general tendency to overestimate the QT interval. It also showed the largest SD of differences, resulting in the widest LoA. Moreover, the magnitude of the error increased with increasing mean QT interval, suggesting a length-dependent bias. In contrast, (b) the PCDTW (normalized RR, windowed) method demonstrated a bias close to zero, indicating high accuracy, and a substantially narrower LoA compared to method (a), reflecting improved stability and consistency.

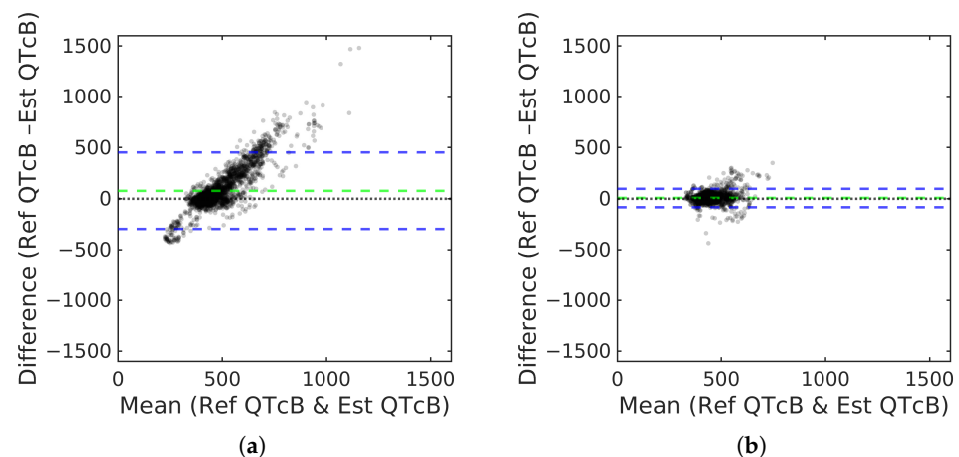


Figure 6. Bland–Altman plots for QTcB estimation ($N = 2912$). (a) DTW (normalized RR, pointwise). (b) PCDTW (normalized RR, windowed).—The green line denotes the mean difference (bias) between reference annotations and algorithm estimates, while the blue lines indicate the 95% limits of agreement defined as bias ± 1.96 standard deviations. Ref QTcB: Bazett corrected QT interval derived from expert annotations (Q onset to T offset). Est QTcB: values automatically obtained using the proposed method.

Figure 7 illustrates the squared errors between the reference QTcB values and those estimated by each algorithm across all cardiac cycles and subjects. For the DTW (normalized RR, pointwise) approach, the error distribution exhibits substantial variability throughout the cardiac cycle, indicating that this method remains sensitive to local temporal misalignments and residual morphological differences even after RR interval normalization. In contrast, the proposed PCDTW (normalized RR, windowed) method consistently yields lower error values across the entire cycle, suggesting that correlation-based window matching more effectively preserves morphological similarity during QTcB estimation.

Overall, PCDTW (normalized RR, windowed) demonstrates both reduced QTcB estimation error and markedly improved consistency across cardiac cycles compared to DTW (normalized RR, pointwise) and DTW (normalized RR, windowed). By aligning ECG waveforms based on window-level morphological correlation rather than pointwise amplitude differences, PCDTW achieves more stable correspondence between cardiac cycles. These results indicate that the proposed method provides a more robust and reliable framework for QTcB estimation under realistic ECG conditions characterized by heart rate variability and inter-subject morphological differences.

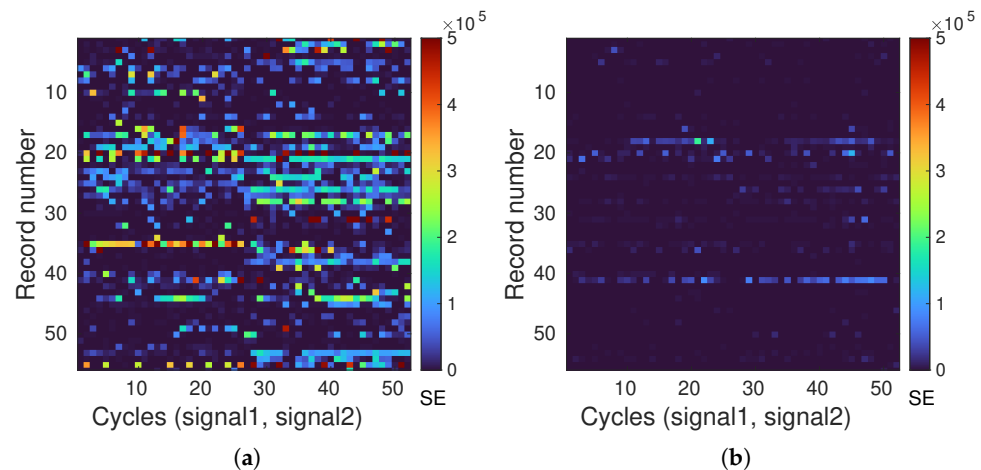


Figure 7. Squared error heatmaps for QTcB interval estimation. (a) DTW (normalized RR, pointwise). (b) PCDTW (normalized RR, windowed).—The color bar on the right represents the magnitude of the SE (squared error) in QTcB interval estimation, where blue indicates smaller errors and red indicates larger errors.

4.2. Sensitivity Analysis with Respect to Window Size

To quantitatively evaluate the effect of window size on the performance of the PCDTW method, a sensitivity analysis was conducted. To ensure experimental consistency, the same 56 QTDB records used throughout this study were employed. Detection performance was evaluated by applying a tolerance window of ± 50 ms between the algorithm-detected points and the expert annotations. Tolerance-based evaluation is commonly used for performance assessment in ECG delineation studies, and related evaluation criteria have been described by the Association for the Advancement of Medical Instrumentation (AAMI) [28]. While a 150 ms tolerance window has been widely used in previous studies [29], a narrower window was applied in this study. Detected points that matched reference annotations within the tolerance window were considered true positives (TP), while unmatched reference annotations and unmatched detected points were counted as false negatives (FN) and false positives (FP), respectively.

The window length was varied to 25, 50, 75, and 100 samples, and the detection performance for Q onset and T offset was evaluated. The results are presented in Figure 8. Overall, sensitivity differences remained within a limited range across all configurations. For Q onset detection, no sensitivity variation was observed in either lead, indicating comparable performance across different window lengths. In contrast, T offset detection showed minor variations across window conditions. The maximum sensitivity difference was 3.39 percentage points in Lead 1 and 3.69 percentage points in Lead 2.

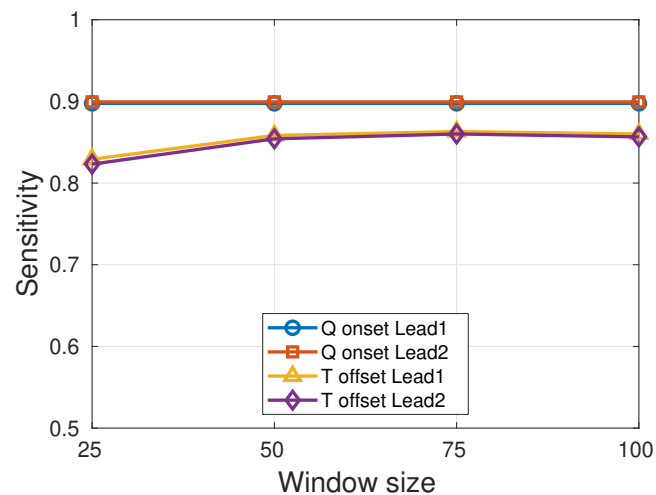


Figure 8. Sensitivity analysis across different window sizes for Q onset and T offset detection on the QT Database.

4.3. Fiducial Point Detection Performance with Deep Learning

We further conducted a performance comparison between the proposed PCDTW method, which had demonstrated improved performance over conventional DTW in previous analyses, and deep learning-based approaches. This comparative study was performed using the LUDB database. Table 2 presents the delineation error comparison results for ECG waveforms (P wave, QRS complex, and T wave) computed from 200 records of the LUDB database based on Lead I.

Table 2. Comparison of P, QRS, and T wave detection errors (ms) between PCDTW and state-of-the-art ECG segmentation methods on the LU database (150-ms tolerance criterion).

Author	Method	P Onset	P Offset	QRS Onset	QRS Offset	T Onset	T Offset	Avg
Abrishami et al. [8]	2BiLSTM	11.92	23.47	19.23	33.75	70.71	46.96	34.34
Londhe et al. [9]	1CNN_2BiLSTM	25.69	13.16	18.66	15.21	30.66	31.83	22.63
Peimankar et al. [10]	3CNN_2BiLSTM	10.92	8.77	10.37	10.39	21.00	14.48	12.32
Nurmaini et al. [11]	4CNN_1BiLSTM	12.20	12.06	13.00	14.00	28.39	19.36	14.34
Camps et al. [12]	CNNs	34.95	38.66	55.07	34.04	30.06	63.19	39.94
Jimenez-Perez et al. [13]	UNet	10.46	9.28	9.37	11.31	29.30	25.05	15.79
Isensee et al. [14]	2-UNet cascade	11.83	7.79	11.99	9.10	25.64	14.25	13.65
Isensee et al. [14]	3-UNet cascade	11.29	9.08	9.19	9.79	25.79	14.79	13.15
Liang et al. [15]	ECG_SegNet	9.72	6.77	9.08	10.34	23.22	14.23	12.23
Our method	PCDTW	12.08	8.26	6.60	7.90	15.27	13.97	10.68

Deep learning-based ECG waveform analysis methods exhibit distinct morphological representation characteristics depending on their model architectures, which in turn lead to differences in robustness to waveform variability and boundary estimation performance. BiLSTM-based models leverage bidirectional temporal context to achieve relatively robust boundary detection under inter-beat temporal variability. However, their emphasis on long-term dependencies tends to smooth fine morphological boundaries such as onsets and offsets, while also incurring high model complexity and training cost. CNN-based models effectively capture local morphological features through limited receptive fields and perform well in regions with strong morphological contrast, such as the QRS complex or T wave. Nevertheless, their ability to handle large beat-to-beat duration variability or nonlinear temporal distortions remains limited due to insufficient modeling of long-range temporal dependencies. U-Net-type architectures combine multi-scale features via encoder-decoder structures and skip connections, achieving high accuracy in segmentation-

based boundary detection. This performance, however, strongly depends on the availability of large, consistently annotated training datasets, and generalization may degrade when data distributions or annotation criteria differ. Overall, while deep learning approaches can achieve high performance by learning diverse waveform variations and noise characteristics, they inherently rely on extensive training data, exhibit sensitivity to generalization, and require substantial computational resources [30].

In contrast to learning-based approaches, the proposed PCDTW framework adopts a structurally different strategy by performing waveform alignment across all cardiac cycles using a single representative reference cycle directly extracted from each record, without requiring any training process. By incorporating a Pearson correlation-based cost function, the proposed method explicitly captures local morphological similarity, enabling stable correspondence of waveform boundaries even in the presence of inter-beat temporal variability or nonlinear temporal distortions. This design allows record-specific morphological characteristics to be naturally embedded into the reference pattern, thereby achieving robust waveform alignment without reliance on external training data or pre-trained models. Although the use of a single reference cycle may lead to reduced performance for a small subset of beats with substantial morphological deviation from the reference, PCDTW nevertheless offers a structural advantage over learning-based methods by constructing reference patterns at the record level and directly exploiting data-dependent morphological information, making it inherently less sensitive to data distribution shifts and generalization issues.

Experimental results demonstrate that PCDTW achieves overall superior performance compared to deep learning-based waveform segmentation methods, particularly by attaining high alignment consistency and boundary estimation accuracy without dependence on external training datasets or pre-trained models. This robustness stems from the use of record-specific reference cycles, which effectively preserve waveform morphology even in datasets such as LUDB, where inter-record morphological variability is pronounced. Consequently, PCDTW is able to mitigate performance degradation caused by distribution mismatch or generalization failure, confirming that reliable waveform boundary estimation can be achieved using only limited, record-internal information.

4.4. Computational Time Comparison Between Deep Learning and PCDTW

To evaluate the applicability of the PCDTW algorithm in real clinical and daily-life environments, this study analyzed not only detection accuracy but also computational complexity and computation time, as summarized in Table 3. Execution time evaluation was conducted using the LUDB dataset.

Table 3. Computational time comparison between Deep Learning and PCDTW methods.

Input Size	Deep Learning			PCDTW
	Train (s)	Test (s)	Total (s)	Total (s)
400 samples (norm RR)	4675.51	3.41	4678.92	40.46 (window = 50)

All experiments were conducted on a system equipped with an Intel Core i5-14400 CPU.

The proposed PCDTW was designed as a training-free framework, requiring no additional model training cost. Furthermore, by adopting a window-based alignment strategy, the computational burden was reduced compared to conventional point-wise DTW, thereby alleviating overall computational complexity. Under the condition where each RR interval was normalized to 400 samples, the total time required to extract fiducial points from 200 LUDB records was 40.46 s.

For comparison, the computational time of a deep learning-based method was also analyzed. A 1D CNN model was trained using 105 records from QTDB and subsequently applied to 200 LUDB records. Under the same 400-sample normalization condition, the inference phase alone required 3.41 s for extracting all fiducial points. However, the training phase required 4675.51 s in a CPU-based environment, resulting in a total processing time (training + inference) of 4678.92 s.

In summary, the deep learning-based method demonstrated fast processing speed during the inference phase but required a comparatively high computational cost during training. In contrast, PCDTW does not require a training process and can be applied without additional training cost due to its reduced computational complexity. Moreover, the average execution time for a single 10-s ECG record was approximately 0.2 s, suggesting that fiducial point detection for individual ECG recordings can be feasibly implemented in real-time or near-real-time environments.

5. Discussion

The objective of this study is to develop a robust and interpretable ECG waveform alignment framework capable of accurately detecting fiducial points even in the presence of temporal distortion and amplitude variability. To this end, we proposed a Pearson correlation-based Dynamic Time Warping (PCDTW) method that focuses on morphological alignment within normalized RR intervals. Experimental results demonstrated that the proposed approach exhibits stable and consistent performance across a wide range of evaluation metrics, including QT interval estimation, QTcB analysis, and the accuracy of multi-waveform boundary detection.

One of the key findings of this study is the structural limitation observed when conventional Euclidean distance-based DTW is applied to ECG signals [16]. Although pointwise DTW can compensate for temporal misalignment, it is highly sensitive to amplitude scaling and baseline fluctuations. This sensitivity leads to instability in the alignment path and large estimation errors, particularly when substantial amplitude differences exist between the reference and target cycles. Window-based DTW partially alleviates these limitations by incorporating local waveform structures into the matching process, thereby reducing noise sensitivity and improving average accuracy. However, because its cost function remains fundamentally based on Euclidean distance, distortions caused by amplitude differences are not completely eliminated, resulting in relatively large variability in QT interval and QTcB estimation.

In contrast, the proposed PCDTW method explicitly decouples waveform similarity from absolute amplitude differences by employing the Pearson correlation coefficient as the matching cost. This design encourages the alignment process to focus on relative morphological patterns rather than magnitude differences, thereby establishing more stable correspondences between cardiac cycles. These characteristics are consistently observed across multiple analyses. In QT interval heatmaps and RMSE comparisons, PCDTW exhibited the lowest error levels and the most uniform error distribution across subjects. Moreover, in QTcB analysis, it achieved the smallest standard deviation and near-zero bias in Bland–Altman plots, indicating enhanced robustness under conditions of heart rate variability.

Another important feature of the proposed framework is its reference-based alignment strategy. By directly constructing a subject-specific reference cycle from each ECG record, the method eliminates dependence on external training data or population-averaged templates. This approach is particularly advantageous in real-world clinical settings, where inter-subject waveform variability and recording conditions can differ substantially.

Conventional rule-based ECG waveform boundary detection methods are typically designed under the assumption of low-noise signals with canonical waveform morphologies and rely on explicit waveform assumptions, such as fixed slope patterns, predefined amplitude thresholds, or empirical temporal relationships between fiducial points [4–6]. However, these assumptions readily break down in cases of large inter-subject variability or atypical pathological waveform deformations. In contrast, the proposed PCDTW framework performs alignment based on relative waveform similarity rather than predefined geometric rules, providing more stable and consistent correspondences even in the presence of waveform distortion, respiratory or motion artifacts, and amplitude fluctuations caused by changes in electrode contact conditions.

Deep learning-based waveform boundary detection methods generally assume that the morphological characteristics of ECG waveforms observed during inference are sufficiently represented within the training data distribution. Under this assumption, waveform boundaries are generalized through population-level parameter optimization. Such models typically require large annotated datasets and extensive training processes to achieve high performance, which can impose practical constraints in terms of data availability and computational resources. In real ECG recordings, however, inter-cycle amplitude variations, baseline drift, atypical T-wave morphologies, and pathological waveform changes frequently occur, leading to distribution mismatches between training and deployment data [8–15].

In contrast, PCDTW operates at the record level by directly exploiting morphological similarity within the same signal, allowing it to adapt naturally to subject-specific waveform characteristics without requiring prior training or large annotated datasets. Comparative results with recent deep learning-based models on the LUDB database further demonstrate that PCDTW achieves comparable or, in some cases, superior waveform boundary detection accuracy despite the absence of a training phase, thereby supporting the effectiveness and clinical applicability of the reference-based alignment strategy.

Considering these characteristics, PCDTW provides more stable and consistent estimation of waveform boundaries. Such improved boundary reliability is particularly important for quantitative ECG analysis, where clinically relevant time intervals depend directly on precise boundary localization. This allows not only the QT interval, which was the primary focus of this study, but also various time-based clinical indices—such as the PR interval and P-wave duration—to be measured with improved accuracy.

The QT interval is a representative metric reflecting both ventricular depolarization and repolarization and is highly dependent on the accuracy of boundary localization. By reducing temporal variability in QT measurement, the PCDTW-based alignment can enhance the reliability of clinical applications, including the assessment of ventricular repolarization abnormalities, monitoring of drug-induced QT prolongation, and risk stratification for life-threatening arrhythmias [31]. Meanwhile, the PR interval represents the conduction time from the onset of the P wave to the beginning of the QRS complex and reflects atrioventricular conduction status, making it useful for evaluating conduction delays or atrioventricular block [32]. In addition, P-wave duration indicates atrial depolarization time and is particularly sensitive to small variations in boundary detection [33]. Therefore, improving the consistency of waveform boundary estimation can increase the reliability of atrial conduction assessment and support more stable identification of atrial abnormalities, such as left atrial enlargement and the risk of atrial fibrillation.

Overall, the proposed framework improves the reliability of quantitative ECG analysis by providing reproducible waveform boundary localization. By enabling stable temporal information, it supports precise estimation of various functional timing indices. These characteristics may facilitate the detection of subtle temporal abnormalities associated with ventricular functional changes and suggest the potential for extension to early diagnosis and risk assessment of cardiovascular diseases, including heart failure.

Despite these advantages, several limitations should be acknowledged. First, the performance of window-based matching methods, including PCDTW, may be affected by the choice of window size, which can introduce a trade-off between robustness and temporal precision. In this study, a fixed window size was determined empirically, and additional analysis showed that performance differences across window sizes were minimal, with consistent overall trends. This suggests that the proposed morphology-based alignment strategy operates robustly under temporal distortions and local signal variations. However, under conditions such as stress, physical activity, or autonomic changes, adaptive windowing may be more appropriate than a fixed window. A systematic evaluation of adaptive window selection under diverse signal conditions was, however, beyond the scope of this study and remains a limitation.

Second, the current implementation employs a single representative reference cycle for each record. This design provides simplicity and interpretability; however, the alignment performance may degrade in recordings with substantial morphological variability or abnormal heartbeats. A preliminary analysis suggested that a multi-reference strategy, which incorporates different morphological patterns, may reduce alignment errors and outliers in complex waveform segments, thereby potentially improving estimation accuracy. Nevertheless, in this study, the single-reference structure was retained to maintain structural simplicity and stability. Meanwhile, morphologically abnormal beats tend to exhibit low correlation with the reference cycle, allowing them to be naturally identified during the alignment process and handled through exclusion or separate analysis in post-processing. Therefore, the proposed framework suggests the potential for extension to a multi-reference-based alignment strategy to further enhance robustness across diverse ECG morphologies.

Finally, although the proposed method was validated using two public databases, limitations were observed in alignment accuracy and boundary estimation when the morphological similarity between heartbeats was reduced. As shown in Figure 9, such cases mainly occurred when waveform shapes were ambiguous or distorted [34], or when signal quality was degraded by noise. These limitations are considered to stem from the inherent reliance of the algorithm on morphological similarity between waveforms. Based on these observations, further validation is required in real-world environments characterized by high physiological variability—such as during physical activity, exercise, or stress—as well as increased noise conditions. In addition, the practical utility of the system could be further improved by enhancing noise robustness, incorporating Signal Quality Index (SQI)-based preprocessing, and introducing confidence assessment techniques for the estimation results [35].

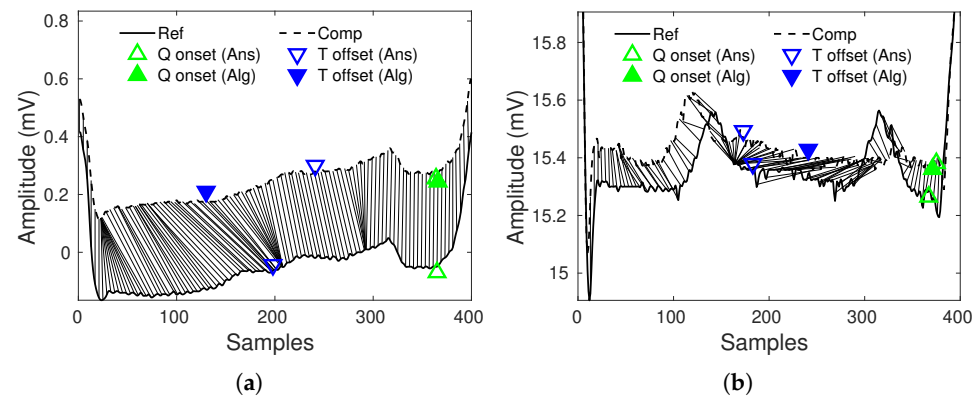


Figure 9. Representative cases showing performance limitations under challenging ECG conditions (a) Poorly defined characteristic waveforms. (b) Degraded signal quality.

6. Conclusions

This study proposed a morphology-oriented ECG waveform alignment method based on Pearson correlation-based Dynamic Time Warping (PCDTW) for robust fiducial point detection. By integrating window-based matching with a correlation-driven cost function, the proposed approach effectively addresses the limitations of conventional Euclidean distance-based DTW methods, particularly their sensitivity to amplitude variations and baseline distortions.

Comprehensive evaluations using publicly available ECG databases demonstrated that PCDTW achieves more stable and consistent estimation of QT interval and QTcB compared with conventional DTW variants. Furthermore, the proposed method outperformed or matched state-of-the-art deep learning-based ECG delineation approaches in multi-waveform boundary detection, despite requiring no training data. These results highlight the effectiveness of morphology-aware alignment for ECG analysis and emphasize the potential of non-learning-based methods as reliable and interpretable alternatives in biomedical signal processing.

Overall, the proposed PCDTW framework provides a robust and scalable solution for ECG waveform alignment and fiducial point detection, particularly in scenarios involving heart rate variability, amplitude fluctuations, and limited annotation availability. Future work will focus on extending the method to multi-reference alignment, adaptive window strategies, and real-time implementation for long-term ECG monitoring applications.

Author Contributions: Conceptualization, R.L. and D.K. (DaeEun Kim); methodology, R.L.; software, R.L.; validation, R.L., D.K. (DongHyeon Kim), D.K. (DaeEun Kim) and B.K.; formal analysis, R.L.; investigation, R.L.; resources, D.K. (DaeEun Kim); data curation, R.L.; writing—original draft preparation, R.L.; writing—review and editing, R.L., D.K. (DongHyeon Kim), D.K. (DaeEun Kim) and B.K.; visualization, R.L.; supervision, D.K. (DaeEun Kim) and B.K.; project administration, D.K. (DaeEun Kim); funding acquisition, D.K. (DaeEun Kim). All authors have read and agreed to the published version of the manuscript.

Funding: This paper was supported by Korea Institute for Advancement of Technology (KIAT) grant funded by the Korea Government (MOTIE) (P0020535, HRD Program for Industrial Innovation).

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: The data used in this study are publicly available from the QT Database [20] and the Lobachevsky University Electrocardiography Database [21], both of which are available via PhysioNet [19].

Conflicts of Interest: The authors declare no conflicts of interest.

Appendix A. PCDTW Algorithm Description

Algorithm A1: PCDTW-based fiducial point mapping

Input: Normalized ECG cycles $\mathbf{X} \in \mathbb{R}^{N \times L}$,
reference cycle index c , reference fiducial indices $\mathbf{p}$, window size w
Output: Mapped fiducial points $\hat{\mathbf{p}}_k$ for all target cycles k
Convert $\mathbf{X}$ to matrix form if necessary;
 $L \leftarrow$ number of samples per cycle;
Extract reference cycles: $\mathbf{a}_{before} \leftarrow \mathbf{X}(c-1, :)$, $\mathbf{a}_{now} \leftarrow \mathbf{X}(c, :)$, $\mathbf{a}_{after} \leftarrow \mathbf{X}(c+1, :)$;
for $k = 2$ **to** $N - 1$ **do**
 Extract target cycles: $\mathbf{b}_{before} \leftarrow \mathbf{X}(k-1, :)$, $\mathbf{b}_{now} \leftarrow \mathbf{X}(k, :)$, $\mathbf{b}_{after} \leftarrow \mathbf{X}(k+1, :)$;
 Initialize DTW cost matrix $\mathbf{D} \in \mathbb{R}^{L \times L}$;
 Set $\mathbf{D}(1, 1) = 0$, others to $+\infty$;
 for $i = 1$ **to** L **do**
 Construct windowed signal $\mathbf{y}_1$ around i using Algorithm A2;
 Compute mean μ_1 and standard deviation σ_1 ;
 for $j = 1$ **to** L **do**
 Construct windowed signal $\mathbf{y}_2$ around j using Algorithm A2;
 Compute mean μ_2 and standard deviation σ_2 ;
 if $\sigma_1 = 0$ **or** $\sigma_2 = 0$ **then**
 $r \leftarrow 0$;
 else
 $r \leftarrow \text{PearsonCorr}(\mathbf{y}_1, \mathbf{y}_2)$;
 $cost \leftarrow 1 - r$;
 $\mathbf{D}(i, j) \leftarrow cost + \min\{\mathbf{D}(i-1, j), \mathbf{D}(i, j-1), \mathbf{D}(i-1, j-1)\}$;
 Backtrack from (L, L) to obtain warping path $\mathcal{P}_k$;
 foreach $p_m \in \mathbf{p}$ **do**
 Find aligned pair $(p_m, q_m) \in \mathcal{P}_k$;
 $\hat{p}_m^{(k)} \leftarrow q_m$;
 Store mapped fiducial points $\hat{\mathbf{p}}_k$;

Algorithm A2: Window construction with adjacent-cycle padding

Input: Current cycle $\mathbf{s} \in \mathbb{R}^L$,
previous cycle $\mathbf{s}^-$, next cycle $\mathbf{s}^+$,
target index i , window size w
Output: Windowed signal $\mathbf{y} \in \mathbb{R}^{2w+1}$
 $L \leftarrow \text{length}(\mathbf{s})$;
if $i \leq w$ **then**
 $pad \leftarrow (2w + 1) - (i + w)$;
 $\mathbf{y} \leftarrow [\mathbf{s}^-(L - pad + 1 : L), \mathbf{s}(1 : i + w)]$;
else
 if $i > L - w$ **then**
 $pad \leftarrow (2w + 1) - (L - (i - w) + 1)$;
 $\mathbf{y} \leftarrow [\mathbf{s}(i - w : L), \mathbf{s}^+(1 : pad)]$;
 else
 $\mathbf{y} \leftarrow \mathbf{s}(i - w : i + w)$;

References

- Kligfield, P.; Gettes, L.S.; Bailey, J.J.; Childers, R.; Deal, B.J.; Hancock, E.W.; Van Herpen, G.; Kors, J.A.; Macfarlane, P.; Mirvis, D.M.; et al. Recommendations for the standardization and interpretation of the electrocardiogram: Part I: The electrocardiogram and its technology a scientific statement from the American Heart Association Electrocardiography and Arrhythmias Committee, Council on Clinical Cardiology; the American College of Cardiology Foundation; and the Heart Rhythm Society endorsed by the International Society for Computerized Electrocardiology. *J. Am. Coll. Cardiol.* **2007**, *49*, 1109–1127.
- Attia, Z.I.; Harmon, D.M.; Dugan, J.; Manka, L.; Lopez-Jimenez, F.; Lerman, A.; Siontis, K.C.; Noseworthy, P.A.; Yao, X.; Klavetter, E.W.; et al. Prospective evaluation of smartwatch-enabled detection of left ventricular dysfunction. *Nat. Med.* **2022**, *28*, 2497–2503.
- Schijvenaars, B.J.; van Herpen, G.; Kors, J.A. Intraindividual variability in electrocardiograms. *J. Electrocardiol.* **2008**, *41*, 190–196.
- Harun-Ar-Rashid, M.; Mahmud, G.; Rahman, M.M.; Delowar Hossain, A. Classification of ST segment in ECG signals based on cross correlated supervised data. *SN Appl. Sci.* **2020**, *2*, 1224.
- Xu, M.; Wei, S.; Qin, X.; Zhang, Y.; Liu, C. Rule-based method for morphological classification of ST segment in ECG signals. *J. Med. Biol. Eng.* **2015**, *35*, 816–823.
- Zhang, Q.; Manriquez, A.I.; Médigue, C.; Papelier, Y.; Sorine, M. An algorithm for robust and efficient location of T-wave ends in electrocardiograms. *IEEE Trans. Biomed. Eng.* **2006**, *53*, 2544–2552.
- Martínez, A.; Alcaraz, R.; Rieta, J.J. Application of the phasor transform for automatic delineation of single-lead ECG fiducial points. *Physiol. Meas.* **2010**, *31*, 1467–1485.
- Abrishami, H.; Han, C.; Zhou, X.; Campbell, M.; Czosek, R. Supervised ECG interval segmentation using LSTM neural network. In *Proceedings of the International Conference on Bioinformatics & Computational Biology (BIOCOMP)*; The Steering Committee of The World Congress in Computer Science, Computer Engineering and Applied Computing (WorldComp): Las Vegas, NV, USA, 2018; pp. 71–77.
- Londhe, A.N.; Atulkar, M. Semantic segmentation of ECG waves using hybrid channel-mix convolutional and bidirectional LSTM. *Biomed. Signal Process. Control* **2021**, *63*, 102162.
- Peimankar, A.; Puthusserypady, S. DENS-ECG: A deep learning approach for ECG signal delineation. *Expert Syst. Appl.* **2021**, *165*, 113911.
- Nurmaini, S.; Darmawahyuni, A.; Rachmatullah, M.N.; Effendi, J.; Sapitri, A.I.; Firdaus, F.; Tutuko, B. Beat-to-beat electrocardiogram waveform classification based on a stacked convolutional and bidirectional long short-term memory. *IEEE Access* **2021**, *9*, 92600–92613.
- Camps, J.; McCarthy, A.; Rodriguez, B.; Mincholé, A. ConvNet Based QRS Multilead Delineator in Electrocardiogram Signals. In *Proceedings of the First Joint Workshop on AI in Health organized as part of the Federated AI Meeting (FAIM 2018)*, co-located with AAMAS 2018, ICML 2018, IJCAI 2018 and ICCBR 2018 Stockholm, Sweden, July 13–14, 2018. Available online: <https://ceur-ws.org/Vol-2142/short1.pdf> (accessed on 27 January 2026).
- Jimenez-Perez, G.; Alcaine, A.; Camara, O. U-Net architecture for the automatic detection and delineation of the electrocardiogram. In *Proceedings of the 2019 Computing in Cardiology (CinC)*; IEEE: Piscataway, NJ, USA, 2019; p. 1–4.
- Isensee, F.; Petersen, J.; Klein, A.; Zimmerer, D.; Jaeger, P.F.; Kohl, S.; Wasserthal, J.; Koehler, G.; Norajitra, T.; Wirkert, S.; et al. nnu-net: Self-adapting framework for u-net-based medical image segmentation. *arXiv* **2018**, arXiv:1809.10486.
- Liang, X.; Li, L.; Liu, Y.; Chen, D.; Wang, X.; Hu, S.; Wang, J.; Zhang, H.; Sun, C.; Liu, C. ECG_SegNet: An ECG delineation model based on the encoder-decoder structure. *Comput. Biol. Med.* **2022**, *145*, 105445.
- Sakoe, H.; Chiba, S. Dynamic programming algorithm optimization for spoken word recognition. *IEEE Trans. Acoust. Speech, Signal Process.* **2003**, *26*, 43–49.
- Ding, H.; Trajcevski, G.; Scheuermann, P.; Wang, X.; Keogh, E. Querying and mining of time series data: Experimental comparison of representations and distance measures. *Proc. VLDB Endow.* **2008**, *1*, 1542–1552.
- Pearson, K.X. On the criterion that a given system of deviations from the probable in the case of a correlated system of variables is such that it can be reasonably supposed to have arisen from random sampling. *Lond. Edinb. Dublin Philos. Mag. J. Sci.* **1900**, *50*, 157–175.
- Goldberger, A.L.; Amaral, L.A.; Glass, L.; Hausdorff, J.M.; Ivanov, P.C.; Mark, R.G.; Mietus, J.E.; Moody, G.B.; Peng, C.K.; Stanley, H.E. PhysioBank, PhysioToolkit, and PhysioNet: Components of a new research resource for complex physiologic signals. *Circulation* **2000**, *101*, e215–e220.
- Laguna, P.; Mark, R.G.; Goldberg, A.; Moody, G.B. A database for evaluation of algorithms for measurement of QT and other waveform intervals in the ECG. In *Proceedings of the Computers in Cardiology 1997*; IEEE: Piscataway, NJ, USA, 1997; pp. 673–676.
- Kalyakulina, A.I.; Yusipov, I.I.; Moskalenko, V.A.; Nikolskiy, A.V.; Kosonogov, K.A.; Osipov, G.V.; Zolotykh, N.Y.; Ivanchenko, M.V. LUDB: A new open-access validation tool for electrocardiogram delineation algorithms. *IEEE Access* **2020**, *8*, 186181–186190.
- Hatano, K.; Takata, T.; Takechi, M.; Wada, A.; Taniguchi, H.; Tamura, Y. Advanced QT interval analysis in long-term electrocardiography using shape-based clustering and template matching: A novel approach for Holter monitoring. *Heliyon* **2025**, *11*, e42662.

23. Vullings, H.; Verhaegen, M.H.; Verbruggen, H. Automated ECG segmentation with dynamic time warping. In *Proceedings of the 20th Annual International Conference of the IEEE Engineering in Medicine and Biology Society. Vol. 20 Biomedical Engineering Towards the Year 2000 and Beyond (Cat. No. 98CH36286)*; IEEE: Piscataway, NJ, USA, 1998; pp. 163–166.
24. Zhao, J.; Itti, L. shapeDTW: Shape dynamic time warping. *Pattern Recognit.* **2018**, *74*, 171–184.
25. Keogh, E.J.; Pazzani, M.J. Scaling up dynamic time warping for datamining applications. In *Proceedings of the Sixth ACM SIGKDD International Conference on Knowledge Discovery and Data Mining*, Boston, MA, USA, 20–23 August 2000; pp. 285–289.
26. Vandenberk, B.; Vandael, E.; Robyns, T.; Vandenberghe, J.; Garweg, C.; Foulon, V.; Ector, J.; Willems, R. Which QT correction formulae to use for QT monitoring? *J. Am. Heart Assoc.* **2016**, *5*, e003264.
27. Bland, J.M.; Altman, D. Statistical methods for assessing agreement between two methods of clinical measurement. *Lancet* **1986**, *327*, 307–310.
28. Association for the Advancement of Medical Instrumentation. ANSI/AAMI EC57:1998/(R)2008: *Testing and Reporting Performance Results of Cardiac Rhythm and ST Segment Measurement Algorithms*; Technical report; Revision of AAMI ECAR:1987; Association for the Advancement of Medical Instrumentation: Arlington, VA, USA, 1999.
29. Kalyakulina, A.I.; Yusipov, I.I.; Moskalenko, V.A.; Nikolskiy, A.V.; Kozlov, A.A.; Zolotykh, N.Y.; Ivanchenko, M.V. Finding morphology points of electrocardiographic-signal waves using wavelet analysis. *Radiophys. Quantum Electron.* **2019**, *61*, 689–703.
30. Siontis, K.C.; Noseworthy, P.A.; Attia, Z.I.; Friedman, P.A. Artificial intelligence-enhanced electrocardiography in cardiovascular disease management. *Nat. Rev. Cardiol.* **2021**, *18*, 465–478.
31. Zhang, Y.; Post, W.S.; Blasco-Colmenares, E.; Dalal, D.; Tomaselli, G.F.; Guallar, E. Electrocardiographic QT interval and mortality: A meta-analysis. *Epidemiology* **2011**, *22*, 660–670.
32. Cheng, S.; Keyes, M.J.; Larson, M.G.; McCabe, E.L.; Newton-Cheh, C.; Levy, D.; Benjamin, E.J.; Vasan, R.S.; Wang, T.J. Long-term outcomes in individuals with prolonged PR interval or first-degree atrioventricular block. *JAMA* **2009**, *301*, 2571–2577.
33. Nielsen, J.B.; Kühl, J.T.; Pietersen, A.; Graff, C.; Lind, B.; Struijk, J.J.; Olesen, M.S.; Sinner, M.F.; Bachmann, T.N.; Haunsø, S.; et al. P-wave duration and the risk of atrial fibrillation: Results from the Copenhagen ECG Study. *Heart Rhythm* **2015**, *12*, 1887–1895.
34. Isaksen, J.L.; Ghouse, J.; Graff, C.; Olesen, M.S.; Holst, A.G.; Pietersen, A.; Nielsen, J.B.; Skov, M.W.; Kanters, J.K. Electrocardiographic T-wave morphology and risk of mortality. *Int. J. Cardiol.* **2021**, *328*, 199–205.
35. Satija, U.; Ramkumar, B.; Manikandan, M.S. A review of signal processing techniques for electrocardiogram signal quality assessment. *IEEE Rev. Biomed. Eng.* **2018**, *11*, 36–52.

Disclaimer/Publisher’s Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.