

DOI: <https://doi.org/10.15276/ict.03.2026.89>

UDC 004.85:616.12-073.97

Self-supervised cardiac cycle phase learning for ECG delineation

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ABSTRACT

Computational methods play an important role in cardiology, supporting the analysis and interpretation of electrocardiographic data. Automated ECG delineation, including the localization of P-wave, QRS-complex, and T-wave boundaries, is particularly important for extracting clinically relevant temporal and morphological information from ECG recordings. However, accurate delineation remains challenging due to substantial variability in ECG morphology, low signal amplitudes near wave boundaries, and ambiguity in the definition of onset and offset points. Recent advances in machine learning show promising progress in biomedical data processing. Most existing machine learning approaches to ECG delineation rely on supervised learning and therefore require detailed expert annotations. In contrast, self-supervised methods can exploit large collections of unlabeled recordings. In this work, a self-supervised method for learning the physiological phase of the cardiac cycle directly from unlabeled ECG recordings is proposed. The model is trained to predict monotonically increasing phase positions on a unit circle, minimizing morphological distance for signals at similar phase points. Morphology is compared using delay embeddings defined at fixed phase lags. Monotonicity constraints further regularize physiologically consistent phase progression. The method is trained on 12-lead MIMIC-IV-ECG recordings without annotations and evaluated for ECG delineation on the QT Database. Without retraining, phase anchors calibrated on only 10 annotated records provide QRS-boundary localization with precision comparable to supervised models. The weights learned on the self-supervised task also improve a supervised delineation model when used for initialization. These results demonstrate the potential of self-supervised physiological phase learning as an annotation-efficient method for ECG delineation and further automated cardiac signal analysis.

Keywords: ECG; delineation; machine learning; self-supervised learning; learned phase; QT Database

For citation: Stavychenko S. G., Filatova A. E. “Self-supervised cardiac cycle phase learning for ECG delineation”. *Informatics. Culture. Technology*. 2026; Vol. 3 No. 2(4): 1148–1155. DOI: <https://doi.org/10.15276/ict.03.2026.89>

In cardiology, computational algorithms play an important role in the initial processing of diagnostic data, such as the ECG signal. One of the key problems in ECG analysis is signal delineation, i.e., identifying clinically relevant points and intervals, such as the onsets and offsets of the P wave, QRS complex, and T wave.

Research relevance and literature overview. Although ECG delineation is relatively straightforward for an experienced clinician, it remains challenging to automate. ECG morphology varies substantially across recordings, while the signal amplitude near wave boundaries can be very low and comparable to the noise level [1]. In addition, there is no universally accepted rule for defining the onset and offset of ECG waves. As shown in [2] this ambiguity is also reflected in manual annotations, whose timing can be affected by noise, particularly for low-amplitude waves such as the P wave.

Automated ECG delineation builds on manual conventions such as the tangent method for locating the T-wave end [3]. In the first computer analyzers, waves were detected using amplitude and slope thresholds applied to the signal and its derivative [4]. An annotated reference database, together with tolerance limits that remain the standard for evaluation, was then provided within the CSE project [5]. A QRS detection scheme combining band-pass filtering, differentiation, and adaptive thresholds was introduced in [6] and refined in [7], and it became the standard first stage of delineation pipelines. Domain-specific signal preprocessing techniques such as synthesis of an integral ECG signal from all leads to compensate for patient-specific electrical heart axis deviations are also studied [8]. Alternatively, the ECG was modeled as a sequence of hidden Markov states [9], an approach that anticipated later statistical and deep-learning segmentation methods. A second widely used benchmark, with manual annotations of P, QRS, and T boundaries, was provided by the QT database [10]. A wavelet-based delineator, in which wave peaks and boundaries are located

from the extrema of the smoothed signal derivative computed at several successively doubled scales, was validated, and this method has since served as the main reference for comparison. In a related line of work, delineation is treated as structural identification by nonlinear filtering based on models of the useful signal. A generalized two-level scheme was proposed in [11]. First, the signal is mapped by a model-based transform, for example into phase space or into an adaptive parameter space of approximating functions. The result is then converted into a new time-domain function that a decision rule analyzes, and partial rules derived from different signal models are combined into an ensemble.

Machine learning (ML) methods have enabled significant progress in many areas of biomedical signal processing, including automated ECG analysis. For ECG delineation, deep learning models are typically trained in a supervised manner, with the task formulated as sample-wise segmentation of the signal into the P wave, QRS complex, T wave, and background. Jimenez-Perez et al. [12] trained a U-Net-based convolutional network on data with annotations of mixed quality and evaluated it following the protocol introduced by Martinez et al. [1] on the QT Database [10], which has become a common reference for comparing delineation methods. Joung et al. [13] applied deep learning-based segmentation to recordings with diverse arrhythmias, in which wave morphology and timing deviate substantially from normal sinus rhythm.

However, supervised learning methods typically require large amounts of annotated data. Creating such datasets is expensive and time-consuming, as detailed annotations often require trained medical experts [14]. To reduce this cost, automated algorithms are increasingly used to generate annotations for large datasets, which may contain substantial, algorithm-specific errors. Such errors can be learned by new ML models, leading to the confirmation bias problem [15].

Self-supervised learning (SSL) provides a way to reduce the dependence on manually annotated data by learning representations directly from unlabeled data. However, the effectiveness of SSL strongly depends on the choice of the self-supervised objective. Recent self-supervised learning studies in ECG analysis have mainly focused on learning general-purpose representations from large collections of unlabeled recordings. The learned representations are then transferred to specific downstream tasks, typically by fine-tuning the pre-trained model on a smaller labeled dataset. For ECG delineation, a similar strategy has been explored by pre-training on unlabeled ECG recordings using signal transformations as a self-supervised task, followed by supervised localization of characteristic points in the QT Database [10] via transfer learning [16].

The ECG signal, however, has a strong structural prior: it is quasi-periodic, and every cardiac cycle passes through the same sequence of physiological states in the same order. This suggests describing each sample by its position within the cardiac cycle, i.e., by a physiological phase. Unlike time, phase is directly comparable across cycles and recordings, even when heart rate and interval durations differ. Importantly, changes in cycle duration are not distributed uniformly: they are absorbed mainly by the TP segment, to a lesser extent by the PQ segment, and least by the waves themselves. The mapping between time and phase is therefore non-linear and cannot be obtained by simple rescaling of the cycle.

Research purpose and objectives. The **goal** of this research is to develop a machine-learning approach to ECG delineation that requires only a limited amount of labeled data. To achieve this goal, the following **objectives** are defined:

- 1) to formulate the machine-learning problem;
- 2) to develop an ECG delineation approach based on the trained model;
- 3) to develop an experimental protocol and evaluate the proposed approach.

Proposed approach. A self-supervised method for learning the cardiac cycle phase from unlabeled ECG recordings is proposed. The model maps each sample of the signal to a point on the unit circle. It is trained so that samples with similar predicted phase have similar local morphology (Fig. 1), where morphology is described by delay embeddings taken at fixed phase lags on the predicted phase. This makes the comparison invariant to variations in cycle and segment duration and allows cycles to be compared across different recordings. A monotonicity constraint ensures that the phase advances consistently over time. The scientific novelty of this work lies in developing

a method to identify ECG structural elements and localize their fiducial points using self-supervised learning of the physiological phase of the cardiac cycle. Unlike existing approaches, the proposed method learns a common phase representation of ECG signals without using annotated data, in which fiducial points of structural elements correspond to specific phase positions. After calibrating these phase positions using a limited number of annotated recordings, the fiducial ECG points can be localized without additional training of the model on an annotated dataset.

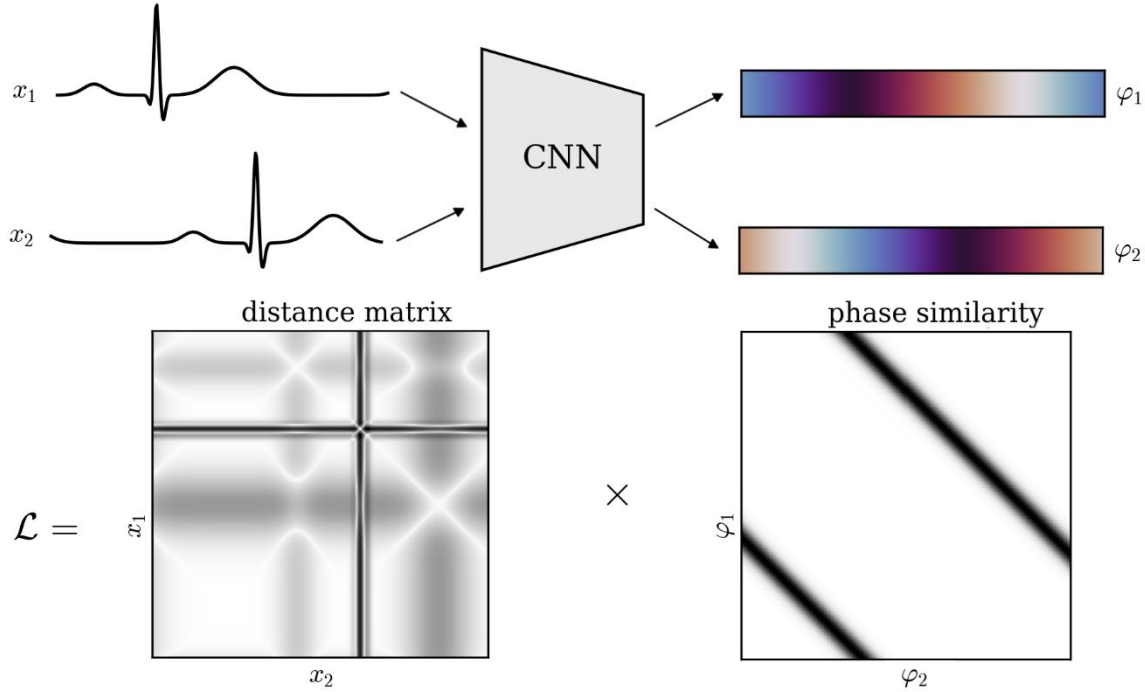


Fig. 1. Title: SSL task objective function schema

Source: compiled by the authors

A 1D U-Net (four stride-2 levels, 32 channels, residual blocks, dilated bottleneck; ≈ 0.14 M parameters) maps a single-lead segment $x \in \mathbb{R}^T$ ($T = 4096$ samples at 500 Hz, median-centered, unit variance) to a unit vector per sample, $p_t = (\cos \varphi_t, \sin \varphi_t)$.

Within window W of the segment, the signal is resampled at phase $\varphi_t + \delta$ with a von Mises kernel on the predicted phases:

$$\tilde{x}_t(\delta) = \frac{\sum_{s \in W} k_{ts}(\delta) x_s}{\sum_{s \in W} k_{ts}(\delta)}, \quad k_{ts}(\delta) = \exp(\kappa [\cos(\varphi_t + \delta - \varphi_s) - 1]),$$

with $\kappa = 400$ (approx. 0.05 rad). The morphology of sample t is the centered vector of the signal values at the phase lags $\delta \in \Delta = \{0, \pm\pi/3, \pm 2\pi/3\}$, $e_t = (v_t - \bar{v}_t \mathbf{1}) / \sqrt{|\Delta|}$, $v_t = (\tilde{x}_t(\delta))_{\delta \in \Delta}$, which spans most of the cycle and stretches with the phase; a sample with a lag not represented in W (kernel mass below 0.5) is masked out ($m_t = 0$).

Two windows W, W' of 512 samples (approx. one cycle), at least 256 samples apart, are compared sample by sample: every pair is charged for its morphological difference, weighted by how close their phases are by Gaussian kernel:

$$\ell(W, W') = \frac{1}{|W||W'|} \sum_{i \in W} \sum_{j \in W'} m_i m_j \|e_i - e_j\|^2 \exp\left(-\frac{\|p_i - p_j\|^2}{2\sigma^2}\right), \quad \sigma = 0.03,$$

W' is taken either from the same recording or from another recording in the batch, so the signal loss is $\mathcal{L}_{\text{sig}} = (1 - \lambda_{\times}) \ell(W, W'_{\text{same}}) + \lambda_{\times} \ell(W, W'_{\text{cross}})$; the cross-recording term ties each phase angle to the same morphology in different recordings, so that a landmark falls at the same phase even where its timing within the cycle differs due to individual traits of a patient.

A batch holds $L = 4$ randomly chosen leads of each 12-lead recording, cut at the same time moments. Since the cardiac cycle is common to all leads, a lead agreement constraint is introduced. The phases are pulled together by the regularization of the variance of the unit vectors over the leads,

$$\mathcal{L}_{\text{agr}} = \frac{1}{TL} \sum_{t=1}^T \sum_{l=1}^L \left\| p_t^{(l)} - \bar{p}_t \right\|^2, \quad \bar{p}_t = \frac{1}{L} \sum_{l=1}^L p_t^{(l)},$$

where $p_t^{(l)}$ is the phase of sample t in lead l .

Two additional terms constrain the direction and the speed of the phase. With $\Delta\varphi_t \in (-\pi, \pi]$ the phase increment between consecutive samples and $s_t = \sin \Delta\varphi_t = p_t \times p_{t+1}$:

$$\mathcal{L}_{\text{back}} = \frac{\sum_t [-s_t]_+}{\sum_t |s_t|}, \quad \mathcal{L}_{\text{jump}} = \frac{1}{T} \sum_t [|\Delta\varphi_t| - \omega_{\text{max}}]_+, \quad \omega_{\text{max}} = 0.3 \text{ rad/sample},$$

penalizing the backward share of the path and increments beyond a ceiling far above a physiological rate. The final loss is: $\mathcal{L} = \mathcal{L}_{\text{sig}} + 0.05 \mathcal{L}_{\text{agr}} + 0.1 \mathcal{L}_{\text{back}} + \mathcal{L}_{\text{jump}}$.

Evaluation. The model is trained on MIMIC-IV-ECG [17]: 800 035 10-s 12-lead recordings at 500 Hz, screened per lead (no missing samples, standard deviation 0.02-2.5 mV, no flat run of 0.5 s, crest factor below 20). Batches hold 32 recordings $\times$ 4 leads, each cut at a random 4096-sample offset. Adam; 60 epochs of 200 steps with $\lambda_x = 1$ on a 100k-recording subset with learning rate (LR) from $3 \cdot 10^{-4}$ to 10^{-5} , and then $\lambda_x = 0.5$ for 20 epochs on the subset and 60 epochs on all recordings (LR from 10^{-4} to 10^{-5}). The training takes about 70 min on a single RTX 4060 Ti.

Delineation is evaluated on the QT Database [10] (the 104 two-lead records annotated by the first annotator, resampled to 500 Hz) initially proposed by PhysioNet [18], following Martinez et al. [1]: P onset/offset, QRS onset/offset and T offset; a detection matches an annotation within 150 ms, the better of the two leads is taken per annotated point, and sensitivity (Se), positive predictive value (PPV) and the mean $\pm$ standard deviation of the error are reported. The trained phase model is applied to the target task in two ways: with no further training, in a few-shot manner, where the labels only fit one phase angle per landmark; and by fine-tuning, where its weights initialize a U-Net with a heatmap head that is trained on QTDB, either with the encoder frozen or with all layers trainable.

With a calibration approach, labels from a small number of records are used to assign one angle on the phase circle to each annotated point k , the circular mean of the predicted phase $\hat{\varphi}_k$ at its annotated positions. A point is then predicted at every crossing of $\hat{\varphi}_k$ by the increasing phase, taken from the raw predicted phase with no signal-based refinement. Angles are calibrated for each lead on the records of four folds and applied to the fifth, using the same five folds as in the supervised baselines. An example of phase prediction is presented in Fig. 2.

Two classical delineators are taken from NeuroKit2 [19], a popular open-source library for neurophysiological signal analysis: its discrete wavelet transform (DWT) delineator, an open-source implementation of the wavelet-based approach of the family originally proposed by Martinez et al. [1] alongside an evaluation protocol, and the recently proposed peak-prominence delineator, which searches prominent peaks in physiologically defined windows [20] and produces the most stable results among classical methods in the authors' practice. The supervised references include the same heatmap U-Net trained on QTDB from random initialization using the same five folds, as well as the results reported by Joung et al. [13]. The evaluation results are reported in Table 1.

Among the classical methods, peak prominence achieves lower SD and higher sensitivity than DWT for all landmarks except QRS offset, where it shows a -19 ms bias, and is therefore used as the primary classical reference. The raw phase, without any network trained on QTDB, localizes QRS onset and offset with SDs of 10.2 and 13.2 ms, respectively, outperforming both classical methods and achieving precision comparable to the supervised U-Net trained on QTDB (10.4 and 14.4 ms) and Joung et al. (11.2 and 17.3 ms), with 100% sensitivity for both boundaries. P-wave boundaries and T offset are less precise: their SDs of 28-43 ms exceed those of the supervised models and peak prominence (16-32 ms).

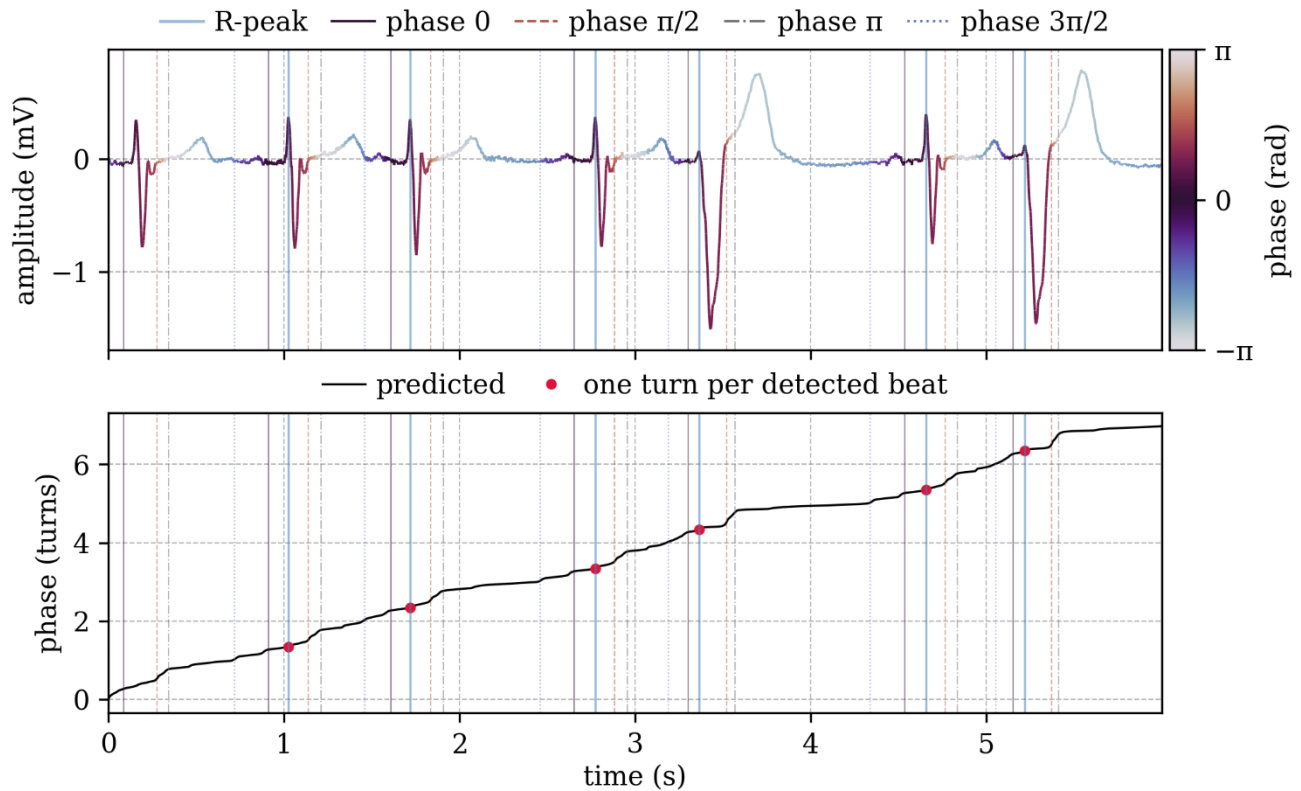


Fig. 2. Title: Phase predictions

Source: compiled by the authors

Table 1. Evaluation result

Method	Labels	P on	P off	QRS on	QRS off	T off
Joung et al. [13]	supervised	13.0 ± 16.1 (96.5/97.9)	-3.3 ± 18.5 (96.6/98.0)	4.1 ± 11.2 (100/-)	2.8 ± 17.3 (100/-)	-0.4 ± 35.1 (97.5/95.3)
NeuroKit2, DWT	none	5.7 ± 22.3 (98.8/85.3)	-3.1 ± 24.2 (98.5/85.5)	-41.2 ± 46.1 (95.3/92.6)	3.6 ± 19.3 (92.0/96.2)	-15.1 ± 30.8 (83.7/83.2)
NeuroKit2, prominence	none	10.5 ± 20.0 (99.5/84.8)	-6.2 ± 21.0 (99.4/84.6)	1.0 ± 14.4 (100/97.6)	-19.0 ± 30.1 (99.8/98.4)	-5.8 ± 32.0 (94.7/93.4)
U-Net heatmaps, from scratch	QTDB, 5-fold	1.0 ± 16.1 (94.1/92.9)	0.8 ± 18.3 (95.7/92.2)	1.2 ± 10.4 (99.5/99.2)	-1.6 ± 14.4 (99.6/99.3)	-4.3 ± 29.4 (93.3/94.4)
U-Net heatmaps, frozen enc.	QTDB, 5-fold	3.0 ± 19.0 (95.0/91.1)	2.7 ± 19.7 (95.5/91.5)	0.4 ± 8.8 (99.8/99.1)	-2.0 ± 11.5 (99.2/99.8)	-7.0 ± 26.9 (91.7/96.4)
U-Net heatmaps, fine-tuned	QTDB, 5-fold	2.1 ± 17.8 (93.6/92.5)	1.8 ± 16.9 (95.2/92.9)	1.0 ± 9.3 (99.7/99.4)	-1.1 ± 12.7 (99.7/99.7)	-4.6 ± 28.5 (94.5/94.7)
phase (ours), raw crossings	angles, 4 folds	-6.9 ± 36.7 (99.0/88.3)	-7.2 ± 27.9 (99.9/88.6)	1.2 ± 10.2 (100/98.8)	3.2 ± 13.2 (100/99.7)	11.4 ± 43.2 (96.8/96.4)
phase (ours), raw crossings	angles, 10 records	-3.7 ± 37.2 (98.7/86.7)	-1.8 ± 27.8 (99.8/88.1)	2.1 ± 10.4 (100/99.0)	-0.7 ± 12.7 (100/99.7)	15.7 ± 43.7 (96.4/96.3)

Source: compiled by the authors

The P-wave PPV of 88% reflects an intrinsic property of the phase representation: the characteristic P-wave phase angle is present in every cycle, so a P-wave crossing is produced even when no P-wave is visible or annotated. As an initialization, the learned phase improves supervised delineation. With the phase encoder frozen and only the decoder and heatmap head trained on QTDB, the model achieves the lowest SDs in Table 1 for QRS onset, QRS offset, and T offset (8.8, 11.5, and 26.9 ms, respectively), while P-wave SD is slightly higher than for training from scratch.

Discussion and conclusion. A cardiac phase learned without annotations from unlabeled 12-lead recordings can localize QRS boundaries using a single calibrated phase angle per landmark, achieving precision comparable to supervised models. The phase representation also provides a useful initialization for supervised delineation. Notably, only 10 annotated records are sufficient for calibration: across five random draws, QRS onset and offset errors are 2.1 ± 10.4 and -0.7 ± 12.7 ms, respectively, comparable to calibration on the full training folds. The corresponding bias varies by only 2-4 ms between draws, whereas P and T angles are less stable, with bias variations of 11-24 ms. Thus, new landmarks can be defined by annotating a small number of recordings and subsequently localized in new recordings without retraining the network, including landmarks not covered by existing public annotations. Improving P-wave and T-offset localization and extending the common phase representation to multi-lead delineation are the main directions for future work.

Conflict of interests: Authors declare that they do not have conflict of interests, in particular financial, personal, copyright or any of a different nature, which could have influenced the research, as well as the results published in this articles

Financing: Research was carried out without financial support

Accessibility data: All data available in digital or graphic form in the main text manuscript

Using artificial intelligence tools: During the preparation of the manuscript, the GPT-5.6 Luna artificial intelligence (AI) tool was used for grammatical and stylistic text checks. All fragments processed using this tool were checked and edited by the authors. AI was not used to generate text, formulas, or tables, formulate scientific statements, obtain results, or draw conclusions. The scientific statements, results, and conclusions are the authors' own intellectual contributions

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Received 27.08.2026

Received after revision 30.09.2026

Accepted 06.10.2026

DOI: <https://doi.org/10.15276/ict.03.2026.89>

УДК 004.85:616.12-073.97

Самокероване навчання фази серцевого циклу для визначення структурних елементів ЕКГ

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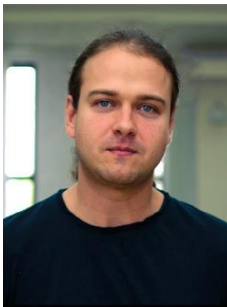
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АНОТАЦІЯ

Обчислювальні методи відіграють важливу роль у кардіології, підтримуючи аналіз та інтерпретацію електрокардіографічних даних. Автоматизоване визначення структурних елементів ЕКГ, зокрема локалізація меж зубця Р, комплексу QRS та зубця Т, є особливо важливим для вилучення клінічно значущої часової та морфологічної інформації із записів ЕКГ. Однак точне визначення меж структурних елементів залишається складним завданням через значну варіабельність морфології ЕКГ, низькі амплітуди сигналу поблизу меж зубців та неоднозначність у визначенні точок початку й закінчення. Останні досягнення в галузі машинного навчання демонструють перспективний прогрес в обробці біомедичних даних. Більшість наявних підходів машинного навчання до визначення структурних елементів ЕКГ ґрунтуються на навчанні з учителем і, отже, потребує детальних експертних анотацій. Натомість методи самокерованого навчання можуть використовувати великі колекції нерозмічених записів. У цій роботі ми пропонуємо метод самокерованого навчання для вивчення фізіологічної фази серцевого циклу безпосередньо з нерозмічених записів ЕКГ. Модель навчається передбачати монотонно зростаючі фазові позиції на одиничному колі, мінімізуючи морфологічну відстань для сигналів у подібних фазових точках. Морфологія порівнюється за допомогою вкладень із затримкою, визначених на фіксованих фазових зсувах. Обмеження монотонності додатково регуляризують фізіологічно узгоджене просування фази. Метод навчено на 12-канальних записах MIMIC-IV-ECG без анотацій і оцінено для визначення структурних елементів ЕКГ на базі даних QT Database. Без перенавчання фазові опорні точки, відкалібровані лише на 10 анотованих записах, забезпечують локалізацію меж QRS з точністю, порівнянню з моделями з вчителем. Ваги, вивчені в задачі самонавчання, також покращують модель визначення структурних елементів з вчителем, коли використовуються для ініціалізації. Ці результати демонструють потенціал самонавчання фізіологічної фази як методу, економного щодо анотацій, для визначення структурних елементів ЕКГ та подальшого автоматизованого аналізу серцевих сигналів.

Ключові слова: ЕКГ; визначення структурних елементів; машинне навчання; самокероване навчання; вивчення фази; QT Database

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