Self-Supervised and Topological Signal-Quality Assessment for Any PPG Device Revision Summary and Tracked Changes

Aug 29, 2025

We thank all reviewers for their constructive feedback. Based on each concern, we have made and summarized the following revisions.

1 Reviewer Tsty

1.1 Concern: How the stage 2 works based on the representation learning is not clear.

We clarified the end-to-end data flow and wording: Stage 1 trains a contrastive encoder so that each 8 s PPG window is mapped to a 512-dimensional embedding that is stable across device settings and motion artifacts; Stage 2, grounded in the invariance learned in Stage 1, we operate on these encoder-derived representations rather than on the raw waveforms. Specifically, we freeze the encoder, treat each 512-D embedding as a one-dimensional signal, compute a four-scalar persistent-homology (PH) signature that captures morphology/regularity, and cluster these 4-D signatures with HDBSCAN; the largest dense cluster is labeled as clean, while all other points are labeled poor.

1.2 Concern: More evidences are required to convince readers that the augmentation strategy can generate similar signal interferences to motion, perfusion loss, and ambient light.

We revised the description for each augmentation (jitter/Gaussian noise, magnitude scaling, time-warp, blackout, frequency dropout, circular shift/polarity, crop) to map to the real nuisance it approximates, and cited prior work that validates these choices in biosignal.

2 Reviewer LtAH

2.1 Concern: The dominant-cluster heuristic (largest/densest cluster = clean) is fragile in regimes where noise overwhelms signal.

We explicitly documented this limitation and outlined practical safeguards that fit our framework without retraining: (i) density-ratio checks between top clusters, (ii) weighting by intra-cluster persistence rather than count, and (iii) Bayesian non-parametric mixtures to relax the largest-cluster assumption.

2.2 Concern: Lack of empirical validation of downstream benefit, making the practical utility claim partially speculative.

We addressed this by clarifying how the SQI is used and why it should help in practice: the SQI serves as a modular pre-filter that removes morphology-unstable windows before heart-rate, rhythm, or biometric pipelines; this is consistent with prior evidence that gating low-quality biosignal segments reduces HR/rhythm errors and improves biometric robustness. Operationally, our SQI filters $\sim$24% of We-Be windows (dominated

by motion/perfusion loss), a tunable trade-off between coverage and accuracy; the gate can be used in binary or multi-level form depending on latency/tolerance requirements.

2.3 Concern: No head-to-head quantitative comparison to existing heuristic and supervised baselines.

Beyond the deployment-focused comparison table (label cost, cross-device portability, interpretability), we now provide an unlabeled, quantitative comparison via convergent validity with two public SQIs. Using prevalence-matched binarization at $q = 0.24$ on $N = 3600$ windows, our SSL-TDA gate agreed with NeuroKit2 on 82.22% and with pyPPG on 87.44% of windows. This evaluates inter-SQI agreement and shows that our label-free method reaches decisions consistent with established toolkits. We also continue to report unsupervised clustering validity metrics (Silhouette ↑, Davies–Bouldin ↓, Calinski–Harabasz ↑) and avoid cross-paper accuracy claims that would conflate differing datasets and label definitions.

3 Reviewer DavL

3.1 Concern: Unclear role of the SSL encoder.

We clarified the role of SSL and end-to-end data flow. See Section 1.1 for the full pipeline clarification.

3.2 Concern: Binary output only

We noted that HDBSCAN naturally yields multiple clusters and outlier scores; these can be mapped to clean/borderline/poor or to a continuous index based on cluster density or distance-to-center, and we flagged this as a straightforward extension.

3.3 Concern: Limited evaluation scope.

We clarified and justified the evaluation scope in light of our goals: the contribution targets scalability (label-free), portability (cross-device/rate without re-tuning), and interpretability (four-scalar signature). Accordingly, we prioritize unlabeled, cross-device validation and standard clustering validity metrics (Silhouette ↑, Davies–Bouldin ↓, Calinski–Harabasz ↑) over supervised accuracy on device-specific corpora, and we now add an unlabeled, quantitative comparison via convergent validity with two public SQIs (NeuroKit2, pyPPG), showing 82.22% and 87.44% agreement on N=3600 windows at q=0.24. The manuscript reports structure quality across heterogeneous datasets and sampling rates (25–128 Hz) and includes ablations isolating the impact of PH and clustering choices. Next steps are explicit: (i) pre/post SQI studies on shared labeled corpora for HR/Rhythm/Biometrics, (ii) multi-level/continuous SQIs for tunable coverage–latency trade-offs, and (iii) clinical validation with multi-LED and accelerometer fusion.

4 Additional Changes

- Tightened SSL, Augmentations, Topological signature, and Unsupervised quality discovery sections for readability and space.
- Merged repeated content across the paper such as pipeline descriptions.
- Removed the separate subsection "Why topology after contrastive learning?" since its rationale is already integrated earlier in the pipeline description.
- Removed Figures on training and cosine-similarity trace to prioritize core contributions.
- Removed the cosine-similarity discussion, which is not in the direct scope of the paper, to prioritize core contributions.
- Editorial improvements.

Self-Supervised and Topological Signal-Quality Assessment for Any PPG Device

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***Abstract*—Wearable photoplethysmography (PPG) is embedded in billions of devices, yet its optical waveform is easily corrupted by motion, perfusion loss, and ambient light—jeopardizing downstream cardiometric analytics. Existing signal-quality assessment (SQA) methods rely either on brittle heuristics or on data-hungry supervised models. We introduce the first fully unsupervised SQA pipeline for wrist PPG. Stage 1 trains a contrastive 1-D ResNet-18 on 276 h of raw, unlabeled data from heterogeneous sources (varying in device and sampling frequency), yielding optical-emitter– and motion-invariant embeddings (i.e., the learned representation is stable across differences in LED wavelength, drive intensity, and device optics, as well as wrist motion). Stage 2 converts each ~~8 s window~~ 512-D encoder embedding into a 4-D topological signature via persistent homology (PH) and clusters these signatures with HDBSCAN. To produce a binary signal-quality index (SQI), the acceptable PPG signals are represented by the densest cluster while the ~~remainder~~ remaining clusters are assumed to mainly contain ~~poor~~ poor-quality PPG signals. Without re-tuning, the SQI attains Silhouette, Davies–Bouldin, and Calinski–Harabasz scores of 0.72, 0.34, and 6,173, respectively, on a stratified sample of 10,000 windows. In this study, we propose a hybrid self-supervised-learning–topological-data-analysis (SSL–TDA) framework that offers a drop-in, scalable, cross-device quality gate for PPG signals.**

***Index Terms*—photoplethysmography, signal quality, self-supervised learning, persistent homology, wearable sensing**

I. Introduction

Wearable photoplethysmography (PPG) underpins today's cardiometric ecosystem—delivering heart rate, SpO_2, respiration, and nascent cuff-less blood-pressure estimates in smartwatches, rings, and earbuds. Global shipments already exceed millions of units per year, generating petabyte-scale PPG streams. Yet the optical waveform is notoriously fragile: motion artifacts, ambient-light leakage, skin–sensor decoupling, and perfusion changes routinely degrade signal quality [1]–[3]. Without timely filtering, downstream algorithms can yield grossly erroneous vitals, undermining user trust and clinical adoption.

Commercial firmware embeds hand-tuned ~~SQA~~ signal-quality assessment (SQA) heuristics—thresholds on amplitude, template correlation, or derivative energy—engineered per LED wavelength and mechanical stack; a firmware update or strap relocation can break these rules. Supervised CNNs detect artifacts reliably [4], but each hardware generation demands thousands of freshly labeled windows, rendering cross-device scaling impractical.

Wearables already store hundreds of hours of unlabeled wrist-PPG per user. Contrastive self-supervised learning (SSL) can harness this ~~*free*~~ free data, but SSL alone does not output a human-interpretable ~~SQI~~signal-quality index (SQI). Conversely, topology-based descriptors capture waveform morphology in a few numbers, yet they have never been paired with modern deep encoders. Persistent homology (PH) has characterized cardiac periodicity and gait regularity [5]; to our knowledge, we are the first to use PH as a morphology prior for wrist-PPG quality.

We fuse SSL and topological data analysis (TDA) into the first ~~*fully unsupervised, device-agnostic*~~ fully unsupervised, device-agnostic SQA pipeline, shown in Fig. 1:

1) **Contrastive representation learning:** ~~A 1-D ResNet-18 trained with NT-Xent on 276 h of heterogeneous data learns embeddings invariant to amplitude, phase, and sampling-rate differences.~~
2) **~~Topology-driven quality discovery:~~** ~~Each~~ trains a contrastive encoder so that each 8 s ~~window is distilled into a~~ PPG window is mapped to a 512-dimensional embedding that is stable across device settings and motion artifacts.
3) **Topology-driven quality discovery:** grounded in the invariance learned in Stage 1, we operate on these encoder-derived representations rather than on the raw waveforms. Specifically, we freeze the encoder, treat each 512-D embedding as a one-dimensional signal, compute a four-scalar PH ~~vector and clustered via HDBSCAN. The densest cluster is deemed *clean*; everything else, *poor*, yielding a binary SQI.~~ signature of the embedding landscape and cluster these 4-D signatures with HDBSCAN; the largest dense cluster is labeled clean, while all other points are labeled poor.

~~Key~~

The key novelties are (i) the first SSL–TDA fusion for SQA, (ii) cross-device ~~validation (sampling rate of 25 to 128 Hz)~~

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and -sampling rate portability without re-tuning, and (iii) ~~a~~ an interpretable four-number signature enabling MCU-level inference.

II. Background

A. Self-supervised learning for physiological signals

Contrastive objectives such as SimCLR [6] and BYOL [7] maximize agreement between two independently augmented views of the same instance; this technique outperforms autoencoders on ECG and PPG [8], [9] and on other biosignals by capturing invariance to amplitude scaling and temporal distortion with ~~*zero*~~ zero annotation effort.

B. Persistent homology in time-series

~~Topological data analysis (TDA)~~ TDA quantifies the shape of data. Sublevel-set PH has characterized cardiac periodicity and gait regularity [5], [10]. Clean, quasi-periodic PPG produces long-lived H_1 loops, whereas noisy windows do not, making PH an attractive ~~*unsupervised*~~ unsupervised morphology cue. In addition, PH reduces encoder embeddings to morphology-aware scalars, adding an explicit morphological prior—capturing beat regularity versus artifact, and providing a compact and interpretable input to clustering.

C. Density-based clustering for quality discovery

HDBSCAN extends DBSCAN with variable-density cluster extraction and explicit noise labeling [11]. It automatically chooses the number of clusters and handles non-Gaussian shapes—ideal for heterogeneous wrist data where artifacts are rare and scattered.

III. Methodology

A. ~~*Pipeline Overview*~~

~~Our goal is to estimate PPG signal quality *without* expert labels. Accordingly, we build a two-stage unsupervised pipeline:~~

1) ~~**Representation learning.** A self-supervised 1-D ResNet is trained with strong temporal augmentations so that windows containing the *same* physiology map to nearby points in embedding space, regardless of amplitude, phase, or motion artifact.~~
2) ~~**Topology-driven quality discovery.** Persistent-homology features are extracted from each raw window and clustered with HDBSCAN. The largest, densest cluster is interpreted as *clean* PPG; all others are labelled *poor* (noise), yielding a binary signal-quality index (SQI).~~

~~The remainder of this section justifies each design choice.~~

A. Corpora and signal conditioning

TABLE I lists the two datasets used in this study.

Why these datasets: WildPPG offers long, mostly clean wrist recordings, whereas We-Be provides lower-rate, motion-rich wrist data. Joint training therefore encourages the encoder to ~~generalise~~ generalize across hardware and noise regimes.

Signal conditioning: A 0.5–8 Hz third-order, zero-phase Butterworth filter removes baseline wander and LED noise. Traces are resampled to a common 25 Hz, z-scored, and segmented into 8 s windows (200 samples, 50 % overlap)

B. Self-supervised representation learning (Contrastive Learning)

a) ~~Contrastive learning~~Loss function: ~~Contrastive objectives have proved effective for ECG arrhythmia detection [15], [16]. In PPG, early work focused solely on heart-rate classification [9]; none produced an interpretable, device-agnostic SQI.~~ The NT-Xent loss encourages invariance to amplitude and phase jitter—precisely the nuisance factors in wrist PPG—while requiring no annotations.

b) Encoder: A 1-D ResNet-18 processes 1×200 inputs, followed by a projection MLP (512→512→512). The output is ℓ_2 ~~-normalised~~ -normalized with $\varepsilon = 10^{-6}$.

c) Augmentation strategy: Each view applies ~~the~~ a deterministic band-pass filter, then draws ~~*two to four*~~ two to four of the following transforms:

- **~~Band-pass~~ Random crop (~~always~~keep 50–70%)**~~:ensures the network never sees drift or high-frequency noise.~~
- ~~**Random crop (50–70 %):** mimics packet drop / screen blackouts~~: packet loss, strap adjustment, transient motion gaps.
- **Time-warp (~~±~~±3%)**~~:models~~ : natural heart-rate variability, slow sensor drift.
- **Jitter / Gaussian noise (1% ~~σ~~SD)**~~:injects sensor noise~~: sensor electronic noise, ambient light flicker.
- **Magnitude scaling (~~±~~±5%)**~~:emulates LED-current fluctuations~~: LED drive-current fluctuations, skin perfusion changes.
- **Frequency dropout ~~:~~(narrowband removal)**~~randomly removes harmonicsto prevent shortcut learning in the frequency domain~~: ambient light interference, missing harmonics.
- **Circular shift (~~±~~±1 s) and polarity inversion**~~:cover strap-orientation errors~~: strap orientation errors, polarity mismatches.
- **Segment blackout (10–40 samples)**~~:imitates transient motion artifact~~: short motion spikes (e.g., hand taps).

Empirical studies confirm that augmentations including jitter (Gaussian noise), scaling, time-warp, and polarity inversion reliably mimic motion, noise, and perfusion artifacts in contrastive learning for ECG/PPG signals [9], [17].

TABLE I
UNLABELLED PPG CORPORA USED FOR PIPELINE DEVELOPMENT.

Corpus	Site	Native f_s	Hours	LED
WildPPG [12]	wrist	128 Hz	216	green
We-Be [13], [14]	wrist	25 Hz	60	green

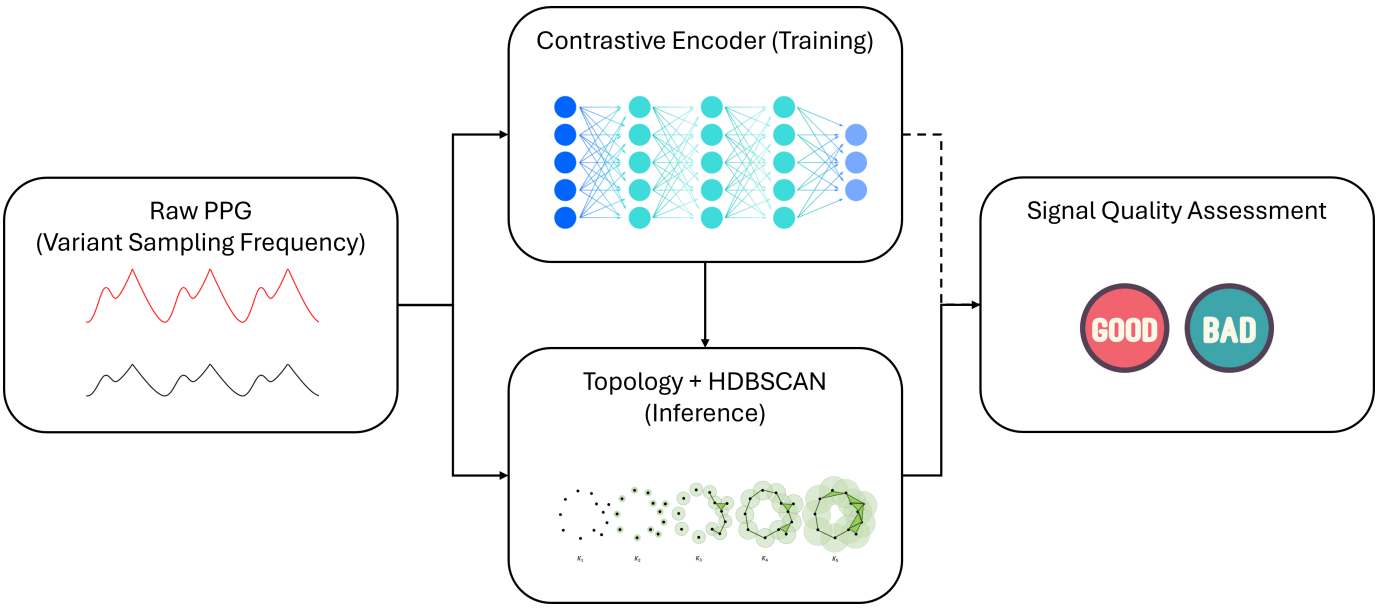

Fig. 1. Proposed two-stage pipeline

d) Training details: By exploring hyperparameter tuning, we use the ~~followings~~following: NT-Xent with $\tau = 0.1$; batch size 512; AdamW (learning rate 2×10^{-4}, weight decay 10^{-4}); 200 epochs; mixed precision.

C. Topological signature

~~Clean, quasi-periodic PPG traces generate pronounced one-dimensional loops (H_1) in their sublevel filtrations, whereas noisy windows do not. For~~ We convert each 8~~s window~~s window into a 512-D embedding using the trained encoder (frozen). Interpreting this embedding as a one-dimensional scalar signal, we compute persistent homology on a 1-D cubical complex (GUDHI) and retain four interpretable features:

$$\left[n_{H_1},\ \Sigma H_1,\ \max H_0,\ \text{mean}\, H_0\right] \in \mathbb{R}^4.$$

These four values summarize the structure in the embedding and are the inputs to HDBSCAN in Stage 2.

D. Unsupervised quality discovery

The 4-D persistence vectors are clustered with HDBSCAN. It adapts the number of clusters automatically, flags sparse points as noise, and handles non-Gaussian shapes—desirable for heterogeneous wrist PPG.

A binary SQI is assigned ~~as~~ such that the largest non-noise cluster is deemed ~~*clean*~~clean, and the remaining points (noise plus smaller clusters) are ~~*poor.*~~ poor.

E. Overall Performance

Because the pipeline is label-free and device-agnostic by design, we evaluate structure quality using standard clustering validity scores (silhouette, Davies–Bouldin, Calinski–Harabasz) rather than supervised accuracy. These metrics capture separability and compactness of the discovered quality strata, which is appropriate when the objective is scalable, cross-device gating without annotation.

IV. Evaluation

A. Encoder convergence

~~Fig. ?? shows the~~ The NT-Xent loss ~~decreasing~~ decreases smoothly from $3.44 \rightarrow 0.95$ across 200 epochs, while the mean cosine similarity $(\overline{\cos})$ between the two augmented views rises from $0.67 \rightarrow 0.77$~~shown in Fig. ??.~~ . The coupled evolution of loss ~~*and*~~ and cosine confirms that the encoder learns discriminative directions rather than collapsing to a trivial representation.

~~NT-Xent loss over 200 epochs.~~

B. Quality of topological features

The $150\,000 \times 4$ persistence matrix exhibits a clear morphology gradient: clean windows populate the high-n_{H_1}, high-$\sum H_1$ corner, whereas noisy windows cluster near the origin.

Fig. 2 shows a representative visualization of the clustering outcome: the densest HDBSCAN cluster comprises 76 % of all windows and corresponds to textbook pulsatile traces, explaining the great performance achieved by the SSL–TDA configuration.

C. Ablation study

TABLE II shows the ablation study results. Removing the topological signature (~~*SSL + HDBSCAN*~~SSL + HDBSCAN) collapses the ~~silhouette~~ Silhouette from 0.72 to 0.05: in 512 D, the contrastive embeddings form a diffuse manifold that density-based clustering labels as almost homogeneous. Conversely, retaining PH but swapping HDBSCAN for k-means halves the ~~silhouette~~Silhouette, showing that the density prior is also essential. The full ~~**SSL–TDA fusion**~~ SSL–TDA

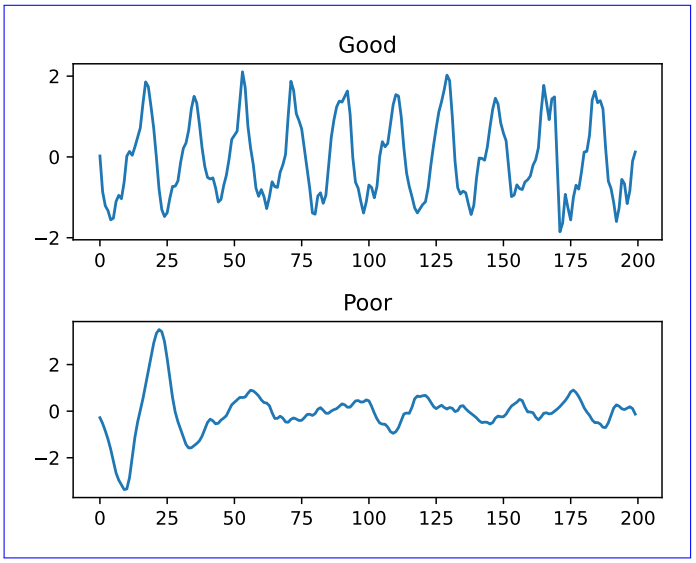

Fig. 2. ~~Mean cosine similarity trace~~Visualization of the clustering result.

TABLE II
ABLATION ON 10 K WINDOWS~~—HIGHER IS BETTER FOR SILHOUETTE AND CALINSKI–HARABASZ (CH), LOWER FOR DAVIES–BOULDIN (DB).~~

Configuration	Sil.(↑)	DB(↓)	CH(↑)
SSL+PH+HDBSCAN (~~ours~~SSL-TDA)	**0.72**	**0.34**	6 173
SSL+HDBSCAN (no PH)	0.05	4.60	29
SSL+PH+k-means (no density)	0.39	0.89	**7 177**
SSL+k-means (SSL only)	0.01	7.33	141

fusion therefore yields the most compact and well-separated clusters.

D. ~~*Quality of topological features*~~

~~The $150\,000 \times 4$ persistence matrix exhibits a clear morphology gradient: clean windows populate the high-n_{H_1}, high-$\sum H_1$ corner, whereas noisy windows cluster near the origin.~~

D. *Unlabeled comparison with existing works*

We assess convergent validity by comparing our SSL-TDA pipeline with two baselines on the same unlabeled corpus. For NeuroKit2 [18], we compute per-beat PPG template-matching scores and aggregate them to per-window values (median); for pyPPG [19], we use its 0-1 template-matching SQI. To obtain binary outputs without labels, we prevalence-match thresholds so each method accepts the same fraction $q = 0.24$ of windows (equal to our acceptance rate). On $N = 3600$ windows, it agreed with NeuroKit2 on 82.22% and with pyPPG on 87.44%. These agreements indicate that our label-free method aligns with existing methods on most windows.

~~Visualization of the clustering result.~~

~~Fig. 2 shows a representative visualization of the clustering outcome: the densest HDBSCAN cluster comprises 76 % of all windows and corresponds to textbook pulsatile traces, explaining the great performance achieved by the PH + HDBSCAN configuration.~~

V. DISCUSSION

a) ~~Why topology after contrastive learning?~~Dominant-cluster heuristic: ~~Contrastive learning yields a *feature space* in which pulses with the same underlying haemodynamics are close, yet it is agnostic to the absolute shape of the signal. Persistent homology adds an explicit morphological prior—capturing beat regularity versus artifact—while compressing a 512-D embedding to only four scalars. This hybrid design outperforms~~ Our current implementation assumes that the largest and densest cluster discovered by HDBSCAN corresponds to physiologically clean PPG, while smaller or scattered clusters correspond to artifacts. This assumption holds in our corpora, where most windows contain usable signal, but it may break down in regimes dominated by noise. In such cases, the "clean = largest cluster" rule could invert. To mitigate this, one can (i) ~~clustering directly in embedding space and~~ compute density ratios between the top two clusters and reject segments when the ratio falls below a threshold, (ii) ~~PH alone without SSL; both configurations achieve markedly lower silhouette scores.~~ weight clusters by intra-cluster persistence rather than point count, or (iii) use Bayesian non-parametric mixtures that relax the largest-cluster assumption. We note that the clustering framework can accommodate them without retraining the encoder.

b) ~~Dominant-cluster heuristic~~Practical utility and downstream effects: ~~Selecting the largest, densest HDBSCAN cluster as clean is justified by the empirical observation that true physiology occupies a contiguous, high-density region of feature space, whereas motion artifacts are sporadic and diverse. On datasets where noise *dominates* (e.g. ICU data), one could invert the rule or re-weight clusters by intra-cluster persistence instead of count~~A natural question is whether the proposed SQA improves downstream analytics such as heart-rate estimation, rhythm classification, or biometric authentication. While we do not include full downstream validation here, prior studies have established that discarding poor-quality PPG segments reduces error rates in heart-rate monitoring and arrhythmia detection, and improves biometric authentication accuracy [4], [15], [20]. Our binary SQI removes roughly 24% of windows in the We-Be dataset; in practice, this would filter the inputs to cardiometric pipelines so that algorithms operate on cleaner segments, reducing spurious beats and missed intervals. We position this work as a modular "quality gate" that can be inserted before such pipelines. A systematic evaluation of downstream benefits, such as pre/post SQI studies on shared labeled corpora—heart rate, rhythm classification, and biometrics, is an important direction for future work.

c) ~~Future work~~Beyond binary quality: ~~Now we assume the clean cluster is densest; long recordings dominated by corruption may violate this. Density-ratio tricks or Bayesian non-parametrics could relax the assumption. In addition,~~

~~fusing~~ In this paper we report a binary SQI for clarity, assigning the largest dense cluster as clean and all others as poor. However, the clustering framework naturally produces multiple clusters and outlier scores, which could be mapped to finer-grained categories (e.g., clean / borderline / poor) or even a continuous quality index based on cluster density or silhouette distance. Such multi-level outputs may better match downstream applications (e.g., arrhythmia screening, where "borderline" segments should be flagged but not discarded).

d) Multi-modality: Fusing accelerometer and PPG embeddings during contrastive pre-training may boost robustness to motion spikes that currently leak into the clean cluster. In addition, We-Be's LED channels other than ~~*green*~~ green were not exploited; multi-channel PH may further improve robustness. Finally, clinical validation against simultaneous ECG or invasive pressure would solidify the findings.

~~*e) Why does the cosine similarity start high yet still work:* In natural-image SimCLR the two random crops of a photo share only ∼10 % of pixels, so the initial view–view cosine is low (∼0.1). Here, both views receive the *same* band-pass and contain the *same* cardiac activity, differing only by mild time-warp, crop–pad, magnitude scaling, and related transforms. Consequently, two randomly initialised encoder paths already observe highly correlated waveforms, and their embeddings begin with a non-trivial alignment: $\overline{\cos}(z_1, z_2) \approx 0.58 - 0.65$ across five random seeds.~~

~~The critical check for representation *collapse* is whether $\overline{\cos}$ quickly approaches 1.0 *without a simultaneous drop in loss*. In our curves, the NT-Xent loss decreases monotonically ($3.44 \rightarrow 0.95$) while $\overline{\cos}$ rises only modestly ($0.67 \rightarrow 0.77$), indicating that the encoder is learning new discriminative directions rather than mapping every input to an identical point. Empirically, windows from different subjects remain well separated in embedding space even at epoch 100, confirming that the higher baseline cosine is a benign consequence of domain-specific augmentations—not collapse.~~

VI. Conclusion

We presented the first fully unsupervised two-stage pipeline that converts raw wrist-PPG into a binary ~~signal-quality index~~ SQI without device-specific thresholds or expert labels~~—~~. Rather than optimizing supervised SQA accuracy, we prioritize scalability (no labels), portability (no device-specific re-tuning across 25–128 Hz), and interpretability (four-scalar signature), positioning the method as a practical quality gate for diverse PPG devices, achieving Silhouette 0.72, Davies–Bouldin 0.34, and Calinski–Harabasz 6,173 on 276 h of heterogeneous data. Since it requires ~~*zero*~~ zero labels and no hardware calibration, the SSL–TDA framework can serve as a drop-in quality gate for any wrist-based ~~photoplethysmography~~ PPG pipeline—paving the way for more reliable heart-rate, rhythm, and biometric-security analytics across the billions of wearables already in use.

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