

# VERIFICATION BASED ECG BIOMETRICS WITH CARDIAC IRREGULAR CONDITIONS USING HEARTBEAT LEVEL AND SEGMENT LEVEL INFORMATION FUSION

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## ABSTRACT

We propose an ECG based robust human verification system for both healthy and cardiac irregular conditions using the heartbeat level and segment level information fusion. At the heartbeat level, we first propose a novel beat normalization and outlier removal algorithm after peak detection to extract normalized representative beats. Then after principal component analysis (PCA), we apply linear discriminant analysis (LDA) and within-class covariance normalization (WCCN) for beat variability compensation followed by cosine similarity and Snorm as scoring. At the segment level, we adopt the hierarchical Dirichlet process auto-regressive hidden Markov model (HDP-AR-HMM) in the Bayesian non-parametric framework for unsupervised joint segmentation and clustering without any peak detection. It automatically decodes each raw signal into a string vector. We then apply n-gram language model and hypothesis testing for scoring. Combining the aforementioned two subsystems together further improved the performance and outperformed the PCA baseline by 25% relatively on the PTB database.

**Index Terms**— ECG biometrics, beat normalization, outlier removal, nonparametric Bayesian, n-gram language model

## 1. INTRODUCTION

The ECG signal is an emerging novel behavior biometrics for human identification [1]. The differences of heart, such as chest geometry, position, size, for different individuals manifest unique characteristics in their ECG signals which can be used as a biometric trait. Furthermore, the ECG signal is difficult for counterfeit credentials and can provide continuous liveness feedback which makes it promising in multimodal biometrics fusion and possible for continuous identity unlock without repeated authentications. Moreover, ECG is an important diagnostic physiological measure in mobile health and body area sensor networks, thus ECG based subject verification is also useful in personalized healthcare service.

ECG biometrics is a challenging task since the ECG signal inherently varies at different heartbeats of the same subject due to cardiovascular conditions [2], variations in physical [3, 4], mental and emotional states [5, 6] as well as variabilities caused by sensor placement and long term gap between visits. Therefore, most existing works used a sequence of heartbeats in normal rest condition to model individuals. Compared to systems using multiple leads [7, 8], promising results based on a single lead ECG signal have also been demonstrated in [1, 6, 9, 10, 11, 12, 13, 14]. A recent comparative literature review on ECG biometrics is provided in [15].

In general, with single lead signals, ECG biometrics methods could be classified into two main categories depending on whether

QRS detection is required. With QRS detection, ECG signal is segmented into multiple cardiac heartbeats and a variety of reduced feature sets derived from the morphological characteristics of these heartbeats are proposed as features for subsequent supervised learning. Those features include fiducial points [1, 6, 9, 11], principal component analysis (PCA) coefficients [10], Hermite polynomial expansion coefficients [13], discrete wavelet transform coefficients [8], short time Fourier transform (STFT) log energy [14], Pulse Active Ratio [16], etc. Due to the QRS detector's unreliable performance for noisy and cardiac irregular data, several methods without this computationally expensive segmentation/delineation frontend are also proposed, for instance, autocorrelation with discrete cosine transform (DCT) in [11] and STFT based cepstral features in [13].

As mentioned in [15], most ECG biometrics modeling methods for the aforementioned features rely on supervised classifiers (K nearest neighbor, support vector machine, neural networks, etc.) under the closed set identification framework. However, these classifiers may not work well for the unseen out-of-set testing samples in the verification task. Recently, Gao, et.al [17] proposed a verification method by scoring each testing sample on LDA based multi-class classifiers, each trained by a particular target sample against all the background samples. To the best of our knowledge, there is no existing work on directly calculating the similarity between target and test samples and comparing it with a global threshold in the ECG verification task including out-of-set testing samples. Furthermore, despite [2, 18, 19], the majority of the currently available algorithms only work well on healthy subjects rather than patients with cardiac irregular conditions. The high accuracy reported in the literatures (within session testing) may not hold for cross session scenarios [15]. It is in this context that we study the verification problem with cardiac irregular data and cross session evaluation. The overview of the proposed system is depicted in Figure 1.

At the heartbeat level, in order to handle the variabilities caused by unreliable R peak detectors, artifacts, noises, and abnormal morphologies in the cardiac irregular data, robust beat normalization with quality check or outlier removal is needed [2, 18, 19, 20, 21]. In this work, we propose a novel shift-invariant beat normalization and outlier removal method utilizing the outputs from two different R peak detectors. Moreover, we apply PCA on the normalized ECG beat waveforms to extract the low dimensional features followed by linear discriminant analysis (LDA) and within-class covariance normalization (WCCN) [22, 23, 24] for beat variability compensation. Finally, cosine similarity with Snorm score normalization [23, 25, 24] is adopted for verification scoring.

At the segment level, we directly apply the hierarchical Dirichlet process auto-regressive hidden Markov model (HDP-AR-HMM) [26, 27] in the Bayesian non-parametric framework to the filtered raw data for unsupervised joint segmentation and clustering without any peak detection. It automatically decodes each raw ECG signal into a long string vector. We then apply the n-gram language

This research is supported in part by the CMU-SYSU Collaborative Innovation Research Center at Carnegie Mellon University.

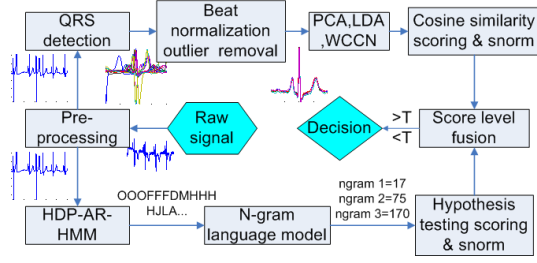


Fig. 1. The overview of the proposed system.

Table 1. PTB database partition and evaluation protocol

	"original"			"refined"		
	subjects	records/segments		subjects	records/segments	
target	82	82	248	80	80	230
test	119	251	798	119	241	733
background	101	146	388	92	131	333
Snorm	70	70	227	65	65	204
Total	290	549	1611	276	517	1500

model and log likelihood ratio based hypothesis testing for verification scoring followed by the Snorm score normalization.

Since heartbeat and segment level subsystems model the ECG signal from different views and the latter one also covers information from those irregular beats, we perform score level fusion to utilize their complementary information and improve the performance.

## 2. DATABASE

To investigate the performance of the proposed system, we used the public available PTB database from PhysioNet[28]. The reasons to select the PTB database for evaluation is as follows: (1) PTB database contains 549 recordings from 290 individuals, among which 52 subjects are healthy and the rest 238 subjects suffer from a variety of cardiac disorders which enables us to evaluate the performance for cardiac irregular conditions. (2) 113 individuals of those 290 subjects have more than one recordings, and the average time interval between any two ECG recording sessions of the same subject is about 500 days [7] which is important for our cross session evaluation. In this work, we only perform cross session testing (target and test segments must come from different recording sessions) for experimental results. (3) Lead I setup is included and sampled at 1000 hz. This could provide guidance for the real world mobile platform or finger based ECG biometrics systems [29, 30, 21].

The "original" and "refined" evaluation protocols are defined in Table 1. In the "original" protocol, all 549 recordings are divided into 4 non-overlapping sets, namely target, test, background and snorm. The test set has 119 subjects which not only covers all 82 subjects in the target set but also includes 37 out-of-set subjects. We only use one recording session for each target subject. Target and test sets must be excluded from any kinds of training and are only used for scoring. All the subjects that have only one recording session are divided into background and snorm sets for training. We also add 35 subjects that have multiple recording sessions to the background set to enable session variability compensation. The duration of each recording is from 32s to 120s, therefore we divide each recording session into multiple non-overlapping 30s-long segments. The signals of some recordings are highly noisy and severely contaminated which is not suitable for biometrics application, thus we rejected 10% of the total segments to form the "refined" protocol. In this protocol, there are totally  $230 \times 733 = 168590$  trials among which 1721 trials are true, the rest are false. All the list files, score files and HDP-AR-HMM demo codes are shared at [31].

## 3. METHODS

### 3.1. Heartbeat level subsystem

#### 3.1.1. Pre-processing and QRS detection

In the pre-processing, we first estimated and removed the baseline wander by a bandpass filter. Second, we applied the filtering and smoothing frontend in [32] to further clean the data. Then, we adopted two different QRS detectors, namely ecgpuwave from [28] and PeakDetection from [33] for the R-peak detection.

#### 3.1.2. Beat normalization and outlier removal

After QRS R-peak detection, we could get two different sets of R-peaks. For each QRS detector, let us denote the sample frequency  $fs$  as 1000, the number of beats as  $N$ ,  $D_i$  as the data associated with the  $i_{th}$  beat,  $RR_i^{pre}$  and  $RR_i^{post}$  as the RR interval of the  $i_{th}$  beat measured against the previous and post R peaks, respectively. The proposed shift-invariant beat normalization and outlier removal algorithm for a particular R peak detector is defined in Algorithm 1. In the time domain normalization, each beat is normalized to a 201 dimensional vector based on the associated phase values [33]. Since the phase values are calculated based on the R peaks, the middle point (index 101) corresponds to the detected R peak index.

Algorithm 1 Beat normalization and outlier removal for one peak detector

**Require:**  $D, RR_i^{pre}, RR_i^{post}, fs, N, k = 0, n = 0, T = \emptyset$   
**Ensure:**  $O$

- 1: **for**  $i = 1 \rightarrow N$  **do**
- 2:   **if**  $(0.4 * fs < \text{length}(D_i) < 1.7 * fs)$
- 3:     $\&(|RR_i^{pre} - RR_i^{post}| < 1/20(RR_i^{pre} + RR_i^{post}))$  **then**
- 4:      $D_i \leftarrow$  time domain normalization (201 bins) of  $D_i$
- 5:      $D_i \leftarrow D_i - \text{mean}(D_i); n \leftarrow n + 1$
- 6:      $[V_n^{max}, I_n^{max}] \leftarrow \max(D_i)$
- 7:      $[V_n^{min}, I_n^{min}] \leftarrow \min(D_i)$
- 8:      $T_n \leftarrow (D_i - (V_n^{max} + V_n^{min})/2) / (V_n^{max} - V_n^{min})/2$
- 9:   **end if**
- 10: **end for**
- 11:  $V_{median}^{max} \leftarrow \text{median}(V^{max}); V_{median}^{min} \leftarrow \text{median}(V^{min})$
- 12: **for**  $j = 1 \rightarrow n$  **do**
- 13:   **if**  $0.5 < \frac{V_j^{max}}{V_{median}^{max}} < 1.5$  and  $0.5 < \frac{V_j^{min}}{V_{median}^{min}} < 1.5$  **then**
- 14:     **if**  $|V_{median}^{max}| > |V_{median}^{min}|$  **then**
- 15:       **if**  $I_j^{max} == 101$  (middle of the 201 bins) **then**
- 16:          $k \leftarrow k + 1; O_k = T_j$
- 17:       **else if**  $(I_j^{min} == 101) \& (mode(I^{max}) == I_j^{max})$  **then**
- 18:          $k \leftarrow k + 1; O_k = \text{circshift}(T_j, 101 - I_j^{max})$
- 19:       **end if**
- 20:     **else**
- 21:       **if**  $I_j^{min} == 101$  (middle of the 201 bins) **then**
- 22:          $k \leftarrow k + 1; O_k = -T_j$
- 23:       **else if**  $(I_j^{max} == 101) \& (mode(I^{min}) == I_j^{min})$  **then**
- 24:          $k \leftarrow k + 1; O_k = \text{circshift}(-T_j, 101 - I_j^{min})$
- 25:       **end if**
- 26:     **end if**
- 27:   **end if**
- 28: **end for**

In the first stage (lines 1-10), we selected those stable beats with reasonable heart rate, perform time-scale and amplitude-scale normalization into template candidates  $T$  and calculate both positive and negative peak values and indexes. Then in the second stage (line 12-28), we perform quality check and circular shifts based on the peak indexes for shift-invariant outputs. Since we do not know whether the detected R peak is true or some irregular T/P/S peaks, we can only guarantee that the positive peak lies in the middle of the template (dim 101) and has the biggest distance to the beat mean.

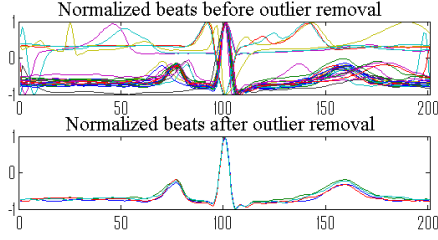


Fig. 2. Beat normalization and outlier removal for s0553.rem

Thus, we treat those beats with normal peak values in the candidates pool  $T$  separately based on the relation of their global peak values. Line 18 and 24 are for some special abnormal beat cases (e.g., the S peak is misidentified as the R peak by the detector in some myocardial infarction cases). It can recover some shift errors by the peak detector to make the proposed normalization shift-invariant.

Due to the R peak detector's unreliable performance in cardiac irregular data, we adopt two different detectors. We perform Algorithm 1 for each detector, and then select the one with the most qualified beats. Finally, we fit each dimension (total 201 bins) of those multiple qualified normalized beats independently into a single gaussian distribution with maximum likelihood estimation and only keep those beats always within the 2 sigma range. Figure 2 shows the normalized beat waveforms before and after outlier removal which indicates the effectiveness of the proposed algorithm.

### 3.1.3. Robust feature extraction and verification scoring

Once we get the outlier-removed normalized beat waveforms, we performed the PCA [10], LDA and WCCN [22] using the background and Snorm data sets to extract robust features for lower dimensional and better discriminative representation. The reason to choose LDA after PCA is because PCA preserves most of the variance after the projection but not necessarily make the coefficients more discriminative. WCCN is typically useful for verification tasks since it helps to cancel out the directions related to the variabilities [22]. Similar to the works in speaker recognition [23, 24] and face recognition [34], we hereby perform LDA and WCCN on top of the PCA to further compensate the beat variability and derive better subject-wise discriminative low-dimensional features. We applied the cosine similarity instead of the inner product for scoring [23] and normalized all the feature vectors into unit L2 norm after each stage of PCA, LDA and WCCN. Finally, Snorm based score normalization (in Equation 1) is employed to further reduce the error rate in the verification task [23, 25]. By scoring the target segment against the whole Snorm cohort set, we can retain the mean  $\mu_1$  and standard deviation  $\sigma_1$  of these scores, vice versa for the test segment in terms of  $\mu_2$  and  $\sigma_2$ .

$$\text{Snorm}(\text{rawscore}(\text{target}, \text{test})) = \frac{\text{rawscore} - \mu_1}{\sigma_1} + \frac{\text{rawscore} - \mu_2}{\sigma_2} \quad (1)$$

### 3.2. Segment level subsystem and information fusion

As depicted in Figure 3 that the proposed segment level approach consists of three main blocks, namely HDP-AR-HMM frontend, n-gram language model and the hypothesis testing based likelihood ratio scoring. HDP-AR-HMM is adopted to map the raw ECG data into a sequence of state labels (strings) by performing joint segmentation and clustering [27] rather than simple quantization [35]. Compared to the traditional HMM model for ECG segmentation [36], this unsupervised HDP-AR-HMM does not require pre-annotated segment labels and boundaries for training and can au-

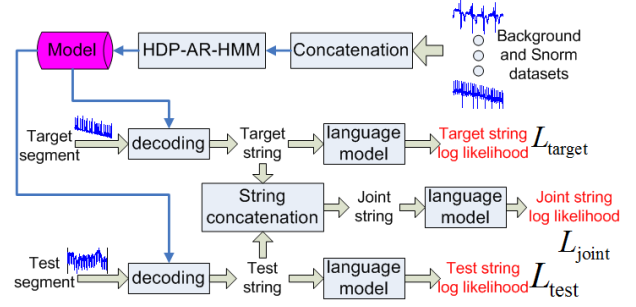


Fig. 3. Overview of the proposed segment level approach

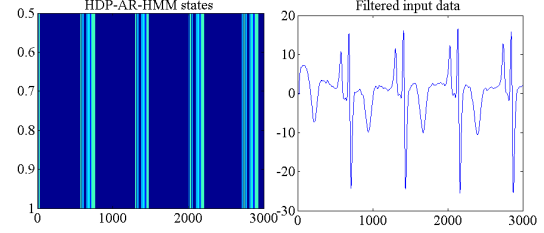


Fig. 4. The filtered waveform and state sequence after 3000 iterations trained/tested on the first 30s of s00151rem. Code is in [31].

tomatically determine the model size and refine model for new unseen data [26, 27]. Particularly, in our model, each state is represented by an order-2 auto-regressive curve which fits the continuous ECG data very well and the quasi-periodic characteristics of ECG signal make the transition probability matrix estimation accurate. Although HDP-AR-HMM has been successfully applied to motion capture and financial data analysis [37, 27], this is the first time to use HDP-AR-HMM on the ECG data to our best knowledge. We show one example in Figure 4 and provide the demo code in [31]. After mapping ECG signals into a set of strings, we use n-gram language model and hypertension testing based log likelihood ratio (see Figure 3) for scoring. Joint and individual language models are for the same subject and different subjects hypothesis testing. SRILM [38] with smoothing is used for n-gram language modeling.

$$\text{rawscore}(\text{target}, \text{test}) = \frac{P(\text{same subject})}{P(\text{different subjects})} = L_{\text{joint}} - L_{\text{target}} - L_{\text{test}}$$

Finally, we simply summed the aforementioned two subsystems' normalized (Snorm) scores in equal weight as our final score.

### 3.3. Relation to prior works

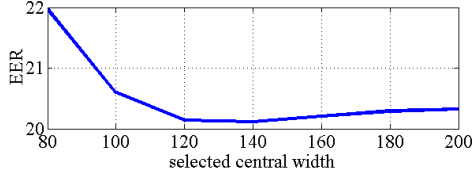
First, we focus on the cross session verification task including unseen out-of-set testing samples and cardiac irregular data rather than the conventional within session in-set identification task with healthy subjects. Second, we propose a novel shift-invariant beat normalization and outlier removal algorithm. Third, we apply LDA, WCCN on top of PCA to further improve the performance. Fourth, we propose a novel peak detection free framework by using HDP-AR-HMM based frontend for joint segmentation and clustering and followed by the n-gram language model based hypothesis testing scoring. Finally, we show that heartbeat and segment level subsystems are complementary, thus fusion enhances the performance.

## 4. EXPERIMENTAL RESULTS

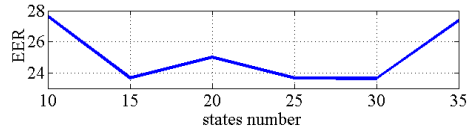
As introduced in Section 2 that we evaluate the proposed methods using Equal Error Rate (EER) by the "refined" protocol on the PTB

**Table 2.** Heartbeat level performance with or without outlier removal and Snorm on the normalized waveforms (width=201)

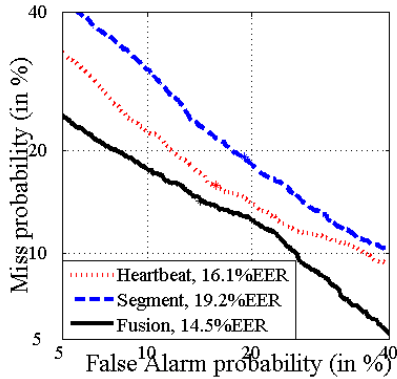
Methods	Cosine	Cosine+Snorm
without Outlier Removal	EER=25.1%	EER=22.0%
with Outlier Removal	EER=23.6%	EER=20.3%



**Fig. 5.** Heartbeat level performance of cosine scoring on the selected central waveforms with outlier removal and Snorm



**Fig. 6.** Segment level small subset performance using 3-gram language model (smoothed), 2500 frontend iterations and no Snorm



**Fig. 7.** Segment level fullset performance and information fusion

database. Heartbeat level subsystem performances are shown in Table 2, 3 and Figure 5, respectively. From Table 2, we can see that both outlier removal and Snorm score normalization improved the verification system performance significantly. In Figure 5, we show that using the entire normalized waveform may not generate better performance than just cropping the central part. The best result was obtained by using the central 141 dimensions which covers the PQRS main cardiac cycle. Results in table 3 demonstrate the effectiveness of PCA, LDA and WCCN for both dimension reduction and discriminative feature extraction. The central cropped version (width 141) achieved the best result. Dual cosine scoring is for a few segments that the sign condition (line 14) in Algorithm 1 may be unreliable determined (R peak and S peak have almost the same relative amplitudes), so we allow them to have an alternative model trained by the normalized waveform with the opposite direction.

Since evaluating the segment level subsystem on the full trial set is computationally expensive, we first adopted an internal small trial set with 2784 trials for parameter tuning in Table 4, 5 and Figure 6, then use the full set for the final subsystem evaluation and

**Table 3.** Heartbeat level performance with outlier removal

	Width=201	Width=141
Methods	dim/EER%	dim/EER%
Cosine	201/23.6	141/22.8
Cosine+Snorm	201/20.3	141/20.1
PCA+Cosine+Snorm	13/20.6	12/20.4
PCA+LDA+Cosine+Snorm	9/19.0	9/18.1
PCA+LDA+WCCN+Cosine+Snorm	9/17.7	9/17.2
PCA+LDA+WCCN+dual Cosine+Snorm	9/16.6	9/16.1

**Table 4.** Segment level small subset performance using 3-gram language model (smoothed) on 15 states frontend without Snorm

Iterations	800	1600	2500	5000	7000
EER (%)	27.6	27.6	25.0	24.9	26.4

**Table 5.** Segment level small subset performance using n-gram language model on 15 states 2500 iterations frontend without Snorm

Methods	N-gram	EER%
SRILM default smoothing	3-gram	38.4
Witten-Bell smoothing	3-gram	25.0
Witten-Bell interpolated smoothing	3-gram	23.7
Kneser-Ney interpolated smoothing	3-gram	25.0
Witten-Bell interpolated smoothing	2-gram	27.7
Witten-Bell interpolated smoothing	4-gram	23.7
Witten-Bell interpolated smoothing	5-gram	25.5

fusion in Figure 7. Table 4 shows that after 2500 iterations sampling, the HDP-AR-HMM becomes stable. Various language model smoothing techniques [38] as well as different n-gram orders are evaluated in Table 5. We can observe that Witten-Bell interpolated smoothing based 3-gram language model has the best performance. Extending the model order beyond 3-gram did not improve the results. In Figure 6 we observe that setting states number between 15 and 30 yielded good results which is reasonable. With less states, the model may not be able to represent all those different ECG patterns; with more states, there might be multiple states associated with similar patterns which reduces the discriminative power.

Finally, on the full trial set (Figure 7) with Snorm, the segment level subsystem achieved 19.1% EER which is comparable to the heartbeat level one with 16.1% EER. By fusing both with equal weight, we observe a significant EER reduction to 14.5% which is more than 25% relatively lower than the PCA baseline in Table 3 and outperformed the state-of-art results (19.2% EER) in [16].

## 5. CONCLUSIONS

We propose a heartbeat and segment level fusion system for the cross session verification task including unseen out-of-set testing samples and cardiac irregular data. At the heartbeat level, beat normalization with outlier removal is crucial and LDA, WCCN, Snorm could be applied on top of PCA for better performance. At the segment level, HDP-AR-HMM performs excellent unsupervised joint segmentation and clustering which decodes the ECG raw data into string vectors. Smoothed 3-gram language model with log likelihood ratio based hypothesis testing scoring on those strings provide good results and can be combined with heartbeat level system together for further improving the overall system performance.

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