ONLINE ECG BIOMETRICS VIA HADAMARD CODE

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ABSTRACT

In recent years, Electrocardiogram (ECG) biometrics has gained extensive attention. However, most existing methods adopted offline batch learning, which means that they need to accumulate all data and retrain the model when new data comes. Therefore, it is inefficient and unpractical for them to handle the online scenario where new data may continually come. To overcome the above limitation, we propose a novel ECG biometrics framework, termed Online ECG Biometrics based on Hadamard Codes. Firstly, we leverage matrix factorization to learn discriminative representations for ECG signals from their base feature space. Considering to leverage the orthogonal property of the Hadamard matrix, we use it to construct Hadamard codes to represent individuals and further guide the learning of representations. Furthermore, we develop an online optimization algorithm, which is efficient and effective to investigate the incremental problem in the context of ECG biometrics. The experimental results on two benchmark datasets indicate the merits of the proposed framework over the state-of-the-art.

***Index Terms*—** Online Learning, Hadamard Matrix, ECG Biometrics

1. INTRODUCTION

In the past few years, ECG biometrics has attracted a lot of attention with the advantage of universality, uniqueness, acceptability, and collectability [1]. To be specific, the existing ECG biometrics methods can be mainly categorized into two groups: fiducial methods and non-fiducial methods. Particularly, fiducial methods [2, 3, 4] extract features by delineating dominant fiducials while non-fiducial methods do not use the fiducial points to generate the feature set [5, 6, 7].

As subspace-based approach aims to extract representations keeping the maximum discriminant power to improve the recognition performance, several works with sparse representation [8, 9, 10] and matrix factorization [11, 12] have shown the success on ECG Biometrics. Although these research works have gained promising performance, one limitation is that they assume all training data are already available before training. Such strategy learns models in batch-based mode. However, when new individuals come for biometric recognition, they have to accumulate all (including both old and new) data and re-learn the models. In real applications, new individuals may continually come and they may re-learn models based on old data many times [13, 14]. In other words, existing batch-based methods are inefficient for **online scenario** where data may come in streaming fashion. In addition, the identification performance is affected by the heterogeneity and diversity within the homogeneous ECG samples and it is essential to learn the discriminative representations.

To handle the above issues, we propose a novel framework for ECG biometrics, termed Online ECG Biometrics based on Hadamard Codes. The main contributions of this paper are summarized as follows: 1) Our method could learn the discriminative representations for ECG signals. 2) To the best of our knowledge, this is the first work to tackle the incremental learning problem for ECG biometrics and such online biometric setting is practical in real-world ECG biometrics tasks. We utilize the Hadamard Matrix to generate distinct Hadamard code for all individuals to guide the learning. Then, a well-designed online optimization algorithm is proposed to incrementally learn from streaming data. 3) Extensive experiments conducted on two datasets demonstrate that the proposed framework achieves satisfying performance.

2. PROPOSED METHOD

2.1. Notations

Suppose we have samples and their base features are extracted from ECG signal for learning. It's worth noting that samples come in a streaming fashion and we learn our model incrementally rather than the batch-based mode. Without loss of generality, we present how our method to be learned at the t-th round. At round t, we use $\vec{\mathbf{X}}^{(t)} \in \mathbb{R}^{m\times n_t}$ denote newly coming data chunk and $\tilde{\mathbf{X}}^{(t)} \in \mathbb{R}^{m\times(N_t-n_t)}$ represent the old data samples accumulated before current round, where n_t is the number of samples coming at round t, $N_t = n_1 + \cdots + n_t$

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is the total number of collected samples at round t, and m is the dimensionality of the base feature space. Throughout this paper, $Tr(\cdot)$ is the trace of a square matrix and $\mathbf{I}$ denotes an identity matrix.

2.2. Model Formulation

To derive a more discriminative representation for ECG biometrics, we can leverage the matrix factorization technique to remove the redundant information in the original base feature to generate the low-rank vectorial representations in latent space. For the sake of accommodating to online ECG biometrics, the corresponding objective at round t can be formulated as:

$$\mathcal{O}_1 = \beta(\left\|\tilde{\mathbf{X}}^{(t)} - \mathbf{G}^{(t)}\tilde{\mathbf{V}}^{(t)\top}\right\|_F^2 + \left\|\vec{\mathbf{X}}^{(t)} - \mathbf{G}^{(t)}\vec{\mathbf{V}}^{(t)\top}\right\|_F^2), \tag{1}$$

where $\tilde{\mathbf{V}}^{(t)} \in \mathbb{R}^{(N_t - n_t)\times r}$ and $\vec{\mathbf{V}}^{(t)} \in \mathbb{R}^{n_t \times r}$ are the learned representations of old and new samples, $\mathbf{G}^{(t)} \in \mathbb{R}^{m\times r}$ is redundant information, r is the dimension of learned representation, and β is the trade-off parameter. With Eq.(1), we can learn the powerful representations $\vec{\mathbf{V}}^{(t)}$ in an online manner by maintaining the information in the original base feature of the old accumulated samples and the newly arrived samples.

Meanwhile, the goal of our method is to learn the projection to transform the out of samples into the latent space, *i.e.*, query samples. With this in consideration, we construct the projection from base feature space to the latent representation space and the function at the t-th round can be written as:

$$\mathcal{O}_2 = \alpha(\left\|\tilde{\mathbf{V}}^{(t)} - \tilde{\mathbf{X}}^{(t)\top}\mathbf{W}^{(t)}\right\|_F^2 + \left\|\vec{\mathbf{V}}^{(t)} - \vec{\mathbf{X}}^{(t)\top}\mathbf{W}^{(t)}\right\|_F^2), \tag{2}$$

where $\mathbf{W}^{(t)} \in \mathbb{R}^{m\times r}$ is the projection matrix learned at round t and α is the trade-off parameter. In online ECG biometrics settings, $\mathbf{W}^{(t)}$ is dynamically updating along with the training procedure and we use the same mapping matrix for both old $\tilde{\mathbf{X}}^{(t)}$ and new samples $\vec{\mathbf{X}}^{(t)}$ so that knowledge previously learned could be compatible with new knowledge.

In general, we want the representations of different individuals to be different as much as possible. In other words, different individuals' learned representations should be discriminative. Meanwhile, samples' representations of the same individual should be similar. To attain this goal, we utilize the Hadamard matrix [15] to generate prototype code for all individuals. In particular, the Hadamard matrix [15] is a n-order orthogonal matrix, the entry in the i-th row and the j-th column can be defined as: $(-1)^{(i-1)\times(j-1)}$. Based on the definition of the Hadamard matrix, we can find that column vectors in a Hadamard matrix are orthogonal and linearly independent. Thus, we randomly designate column vectors of Hadamard matrix as the prototype codes for individuals and one individual corresponds to one code. Then, to make the learned representations more discriminative, we force them to be similar with corresponding Hadamard prototype codes:

$$\mathcal{O}_3 = \theta(\left\|\tilde{\mathbf{H}}^{(t)} - \tilde{\mathbf{V}}^{(t)}\right\|_F^2 + \left\|\vec{\mathbf{H}}^{(t)} - \vec{\mathbf{V}}^{(t)}\right\|_F^2), \tag{3}$$

where $\tilde{\mathbf{H}}^{(t)} \in \mathbb{R}^{(N_t - n_t)\times r}$ and $\vec{\mathbf{H}}^{(t)} \in \mathbb{R}^{n_t \times r}$ denote the assigned Hadamard code matrix of old samples and new samples at round t, and θ is the trade-off parameter. Specifically, samples of the same individual share the same Hadamard code while samples of different individuals correspond to different Hadamard code. In light of the property of Hadamard matrix, Eq.(3) can learn more discriminative representations.

If samples of new individual are observed in round t, we randomly and non-repeatedly select a new column vector from Hadamard matrix to represent the new individual. Then, we can construct Hadamard code matrix $\vec{\mathbf{H}}^{(t)}$. From this, we can find that our method may handle the situation where new individual comes and such situation may be quite common in practice for ECG Biometrics.

Overall Objective Function By combining Eq.(1), Eq.(2), and Eq.(3), the overall objective function can be written as:

$$\min_{\mathbf{W}^{(t)},\mathbf{G}^{(t)},\vec{\mathbf{V}}^{(t)}} \mathcal{O}_1 + \mathcal{O}_2 + \mathcal{O}_3 + \delta Re(\mathbf{W}^{(t)}, \mathbf{G}^{(t)}), \tag{4}$$

where δ is a parameter and $Re(\cdot)$ is regularization item.

2.3. Optimization

We propose an online optimization algorithm for Eq.(4) and the optimization steps at the t-th round are shown as follows.

Step 1: Update $\mathbf{W}^{(t)}$. The sub-problem of $\mathbf{W}^{(t)}$ can be rewritten as:

$$\begin{aligned}\min_{\mathbf{W}^{(t)}} \quad & \alpha\left\|\tilde{\mathbf{V}}^{(t)} - \tilde{\mathbf{X}}^{(t)\top}\mathbf{W}^{(t)}\right\|_F^2 + \\ & \alpha\left\|\vec{\mathbf{V}}^{(t)} - \vec{\mathbf{X}}^{(t)\top}\mathbf{W}^{(t)}\right\|_F^2 + \delta\left\|\mathbf{W}^{(t)}\right\|_F^2,\end{aligned} \tag{5}$$

By setting the gradient of the objective with respect to $\mathbf{W}^{(t)}$ to zero, we have the solution,

$$\mathbf{W}^{(t)} = (\mathbf{C}_1^{(t)} + \tfrac{\delta}{\alpha}\mathbf{I})^{-1}\mathbf{C}_2^{(t)}, \tag{6}$$

where $\mathbf{C}_1^{(t)} = \tilde{\mathbf{X}}^{(t)}\tilde{\mathbf{X}}^{(t)\top} + \vec{\mathbf{X}}^{(t)}\vec{\mathbf{X}}^{(t)\top}$ and $\mathbf{C}_2^{(t)} = \tilde{\mathbf{X}}^{(t)}\tilde{\mathbf{V}}^{(t)} + \vec{\mathbf{X}}^{(t)}\vec{\mathbf{V}}^{(t)}$. Obviously, we can transform $\mathbf{C}_1^{(t)}$ into the following scheme:

$$\begin{aligned}\mathbf{C}_1^{(t)} &= \tilde{\mathbf{X}}^{(t)}\tilde{\mathbf{X}}^{(t)\top} + \vec{\mathbf{X}}^{(t)}\vec{\mathbf{X}}^{(t)\top} \\ &= [\tilde{\mathbf{X}}^{(t-1)}; \vec{\mathbf{X}}^{(t-1)}][\tilde{\mathbf{X}}^{(t-1)}; \vec{\mathbf{X}}^{(t-1)}]^\top + \vec{\mathbf{X}}^{(t)}\vec{\mathbf{X}}^{(t)\top} \\ &= \mathbf{C}_1^{(t-1)} + \vec{\mathbf{X}}^{(t)}\vec{\mathbf{X}}^{(t)\top}.\end{aligned} \tag{7}$$

Similarly, we have $\mathbf{C}_2^{(t)} = \mathbf{C}_2^{(t-1)} + \vec{\mathbf{X}}^{(t)}\vec{\mathbf{V}}^{(t)}$. Notably, $\mathbf{C}_1^{(t-1)}$ is calculated at the previous round ($t-1$ round) and can be directly used at the current t-th round. Hence, we just need to calculate $\vec{\mathbf{X}}^{(t)}\vec{\mathbf{X}}^{(t)\top}$ at round t and the calculation of

$\mathbf{C}_1^{(t)}$ can be very efficient. These temporary variables, *e.g.*, $\mathbf{C}_1^{(t-1)}$ and $\mathbf{C}_2^{(t-1)}$, could carry knowledge from old data and help our method incrementally learn from streaming data.

Step 2: Update $\mathbf{G}^{(t)}$. Analogous to $\mathbf{W}^{(t)}$, we set the derivative of the $\mathbf{G}^{(t)}$ sub-problem with respect to $\mathbf{G}^{(t)}$ to zero. Then, the closed-form solution of $\mathbf{G}^{(t)}$ can be obtained:

$$\mathbf{G}^{(t)} = \mathbf{C}_2^{(t)}(\mathbf{C}_3^{(t)} + \tfrac{\delta}{\beta}\mathbf{I})^{-1}, \tag{8}$$

where $\mathbf{C}_3^{(t)} = \mathbf{C}_3^{(t-1)} + \vec{\mathbf{V}}^{(t)\top}\vec{\mathbf{V}}^{(t)}$. Notably, we can temporarily store these variables at last round and directly use them to get the variables at current round, which ensures the online optimization being extremely efficient.

Step 3: Update $\vec{\mathbf{V}}^{(t)}$. Since $\vec{\mathbf{V}}^{(t)}$ is known, we only need to update $\vec{\mathbf{V}}^{(t)}$ of the newly coming data. When $\mathbf{W}^{(t)}$ and $\mathbf{G}^{(t)}$ are fixed, the objective function to solve $\vec{\mathbf{V}}^{(t)}$ can be rewritten as:

$$\begin{aligned}\min_{\vec{\mathbf{V}}^{(t)}} \ & \beta\left\|\vec{\mathbf{X}}^{(t)} - \mathbf{G}^{(t)}\vec{\mathbf{V}}^{(t)\top}\right\|_F^2 + \alpha\left\|\vec{\mathbf{V}}^{(t)} - \vec{\mathbf{X}}^{(t)\top}\mathbf{W}^{(t)}\right\|_F^2 \\ & + \theta\left\|\vec{\mathbf{H}}^{(t)} - \vec{\mathbf{V}}^{(t)}\right\|_F^2.\end{aligned} \tag{9}$$

Similarly, we can obtain the closed-solution of $\vec{\mathbf{V}}^{(t)}$ as:

$$\begin{aligned}\vec{\mathbf{V}}^{(t)} = & (\alpha\vec{\mathbf{X}}^{(t)\top}\mathbf{W}^{(t)} + \beta\vec{\mathbf{X}}^{(t)\top}\mathbf{G}^{(t)} \\ & + \theta\vec{\mathbf{H}}^{(t)})((\alpha+\theta)\mathbf{I} + \beta\mathbf{G}^{(t)\top}\mathbf{G}^{(t)})^{-1}.\end{aligned} \tag{10}$$

By the above steps, we can update all variables and repeat the process iteratively until the objective function converges.

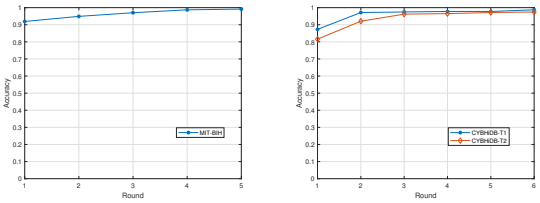
2.4. Matching

After training, the latest projection matrix $\mathbf{W}^{(t)}$ can be learnt to construct the discriminative representations for query samples and enroll samples, which can be represented as $\mathbf{X}_q^\top\mathbf{W}^{(t)}$ and $\mathbf{X}_e^\top\mathbf{W}^{(t)}$, respectively. In the matching stage, we compute the Euclidean distance among heartbeat vector of query sample and all enroll samples. If the distance between one individual's enroll and query is the smallest, we then believe that the query belongs to this individual.

3. EXPERIMENTS

3.1. Experimental Settings

Datasets. We conducted the experiments on two datasets to evaluate the effectiveness of our method. **MIT-BIH** [16] is one of the most used dataset for ECG biometrics and it is available at the Physionet [17] repository. It contains 48 two-channel ambulatory ECG recordings, obtained from 47 individuals. **CYBHiDB** [18] is regarded as a challenging off-the-person dataset, acquired from hand palms and fingertips. In this paper, we used the data in long-term with 63 healthy participants, including two distinct sessions separated by three months, and we called them T1 and T2, respectively. For both datasets, we randomly selected 5 homogenous samples for each individual to form the test set and left the remaining samples as the training set.



(a) MIT-BIH. (b) CYBHiDB.

Fig. 1. Accuracy results at all rounds.

Evaluation metrics. For the identification mode, the accuracy is used as the evaluation criteria, which is the percentage of correctly classified testing samples. For the verification mode, Equal Error Rate (EER) is employed to evaluate the performance.

Implementation details. The heartbeats are segmented with a number of sampling points from each side of the R peak, which is detected by Pan-Tompkin [19]. One heartbeat is composed of 260 sampling points for MIT-BIH and 600 sampling points for CYBHiDB. We extracted 1DMRLBP[7] served as the input of the proposed framework and the enroll sample for each individual is generated by the mean homologous heartbeat in the training set. We generate 2^7-order Hadamard matrix and the dimension of the learned representation r is set to 128. The iteration is set to 6 and the trade-off parameters α, β, θ, and δ are selected by a validation procedure in the experiment.

Online setting. Inspired by the online setting of other research domains [20], we split the training set into several data chunks to support the online scenario. For MIT-BIH, the training set is divided into 5 data chunks. Specially, each of the first 4 chunks has 70 samples and the last chunk has 49 samples. For CYBHiDB, it has 6 chunks with each of the first 5 chunks containing 108 samples and the last chunk containing 27 samples. For our method, we used these data chunks to simulate data streaming and learned from training data incrementally.

3.2. Comparison with state-of-the-arts

We compared our method with several state-of-the-arts on MIT-BIH, including non-deep methods [21, 22, 11] and deep-learning based methods [1, 23]. For all baselines, the results are copied from their original papers. Experimental results are summarized in Table 1 and we have the following observations: 1) Our method outperforms all non-deep baselines on MIT-BIH, demonstrating its effectiveness for ECG biometrics. 2) Compared with deep-learning methods, our model achieves comparable performance. Especially, the experimental results are superior to the deep baseline [1]. The

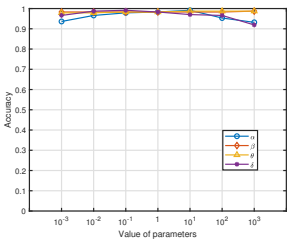


Fig. 2. Balance parameters analysis.

Table 1. **Performance analysis on MIT-BIH.**

Dataset	Method	EER(%)	Accuracy(%)
MIT-BIH	[21]	-	93.1
	[11]	2.73	94.68
	[22]	-	98.2
	[23]	0.02	99.7
	[1]	-	96.5
	OURS	0.64	99.15

deep model [23] achieves the satisfying performance at the cost of much more training time and it is not suitable to handle incremental datasets with new instances. Therefore, our method can generate a more discriminative representation in an online manner and it works well for ECG biometrics.

We also conducted the experiments on the challenging off-the-person dataset CYBHiDB under two situations, *i.e.*, within-session and across-session. The experiments under within-session situation use training data and testing data in the same session, *i.e.*, all training data and testing data come from T1 session or T2 session. For the across-session situation, training data and testing data come from different sessions. The baselines include non-deep methods [9, 24, 26, 27] and deep method [25]. Experimental results are summarized in Table 2 and Table 3. For all baselines, the results are those reported in previous work [9]. From Table 2, we can observe that our model achieves the satisfying accuracy and EER results compared with all non-deep and deep methods under the within-session situation. For the across-session situation, the experimental results are summarized in Table 3. It is worth noting that our model has an extraordinary performance in all cases, demonstrating the effectiveness of our model.

Note that the results of our method are obtained in an online fashion while other baselines are all learned in batch-based mode. Generally, batch-based learning strategy may bring better performance but is unpractical and inefficient for online scenario. That is one of the motivations to propose our method. To better display the online learning setting of our method, we further plotted accuracy results versus every round in Figure 1. From this figure, we can find the performance is always satisfactory and gets better with more rounds. It confirms that our method is able to incrementally learn from streaming data for ECG biometrics.

In summary, our method outperforms existing methods. Besides, our method is the first attempt to handle the online scenario where training samples continually appear along with new data chunks for ECG biometrics and such scenario is valuable to real-world ECG biometrics.

Table 2. **Within-session analysis on CYBHiDB.**

Dataset	Method	EER(%)		Accuracy(%)	
		T1	T2	T1	T2
CYBHiDB	[9]	1.26	2.28	97.43	95.32
	[24]	3.12	4.53	95.51	93.26
	[25]	1.85	3.35	97.12	94.95
	[26]	2.52	3.89	96.07	94.23
	[27]	5.45	6.53	93.52	91.41
	OURS	1.58	1.71	98.73	97.78

Table 3. **Across-session analysis on CYBHiDB.**

Method	Training	Testing	EER(%)	Accuracy(%)
[9]	T1	T2	10.26	87.75
	T2	T1	11.14	86.24
[24]	T1	T2	14.04	83.23
	T2	T1	13.18	84.35
[25]	T1	T2	12.78	85.46
	T2	T1	12.83	84.46
[26]	T1	T2	13.87	84.35
	T2	T1	14.56	83.92
[27]	T1	T2	15.23	82.49
	T2	T1	14.78	83.83
OURS	T1	T2	3.17	96.51
	T2	T1	2.70	96.19

3.3. Parameters sensitive analysis

We also conducted experiments to analyze the sensitivity of parameters and the results on MIT-BIH are plotted in Figure 2. It can be seen that our method is robust to almost all parameters. Thus, we can conclude that our model is not sensitive to parameters and could be easily applied in practice. We finally set α, β, θ, and δ to 1 in our experiment, respectively.

4. CONCLUSIONS

In this paper, we propose a novel ECG biometrics framework termed Online ECG Biometrics based on Hadamard Codes. We learn the representations for ECG signals from base feature space and assigned individuals' Hadamard codes. To be compatible with the incremental setting, we present our objective loss function in online mode and design a novel online optimization algorithm to solve it. As far as we know, this is the first online model for ECG biometrics which could incrementally learn from streaming data. Extensive experiments on two benchmark datasets have demonstrated the effectiveness of the proposed method.

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