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Time series for blind biosignal classification model ☆

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ABSTRACT

Biosignals such as electrocardiograms (ECG), electroencephalograms (EEG), and electromyograms (EMG), are important noninvasive measurements useful for making diagnostic decisions. Recently, considerable research has been conducted in order to potentially automate signal classification for assisting in disease diagnosis. However, the biosignal type (ECG, EEG, EMG or other) needs to be known prior to the classification process. If the given biosignal is of an unknown type, none of the existing methodologies can be utilized. In this paper, a blind biosignal classification model (*B²SC Model*) is proposed in order to identify the source biosignal type automatically, and thus ultimately benefit the diagnostic decision. The approach employs time series algorithms for constructing the model. It uses a dynamic time warping (DTW) algorithm with clustering to discover the similarity between two biosignals, and consequently classifies disease without prior knowledge of the source signal type. The empirical experiments presented in this paper demonstrate the effectiveness of the method as well as the scalability of the approach.

1. Introduction

The term 'biosignal' refers to all kinds of signals that can be measured and monitored from biological beings, including electrocardiogram (ECG), electroencephalogram (EEG), electromyogram (EMG), and electrooculography (EOG). The signals are the recordings of the electrical activity of the heart, brain, muscles, and eyes, respectively, which can be used in making diagnostic decisions. Research into ECG classification has proliferated since the discovery of the automatic recognition of electrocardiogram waves by Stallman and Pipberger [1]. After this discovery, a rule-based rough-set decision system was developed to generate an inference engine for ECG classification from different standard time-plane features [2]. Then, ECG classification was optimized by applying a feature selection method with a new criterion function index to improve performance [3]. ECG signal classification using parallel genetic algorithms and neural networks [4], as well as using block-based neural networks, was proposed [5]. Although EEG classification is more difficult due to the high dimensional feature space, a certain amount of research is underway in order to benefit the biomedical community. For example, Subasi [6] developed a Mixture of Expert (ME) network structure to improve the accuracy of epileptic seizure detection in EEG, and the overall predictive performance was superior to any of the individual experts. An automatic recognition method for Alzheimer's disease (AD) with single-channel EEG recording using combined genetic algorithms (GA) and artificial neural networks (ANN) was proposed by Cho et al. [7]. Similar signals are obtained in EMG and EOG classification, however, the complex nature of the signals often means that their analysis and classification is difficult [8]. Lucas et al. employed a support vector machine (SVM) approach to classify multi-channel surface EMG signals. The experimental results showed that their method is suitable for real-time applications [9]. Then, the authors established an EMG signal classification system to discriminate finger motions by using linear neural networks [10]. It showed promising performance for classifying motions based on biosignal patterns. Recently, Alkan and Günay proposed a surface EMG signal classification system, which used five discriminant functions and an SVM classifier [11]. Their system is used to classify EMG signals in prosthetic arm control. Furthermore, EOG is an efficient measurement technique to detect eye movement for human activity recognition as shown by the use of EOG signals for the realization of a Human Computer Interface (HCI) device [12], which is able to recognize a patient's eye movements and thus restore some communication abilities. Güven and Kara [13] used Artificial Neural Networks to analyze EOG signals, which can be used to diagnose subnormal vision. Then Bulling et al. proposed a method for analyzing repetitive eye movement patterns [14]. They used EOG signals to detect three basic eye movement types (saccades, fixations, and blinks) and proved that the recognition methodology could successfully identify five office activities.

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However, all of the aforementioned studies concentrated on a single type of biosignal, where the source of the biosignal was known (ECG, EEG, EMG, or EOG) to the classifier, and the classification was conducted based on the nature of the specific type of biosignal. However, to our knowledge, there is not any literature about automatically identifying biosignals, which would be useful when the type of biosignal is unknown. To bridge this gap, this study proposes an automatic approach for identifying an unknown biosignal and typing it as ECG, EEG etc., in addition to conventional biosignal classification. The approach incorporates a DTW (dynamic time warping) algorithm of time series classification, which is capable of identifying a specific disease or symptom regardless of the type of source biosignal. The organization of this paper is as follows: in Section 2, the proposed approach and its three major phases are presented in detail. After that, the empirical results are discussed in Section 3, followed by the conclusion and future work sections.

2. Blind biosignal classification model

An emerging trend is that not only do professionals use medical technologies and tools, but also patients and others [15]. The rapid development of innovative information and communication technologies has led to home-based healthcare, which is feasible and preferable, particularly for the elderly and patients with chronic diseases who self-manage their health at home rather than in a hospital. However, home-based users of medical technology are usually non-professional and not well trained, so they may incorrectly attach ECG sensors to their bodies for example. Furthermore, multiple biosignals may be acquired simultaneously and mixed or combined into one, which may result in unknown or ambiguous source biosignals with only their temporal waveforms or time-frequency patterns known, but not their types [16]. Inspired by these facts, a blind biosignal classification model (*B²SC Model*) is proposed, which serves as a partial implementation of an integrated multi-function biosignal measurement device for such home-based healthcare paradigms. *B²SC Model* can automatically identify an unknown (blind) mixed biosignal for further detailed analysis and diagnosis, and its purpose is multifold: (1) enabling non-skilled home-based users to operate a multi-function biosignal acquisition device easily for monitoring and managing their health conditions; (2) helping to improve the diagnostic capability of a disease or symptom without knowing the exact type of source biosignal; and (3) allowing the use of only one device and one sensor which could adapt to multiple biosignals. *B²SC Model* is composed of three major phases: biosignal template construction, template optimization and management, and pattern matching. The details of each phase will be described below.

2.1. Biosignal template construction

As previously discussed, the quality and quantity of a training dataset in a classification problem severely affects the efficiency and performance of a classification algorithm. The biosignal template construction phase aims at constructing a library of biosignal templates using all available raw data from biosignals, and such templates will be ultimately used for guidance in accurately classifying an unknown biosignal. The raw biosignals usually have long signal lengths and the datasets often have large file sizes, meaning that it is impossible for the raw data to be used directly in training the classification model. Moreover, a single type of biosignal may have diverse patterns. Fig. 1 shows an example of this: all four patterns are ECG signals. The first pattern indicates a normal ECG signal, and the other three reveal the different stages of ischemic heart disease. Therefore, the construction of a variety of biosignal templates as training datasets is critical for the subsequent task of classification.

The benchmark datasets, downloaded from the MIT-BIH Arrhythmia Database [17], the CHB-MIT Scalp EEG Database [18] and the EMG Datasets Repository [19] were used to produce the ECG, EEG, and EMG templates, respectively. The MIT-BIH Arrhythmia Database provides standard test materials for the evaluation of arrhythmia detectors as well as for basic research in cardiac dynamics. The CHB-MIT Scalp EEG Database collects the EEG recordings from pediatric patients who suffered from intractable epilepsy. Furthermore, the CAP (Cyclic Alternating Pattern) Sleep Database records EMG and EOG signals as well as EEG signals. It is intended to provide a useful number of carefully annotated examples of CAP in a representative variety of pathophysiologic contexts, which is vital for the study of CAP dynamics, and in particular for the development and evaluation of CAP analysis. In this paper, we use ECG as an example, to describe the entire process of the *B²SC Model*. EEG or EMG datasets are used for construction and training in exactly the same way as ECG signals.

The essential tasks of template construction include biosignal segmentation and template formation. Segmentation partitions each ECG signal into small pieces so that each piece contains only one cycle of an ECG recording, representing one candidate template. As a result, there are in total 240,000 one-cycle ECG signals generated from the entire MIT-BIH Arrhythmia Database. All of these one-cycle ECG signals are used as the source for generating the library of ECG templates. Nonetheless, the number of candidate biosignal templates determines the efficiency and performance of the subsequent classification tasks: too few templates for each category may lead to underfitting, which misclassifies some important biosignal patterns; but too many templates may cause redundancy and wastage of resources. To this end, the existing ECG categories defined by Jenkins and Gerred [20] are used as guidelines to determine the groups of templates, which describe nine major common categories for ECG signals. We have ignored the minor subcategories in this study. Similarly, the general categories specified by Niedermeyer and da Silva [21] and Khushaba et al. [19] are used to determine the classes for EEG and EMG in this study. Therefore, in the template formation stage, all candidate ECG templates are roughly divided into nine groups. The widely used clustering methodology, *k*-nearest neighbors (*k*NN) algorithm [22], was employed for classifying a template by the major label amongst its *k*-nearest neighbors in the ECG database.

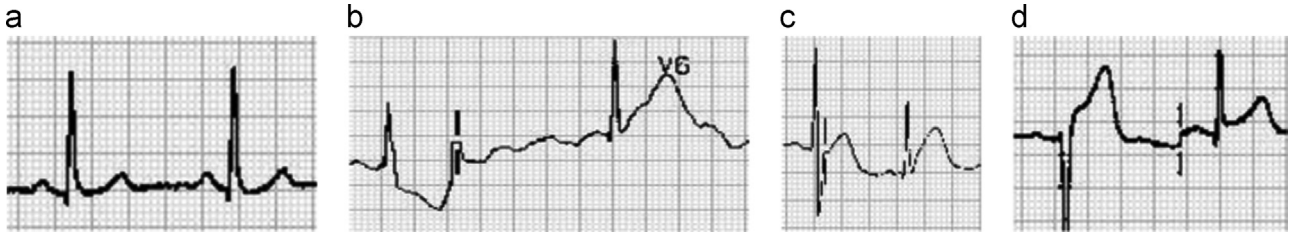

Fig. 1. Samples of different patterns from ECG signals: (a) normal ECG; (b) acute inferior myocardial infarction; (c) acute posterior myocardial infarction, and (d) acute anterior myocardial infarction.

2.2. Template optimization and management

This phase refines the library of ECG signal templates that were generated in the above template construction step, into a set of optimal ECG templates (*OpTem*) which represent the majority of ECG signals in the database. To discover the optimal representatives from each category of various ECG patterns, the *k*-medoids algorithm [23] was employed. The *k*-medoids method is a traditional clustering algorithm, which finds one central object as a representative for all other samples within the cluster. However, the quality of this algorithm relies heavily on several factors. First, the initial central object for each cluster is determined randomly, which may result in the local maxima. Second, the choice about how many clusters are used may affect the efficiency of the algorithm. Furthermore, the distance measure method and stopping criterion for large datasets may also influence the performance. Because of these shortages, we have amended the *k*-medoids method by using the following refinements:

- The number of ECG clusters (k value) depends on the number of existing categories of ECG signals in the database, i.e. nine common categories. No user input parameter is needed.
- The initial central ECG template for each cluster is extracted from each ECG signal category in the library of signal templates. This prevents local maxima from being produced.
- A stopping criterion is employed to restrict the search space in terms of the number of candidates for ECG template. This decreases the number of candidates to be visited without sacrificing the quality of the resultant optimal templates, meanwhile increasing the performance of the algorithm.

  In fact, the template construction phase and this optimization phase can be combined into one from an implementation point of view. Fig. 2 illustrates the proposed template construction and optimization phases, which attempt to produce a set of optimal ECG templates.

2.3. Pattern matching

This phase is a kernel component of our *B²SC Model*. It is aimed at identifying an unknown biosignal into ECG, EEG, or other type, by comparing the similarity of an input biosignal with various datasets of representative biosignal templates. Fig. 3 describes the detailed procedure of the pattern matching algorithm. Given a source blind biosignal $S=\{s_1, s_2, \ldots, s_m\}$ with m sample segments and a set of optimal representative templates $OpTem=\{P_{ecg}(i),\ P_{eeg}(j);\ 1\le i\le k,\ 1\le j\le w\}$, where P_{ecg} denotes the ECG template collection with k optimal templates, and P_{eeg} indicates an EEG template collection with w optimal templates. A parameter λ is declared as a threshold for discriminating amongst ECG, EEG and other biosignals. This process is in fact regarded as a floating window that shifts from the starting point of S to the end, and matches each slice of S with a template P, where the window size equals $|P|$. The process enumerates every cluster in the *OpTem*, and meanwhile the local minimum similarity scores min_{ecg} and min_{eeg} are further compared and evaluated. The global minimum similarity score min_{tp} is eventually obtained, for identifying a biosignal other than ECG/EEG.

The goal of the pattern matching phase is to optimize the similarity function in Eq. (1). The function minimizes the distance (similarity score) between the samples and the templates by comparing each segment of a source blind biosignal S iteratively with a template P in *OpTem*. The notation $|.|$ refers to the length (number of segments) of a sample, where $P\in\{P_{ecg}; P_{eeg}\}$, $S_{b,e}$ depicts a segment that is an interval between bth and eth of sample S, i.e., $S_{b,e}\in S$, whereas $|S_{b,e}|=|P|$.

$$Sim(P,\ S)=\min_{0\le b\le |S|-|P|;b+|P|\le e\le |S|} DTW(P,\ S_{b,e}) \tag{1}$$

In Eq. (1), an auto-aligned dynamic time warping (DTW) algorithm as defined in Eq. (2) is applied to evaluate the degree of similarity between two comparable biosignals. DTW is an algorithm for measuring similarity between two sequences, which may vary in time or speed. It is a robust distance measure for time series data, allowing two signals with similar patterns to align even if they are not on the same time axis. DTW is widely used in a variety of domains including speech recognition, word image matching, handwriting recognition, heart rhythm change detection, ECG segmentation and classification [24–27]. Detailed information about DTW can be found in Han and Kamber [28]. Eq. (2) assumes that there are two ECG signals, $ET=et_1,\ldots,et_i,\ldots,et_n$ and $EU=eu_1,\ldots,eu_j,\ldots,eu_m$ of length n and m, respectively. To compare their similarity, an n-by-m matrix is constructed where the (ith, jth) element of the matrix contains the distance $d(et_i,\ eu_j)$ between two points et_i and eu_j.

$$DTW(ET,\ EU)=\ \min\sqrt{\sum_{l=1}^{K} d(w_l)},\ \text{and}\ \max(m,n)\le K\le m+n \tag{2}$$

where w_l is the lth element of a warping path W, which is a contiguous set of matrix elements that provide mapping between ET and EU, hence;

$$d(w_l)=d(et_i,\ eu_j)=(et_i,\ eu_j)^2 \tag{3}$$

The smaller the value of d is, the higher the similarity of two biosignals. There are many warping paths that satisfy the condition, but we are only interested in the optimal path that minimizes an accumulated distance along the warping path, as defined in Eq. (2). An efficient technique for determining the shortest warping path is dynamic programming. As depicted in Eq. (4), it is able to determine the cumulative distance D_T recursively as the distance d and the minimal accumulated distances of the adjacent elements. This enables the search space of warping paths to be greatly reduced, and the complexity for computing an optimal warping path is decreased to $O(nm)$.

$$D_T(et_i,\ eu_j)=d(et_i,\ eu_j)+\ \min\{D_T(et_{i-1}, eu_{j-1}),\ D_T(et_i,\ eu_{j-1}),\ D_T(et_{i-1}, eu_j)\} \tag{4}$$

```
1. initialize k = # of categories for each type of biosignal;
2. segment each biosignal into a number of one-cycle patterns;
3. cluster all patterns into k classes by kNN algorithm;
4. for each k cluster
      find a central (medoids) pattern of the cluster;
5. for each pattern p
      calculate the distance between p and each medoids;
      re-assign p to a cluster with nearest medoids;
6. for each cluster
      calculate the distance among all p within a cluster;
      assign a new medoids to p that has the minimum distance to other patterns;
7. if no more pattern can change the structure of clusters
      retrieve the medoids and l nearest patterns for each cluster as the representatives;
   otherwise, repeat step 6.
```

Fig. 2. Templates construction and optimization algorithm.

Input:
1) $S = \{s_1, s_2, \ldots, s_m\}$: a blind biosignal
2) $OpTem = \{P_{ecg}(i), P_{eeg}(j); 0 \le i \le k, 0 \le j \le w\}$: the optimal representative biosignal templates
3) λ: threshold for determining the type of an input biosignal

Output: $Class$ = {ECG, EEG and Other}: the signal class

1. $min_{ecg} \leftarrow$ Matching ECG templates and get the minimum similarity measurement
   For each optimal ECG template in P_{ecg}
   Compute the similarity with the blind biosignal S
   End For
   Tentatively classify S into one of the ECG categories
2. $min_{eeg} \leftarrow$ Matching EEG templates and get the minimum similarity measurement
   For each optimal EEG template in P_{eeg}
   Compute the similarity with the blind biosignal S
   End for
   Tentatively classify S into one of the EEG categories
3. $min_{tp} \leftarrow$ Compare min_{ecg} and min_{eeg} to get the minimum similarity measurement among the signal templates
4. If $min_{tp} < \lambda$
   If $min_{tp} = min_{ecg}$, output is ECG
   Else output is EEG
5. If $min_{tp} > \lambda$, output is Other biosignal

Fig. 3. Pattern matching phase of *B²SC Model*.

Table 1
The classification performance of *B²SC Model*.

Biosignals	Number of signals	Classification performance		
		Recall	Precision	*F*-score
ECG	1018	0.951866	0.923737	0.937591
EEG	761	0.893561	0.956399	0.923913
Other	572	0.944056	0.913706	0.928633

3. Results

3.1. Experimental setting

To demonstrate the effectiveness of the proposed *B²SC Model*, experiments were performed on datasets which included EMG signals from the EMG Datasets Repository [19], in addition to ECG and EEG signals. Note that EMG signals are analyzed in the same manner as other signals in evaluating the effectiveness of the *B²SC Model*. Throughout the experiments, all data were divided into two disjunctive partitions: *training set* and *test set*, based on the 10-fold cross validation method, and the ratio for training and test sets was 80% vs. 20%. The training set was used to construct the optimal biosignal templates, *OpTem,* and included ECG and EEG signals, whereas the test set was used for validation. The threshold λ was computed automatically by taking the maximum similarity score among all pairs of the optimal templates. Classification performance was evaluated in terms of recall, precision and *f*-score.

3.2. Classification results

The results depicted in Table 1 reveal that the *B²SC Model* can correctly identify ECG and EEG signals from other biosignals by incorporating the optimal template generation method and prior auto-alignment strategy into the DTW algorithm. Moreover, several observations can be drawn from the experimental results as follows: (a) the classification performance with respect to ECG signals is the best among all biosignals, where both the recall rate (0.951866) and the *f*-score value (0.937591) are the highest. Two possible reasons lead to such a situation: first, there are sufficient categories and a sufficient number of ECG signals that are selected into the library, meaning that the template optimization phase is able to produce practical clusters. Second, an ECG signal possesses several significant characteristics that make it amenable for achieving a high matching accuracy, such as the morphological periodicity and the feature points (P, Q, R, S and T [29]); (b) the performance for classifying EEG signals is slightly degraded, especially the recall rate. This may be caused by the fact that EEG signals tend to have more complex patterns, which complicates the pattern matching process; (c) the further expansion of *B²SC Model* is straightforward, so new categories of ECG and EEG signals or new types of biosignals can be added without limitations. This property of the *B²SC Model* means that the proposed approach is superior to other biosignal classification methods, which are only able to classify a single source biosignal.

4. Conclusion

We have presented a *B²SC Model* that can automatically identify the type (ECG, EEG, EMG or others) of a blind biosignal, and thus can classify a disease or symptom without knowing the type of the source biosignal. Some refinements to the time series algorithm have been proposed, such as template optimization and prior auto-alignment. The performance and efficiency in classifying ECG, EEG and other types of biosignals can also be improved by generating a small set of optimal representative biosignal templates, which restrict the processing space for pattern matching and classification. To our knowledge, this study is novel since there is no similar research reported in the literature to date. In the future, EMG, EOG and other general biosignals will be introduced into the model and large-scale biosignal data will be considered.

Conflict of interest statement

None declared.

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