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Singular Value Decomposition Based Feature Extraction Technique for Physiological Signal Analysis

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Abstract Multiscale entropy (MSE) is one of the popular techniques to calculate and describe the complexity of the physiological signal. Many studies use this approach to detect changes in the physiological conditions in the human body. However, MSE results are easily affected by noise and trends, leading to incorrect estimation of MSE values. In this paper, singular value decomposition (SVD) is adopted to replace MSE to extract the features of physiological signals, and adopt the support vector machine (SVM) to classify the different physiological states. A test data set based on the PhysioNet website was used, and the classification results showed that using SVD to extract features of the physiological signal could attain a classification accuracy rate of 89.157%, which is higher than that using the MSE value (71.084%). The results show the proposed analysis procedure is effective and appropriate for distinguishing different physiological states. This promising result could be used as a reference for doctors in diagnosis of congestive heart failure (CHF) disease.

Keywords Physiological signal · Multiscale entropy · Support vector machine · Feature selection

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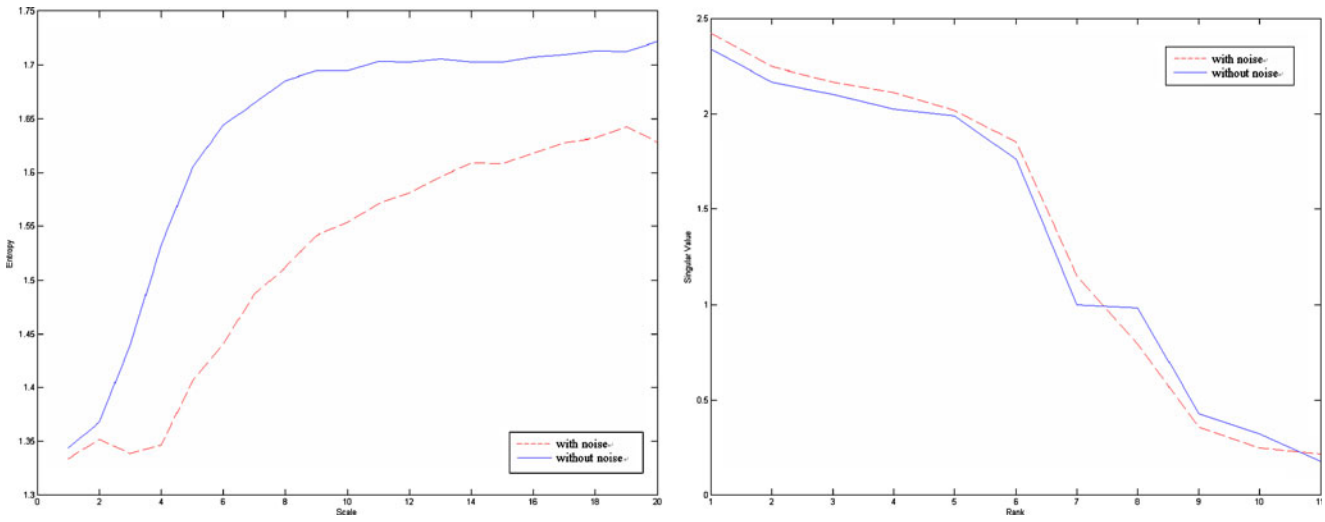
Introduction

Physiological signals like electrocardiogram (ECG), electromyography (EMG), and electroencephalograph (EEG) are one of the ways to describe the physiological condition of the human body. Because the physiological signal must be continuously collected during a set time period, analysis of the signal could provide hidden information that is not easy to determine from a physical index such as body mass index (BMI) or Systolic Blood Pressure (SBP). The multiscale entropy (MSE) analysis method was proposed by M. Costa *et al.* (2002) to present the information hidden in physiological signals [1]. This method quantifies complexity, irregularity, or randomness of the physiological time-series signal. Many studies have used this method to describe the complexity of signals and compare the different physiological conditions of the human body. Costa *et al.* (2002) used the MSE to separate different cardiac interest interval time-series signals by age and diseases. They found that a higher value of entropy was assigned to healthy subjects than to patients on all scales, and also that the healthy young subjects had higher entropy values than healthy elderly subjects. Ferrario *et al.* (2006) used MSE to analyze fetal heart rate signals for identification of fetal distress [2]. Norris *et al.* (2008) used MSE to present heart rates of trauma patients and found that survivors had higher MSE values than patients who would die within three hours [3]. Hung and Jiang (2009) used MSE to investigate the effect of fatigue on cardiac dynamics during long-term web browsing. They found that the cardiac dynamics of subjects during Web browsing were less complex than those of healthy young subjects under free-running conditions [4]. Moreover, some researchers have used MSE on other physical signals, such as EEG or physiological indexes. Trunkvalterova *et al.* (2008) used

MSE to detect autonomic deregulation in young patients with type 1 diabetes mellitus (DM) [5]. They found that using MSE to analyze the heart rate, SBP, and diastolic blood pressure (DBP) oscillations allowed the detection of subtle abnormalities in cardiovascular control in young patients with DM. Park *et al.* (2007) used MSE of human EEG from patients with different pathological conditions of Alzheimer's disease (AD) to measure the complexity of the signal [6]. Costa *et al.* (2003) compared the complexity of human gait time series from healthy subjects under different conditions by MSE, and observed that normal spontaneous walking had the highest complexity in comparison to slow and fast walking, and also in comparison to walking paced by a metronome [7].

Although MSE can easily present the complexity of the different physiological conditions, this method still has some imperfections. Valencia *et al.* (2009) revealed the shortcomings of MSE. First, the course of the entropy-based complexity as a function of the time scale is partially linked to the reduction of variance inherent to the procedure for the elimination of the fast temporal scales. Second, the procedure for the elimination of the fast temporal scales exploits a filter with a frequency response that cannot prevent aliasing, and is thus suboptimal, especially in the presence of fast oscillations [8]. Because the MSE approach depends on variance, noise interference in the signal can cause misjudgment of complexity. This paper adopted singular value decomposition (SVD) approach as a comparison for MSE. Figure 1 shows a detrend signal processed with the MSE and SVD approaches. In Fig. 1, the source of a physiological signal comes from a database in PhysioNet website. The dotted lines represent the signal with noise (raw signal), and solid lines are the signal eliminated the affect of noise in the raw signal by impulse rejection filter [9]. Figure 1(a) shows the results of processing with the MSE approach, the large gap between the solid and dotted lines shows that the entropy values of this signal could easily be misjudged. However, the same signal processed with the SVD approach is shown in Fig. 1(b); clearly, the impact of noise is not significant. Thus, using SVD to analyze the signal appears to be more reliable than using the MSE approach. On the other hand, when using MSE, it is sometimes necessary to use empirical mode decomposition (EMD) to extend some specific unimportant frequencies by removing a few intrinsic mode functions (IMFs). However, in removing IMFs, one should not ignore some important information, and avoiding the effects of trends is also essential.

SVD is a data decomposition approach similar to principal component analysis (PCA). It has many applications in signal processing and statistics, such as feature extraction of a signal, matrix approximation, and pattern recognition. However, PCA cannot use a single signal to pick up features and cannot provide details of the features in each different frequency signal. Moreover, the different physiological conditions are usually hidden in certain specific frequencies, so using SVD to extract the features allows the collection of more comprehensive information than does using PCA. In past applications of SVD on ECG analysis, Kanjilal *et al.* (1997) extracted fetal ECG from single-channel maternal ECG [10], and Ayat *et al.* (2008) extracted fetal ECG from single abdominal ECG signals [11]. In addition, Bart De Moor (1993) showed that the SVD approach is robust for signals containing noise [12]. This study is the first to use the SVD and MSE approaches to extract the features of ECG signals. The ECG signals



(a) Result of using MSE approach (b) Result of using SVD approach

Fig. 1 The MSE and SVD approaches affected by noise. **a** Result of using MSE approach. **b** Result of using SVD approach

were gathered from two groups that the healthy subjects group and the congestive heart failure (CHF) patients group. After the completion of the feature-extraction stage, the support vector machine (SVM) classifier was used to evaluate the effect of features extracted by SVD and MSE. The results show that the features of physiological signals extracted by SVD can provide more information for diagnosis of disease.

Materials and methods

Data description

In this study, a data set from the "PhysioNet" website was used to statement the proposed method. This data set had 83 subjects composed of two groups. The first group had lead II ECG signals for 54 healthy subjects, including 46 (22 male and 24 female, aged 65.87±3.97 years, range 56–78 years) elderly and eight (aged 35.44±4.52 years, range 28.5–40 years) young male subjects [13]. The other group included lead II ECG signals for 29 (aged 55.28± 11.60 years) CHF patients [14]. The data were obtained from 24-h holster recordings (sampled at 128 Hz) of continuous supine resting during ECG. Since the patterns and the characteristics of ECG signals might vary with the subject's mental state, such as sleep or consciousness, only the four hours of signals recorded when the subjects were awake were used.

Proposed research procedure

This study extracted features of ECG signals and classified them into two groups. First, the ECG signals were described by the interbeat interval (R-R interval). Next, the R-R interval was decomposed into different frequency IMFs by EMD. All IMFs were presented per subject in a matrix and then SVD was used to extract the ranked singular values for the signal. Finally, the ranked singular values of healthy and CHF groups were compared by two-sample *t*-test, and significant singular values were used as input for the SVM classifier to determine the two different physiological states (healthy and CHF). The procedure of the proposed method is described as follows:

Step 1: Describing the ECG signal by R-R interval

The ECG signal includes much information on heart activity. The P wave presents the depolarization of the atrium, and the QRS complex shows the depolarization of the ventricle. The T wave displays the repolarization of the ventricle. Because CHF is related to the heart's inability to normally eject the blood, it can be detected by checking the heart rate. Since the R-R interval is a common index of heart rate, the R-R interval was used to describe the ECG signal. The electrocardiogram signal is presented in Fig. 2.

Step 2: Decomposition of R-R interval to IMFs by EMD method

The EMD method uses the local characteristic time scale to decompose complicated data sets into a finite number of components, which is a collection of IMFs. Each IMF represents a simple oscillatory mode as a counterpart to the simple harmonic function, but it is much more common that an IMF has variable amplitude and frequency along the time axis. Thus, IMFs can illuminate data trends on different time scales. An IMF is defined as a function that satisfies the following: (1) In the whole data set, the number of extrema and the number of zero-crossings must either be equal, or differ at most by one; (2) At any point, the mean value of the envelope defined by the local maxima and the envelope defined by the local minima is zero.

The procedure of extracting an IMF is called sifting. The execution process is described as follows:

1. Between each successive pair of zero crossings in signal $x(t)$, identify a local extreme in the data.
2. Connect all local maxima and local minima as an upper envelope u_k (t) and lower envelope l_k (t) by cubic spline, respectively.
3. Calculate the mean of envelopes: $m_k(t) = (u_k(t) + l_k(t))/2$
4. Extract the first component by calculating the difference between raw signal and the mean of envelopes: $h_k(t) = x(t) - m_k(t)$
5. Repeat step 1 to step 4 until h_k (t) satisfies the definition of IMF, and record c_k (t)=h_k (t)
6. Calculate the residual value: $r_k(t) = x(t) - c_k(t)$
7. If r_k (t) is a monotone function, then stop the process. Otherwise, repeat steps 1–4 to find all IMFs.

After using the sifting process, the signal can divide into n IMFs and a monotone function as follows:

$$x(t) = \sum_{k=1}^{n} c_k(t) + r_n(t), \tag{1}$$

where c_k (t) represents the kth IMF, and $r_n(t)$ is a monotonic function that cannot be decomposed to any IMF. Huang *et al.* (2003) proposed a stopping criterion called the S-number criterion to avoid over decomposition of the signal.

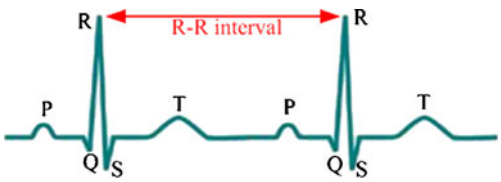


Fig. 2 The ECG signal

The S-number is defined as the number of consecutive siftings when the numbers of zero-crossings and extrema stay the same. The sifting process will stop only if the numbers are equal or differ at most by one [15].

In this paper, four hours of R-R interval data from conscious subjects were used, and each subject's data were decomposed into several IMFs. Each IMF represented different time scales to avoid the phenomenon of abnormal heart rates in some specific time scales being eliminated or ignored in the raw complicated R-R interval data.

Step 3: Feature extraction via SVD approach

With the R-R interval signal decomposed into several IMFs, each signal was described by an $n \times p$ matrix A, composed of n IMFs, with each IMF having p data points. There exist orthogonal matrices $U = [u_1, u_2, \cdots, u_n] \in R^{n \times n}$ and $V = [v_1, v_2, \cdots, v_p] \in R^{p \times p}$, such that

$$U^T A V = \begin{cases} \begin{bmatrix} diag(\sigma_1, \sigma_2, \cdots, \sigma_m) \\ 0 \end{bmatrix} & \text{if } n \geq p \\ [\, diag(\sigma_1, \sigma_2, \cdots, \sigma_m) \;\; 0 \,] & \text{if } n \leq p \end{cases} \quad (2)$$

where $m = min\ (n, p)$, and $\sigma_1, \sigma_2, \cdots, \sigma_m$ are the ranked singular values of A such that $\sigma_1 \geq \sigma_2 \geq \cdots \geq \sigma_m \geq 0$. In this study, these singular values were used as the features for comparison of different groups (healthy and CHF) of subjects. A physiological R-R interval signal was decomposed into 11 IMFs, so there were eleven ranked singular values for a signal. Those ranked singular values were used as the features, which in turn were used to classify the different physiological situations.

Step 4: Comparison of singular values in different physiological states in each rank

Because each different physiological state had m ranked singular values, a two-sample t-test was used to compare the differences in these singular values for the healthy and CHF groups in each rank. In the two-sample t-test, the study assumed the null hypothesis that the means of a singular value in different physiological states were the same, and set the significant level at $\alpha = 0.05$. After the statistical test, some significant ranks wherein the singular values of different physiological states were obtained had difference. These significant ranked singular values could be used to distinguish the different groups of physiological situations.

Step 5: Using SVM to classify the different physiological states

Finally, the significant ranked singular values and all ranked singular values were used as the features, and these features were processed with SVM to classify the different physiological states. SVM is a supervised learning method for classification. It performs well on problems with low training sets, with nonlinear and multi-dimensional data, so SVM was used to test the classification accuracy of using SVD features to diagnose CHF disease. Assume a set of points as follows:

$$D = \{(\mathbf{x}_i, c_i) | \mathbf{x}_i \in R^p, c_i \in \{\text{healthy}, \text{CHF}\}\}_{i=1}^{83} \quad (3)$$

where c_i indicates the class of subject $\mathbf{x}_i$, and each $\mathbf{x}_i$ is a p-dimensional singular values vector. The aim of the SVM is to find a maximum-margin hyperplane that divides the points having c_i = healthy or c_i = CHF, i=1, 2, ..., 83. This hyperplane can be written as the set of points $\mathbf{x}$, expressed as:

$$\mathbf{w} \cdot \mathbf{x} - b = 0 \quad (4)$$

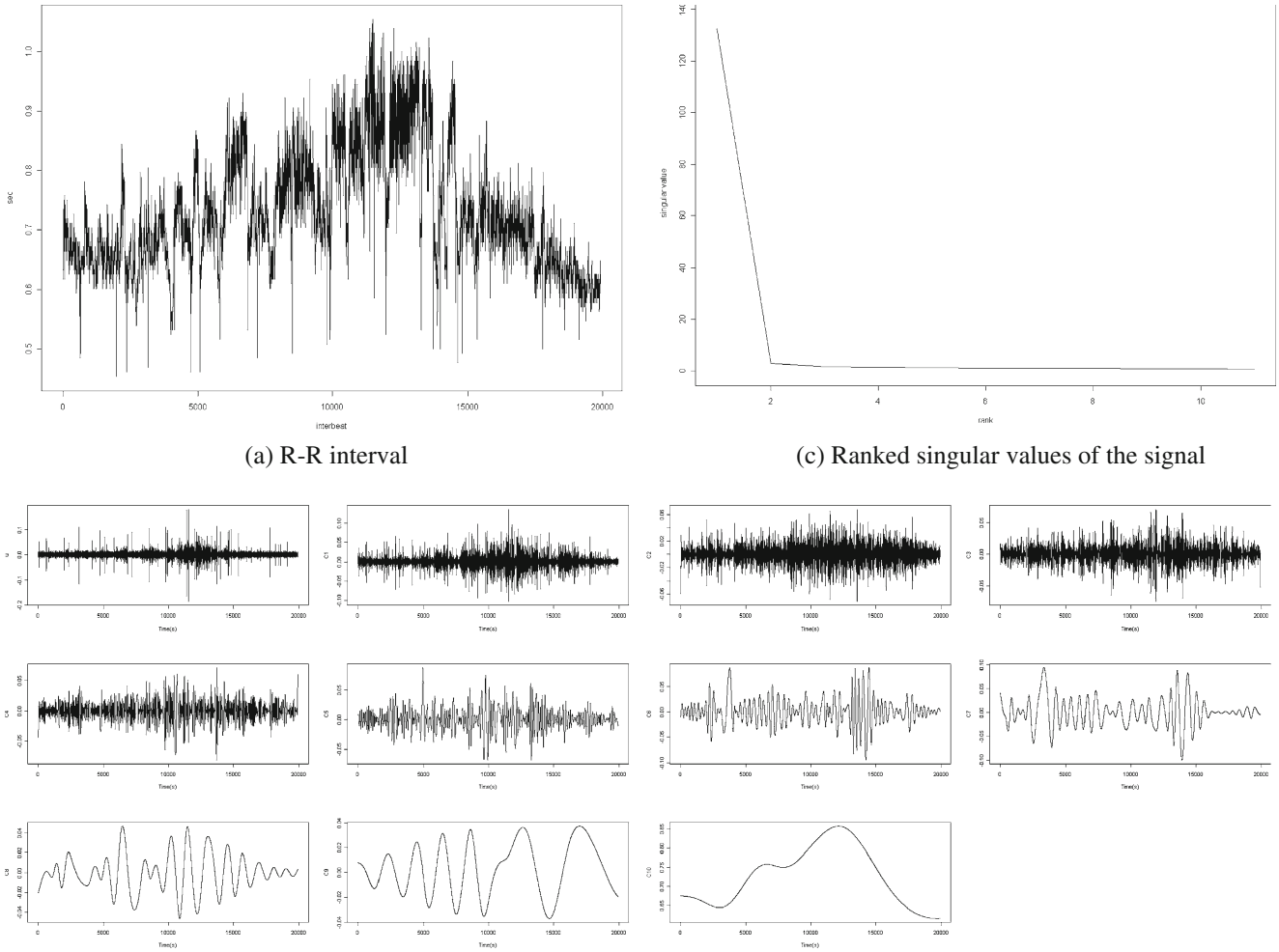
where $\mathbf{w}$ is a normal vector perpendicular to the hyperplane, and $b/\|\mathbf{w}\|$ is the offset of the hyperplane from the origin along the normal vector $\mathbf{w}$. With geometry, it can be found that the width of the margin is $2/\|\mathbf{w}\|$ under the minimum $\|\mathbf{w}\|$.

Results

The feature-extraction process is shown in Fig. 3. In Fig. 3 (a), the raw R-R interval signal has a trend that the interval time becomes longer before the first 14,000 interbeats and progressively shorter after 15,000 interbeats. The signal was decomposed by EMD method implementation in Visual Signal® (version: 1.1.8.307) into ten components (C1–C10) and one noise, as shown in Fig. 3(b). Using SVD to analyze all IMFs produced the ranked singular values shown in Fig. 3(c).

Figure 3(c) has 11 ranked singular values because the EMD decomposed the original R-R interval signal into 11 components. Please note that although the first singular value was significantly higher than the others, the first IMF is not better than the other IMFs. With this approach, each subject's R-R interval signal data in the prepared database was transformed into a ranked singular values curve. Figure 4 shows the ranked singular values curves for all data.

The dotted lines in Fig. 4 represent the ranked singular values of CHF subjects, and the solid lines represent those of healthy subjects. According to Fig. 4(a), every subject had a similar pattern, wherein the value in the first singular value was significantly higher than the others. The greatest difference was that the first singular values of CHF subjects were higher than those of healthy subjects, as illustrated in Fig. 4(b). Based on this finding, the study tested the differences in average singular values between the healthy and CHF groups by two-sample t-test in each rank. Table 1

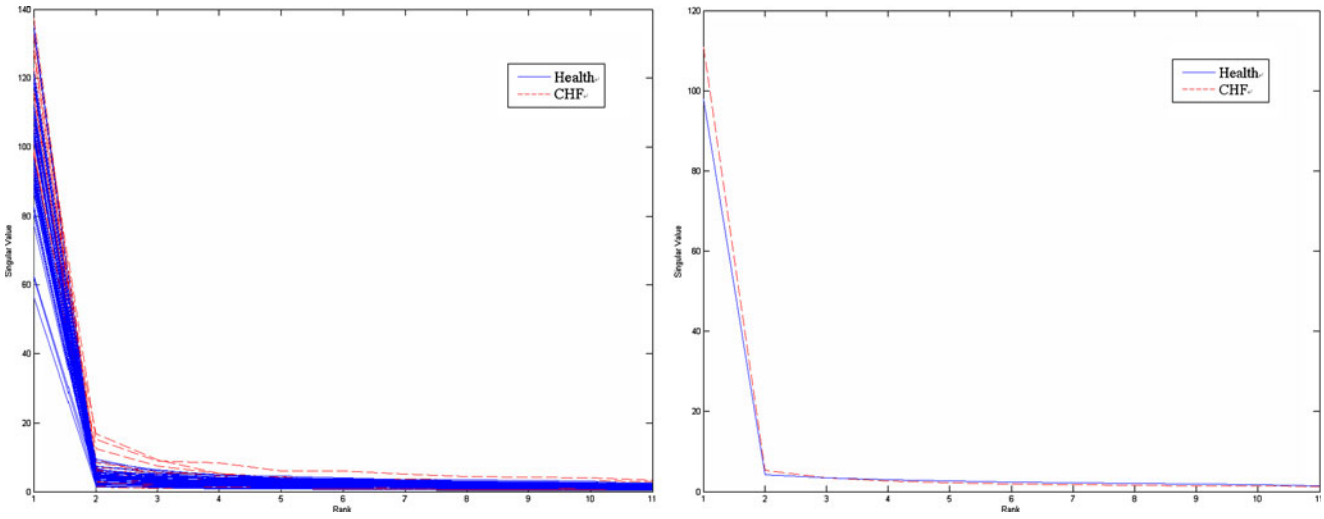


(a) R-R interval

(c) Ranked singular values of the signal

(b) IMFs of R-R interval in (a)

Fig. 3 Prepared method to extract features for R-R interval data. **a** R-R interval. **b** IMFs of R-R interval in (a). **c** Ranked singular values of the signal



(a) All subjects' ranked singular values curves

(b) Average of ranked singular values in each group

Fig. 4 Ranked singular values for all subjects' data. **a** All subjects' ranked singular values curves. **b** Average of ranked singular values in each group

Table 1 Two sample *t*-test for each ranked singular value in different groups

Rank	Physiological situation	Average	Standard deviation	*p*-value
1	CHF	110.9045	13.2479	0.000*
	Healthy	97.9336	15.9765	
2	CHF	5.3153	3.9558	0.211
	Healthy	4.3310	1.7188	
3	CHF	3.4934	2.2526	0.907
	Healthy	3.4404	1.2416	
4	Healthy	2.9809	0.9524	0.543
	CHF	2.7682	1.7303	
5	Healthy	2.6985	0.8332	0.092
	CHF	2.2576	1.2346	
6	Healthy	2.4341	0.7505	0.061
	CHF	1.9812	1.1409	
7	Healthy	2.2350	0.6849	0.040*
	CHF	1.7985	0.9870	
8	Healthy	2.0914	0.6361	0.022*
	CHF	1.6462	0.8934	
9	Healthy	1.9576	0.6073	0.019*
	CHF	1.5220	0.8500	
10	Healthy	1.7924	0.5728	0.027*
	CHF	1.3982	0.8278	
11	Healthy	1.5434	0.5156	0.066
	CHF	1.2519	0.7422	

The asterisk (*) means the *p*-value is significant at α=0.05

presents the two-sample *t*-test results. The asterisk (*) in the *p*-value column indicates that the two groups had a significant difference (α=0.05) in average singular value at the rank. As can be seen from Table 1, the average singular value in the CHF group was higher than that in the healthy group in the first three ranks, but the opposite was true in the following ranks. In other words, the singular values decreased more quickly in the CHF group than in the healthy group.

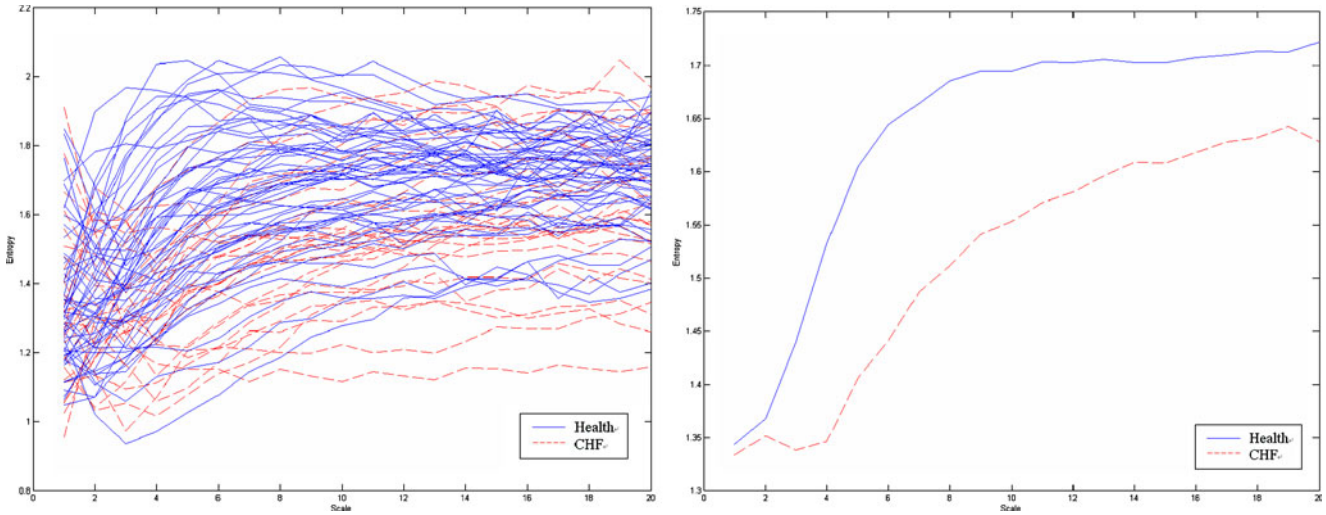
Finally, the SVM method was used to compare the classification accuracy by using the singular values of all ranks and only significant ranks (rank 1 and ranks 7–10) as the features. This paper chose 75% of the data by random sample for the training data in SVM classification, and 62 subjects (23 subjects from the CHF group and 39 subjects from the healthy group) to find the optimal separating hyperplane. The remaining data (six CHF subjects and 15 healthy subjects) were used to test the classification effect. The classification results are presented in Table 2.

As Table 2 shows, the classification accuracy rates of using singular values of all ranks and only significant ranks as features were 87.952% and 89.157%, respectively. Although the classification accuracy rate with significant features was not increased very much above that with all features, the accuracy rate for testing the CHF group was higher (66.667% with all features used, but 83.333% with only significant features). That indicates that using only significant rank singular values to classify these two groups allows higher sensitivity and specificity. On the other hand, the classification results in Table 2 was compared with the results of using MSE as the features for the SVM classification approach. Figure 5 shows the MSE curves, which contained only the first seven IMFs for subjects' R-R interval signals in the same databases.

Table 2 Classification accuracy rate using ranked singular values as features

		Sample size	Accuracy rate (%)
All features	Training	62 (H:39 , C:23)	88.710 (H: 92.308 , C: 82.609)
	Testing	21 (H:15 , C:6)	85.714 (H: 93.333 , C: 66.667)
	Overall	83	87.952
Significant features	Training	62 (H:39 , C:23)	87.089 (H: 92.308 , C: 78.261)
	Testing	21 (H:15 , C:6)	95.238 (H: 100 , C: 83.333)
	Overall	83	89.157

C means the CHF group; H means the healthy group



(a) All subjects' MSE curves (b) Average entropy in each scale of two groups

Fig. 5 MSE curve for all subjects' data. **a** All subjects' MSE curves. **b** Average entropy in each scale of two groups

The dotted lines in Fig. 5(a) represent the MSE values for CHF subjects, and the solid lines represent healthy subjects. Figure 5(b) shows the average entropy in every scale of the two groups. The healthy subjects had higher entropy than did the CHF patients. The same analysis steps were used to rank singular values as the features, and the SVM approach was used to classify the two different physiological conditions. The two-sample *t*-test results for the entropy of each scale and the SVM classification results are presented in Tables 3 and 4.

In Table 3, the significant differences between CHF and healthy groups are visible in scales 3–16 and scale 20, but these two groups' entropies were similar in the first two scales. The average entropy of the CHF group in each scale was lower than the average entropy of the healthy group, indicating that the complexity of heart rate was higher in healthy subjects than in CHF patients. This result is consistent with Costa *et al*. (2002). From Table 4, the accuracy rates for using all and significant MSE values as the features were 72.289% and 71.084%, respectively. Comparing the two classification results in Tables 2 and 4, it is clear that using ranked singular values as the features allows a higher classification accuracy rate than using the MSE values as the features in the SVM classification approach for these two groups. The greatest difference was in the accuracy rate for CHF patients: Using ranked singular values as the features allowed a classification accuracy rate of almost 80%, while one of only about 30% was possible using MSE values as the features. For this reason, as the same physiological condition (like CHF) might have different patterns in MSE curves, and the MSE curve is vulnerable to the impact of noise. Therefore, using SVD to extract the features of the signals is better than using MSE values.

Conclusions

This study proposes using the SVD method to extract features from R-R interval signals. Extracted features were input to SVM for classification and two different types of physiological status, healthy and CHF, were used to evaluate the proposed method in terms of applicability and performance. Experimental results showed that, using all ranked singular values as features, whether the subject was healthy or suffered from CHF could be distinguished with a total accuracy of over 87%. A higher total accuracy (about 89%) was achieved by using only significant ranked singular values for classification. According to the results, this paper has two conclusions: (1) Using SVD to extract the features of physiological signals can achieve good indexes to classify different physiological states. (2) Using only the significant features to classify physiological states can provide better results than using all features.

On the other hand, this study also compared the SVM classification results of using ranked singular values and MSE values as the features. The results showed that using SVD to extract the features of physiological signals was better than using MSE values as the features in classification. A reasonable explanation is that the MSE approach used a ratio of tolerance (r) to calculate the entropy value, and the noises or trends of signal values were underestimated by the leading entropy value. However, the interference was of low importance in the SVD approach,

Table 3 Two sample *t*-test for each scale's entropy values in different groups

Scale	Physiological situation	Average	Standard deviation	*p*-value
1	CHF	1.334	0.2269	0.840
	Healthy	1.344	0.1965	
2	CHF	1.352	0.1813	0.713
	Healthy	1.368	0.1951	
3	CHF	1.339	0.1745	0.038*
	Healthy	1.440	0.2229	
4	CHF	1.347	0.1893	0.000*
	Healthy	1.533	0.2337	
5	CHF	1.407	0.1929	0.000*
	Healthy	1.604	0.2290	
6	CHF	1.441	0.1902	0.000*
	Healthy	1.644	0.2166	
7	CHF	1.487	0.2023	0.000*
	Healthy	1.665	0.1979	
8	CHF	1.512	0.2022	0.000*
	Healthy	1.685	0.1849	
9	CHF	1.541	0.2037	0.001*
	Healthy	1.695	0.1740	
10	CHF	1.553	0.2056	0.001*
	Healthy	1.695	0.1638	
11	CHF	1.571	0.2105	0.002*
	Healthy	1.703	0.1616	
12	CHF	1.581	0.2095	0.008*
	Healthy	1.703	0.1495	
13	CHF	1.596	0.2168	0.018*
	Healthy	1.705	0.1396	
14	CHF	1.608	0.2183	0.041*
	Healthy	1.703	0.1389	
15	CHF	1.608	0.2072	0.033*
	Healthy	1.702	0.1377	
16	CHF	1.618	0.2140	0.046*
	Healthy	1.707	0.1255	
17	CHF	1.628	0.2105	0.065
	Healthy	1.710	0.1351	
18	CHF	1.632	0.2138	0.071
	Healthy	1.713	0.1354	
19	CHF	1.642	0.2165	0.116
	Healthy	1.713	0.1260	
20	CHF	1.628	0.2127	0.037*
	Healthy	1.722	0.1321	

The asterisk (*) means the *p*-value is significant at α=0.05

Table 4 Classification accuracy rate by using MSE values to be features

		Sample size	Accuracy rate (%)
All features	Training	62 (H:39 , C:23)	72.581 (H: 92.308 , C: 39.130)
	Testing	21 (H:15 , C:6)	71.429 (H: 93.333 , C: 16.667)
	Overall	83	72.289
Significant features	Training	62 (H:39 , C:23)	70.968 (H: 92.308 , C: 34.783)
	Testing	21 (H:15 , C:6)	71.429 (H: 93.333 , C: 16.667)
	Overall	83	71.084

C means the CHF group; H means the healthy group

thus leading to lower ranks and small singular values in the proposed method. Therefore, this paper presents an available approach to extracting physiological signal features for distinguishing different physiological states. These promising results indicate that the proposed method can be applied to medical diagnosis of CHF.

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