Identification of Respiratory Phases Using Seismocardiogram: A Machine Learning Approach

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Abstract: *This study was aimed at developing an algorithm that could identify the respiratory phases, i.e. inspiration (I) or expiration (E), by analysing seismocardiogram (SCG) cycles. In order to better assess SCG cycles, it is needed to discriminate the cycles based on their position in the respiratory phases. The total 2146 SCG cycles obtained from 45 subjects were studied, in which 1109 cycles were in phase I, and the rest in phase E. Support vector machine (SVM), a powerful machine learning algorithm, was employed to identify the respiratory phase of SCG cycles. The systolic interval of each SCG cycle was divided to 32 equal bins, and the averages of these bins obtained the feature vector associated with each cycle. The SVM model was trained using half the data, and then was tested on the other half. The developed model could correctly identify 88% of the testing data. The obtained results are promising and can establish a solid ground for further analysis.*

1. Introduction

Seismocardiogram (SCG) is a cardiac signal that can be obtained by placing an accelerometer on the sternum and measuring the vibration of the heart. Previous studies have indicated that SCG is correlated to certain hemodynamic parameters, in particular systolic time intervals (STIs) [1]–[3]. On the other side, it has also been demonstrated that the morphology SCG signal is different in different phases of respiration, i.e. inhale (I) and exhale (E) [4]. Figure 1 shows two SCG cycles in phase I and E. The difference in their morphologies is observable in this figure.

In order to better asses SCG and obtain systolic time intervals appropriately, it is beneficial to identify the respiratory phase of each SCG cycle. Such identification is highly challenging, because it should be conducted without an independent recording of respiration signal as collecting the respiration imposes extra complexity and cost. Therefore, the aim of this study was to develop an algorithm that could identify the respiratory phases (I or E) by analysing seismocardiogram (SCG) cycles.

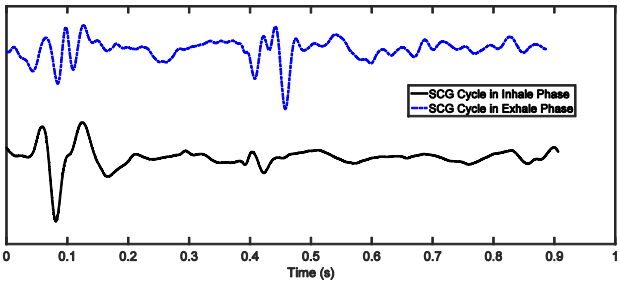

Figure 1. The morphology of SCG cycles is different in different respiratory phases, i.e. inhale and exhale.

2. Methods

In order to identify the respiratory phase of each seismocardiogram (SCG) cycle, different stages were considered that are explained in the following sections.

2.1. Data collection

The dataset was acquired from 45 (19 female and 26 male) mostly old and diagnosed with ischemic heart disease (IHD) (Age: 66.5±9.9, Weight: 83±18.2 and Height: 170±8.5). The ethical approval for this data acquisition was granted by Simon Fraser University and the Fraser Health Authority of British Columbia.

The data acquisition involved measurement of SCG, 12 lead ECG and respiration. All of the signals were acquired by a Biopac biological data acquisition system (www.biopac.com 2007). The SCG signal was measured using a high sensitivity (1000 mV/g) accelerometer, which was positioned on the sternum. The accelerometer sensor was factory calibrated, weighed 54 g and was connected to a charge amplifier. The respiration was recorded using a strain gauge transducer that measures the changes in thoracic circumference, using a belt, which is fastened to the subject's thorax. The subjects were asked to keep the normal pattern of respiration and to pause and hold their breath on maximum inhalation and maximum exhalation respectively for short periods of time not exceeding 4 s.

2.2. Preprocessing, segmentation, and labelling

The acceleration signals were first low-pass filtered with 40 Hz cutoff frequency to obtain seismocardiogram (SCG). Then, SCG signals were segmented to beat to beat cycles using the R peaks of the concurrently recorded electrocardiogram (ECG) signals. Each SCG cycle was considered from two consecutive R peaks delayed by 200 ms.

Based on the position of the corresponding R peak in the respiration signal, each cycle was labelled as inhale (I) or exhale (E).

2.3. Feature extraction

To further analyze the data, it was needed to extract a feature vector from each SCG cycle. The identification model (that is described in the section 2.4.) assigns a label (I or E) to each cycle using the extracted feature vector. In this study, each SCG cycle was first normalized to have a unit length. Then, the first 512 data points of cycle were considered, which included the systole interval. These data points were divided to 32 equal-size bins (16 data points were in each bin). The averages of these bins obtained the feature vector associated with each SCG cycle. Figures 2 shows the extracted features from the systole intervals of two SCG cycles in inhale and exhale phases respectively.

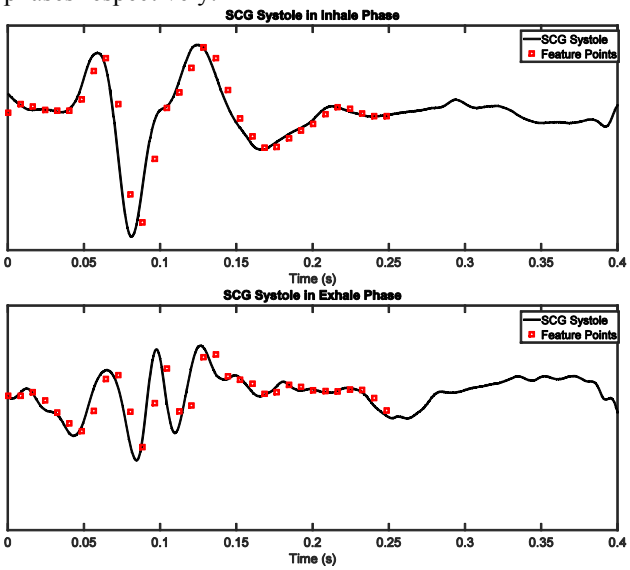

Figure 2. Top: The systole of an SCG cycle in the inhale phase, and its extracted feature points. Bottom: The systole of an SCG cycle in the exhale phase, and its extracted feature points.

2.4. Identification

To identify the corresponding respiration phase of each SCG cycle, support vector machine (SVM), a machine learning algorithm, was used. SVM is very powerful tool for identification problems, and has been widely used for analysing biomedical signals such as heart murmurs identification [5], [6], reducing false alarms during arrhythmia [7], and recently monitoring dental operations [8].

SVM is originally a binary identifier, which separates the data of two categories by a hyper-plane that has the maximum minimum distance to the data [9]. Using SVM involves two stages: training and testing. In the training stage, SVM uses a selective set of data that are denoted as training data to develop the model. Then, in the testing stage, another set of data that is called testing is utilized to evaluate the performance of the developed model. In this study, half of the data was used for training and the other half for testing (there was no overlap between them).

SVM usually transforms the data to a higher dimension to facilitate their separation by using a kernel function. In this study, a radial basis function (RBF) was employed:

$$K(X_i, X_j) = \exp\left(-\gamma \left\| X_i - X_j \right\|^2\right) \qquad \gamma > 0 \tag{1}$$

where X is the input vector, and γ is a hyper-parameter that can modify the results. The SVM with RBF kernel has another hyper-parameter C that controls how much misclassification is acceptable in the training stage [9]. In this study, the software package LIBSVM [10] was used for training and testing of the SVM model. To find the values of the hyper-parameters, the grid search method and a 5–fold cross validation were employed [11]. In the grid search, the values are explored in a wide range to find the solution. In a ν–fold cross validation, the training data are divided to ν equal–sized subsets, in which ν-1 subsets are used for training, and the one remained subset for testing. This process is repeated ν times, and the average identification accuracy is obtained.

3. Results

Among 2146 SCG cycles, 1097 ones were used for training (567 cycles in phase I, and 530 in phase E), and the rest for testing (1049 cycles, 542 cycles in phase I and 507 in phase E). The hyper-parameters C and γ, were varied in the range 2^{-15}, 2^{-13}, . . . to 2^{1} , 2^{3}, and for each pair, a 5-fold cross-validation was utilized in the training data. The optimal values of hyper-parameters were the ones that obtained the highest total accuracy. The obtained values were C=8, and γ= 0.125

The corresponding elements of feature vectors in the training data were scaled to have zero mean and unit variance. The same scaling coefficients were employed on the feature vectors of the testing data. SVM with RBF kernel was used for training, and then the developed

model was used for testing, in which the different identification accuracies were obtained as follows,

Target Inhale Accuracy = 100* (Number of correctly identified inhale cycles / Total number of inhale cycles)

Target Exhale Accuracy = 100* (Number of correctly identified exhale cycles / Total number of exhale cycles)

Output Inhale Accuracy = 100* (Number of correctly identified inhale cycles / Total number of cycles identified as inhale)

Output Exhale Accuracy = 100* (Number of correctly identified exhale cycles / Total number of cycles identified as exhale)

Total Accuracy = 100* ((Number of correctly identified cycles / Total number of cycles)

Figure 3 displays the confusion matrix of this analysis, in which inhale and exhale phases are indicated by "1" and "2" respectively. In this matrix, the entries on the diagonal shows the number and percentage of correctly identified cycles (green color), and the off diagonal entries are corresponded to misidentified cycles (red color). The last row and column entries illustrate target and output accuracies respectively (gray color). Generally speaking, target or output accuracies describe how much of the input or output data are correctly identified. For instance, according to Figure 3, 86.6% of the inhale input data were identified correctly. Also, whenever the output of the developed model was exhale, its accuracy for being correctly identified was 84.8%.

The right-bottom element of this matrix (blue color) shows the total accuracy as 88.4%, which indicates the efficiency of the proposed method.

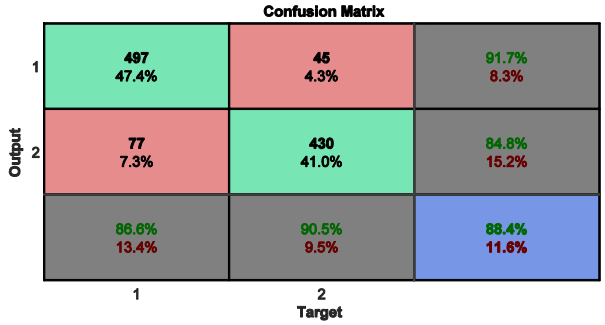

Figure 3. The confusion matrix and different identification accuracies. The inhale and exhale phases are indicated by "1" and "2" labels respectively.

4. Conclusion

In this paper, an algorithm was proposed to identify the respiratory phase of SCG cycles, i.e. inhale or exhale. Support vector machine (SVM) that is a powerful machine learning algorithm was used for identification. The features were extracted from the time-domain and included the average-bins of the systole. The total identification accuracy was 88% that demonstrates the capability of the proposed method in identifying the respiratory phase. The identification accuracies were promising, and can be used as a ground for further analysis. As part of the future works, we would like to modify the algorithm for higher accuracies, and validate the results on more SCG cycles obtained from more subjects.

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