Diagnosis of Sleep Apnea by Evaluating Points Distribution in Poincare Plot of RR Intervals

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Abstract

Sleep apnea detection using ECG-derived parameters is non-invasive and inexpensive. This article presents novel ECG-derived features to be used in conjunction with existing standard features for improving the detection of sleep apnea. The features presented here were derived using Poincare plots of RR intervals. Global features are based on counting number of points above, below, and on the identity line in Poincare plot. Furthermore, local features are based on point to point variations relative to the identity line (i.e., temporal information in Poincare plot). Performance of features in detection of apnea was evaluated using k-nearest neighbor, self-organizing map, and multilayer perceptron neural network. The accuracy of classifiers on test set was respectively 88.89%, 77.77%, and 100%.

1. Introduction

Sleep apnea is a common disorder and a leading cause of excessive daytime sleepiness [1]. The disease process is characterized by one or more pauses in breathing or shallow breaths during sleep. These pauses can last from a few seconds to minutes and they may last 30 times or more in an hour [2]. Sleep is disrupted during these episodes of breathlessness, and as a result, the quality of sleep would decrease, leading to daytime sleepiness.

Sleep apnea is typically chronic, and those affected by it are often unaware. Often times, a family member or bed partner is the first to notice signs of sleep apnea.

The most common type of sleep apnea is obstructive sleep apnea. In this condition, the airway collapses or becomes blocked during sleep, causing shallow breathing or pauses in breathing [3]. During these episodes, air that squeezes past the blockage can cause loud snoring, a common presenting complaint of the disease [1]. While obstructive sleep apnea is more common in people who are overweight, it can affect anyone.

If left untreated, sleep apnea can cause increased risk in a number of serious health conditions. For example, untreated sleep apnea can increase the risk of high blood pressure, heart attack, stroke, heart failure, and diabetes. Additionally, it can lead to arrhythmias or irregular heartbeats, and increased chance of having work-related or driving accidents [4].

Sleep apnea is a chronic condition that requires long-term management. Lifestyle changes, mouthpieces, surgery, and breathing devices can successfully treat sleep apnea in many people. Early recognition of sleep apnea can be done using ambulatory recording methods such as long-term ECG and blood pressure monitoring using dedicated recording systems [5].

Heart rate variability (HRV) analysis in frequency domain is used successfully for automatic detection of sleep apnea [2]. The main purpose of this article is to compare conventional and newer features extracted from Poincare plot of RR time series between healthy and apnea groups and to create a model for detection of sleep apnea.

2. Method and Data

The apnea database from Physionet was used for this study. Multiple features were extracted from Poincare plots is used for HRV analysis to distinguish apnea versus normal.

2.1. Poincare Plot of RR Intervals

Poincare plot is a non-linear method of HRV analysis. Considering RR time series as (RR_1,RR_2,…,RR_n, RR_{n+1}), Poincare plot could be created by $p_i=(x_i, y_i)$ pairs in which:

$$x = (x_1, x_2, \ldots, x_n) = (RR_1, RR_2, \ldots, RR_n) \quad (1)$$

$$y = (y_1, y_2, \ldots, y_n) = (RR_2, RR_3, \ldots, RR_{n+1}) \quad (2)$$

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where, (i=1,2,3, …,n) and *n* is the number of points in the Poincare plot which is one less than the length of the RR time series [6]. Poincare Plot of a healthy subject and patients with apnea is shown on Figure 1.

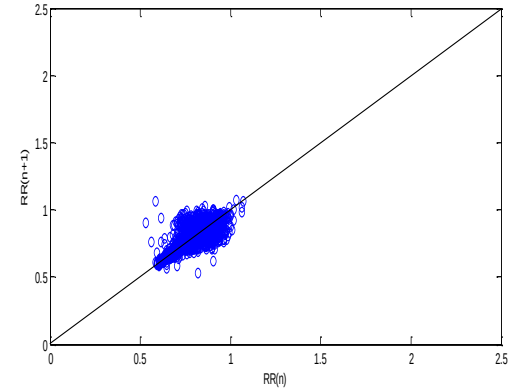
2.1.1. Standard Descriptors of Poincare Plot

Two standard descriptors of Poincare plot are *SD1* and *SD2* which are defined as follows [7]:

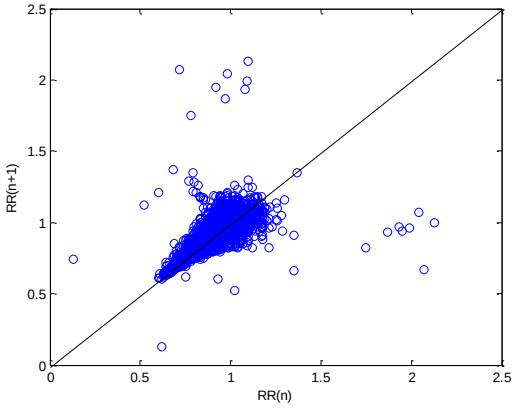
$$SD1 = (Var((x-y) / (2)^{1/2}))^{1/2} \quad (3)$$

$$SD2 = (Var((x+y) / (2)^{1/2}))^{1/2} \quad (4)$$

Where Var is a variance.



(a)



(b)

Figure 1. Poincare plot of RR intervals of a) healthy subject, and b) patient with apnea.

2.1.2. Global Occurrence Matrix (GOM)

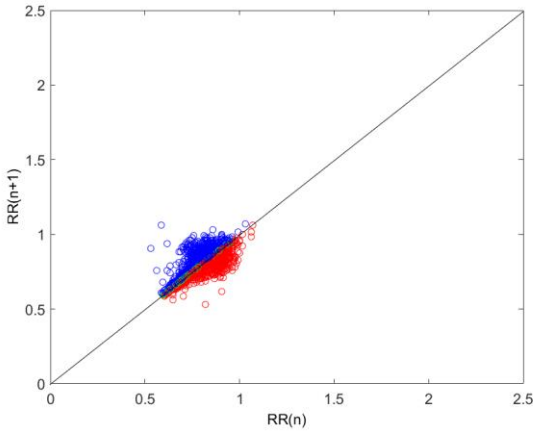
Global occurrence matrix quantifies the distribution of points in Poincare plot relative to identity line. The points' position relative to the identity line (y = x) have different meanings. The points on this line correspond to equal consecutive *RR* intervals, the points above and below it correspond to decreasing and increasing heart rate, respectively [6, 8]. Moharreri *et al.* proposed new features to quantify distribution of points relative to identity line [9]. They performed global and local analyses of points relative to the identity line. In *GOM*, the points in Poincare plot are partitioned into three regions (Figure 2) [9]:

- Points which are above the identity line (A);
- Points which are on the identity line (O);
- Points which are below the identity line (B).

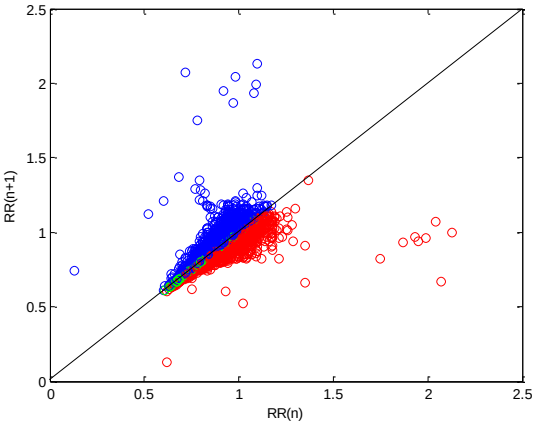
In global method, a *3×1* vector (GOM) was constructed by counting number of points in each region [9]:

$$GOM = [N_A \; N_O \; N_B] \quad (6)$$

In which N_A is the number of points in region *A*, N_O is the number of points in region *O*, and N_B is the number of points in region *B*.



(a)



(b)

Figure 2. Three regions relative to identity line are color coded (Blue, green, and red are respectively region A, O, and B) for a) healthy subject, and b) patient with apnea. GOM will be extracted by counting number of points in each region.

2.1.3. Co-occurrence Matrix (COM)

Moharreri *et al*. also considered every two consecutive points P_i and P_{i+1} in Poincare plot and created nine features (COM) based on position of these two points relative to each other and identity line [9, 10], Figure 3. *COM* is a 3×3 matrix which elements are defined as follows [9]:

$$COM = \begin{bmatrix} AA & AO & AB \\ OA & OO & OB \\ BA & BO & BB \end{bmatrix} \quad (7)$$

For example, AA is number of Poincare points that P_i was above identity line and P_{i+1} was also above identity line.

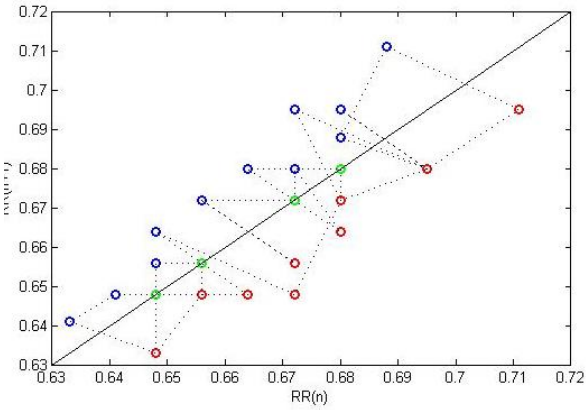


Figure 3. Temporal variations of points in Poincare plot that will be used for extraction of COM.

2.2. Data

The CinC Challenge 2000 data sets (Apnea-ECG database) [11] from the Physionet database [12] was used in this study. This database contains 70 ECG recordings sampled at 100 Hz. Each record is approximately 8 hours with appending annotations acquired from a study of simultaneously recorded respiration signals. The apnea annotation in the recordings was done by sleep disorder experts using standard criteria with respiration signals analysis [12].

The group of apnea (class A) recordings that is used in this article was defined as having 100 or more minutes with disordered breathing. We used 60 minutes signals with labeled parts. The subjects of the class A recordings were fifteen men and one woman, with a mean age of 50 years (29-63 years). Furthermore, we have used 15 long-term ECG recordings of subjects in normal sinus rhythm from Physionet Normal Sinus Rhythm database [12] in order to compare apnea group versus normal group.

2.3. Statistical Analysis and Classifier

Kruskal-Wallis test which is a non-parametric version of the classical one-way ANOVA was used first to compare the extracted features between apnea and healthy groups (statistical significant level equal to 0.05).

Then K-Nearest Neighbor (KNN), Self-Organizing Map (SOM), and Multi-Layer Perceptron (MLP) were used to classify these two groups using extracted features. All the classifiers were trained on 70% of data as a training set, and the accuracy was evaluated on 20% of data as a test set. To avoid over fitting, we used 10% of data as validation data.

3. Results

Mean and standard deviation of extracted features for healthy and apnea groups are reported Table 1. *P*-value for comparison of standard descriptor of Poincare plot, GOM features, and COM features could be found in Table 1. Features with significant differences between two groups are marked by * in these tables.

Table 1. Mean and standard deviation of extracted features for normal and apnea groups and *P*-value for comparison of standard descriptor of Poincare plot, GOM features, and COM features between two groups (significant differences between two groups are marked by *).

	Normal	Apnea	*p*-value
SD1	0.02 ± 0.0001	0.11 ± 0.006	<0.001*
SD2	0.14 ± 0.003	0.28 ± 0.02	0.008*
N_A	147 ± 25	139 ± 40	0.010*
N_O	466 ± 159	663 ± 100	0.024*
N_B	149 ± 118	139 ± 30	0.060
AA	591 ± 89	491 ± 145	<0.001*
AO	200 ± 60	339 ± 50	0.003*
AB	685 ± 82	808 ± 252	0.006*
OA	203 ± 27	216 ± 497	0.001*
OO	85 ± 33	207 ± 32	<0.001*
OB	178 ± 144	239 ± 61	<0.001*
BA	687 ± 57	594 ±138	0.038*
BO	180 ± 119	215 ± 82	0.005*
BB	630 ± 195	582 ± 45	0.003*

GOM and COM features were used with KNN, SOM, and MLP classifiers for detection of apnea from healthy subject. For KNN classifier the parameter *K* was considered as three. The SOM network starts with 40 neurons. The MLP neural network has two layers used for classification. The first layer has twelve neurons as input features, while the output layer has two neurons as two classes of apnea and healthy, and the hidden layer has 50 neurons. The classification performance on test data set are shown in Table 5. The results show that the MLP neural network had the best performance compared to other classifiers and detected apnea with the accuracy, specificity, and sensitivity of 100%.

Table 2. Classification performance for apnea detection on test data set

	Accuracy	Sensitivity	Specificity
KNN	88.89	100	75
SOM	77.77	80	75
MLP	100	100	100

4. Discussion

In this article, standard descriptor features (e.g., SD1 and SD2) and new features (e.g., Global Occurrence Matrix and Co-occurrence Matrix) extracted from Poincare plot of RR intervals were compared between healthy and apnea groups. These features were used with three different classifiers (k-nearest neighbor, self-organizing map, and multilayer perceptron neural network) for detection of apnea and produced promising results. The results of this study suggest that new features that quantify distribution of points in Poincare plot relative to unity line have potential to be used in combination with conventional features in Poincare plot for sleep apnea detection.

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