Classification Methods from Heart Rate Variability to Assist in SAHS Diagnosis

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Abstract-The aim of this study is to analyze different feature classification methods applied to heart rate variability (HRV) signals in order to help in sleep apnea-hypopnea syndrome (SAHS) diagnosis. A total of 240 recordings from patients suspected of suffering from SAHS were available. This initial dataset was divided into training set (96 subjects) and test set (144 subjects). For this study, spectral and nonlinear features have been extracted. Spectral characteristics were obtained from the power spectral density (PSD) from HRV records. On the other hand, the nonlinear features were obtained from HRV records in the time domain. Afterwards, some features were selected automatically by forward stepwise logistic regression (FSLR). We constructed two classifiers based on logistic regression (LR) and support vector machines (SVMs) with the selected features. Our results suggest that there are significant differences in various spectral and nonlinear parameters between SAHS positive and SAHS negative groups. The highest sensitivity, specificity and accuracy values were reached by the SVMs classifier: 70.8%, 79.2% and 73.6%, respectively. Results showed that feature selection of optimum characteristics from HRV signals could be useful to assist in SAHS diagnosis.

Keywords—Sleep apnea hypopnea syndrome, HRV, stepwise feature selection, logistic regression, support vector machines.

I. INTRODUCTION

Sleep apnea-hypopnea syndrome (SAHS) is characterized by repetitive pharyngeal collapse during sleep, causing intermittent cessations of breathing (apnea) or marked reduction (hypopnea) in airflow [1]. These airflow interruptions are related to hypoxemia and variations in heart rate [2]. SAHS has been usually related to major cardiovascular diseases [3], occupational accidents, and motor-vehicle collisions [4]. Epidemiological studies estimate the prevalence of SAHS up to 5% of adult men in western countries [2].

Nocturnal polysomnography (PSG) is the gold standard in SAHS diagnosis. However, it presents some drawbacks. A high number of physiological signals and data are acquired in each polysomnographic test. The specialist conducts an inspection of the signals to derive the apnea-hypopnea index (AHI), which is used to determine SAHS severity. Hence, PSG is complex, costly and time-consuming [5]. In recent years, due to limitations of the PSG, alternative diagnostic approaches have emerged. These alternatives have focused on automatic methods based on a reduced number of biomedical signals. One of them is the analysis of heart rate variability (HRV) derived from electrocardiogram (ECG) [6, 7, 8].

In this study, we performed a feature extraction stage where different spectral and nonlinear features were computed. Then, forward stepwise logistic regression (FSLR) were applied to automatically select optimum features. Finally, these features were classified by two methods: logistic regression (LR) and support vector machines (SVMs).

Relative power (RP), peak amplitude (PA), spectral entropy (SE) and median frequency (MF) were extracted from the power spectral density (PSD) of HRV recordings. Three nonlinear characteristics were also computed: central tendency measure (CTM), Lempel-Ziv complexity (LZC) and sample entropy (CTM).

Our initial hypothesis was that these features could contain complementary information that could be helpful in the diagnosis of SAHS. This study was aimed at assessing the usefulness of the proposed techniques to obtain relevant information from HRV recordings in SAHS diagnosis.

II. DATA SET

The study population used in this work was 240 subjects. All had typical symptomatology of suffering from SAHS. ECG recordings were obtained through a polygraph Alice 5 of Philips Healthcare-Respironics as part of the PSG. The signal acquisition was performed with 200 Hz of sampling frequency. AHI was the average calculated from the number of apneic events detected in PSG. Note that medical specialists have considered positive diagnosis of SHAS provided an AHI \geq 10 events / hour.

A positive diagnosis of SAHS was confirmed in 160 subjects. There were no differences in age and body mass index (BMI) between SAHS positives and negatives. Table 1 summarizes the clinical characteristics of both groups, including age, sex, BMI and AHI (mean \pm standard deviation).

HRV signals were obtained from ECG recordings. Firstly, QRS detection algorithm was applied [9]. Next, physiologically impossible beats no fitting the following criteria were

L.M. Roa Romero (ed.), XIII Mediterranean Conference on Medical and Biological Engineering and Computing 2013, IFMBE Proceedings 41,

DOI: 10.1007/978-3-319-00846-2_450, © Springer International Publishing Switzerland 2014

removed: *i*) 0.33s < interval between beats < 1.5s and *ii*) the maximum difference between consecutive intervals were 0.66 s [2]. In order to perform spectral analysis, the HRV signal was interpolated by a linear interpolation at a frequency of 3.41 Hz [2].

III. METHODOLOGY

A training set with 96 records (40%) and a test set with 144 records (60%) were randomly derived from the initial population to developed and evaluated our algorithm. Accordingly, the training set was used to perform feature extraction and feature selection processes. Once LR and SVMs classifiers were built, the test set was used to evaluate them.

A. Feature Extraction

PSD was calculated using the non-parametric Welch method. This is suitable for the analysis of non-stationary signals [10]. Hamming window of 2^{11} samples (10 minutes), along with a 50% overlap and a 2^{15} points *PSD* was used. Then, each *PSD* was normalized dividing the amplitude by its total power.

Nonlinear characteristics were obtained from HRV recordings in the time domain. Each signal was divided into epochs of 500 samples corresponding to 5 minutes signal because, during an episode of apnea, cyclical heartbeat variations usually appears periodically between 25 and 100 seconds [11]. Hence, the selection of several of this cycles is ensured. We calculate the average of the nonlinear features extracted in all periods of 5 minutes to obtain a single value for each feature.

A1 Spectral Parameters

Firstly, every single frequency of the *PSD* was analyzed to obtain the spectral bands that showed significant differences between SAHS positive and SAHS negative groups (*p*-value < 0.01). We used Mann-Whitney U test in the training set. Two spectral bands were obtained: B₁ \in (0.0242-0.274) Hz. and B₂ \in (0.0309 - 0.0341) Hz. Figure 1 shows the *p*-value for each frequency in the training set.

Next, four spectral features were computed from spectral bands B_1 and B_2 :

- 1. *RP*, which is the ratio of the area enclosed under the *PSD* in the frequency band to the total area under the *PSD*.
- 2. *PA* in the frequency band, which is the local maximum of the spectral content in the apnea frequency range.
- 3. *SE*, which is a disorder quantifier related to the flatness of the spectrum [12]:

Table 1 Clinical data of the study population

Features	All	SAHS	SAHS
		negative	positive
N ^o subjects	240	80	160
Age (years)	52.3 ± 13.7	47.2 ± 12.2	54.8 ± 13.8
Male (%)	77.5	65.0	83.8
$BMI (Kg./m^2)$	29.8 ± 4.4	27.8 ± 3.7	30.8 ± 4.3
AHI (events/hour)	-	3.9 ± 2.4	36.6 ± 25.7



Fig. 1 p-value for each frequency in the training set

$$SE = -\sum_{j} p_j \cdot ln(p_j), \qquad (1)$$

where p_i is the normalized value of the *PSD*.

4. *MF*, which is defined as the spectral component which comprises 50% of the total signal power [12].

A2 Nonlinear Parameters

Three nonlinear characteristics were computed:

1. *CTM*, which provides a variability measure from second order difference plots, assigning larger values to lower variability [13]:

$$CTM = \frac{1}{N-2} \sum_{i=1}^{N-2} \delta(d_i),$$
 (2)

$$\delta(d_i) = \begin{cases} 1 & \text{if } [(x(i+2) - x(i+1))^2 + (x(i+1) - x(i))^2]^{1/2} < \rho \\ 0 & \text{otherwise} \end{cases} , (3)$$

where, in our implementation, $\rho = 0.54$.

2. *LZC*, which is a nonparametric measure of complexity linked with the rate of new subsequences and their repetition along the original sequence [14]. c(n) is increased every time a new subsequence is encountered:

$$LZC(n) = \frac{c(n)}{b(n)} \tag{4}$$

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$$b(n) = \lim_{n \to \infty} c(n) = \frac{n}{\log_2(n)}.$$
(5)

3. *SampEn*, which quantifies irregularity in time series, with larger values corresponding to more irregular data [15]:

$$SampEn(m,r,N) = -\ln\left[\frac{A^m(r)}{B^m(r)}\right],$$
(6)

where A^m and B^m are the average number of (m)-length and (m + 1)-length segments $X_m(i)(1 \le i \le N - m + 1)$ with $d[X_m(i), X_m(j)] \le r(1 \le j \le N - m, j \ne i)$. According to [16], in our algorithm we use m = 3 and r = 0.25because all SampEn values were different from log(0).

B. Feature Selection

Feature selection was performed using the algorithm proposed by Hosmer and Lemeshow based on automatic step forward feature selection [17].

This algorithm chooses the strongest variables in a data set. The likelihood ratio test was used to assess statistical differences (*p*-value) between nested LR models differing in one degree of freedom. Iterative LR processes were applied to describe the relationship between a dependent variable and the independent variables. At each iteration, the stepwise method performs a test for backward elimination followed by a forward selection procedure [17]. Features that contribute with significant information are added to the model, whereas no significant features are removed.

If the likelihood *p*-value of the likelihood ratio is less than a threshold input α_E , FSLR model includes the feature. Also excludes features when the likelihood ratio is greater than a threshold output $\alpha_S > \alpha_E$.

C. Feature Classification

In the classification stage, two classification methodologies were assessed:

- LR relates a set of input features with a categorical dependent variable. The input patterns are classified into two mutually exclusive categories. The probability density function for the response variable can be modelled by a Bernoulli distribution. LR classifier assigns an input vector to the class with the maximum a posteriori probability value. The maximum likelihood criterion is used to optimize the coefficients of the independent input features in the model.
- SVMs map the input data into a much higher dimensional space. The goal is finding an optimal separating hyperplane between outputs belonging to two classes. SVMs attempt to maximize the separation between the

two classes and minimize training error. This is controlled by means of the regularization parameter C. In this study a linear SVM kernel was used. C was obtained by leave-one-out cross validation in the training set. A value of $C = 10^{-8}$ was selected.

D. Statistical Analysis

Statistical differences between groups were evaluated by means of the Mann-Whitney U test. The LR and SVM classifiers were assessed on the test set. Sensitivity (*Se*), specificity (*Sp*), positive predictive value (*PPV*), negative predictive value (*NPV*) and accuracy (*Ac*) were computed to quantify classification performance.

IV. RESULTS

Table 2 shows the average value (mean \pm standard deviation) and the *p*-value for each feature under study in the training set. *RP*, *PA* and *SE* achieved statistical significant differences between SAHS negative and SAHS positive groups in B_1 and B_2 .

Table 3 summarizes the diagnostic results of the two classification algorithms in the test set. It can be seen that the SVM classifier achieved higher diagnostic accuracy than the LR model. Furthermore, the results demonstrate the utility of performing feature selection.

V. DISCUSSION AND CONCLUSIONS

In the present study, were assessed in order to help in SAHS diagnosis two classifiers, based on LR and SVM. Independent training and test sets were used to compose and assess each classifier. A total of 11 spectral and nonlinear features composed the initial feature set. After the feature selection stage, 3 optimum variables were selected: PA_{B_2} , *LZC* and *CTM*. The spectral characteristics were obtained in two very low frequency bands, which showed significant differences.

Our results are consistent with previous studies that evaluated the relationship between changes in HRV (tachycardia, bradycardia) and physiological changes due to periodic hypoxia [6, 7, 8].

The optimal characteristics were extracted from the spectral parameters and the nonlinear parameters, which shows that the information is complementary. The model using SVM performed better than LR, reaching a diagnostic accuracy of 73.6%.

The study has some limitations that must be noted. First, it is clear that it would be appropriate to extend the total number of subjects and the rate of negative SAHS subjects. It would

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Features	SAHS negative	SAHS positive	<i>p</i> -value
RP_{B_1}	0.0128 ± 0.0045	0.0205 ± 0.0158	< 0.01
PA_{B_1}	0.0153 ± 0.0100	0.0340 ± 0.0454	< 0.01
SE_{B_1}	0.0104 ± 0.0033	0.0153 ± 0.0097	< 0.01
MF_{B_1}	0.0257 ± 0.0001	0.0258 ± 0.0001	> 0.01
RP_{B_2}	0.0103 ± 0.0041	0.0161 ± 0.0117	< 0.01
PA_{B_2}	0.0113 ± 0.0065	0.0255 ± 0.0286	< 0.01
SE_{B_2}	0.0086 ± 0.0031	0.0125 ± 0.0076	< 0.01
MF_{B_2}	0.0325 ± 0.0001	0.0325 ± 0.0001	> 0.01
CTM	0.6613 ± 0.2117	0.6923 ± 0.1746	> 0.01
LZC	0.3727 ± 0.0625	0.3546 ± 0.0684	> 0.01
SampEn	0.4121 ± 0.0867	0.4053 ± 0.1034	> 0.01

Table 2 Average (mean \pm standard deviation) for each feature under study

	Ί	able 3	Diagnostic	evaluation	of the	classifiers	(test s	et)
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Model	Se(%)	Sp(%)	PPV(%)	NPV(%)	Ac(%)
$LR (PA_{B_2}, LZC, CTM)$	76.0	58.3	78.5	54.9	70.1
$\mathrm{SVM}_{(PA_{B_2}, LZC, CTM)}$	70.8	79.2	87.0	56.7	73.6
LR (all features)	70.8	47.9	74.7	47.2	63.2
SVM (all features)	51.6	71.9	77.5	41.1	58.3

also be desirable to use other feature selection methods, such as principal component analysis (PCA). Thus, it is possible that other features also provide useful information.

In conclusion, the results reported in this study suggest that the joint analysis of spectral and nonlinear features from HRV recordings obtained from ECG, automatically selected by means of FSLR, could provide additional useful information to help in SAHS detection.

ACKNOWLEDGEMENTS

This research was supported in part by the Proyecto Cero 2011 on Ageing from Fundación General CSIC, Obra Social La Caixa and CSIC, the "Ministerio de Economía y Competitividad" and FEDER under project TEC2011-22987, and project VA111A11-2 from Consejería de Educación (Junta de Castilla y León).

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