Sleep Apnea Detection Directly from Unprocessed ECG through Singular Spectrum Decomposition

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Abstract

ECG-based detection of sleep apnea is generally based on heart rate related indices. Computation of these indices requires an ECG record to be pre-processed and the R-peak locations to be estimated. This study proposes a novel method to detect minute-by-minute sleep apnea episodes directly from an unprocessed ECG through singular spectrum decomposition (SSD). Given an ECG record, SSD was applied to non-overlapping segments and the dominant frequency (DF) of the component in the frequency range 0.02-0.5 Hz was estimated. Each segment was binary classified based on the corresponding DF (1, if DF larger than a defined threshold, 0 otherwise). For every minute, the sum of the corresponding binary values was then used to classify that minute as normal or apnea. Validation was based on the learning set of the Apnea-ECG Database. Two segment lengths, 10s and 20s, were tested, and K-fold cross-validation was used to determine the optimal values for threshold and sum, and for performance analysis. The 20s segment-based analysis proved to be more reliable and provided a sensitivity and a specificity of 67% and 52%, respectively. Although performance of the proposed model is still unsatisfactory, the preliminary results reported in this study suggest that detection of sleep apnea directly from unprocessed ECG may be possible.

1. Introduction

Sleep apnea (SA) is a common sleep disorder. It may occur when tissues in the upper airways come too close to each other during sleep, temporarily blocking the inflow of air (obstructive SA), or because the brain does not send proper signals to the muscles that control the breathing (central SA), or because of both causes (mixed SA). Obstructive SA is the most common form in the general population, with a reported prevalence of 4% in adult men and 2% in adult women. SA is commonly associated with aging and obesity [1]. The most common symptom is an excessive daytime sleepiness, with serious consequences such as traffic accidents. SA has also been proven to be linked with arterial hypertension and is nowadays regarded as an important risk factor for the development of cardiovascular diseases [2]. If treated at an early stage, night-time and day-time blood pressure of patients suffering of SA can be lowered, and adverse health effects reduced [3]. SA is successfully treated with home ventilation using nasal continuous positive airway pressure. SA is traditionally diagnosed by polysomnography studies taken during the duration of one night in a specialized sleep center. This requires dedicated personnel and infrastructure, and special acquisition systems, which make this diagnosis an expensive procedure. Therefore, simpler and home-based ways to assess sleep apnea have been investigated in the last decade. Respiration is well known to induce changes on the heart rate. This influence can be studied by analysing the beat-to-beat series that can be extracted from an ECG recording. This signal contains fluctuations commonly named heart rate variability, which present frequency components between 0 and 0.5 Hz and are linked to the autonomic nervous system. Cyclical variation in heart rate has been described as being characteristic of obstructive SA [4]. Many algorithms have been devised during the last decade to detect SA from ECG recordings. Regardless the diversity of ideas and approaches, the domain of analysis (time or frequency), and the use of additional information, all algorithms make use of the heart rate variability signal [5]. This requires an ECG recording to be processed and the temporal locations of all beats to be correctly identified, increasing the computation time and making the results depending on the accuracy of the beat detection algorithm employed.

In this study, we investigated a method to detect SA episodes directly from a single lead unprocessed ECG recording. The proposed method decomposes an ECG excerpt by means of singular spectrum decomposition (SSD), a recently proposed data-driven and adaptive algorithm for the decomposition of nonlinear and nonstationary time series [6]. The resulting decomposition is used to assess the respiratory activity in the excerpt and discriminate whether

an SA episode is occurring. Although most of the heart rate variability algorithms proposed over the last decade are quite accurate, this alternative approach takes into account the complete signal and may be picking up other frequency characteristics, and reveal more details on the progress of sleep apnea overnight.

2. Methods

2.1. Dataset

The learning set from the Apnea-ECG Database available on Physionet was used in this study [7]. This dataset consists of 35 records (20 apnea recordings, 5 borderline, and 10 control). Each recording includes a single ECG signal digitized at 100 Hz with 12-bit resolution, continuously for approximately 8 hours. Only the first 5 hours of each recording were used in this study. Binary annotation files are also available, containing an annotation for each minute of each recording indicating the presence or absence of apnea at that time. No pre-processing was applied to the ECG signals.

2.2. Singular spectrum decomposition

SSD is a recently proposed adaptive and fully data-driven algorithm for the decomposition of nonlinear and nonstationary time series into physically meaningful narrow-banded components [6, 8]. SSD has been shown to yield physically significant components when applied to time series from diverse domains of science (among which biology and climatology), attesting its robustness and versatility. Given a zero-mean time series $x(n)$, $n = 1, \ldots, N$, the SSD algorithm iteratively extracts a set of component series from $x(n)$ until the total variance of the extracted components reaches a user-defined threshold. Each iteration consists of the following steps:

Embedding. The time series $x(n)$ is embedded in a vector space of dimension m. Given an embedding dimension m, with $1 < m < N$, the embedding procedure forms m lagged vectors $x(i) = [x(i), \ldots, x(N); x(1), \ldots, x(i-1)]$, with $i = 1, \ldots, N - m + 1$. For instance, given the time series $x(n) = \{1, 2, 3, 4, 5\}$, and an embedding dimension $m = 3$, the corresponding trajectory matrix X collecting all lagged vectors will be:

$$X = \begin{bmatrix} 1 & 2 & 3 & 4 & 5 \\ 2 & 3 & 4 & 5 & 1 \\ 3 & 4 & 5 & 1 & 2 \end{bmatrix}$$

Decomposition. The singular value decomposition of the trajectory matrix X is then computed.

Grouping and Reconstruction. Out of the m principal components of X, a subset ($p < m$) is selected to reconstruct a specific component series, in such a way that it describes a well-defined time scale in the original time series (please find more details in [6] about the automated selection of the embedding dimension m and of the subset of p principal components). The estimated component series is then subtracted from $x(n)$, and the procedure is iterated for the residual until a stopping criterion is met, namely when the energy of the residual falls below a pre-defined threshold.

Therefore, at each stage SSD decomposes a time series, or its residual, by extracting all nonlinear and transient periodic patterns (cyclicities) in it, and separates the periodic components from possible trend and noise.

In this study, we used a modified version of the original SSD algorithm proposed in [6] (which will be referred to as SSD-band hereafter), which provides only one SSD component representing a user-defined frequency band. The frequency band of interest was set to [0.02,0.5] Hz to sufficiently account for the range of the heart rate variability and of the respiratory rate at rest.

2.3. Sleep apnea identification

Given an ECG recording, SSD-band was applied to non-overlapping segments and the dominant frequency (DF) was estimated for each segment. In this study, we investigated two possible segment lengths: 10s (6 segments per minute) and 20s (3 segments per minute), respectively. Performance of DF in achieving minute-by-minute sleep apnea episode identification was analyzed as follows. For each minute, each segment was binary classified based on the corresponding value of DF (1, if DF larger than a defined threshold (TH), 0 otherwise), and the sum of the binary values within a minute (SUM) was used to classify that minute as normal (N) or apnea (SA), with the larger the sum the more likely an SA episode is occurring. The idea is to detect somehow the absence of a clear respiration component in the 0.02-0.5 Hz range. The underlying hypothesis is that in absence of respiration related fluctuations on the ECG signal, SSD-band likely starts decomposing noise or QRS like components within the frequency band [0.02,0.5]Hz of an ECG signal, with higher chance of higher DF values. Figures 1 and 2 show an example of the SSD-band analysis of a normal and a sleep apnea segment, respectively. It can be noticed how a component approximating the respiration induced ECG fluctuations can be extracted from the normal segment, with a DF at about 0.2 Hz, while the SSD-band component extracted from the sleep apnea segment misses those fluctuations, since no respiration is present, with the baseline likely corrupted by the low frequency component of some muscular noise and characterized by a larger value of DF.

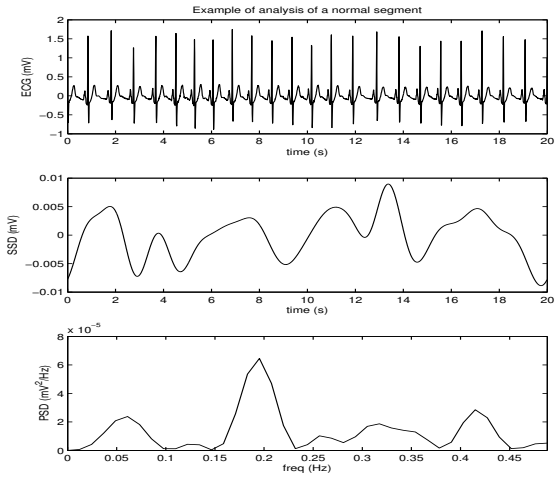

Figure 1. Example of the SSD-band analysis of a normal ECG segment. Top: ECG excerpt; Middle: corresponding component in the frequency range [0.02,0.5] Hz provided by SSD-band; Bottom: Power spectral density (PSD) of the SSD-band component.

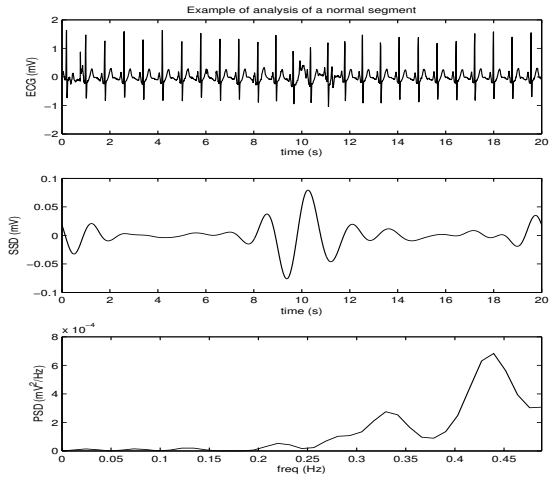

Figure 2. Example of the SSD-band analysis of a sleep apnea ECG segment. Top: ECG excerpt; Middle: corresponding component in the frequency range [0.02,0.5] Hz provided by SSD-band; Bottom: Power spectral density (PSD) of the SSD-band component.

2.4. Statistical analysis

K-fold cross-validation was used to determine the optimal values for TH (in the range 0.02-0.5 Hz) and SUM (in the range 0 to 6 for 10s segments, and 0 to 3 for 20s segments) and for performance analysis. A value of K=5 was used in order to have a proportion of 80% records in the training set (28 records) and 20% records in the test set (7 records) at each iteration (also to agree with the 80-20 Pareto's rule). Generalized linear model regression was also used to determine whether the within a minute variability of DF was a significant predictor of SA episodes, assuming that SA episodes should be characterized by more variability, due to a lack of respiration activity. The median absolute difference (MAD) of DF values per minute were used as input to the model. Lilliefors test was used to test whether DF values followed a normal distribution. The alternative hypothesis was accepted, and Wilcoxon rank-sum test was used to test the difference between SA minutes and N minutes in terms of the median value of DF per minute. Results are given as median(MAD).

3. Results

Table 1 shows the average results of the 5-fold cross-validation, for both segment lengths 10s and 20s. Generalized linear model regression showed that the variability of DF within a minute is a significant predictor of SA episodes ($p < 10^{-4}$, for both 10s and 20s segments. Table 2 summarizes the results of the Wilcoxon rank-sum test for both segment lengths 10s and 20s.

Table 1. Average results of the 5-fold cross-validation. Se: sensitivity; Sp: specificity; TH: optimal threshold for DF; SUM: optimal sum of the binary values within a minute.

	10s	20s
Se (%)	77	67
Sp (%)	28	52
TH (Hz)	0.27	0.25
SUM	3	1

Table 2. Results of the Wilcoxon rank-sum test for both segment lengths 10s and 20s. med: median; MAD: median absolute difference; Wilcoxon: Wilcoxon rank-sum test.

	10s		20s	
	N	SA	N	SA
med(MAD) (Hz)	0.95(1.11)	0.90(1.12)	0.25(0.83)	0.35(0.83)
Wilcoxon	$p < 10^{-3}$		$p < 10^{-4}$	

4. Conclusions

This study investigated an approach for minute-by-minute sleep apnea detection directly from unprocessed ECG, by means of singular spectrum decomposition applied to consecutive non-overlapping ECG excerpts from

each minute. Two segment lengths for the ECG excerpts have been analyzed, namely 10s and 20s. The unrealistic value of median DF showed in Table 2 for the normal 10s segments (0.97 Hz) suggests that 10s is insufficient for the SSD-band method to describe the respiration induced ECG fluctuations, and the corresponding classification showed in Table 1 should be considered unreliable. On the contrary, the analysis carried out on the 20s normal segments provided a more realistic value of respiration induced ECG fluctuation median DF (0.25 Hz). The SSD-band method based on 20s segments showed a sensitivity of 67% and a specificity of 52%, for a frequency threshold of 0.25 Hz. The relatively high value of respiration induced ECG fluctuation median DF (and the corresponding MAD) from the 20s normal segment analysis suggests that non-respiratory high frequency components are still present in the SSD-band derived component, likely affecting classification performance. However, the significant difference in terms of median DF between normal and sleep apnea minutes still supports the hypothesis that SSD-band based DF could be reliably used to discriminate sleep apnea episodes. Following an idea proposed by McNames and Fraser [9], namely that periods of apnea can be visually identified by looking at the spectrogram in 0.02-0.08 Hz range, we also looked at the predictive power of the energy in 0.02-0.08 Hz range of the SSD-band components in each minute. We did not find any significant results in terms of ability of the energy in 0.02-0.08 Hz range to discriminate between normal and sleep apnea minutes. In conclusions, although performance of the proposed model is still unsatisfactory, especially in avoiding false positive, the preliminary results reported in this study suggest that detection of sleep apnea directly from unprocessed ECG may be possible.

References

[1] Young T, Palta M, Dempsey J, Skatrud J, Weber S, Badr S. The Occurrence of Sleep-Disordered Breathing among Middle-Aged Adults. N Engl J Med April 1993; 328(17):1230–1235.

[2] Young T, Peppard PE, Gottlieb DJ. Epidemiology of obstructive sleep apnea: a population health perspective. Am J Respir Crit Care Med 2002 May 1;165(9):1217–39.

[3] Dimsdale JE, Loredo JS, Profant J. Effect of continuous airway pressure on blood pressure. Hypertension 2000 Jan;35(1 Pt 1):144–7.

[4] Guilleminault C, Connolly S, Winkle R, Melvin K, Tilkian A. Cyclical variation of the heart rate in sleep apnoea syndrome. Mechanisms, and usefulness of 24 h electrocardiography as a screening technique. Lancet 1984 Jan 21; 1(8369):126–31.

[5] Penzel T, McNames J, de Chazal P, Raymond B, Murray A, Moody G. Systematic comparison of different algorithms for apnoea detection based on electrocardiogram recordings. Med Biol Eng and Comp 2002;40(4):402–407.

[6] Bonizzi P, Karel JMH, Meste O, Peeters RLM. Singular spectrum decomposition: a new method for time series decomposition. Advances in Adaptive Data Analysis 2014;Vol. 6, No. 4:1450011 (34 pages).

[7] Penzel T, Moody GB, Mark RG, Goldberger AL, Peter JH. The Apnea-ECG Database. In Computers in Cardiology, volume 27. 2000; 255–258.

[8] Bonizzi P, Karel J, De Weerd P, Lowet E, Roberts M, Westra R, Meste O, Peeters R. Singular spectrum analysis improves analysis of local field potentials from macaque V1 in active fixation task. In Proc. IEEE EMBS. 2012; .

[9] McNames JN, Fraser AM. Obstructive sleep apnea classification based on spectrogram patterns in the electrocardiogram. In Computers in Cardiology, volume 27. 2000; 749–752.

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