Sleep apnea syndrome diagnosis by analysis of the cardiac interbeat RR time series

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***Abstract*-**An automatic tool is proposed to help clinicians in the diagnosis of sleep apnea syndrome. The method uses an elementary signal processing of the heart interbeat RR time series, offering the possibility of screening the pathology on the basis of a portable and inexpensive device that can be used at the patient's home.

RR: cardiac interbeat interval; SAS: Sleep Apnea Syndrome; AIM: absolute irregularity measure; RIM: relative irregularity measure; ECG: electrocardiogram; EEG: electroencephalogram; CPAP: Continuous Positive Airway Pressure

I. Introduction

Sleep apnea syndrome — in which the usual complaints are daytime sleepiness, loud snoring, and restless sleep — is believed to affect a significant percentage of the population (4%). With the introduction of nasal Continuous Positive Airway Pressure as an effective treatment, the demand for costly polysomnographic diagnosis is steadily increasing. For that reason, there is a growing interest among clinicians for a portable device that could be used at home and constitute a reliable screening method.

Such a screening tool is the analysis of the RR time series, which provide the heart interbeat intervals between QRS complexes and can be easily recorded (24 hours Holter recording[1]). The significance of the Holter resides in a characteristic pattern of sinus arrhythmia associated with apnea: extended bradycardia followed by abrupt tachycardia.[4] Such apnea patterns are illustrated on Figure 1. Bradycardia corresponds to increased interbeat intervals (higher values in the RR series) while the sudden tachycardia correspond to an abrupt transition to shorter interbeat intervals (abrupt drop in the RR series). Except for patients with abnormalities of the autonomic nervous system, there is thus a one-to-one correspondence between the number of such patterns in the RR time series and the number of apnea cycles. Despite this strong correlation, to our knowledge no reliable automatic tool has emerged for the sleep apnea syndrome diagnosis based on the analysis of the RR time series.

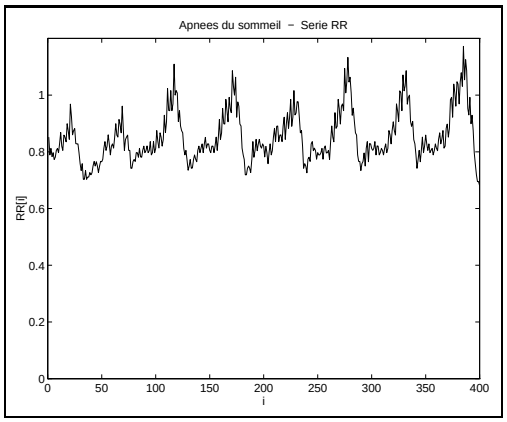

Figure 1: Apnea patterns in the RR series of a patient suffering from SAS. i labels the number of the heart beat, and RR is the beat duration in seconds.

One reason for the lack of such tools is that the characteristic patterns on Figure 1 have to be detected among many other irregularities, arising from the natural heartbeat variability of healthy patients (see Figure 4) or various other phenomena (e.g. extrasystoles, recording failures...). Another and more important reason is that current RR analysis methods used for SAS diagnosis [6] are based on software tools used by cardiologists to study the heart rate variability (for instance, in order to evaluate the risk of sudden cardiac death after myocardial infarction). Heart rate variability is classically studied by a frequency domain analysis of the RR series over 24 hours (after a time-consuming pre-treatment of the signal in order to remove artefacts).[10] More recently, the RR time series analysis has also attracted an increasing number of physicists and various variability indices have been defined based on tools of statistical and dynamical sys-

[1]Our data comes from an Oxford Holter recording system MR 4500P and the signal was digitized at 128 samples/sec by an Oxford analyser Medilog 4500.

tems analysis.[11]

Obvious mathematical arguments — e.g. the fact that the irregular patterns caused by apnea are far from stationary — suggest that the tools used for heart rate variability analysis are not suitable for SAS diagnosis. This is confirmed by a number of validation studies (e.g. [7]).

In this paper, we propose an automatic tool focused on the detection of apnea patterns in the RR time series. An elementary signal processing of the (raw) original RR time series is used to enhance the effect of apnea patterns while smoothing other irregularities. An automatic "counting" of the patterns then provides a cumulated graph of the detected apneas over the night and the evolution of the frequency of apneas over periods of 15 minutes. Such information can be directly interpreted by clinicians and allows for interactive use as opposed to usual heart-rate variability indices. The preliminary validation that we have performed on clinical data suggests that the proposed approach is highly reliable in establishing the diagnosis of sleep apnea syndrome.

II. Construction of an auxiliary signal

The analysis of the RR time series must detect the characteristic apnea pattern illustrated in Figure 1 among a variety of random-like variations due to normal heart rate variability, extrasystoles, or recording failures. To make this task easier, we first generate a new time series which acts as an apnea detector by magnifying the apnea peaks and smoothing down all the rest.

The new signal $s[i]$ is obtained by an elementary convolution operation:

$$s = RR * c \tag{1}$$

where $RR[i]$ is the interbeat time series, and "$*$" stands for the discrete convolution operation, i.e.

$$(a * b)[i] = \sum_{k=-\infty}^{+\infty} a[k]b[i-k] = \sum_{k=-\infty}^{+\infty} a[i-k]b[k]. \tag{2}$$

The signal $c[i]$, which we shall refer to as the "convolution key", is defined by

$$c[i] = \begin{cases} -1 & \text{if } 0 \le i \le \tau - 1 \\ 1 & \text{if } \tau \le i \le 2\tau - 1 \\ 0 & \text{elsewhere} \end{cases} . \tag{3}$$

where the width τ is a design parameter (see Figure 2) fixed to $\tau = 10$ throughout the paper.

The *design of the convolution key* is driven by the idea of "matched filter" in telecommunications. For optimal detection, we should have chosen a key with the same shape as the apnea patterns in the RR series. Unfortunately, apnea patterns tend to exhibit a large diversity, not only between two different patients, but also (although less dramatically) between successive occurrences in the same RR series. The usual trade-off between the selectivity of the filter and its robustness dictated the simple choice that has been retained.

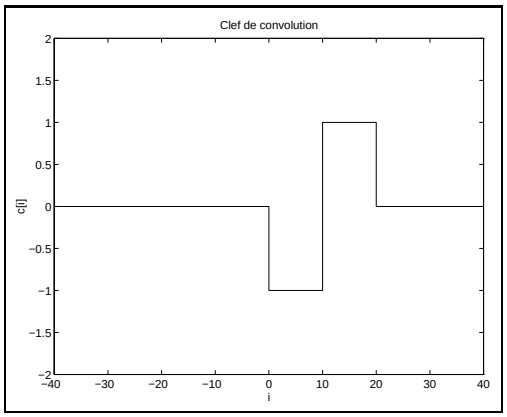

Figure 2: The convolution key $c[i]$ with $\tau = 10$.

Figures 4 and 3 show the effect of the convolution on respectively a healthy and an SAS-suffering patient. In Figure 3, the convoluted signal $s[i]$ is smoother than the original signal $RR[i]$, and it is centered at zero. The number of peaks of $s[i]$ is equal to the number of apnea patterns of $RR[i]$, the height of the peaks depending on the intensity of the transition between slow rate and fast rate. In Figure 4, the signal $s[i]$ is also smoother than $RR[i]$ and centered around zero, but the peaks are lower and less regular.

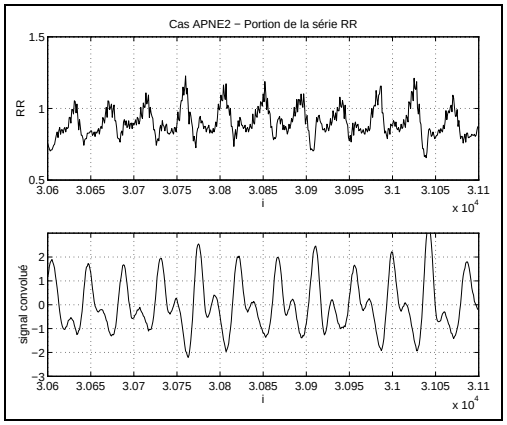

Figure 3: Above: sample of the RR series of a patient showing hard SAS. Lower: signal $s = RR * c$.

III. "Grand peaks" and their time distribution function

We call *grand peak* each positive peak in $s[i]$ whose height h is greater than a value h_{trig} (we shall usually choose h_{trig} around 1) and whose width l is greater or equal to a value l_{trig} (we have chosen $l_{\text{trig}} = 12$). We

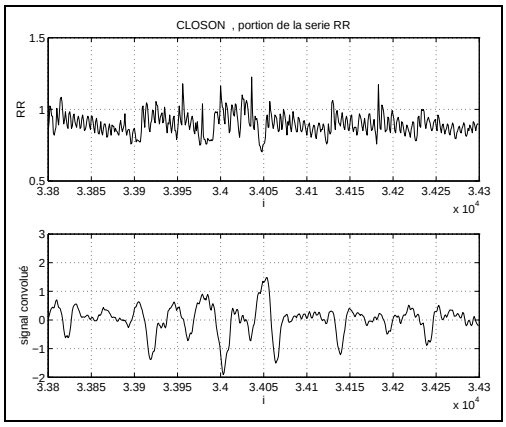

Figure 4: Above: sample of the RR series of a healthy patient. Lower: signal $s = RR * c$.

rely on the correspondance between grand peaks in $s[i]$ and apnea patterns in $RR[i]$, i.e., each apnea pattern in $RR[i]$ will cause a grand peak in $s[i]$ provided the pattern is sufficiently strong, and grand peaks are unlikely to occur in the absence of apnea pattern in $RR[i]$. Hence, by counting the grand peaks, one counts the apnea patterns. For instance, on Figure 3, we count 11 apnea patterns in $RR[i]$ and 11 grand peaks in $s[i]$ (the very first peak corresponds to a pattern occuring just before starting the plot). Only one grand peak is detected (with an amplitude of 1.5) in Figure 4. This peak is not caused by an apnea pattern but by a resembling irregularity of the (normal) RR signal.

We then define the *time distribution function of grand peaks*, which we will call $F(t)$, such that

$F(t)$ = number of grand peaks detected between time t and the beginning of the recording.

From the grand peak distribution function $F(t)$, we derive a *local frequency graph*. It provides the grand peaks frequencies calculated on a 15 minutes basis throughout the record.

To each 15 minutes portion, we associate an *absolute irregularity measure* (AIM) and a *relative irregularity measure* (RIM) defined as

$$AIM = \sigma(1/T_i) \quad (4)$$

$$RIM = \sigma(1/T_i)/(\text{local frequency}) \quad (5)$$

where T_i gives the time (measured in hours) between two grand peaks, and *local frequency* (expressed in Apnea Per Hour) is the frequency of grand peaks as measured on the 15 minutes interval. The symbol σ stands for standard deviation, evaluated on the 15 minutes interval.

IV. Results

The results of our analysis are displayed by using a cumulated graph and a "local frequencies graph" (see Figures 5, 6 and 7).

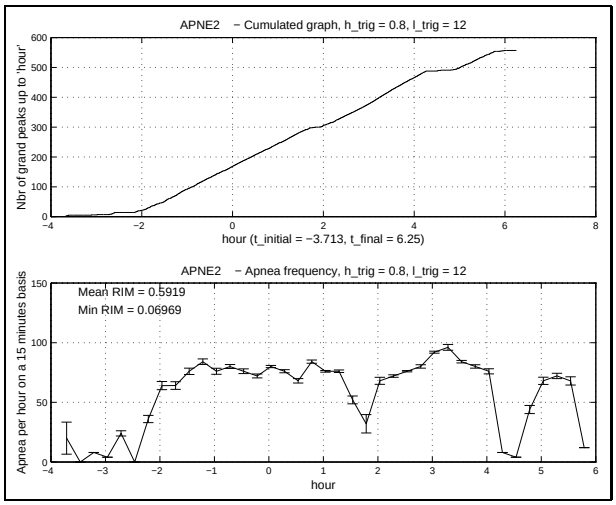

Figure 5: Cumulated graph and local frequencies graph for patient A suffering from sleep apneas.

A. Cumulated graph

The upper graph, called *cumulated graph*, displays the distribution function $F(t)$. The title provides the name of the patient as well as the values of h_{trig} and l_{trig} (see Section III). The X-axis indicates the time in hours (0 stands for midnight), and the Y-axis gives the number of grand peaks detected up to that time.

This graph shows some very typical features for a patient suffering from SAS (Figure 5):

- The slope is very regular over the night, except for the very beginning (the patient was not asleep yet) and two small periods of time during the night (it is likely that the patient was awake during that time).

- The magnitude of the curve is high, which means that many grand peaks, and thus many SAS-like patterns, have been detected.

- The curve is very smooth at small scale, which means that the apnea patterns occur very regularly in time. This helps to distinguish between true SAS and noisy RR series, the latter sometimes exhibiting many SAS-like patterns. These patterns trigger grand peaks in $s[i]$[2] which are recorded in $F(t)$, but they occur less regularly than in true SAS cases. As an illustration, it is instructive to compare Figure 5 and Figure 7. Figure 7 displays the cumulated graph of a healthy patient who presents high variability. The cumulated graph shows a high number of

[2]For example, if we choose $h_{\text{trig}} = 0.8$ and $l_{\text{trig}} = 12$, we see that the healthy RR series in Figure 4 has produced two grand peaks.

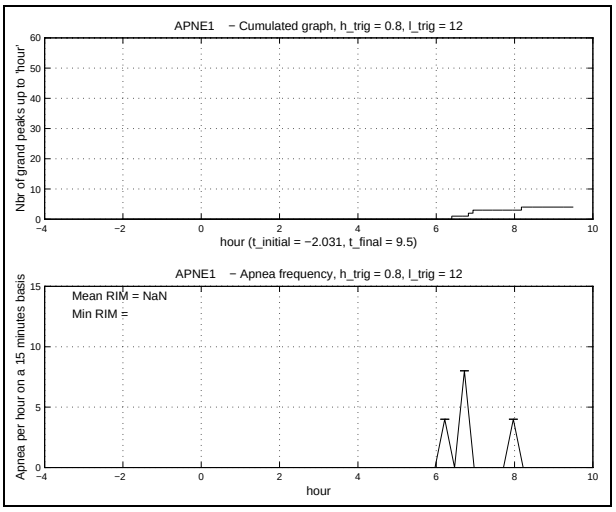

Figure 6: Cumulated graph and local frequencies graph for patient A under CPAP treatement. One sees that the treatment has been very efficient (note the different scale).

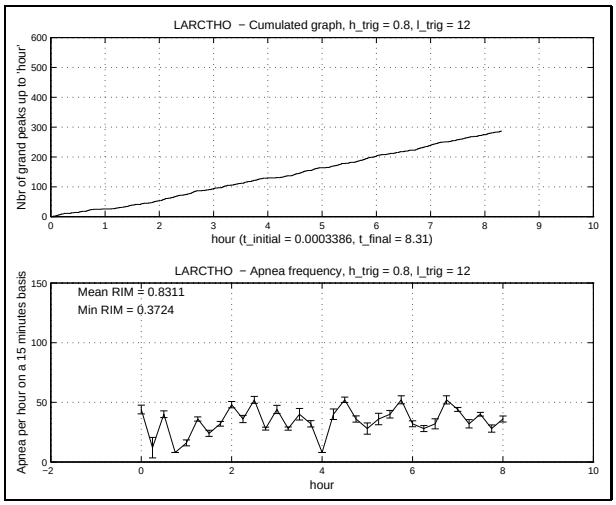

Figure 7: Cumulated graph and local frequencies graph of a healthy patient.

grand peaks. However, the graph is easily differentiated from the corresponding one on Figure 5 through the irregularity of the curve. In order to help quantifying the irregularity of the curve, we have defined two parameters which are displayed in the lower graph of the figure. The first one gives the mean relative irregularity measure (RIM) over the whole record, and the second gives the smallest RIM of all 15 minutes sequences extracted from the whole record. The second irregularity parameter is particularly relevant. Its value is 0.07 on Figure 5 while a normal value for a healthy patient is around 0.4. A low RIM index seems very typical of SAS.

B. Local frequencies

The lower graph in Figures 5, 6 and 7, called *local frequencies graph*, is derived directly from the *cumulated graph*. It provides the grand peak frequencies calculated on a 15 minutes basis.

The error bars give an estimation of the irregularity of the occurence of grand peaks within the 15 minutes time portions. Comparing Figures 5 and 7, one sees that error bars are smaller in the SAS case, i.e., that grand peaks occur more regularly in case of SAS. This is a very characteristic feature. Another typical feature is the amplitude of the curve, which rarely reaches more than 50 apneas per hour with healthy patients.

V. Correlation between grand peaks and apnea patterns

To validate the expected correlation between grand peaks and apnea patterns, Figure 8 illustrates two portions of the original RR time series of patient A (Figure 5).

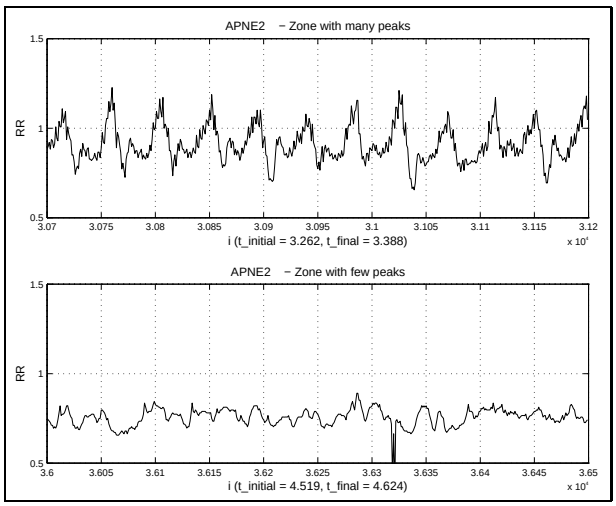

Figure 8: Two portions of the RR series of patient A. Above: high frequency of grand peaks. Lower: low frequency of grand peaks.

The first portion has been selected at a time of the night where our analysis indicates a high frequency of grand peaks. One indeed recognises the correlation with apnea pattern both qualitatively and quantitatively. In contrast, the second portion was selected at a time of the night where our analysis indicates a low frequency of grand peaks. No apnea pattern is present during this period.

Such a validation can be interactively operated by the clinician. The software we have developed has this capability, offering a very convenient way for the clinician to detect the periods of high frequency and to analyse the corresponding apnea patterns directly on

the RR series.

VI. Conclusion

The objective was to design an algorithm for an automatic detection of apnea patterns in an RR interbeat time series. Our solution is to perform a convolution on RR with a dedicated signal c, yielding a filtered signal s. The "grand peak" distribution function over time provides the clinician with relevant information about the frequency of apneas over the night. The results can be directly interpreted by the clinicians and our method offers a tool that can be used interactively. Further validation of the results on a large number of patients and healthy subjects is the object of current work.

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