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Recurrence quantification analysis across sleep stages

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ABSTRACT

In this work we employ a nonlinear data analysis method called recurrence quantification analysis (RQA) to analyze differences between sleep stages and wake using cardio-respiratory signals, only. The data were recorded during full-night polysomnographies of 313 healthy subjects in nine different sleep laboratories. The raw signals are first normalized to common time bases and ranges. Thirteen different RQA and cross-RQA features derived from ECG, respiratory effort, heart rate and their combinations are additionally reconditioned with windowed standard deviation filters and ZSCORE normalization procedures leading to a total feature count of 195. The discriminative power between *Wake*, *NREM* and *REM* of each feature is evaluated using the Cohen's kappa coefficient. Besides kappa performance, sensitivity, specificity, accuracy and inter-correlations of the best 20 features with high discriminative power is also analyzed. The best kappa values for each class versus the other classes are 0.24, 0.12 and 0.31 for *NREM*, *REM* and *Wake*, respectively. Significance is tested with ANOVA *F*-test (mostly $p < 0.001$). The results are compared to known cardio-respiratory features for sleep analysis. We conclude that many RQA features are suited to discriminate between *Wake* and *Sleep*, whereas the differentiation between *REM* and the other classes remains in the midrange.

1. Introduction

In order to diagnose sleep or sleep related disorders, nowadays, polysomnography (PSG) is performed to record physiological data over a whole night in a sleep laboratory. Its key component is the measurement of cerebral activity with electroencephalography (EEG). Several electrodes have to be applied to the patients scalp at defined positions which can only be done by trained persons. In addition, electrocardiogram (ECG), respiratory activity, muscular activation, i.e. electromyogram (EMG), body temperature and eye movements, i.e. electrooculogram (EOG), are monitored. The amount of different parameters already evokes a high complexity of such recordings. With increasing age, chronic illnesses and sleep disorders occur more often. The demographic change will not allow each subject with potential sleep disorder to be analyzed in a sleep laboratory as this is too cost- and time-intensive. Alternatives need to be established to explore sleep in more convenient environments, for example at home. Several studies show that it is possible to perform sleep staging to a certain extent using cardio-respiratory signals and body movements [4,6,25,30,31,41]. For example frequency and time-frequency analysis are applied on cardiac data to determine sleep or sleep-related disorders, such as sleep disordered breathing or sleep apnea [17,23]. The measurement of cardiac and respiratory signals can be transferred to the home environment more easily than EEG measurements, e.g. by using wearable sensor suites [21] or integrating the sensors into the bed mattress or pillow [9]. New methods and algorithms have to be developed to extract relevant data and multi-modal (coupled) signals using less sensors. Park et al. and Mita for example show improved algorithms to derive respiration from ECG measurements [36,38]. The aim of the research in this domain is to get an accurate estimate of sleep stages without the need of EOG, EMG or even EEG recordings. Recording in a familiar environment helps reducing the so-called first night effect biasing the regular sleep behavior. It also allows long-term measurements that are more representative than only one single night.

Sleep is a very complex physiological process, not yet completely understood, in which the parasympathetic nervous system

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(NS) predominantly controls the sleep depth by regulating the body temperature, heart rate and breathing activity. However, the sympathetic NS acts against it, so that the body is always alert to external stimuli [42]. It is obvious that sleep is essential and vital as sleep deprivation results in serious behavioral and psychological disorders that finally lead to obesity, cardiovascular morbidity, traffic accidents and death [1]. In this work we analyze cardio-respiratory signals across wake and sleep stages at night. We employ recurrence quantification analysis (RQA), which is known to be a powerful tool to study complex (physiological) systems. RQA has already successfully been applied to EEG data [44] to distinguish between sleep stages. Smietanoswki et al. determined several RQA features using recurrence plots on heart rate (HR) signals to derive dynamics of the heart rate variability (HRV) in healthy subjects and patients with obstructive sleep apnea (OSA) [43]. They found out that the change of recurrences between healthy and OSA subjects is different, arising from a more complex heart rate dynamic for the rapid eye movement (REM) stage. RQA is also an adequate method to study the nonlinear dynamic properties of QT and RR intervals during acute myocardial ischemia [39].

Terrill et al. apply RQA features, amongst others, solely on respiratory effort (RE) signals to classify 30 s epochs of infant sleep into *Wake*, *REM* and *NREM* stages [46]. They show that most of the computed RQA features are top-rated by a feature selection algorithm and contribute to better performance. Another promising approach for sleep staging is the exploration of phase synchrograms by means of RQA, as proposed by Nguyen et al. [37]. That study was also performed on data acquired from healthy infants and additionally on simulated data to show the improvements of the method compared to conventional methods to analyze synchrograms. Cardio-respiratory phase synchronization (position and number of heartbeats within respiratory cycles), which is often inspected with synchrograms, significantly changes with sleep stages, as discovered by Bartsch et al. [2].

However, to the knowledge of the authors, no work was published employing RQA on both, exclusively raw cardiac and respiratory data, for adult sleep stage investigation. Therefore, in this work, we concentrate on extracting thirteen of the most common RQA features from ECG, RE, HR signals and the two combinations of {ECG+RE} and {RE+HR} to determine the most discriminative features between different sleep stages and wake.

This paper first gives a general overview of RQA as a quantifying description of recurrence plots (RPs), succeeded by a list of extracted RQA features. Then, it describes the employed data set and signal preprocessing steps for RQA, followed by a summary of the RQA embedding parameters. Finally, the ability of 195 computed cardio-respiratory RQA features derived from 313 whole night recordings of different subjects – representing more than 2300 h of data – to distinguish between *NREM*, *REM* and *Wake* stages is presented and discussed.

2. Materials and methods

2.1. Recurrence quantification analysis

Recurrence quantification analysis (RQA) is a method for describing recurring states in the phase space of dynamic systems. The concept of recurrence was introduced by Henri Poincaré in 1890: the trajectory of a classical system will return infinitely many times to a limited region in phase space [15,40]. Often, only one time series $x_n(t)$ of a complex system $\vec{x}$ in d dimensions ($\vec{x} \in \mathbb{R}^D$) is observable. For this case, Takens proposed in 1981 a time delay embedding technique to reconstruct the phase space of the original system. Embedding $m \geq 2 \cdot D + 1$ (correlation dimension D) sampling points of the discrete time series with delay τ for each time t_i, then $\vec{\hat{x}}$ is a reconstruction of the original trajectory:

$$\vec{\hat{x}}(t_i) = \sum_{k=1}^{m} x_n \cdot (t_i + (k-1) \cdot \tau) \cdot \vec{e}_k, \tag{1}$$

with $\vec{e}_k$ as the unit vector of the dimension k. A diffeomorphism exists, so the embedding preserves the properties of the original attractor [34,45].

To visualize recurrences in multidimensional phase space, Eckmann et al. presented recurrence plots (RPs) in 1987 [11]. An RP is an illustration of the binary recurrence matrix $\vec{R}$. The entry $R_{i,j}$ is set to 1 (black pixel in the plot) if two states at different times are similar, i.e. the points $\vec{\hat{x}}(t_i)$ and $\vec{\hat{x}}(t_j)$ in phase space fall inside a ball of radius ε:

$$R_{i,j}(\varepsilon) = \Theta(\varepsilon - \|\vec{\hat{x}}(t_i) - \vec{\hat{x}}(t_j)\|) \qquad i, j = 1, \ldots, N, \tag{2}$$

where Θ is the Heaviside step function and $\|\cdot\|$ is a norm, e.g. the Euclidean. RPs can be interpreted as a generalized form of autocorrelation. The main diagonal line represents the identity. Diagonal lines in general indicate deterministic behavior, regular patterns of parallel lines reveal a periodicity. Isolated points are typical for chaotic systems, whereas a rectangular patch results from an accumulation of subsequent states in a limited region of phase space during laminar sections of a process.

For cross-recurrences of two time series x_n and y_n, embedded in the same phase space, (2) is modified for cross-recurrence plots (CRP) in an analog way [34,48,50]:

$$CR_{i,j}(\varepsilon) = \Theta(\varepsilon - \|\vec{\hat{x}}(t_i) - \vec{\hat{y}}(t_j)\|). \tag{3}$$

Thus, it is possible to study interrelations between the two signals, e.g. synchronization, time shift or distortion. Unlike RPs, CRPs are usually not symmetric and therefore bowed lines may appear. Examples of RPs and CRPs applied to ECG, respiratory effort and heart rate samples are shown in Fig. 1. Their creation and interpretation will be discussed in the upcoming sections.

In order to quantify the two dimensional plots for computerized analysis of complex dynamic systems, Zbilut and Webber offered in the 1990s a few features, that measure the percentage of recurring states *REC* and the amount of diagonal lines: *DET* describes the degree of determinism and *ENT* is the Shannon entropy concerning deterministic sections [47,49]. Additionally, Marwan et al. demonstrated in 2002, that the information contained in vertical structures (laminarity *LAM*, trapping time *TT* and maximum length V_{max}) is useful to detect chaos-chaos transitions. These RQA features were successfully applied to heart-rate variability data to predict life-threatening cardiac arrhythmia [35]. Besides, recurrence times and their entropy describe the periodicity [14,27]. In recent years, features from graph theory were added, which quantify the density of recurring states in phase space [3,10,33].

The Cross Recurrence Plot Toolbox for MATLAB® [32], which is used in this work, provides a way to compute windowed RQA. Especially for long data sets containing several hundreds of thousands data points and to achieve an acceptable resolution it is necessary to analyze small sub-RPs stepping through the signal. A total of thirteen different RQA features is computed. They are *REC*, *DET*, *ENT*, *L*, L_{max}, *LAM*, *TT*, $T(1)$, $T(2)$, V_{max}, T_{rec}, *clust* and *trans*. Detailed descriptions and feature interpretations are specified in the following Section 2.2.

On the one hand, particularly for physiological systems of complex dynamics an important advantage of RQA is that no assumptions on the time series are required, like linearity in Fourier transforms [50]. On the other hand, it is challenging to find optimum embedding parameters, because no strict rules exist. For an adequate embedding dimension to reconstruct the original