Automatic Sleep Arousal Detection using State Distance Analysis in Phase Space

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Abstract

Defective sleep arousal can contribute to significant sleep-related injuries and affect the quality of life. Investigating the arousal process is a challenging task as most of such events may be associated with subtle electrophysiological indications. Thus, developing an accurate model is an essential step toward the diagnosis and assessment of arousals.

Here we introduce a novel approach for automatic arousal detection inspired by the states' recurrences in nonlinear dynamics. We first show how the states distance matrices of a complex system can be reconstructed to decrease the effect of false neighbors. Then, we use a convolutional neural network for probing the correlated structures inside the distance matrices with the arousal occurrences.

Contrary to earlier studies in the literature, the proposed approach focuses on the dynamic behavior of polysomnography recordings rather than frequency analysis. The proposed approach is evaluated on the training dataset in a 3-fold cross-validation scheme and achieved an average of 19.20% and 78.57% for the area under the precision-recall (AUPRC) and area under the ROC curves, respectively. The overall AUPRC on the unseen test dataset is 19%.

1. Introduction

Sleep arousals include a wide spectrum of clinical features ranging from the elevation of blood pressure to nocturnal awakenings. The indications of sleep arousals can be considered as an unconscious reflex to respiratory and non-respiratory stimuli such as ventilator obstruction or periodic limb movement. Thus, accurate detection of such events can lead to revealing the underlying causes and consequently to improve the treatment outcome. While EEG arousals are simply defined as an abrupt shift of EEG frequency [1], various kinds of sleep-interfering processes and class imbalance problem impede robust and reliable automatic arousal detection. The most common methods in the literature on automatic arousal detection are frequency analysis of polysomnography (PSG) signals. Analyzing EEG frequency bands [2], the coherence of different frequency bands between EEG and ECG signals [3], and periodogram of EEG, EMG, and airflow pressure [4] can be named as examples of such methods.

Inspired by the recurrence quantification analysis (RQA) [5], in this work we proposed a method to reconstruct the states distances for PSG signals to characterize the dynamical behavior of such rare arousal events. Although analysis of the states' distances of a dynamical system is well known in deterministic chaos process, we use it here as a tool to investigate the correlation between the sleep arousals and the phase transitions of PSG signals.

It has been shown that the distance between the states of a nonlinear dynamical system can reveal the fundamental features of the system dynamic [5]. Due to the complex patterns of such distance matrices, quantifying them for discerning a distinct regime using hand-engineered features is a challenging task. Therefore, in this work, we use a convolutional neural network (CNN) architecture to learn such critical and complex patterns more effectively.

Although few studies have been used deep learning to study the patterns of states distances [6] [7], to the best of our knowledge, this is the first time that this approach is used for sleep arousal analysis. The main contributions of this paper are as follows: 1) proposing a novel approach for reconstructing the state distance matrix with low embedding dimension while reducing the effect of false neighbors (Section 2.1), 2) analyzing states distance matrices using CNN for discovering the underlying sleep dynamics for arousal detection (Section 2.2).

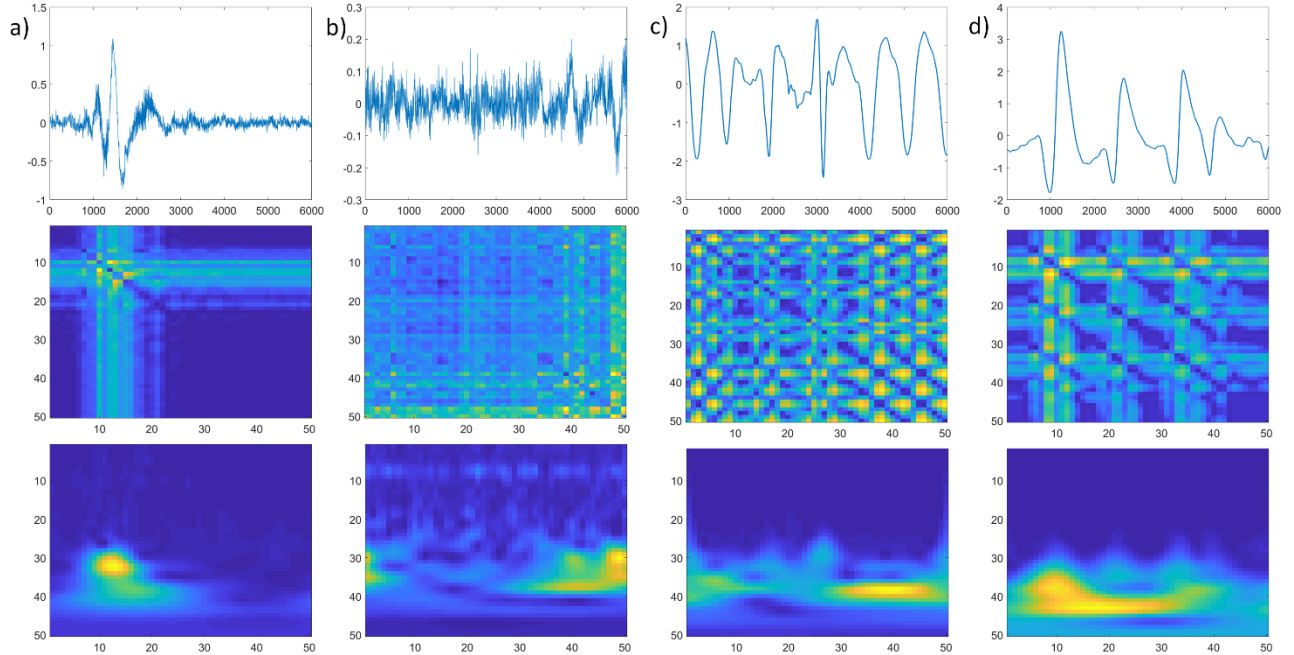[*] The first two authors have contributed equally to this study.

Figure 1. The 30s EEG and EMG time series (upper row), ε-distance matrices (middle row) and CWTs (lower row). Columns a) and b) represent the EEGs during arousal and non-arousal events, respectively. Columns c) and d) represent the abdominal EMGs during arousal and non-arousal events, respectively. The time series are shown in samples (sampling frequency is 200 Hz).

2. Materials and methods

For this challenge, 13 various PSG signals (including 6 EEG, 1 EOG, 3 EMG, 1 airflow, 1 SaO2, and 1 ECG signals) of 994 patients (in the training set) with the sampling frequency of 200 Hz are provided by Physionet/Computing in Cardiology Challenge 2018. The objective of this challenge is to detect the probability of arousal events. More information can be found in [8].

2.1. States distances in phase space

Phase space reconstruction [9] and RQA are powerful techniques to represent the non-stationarity in time series and have been used in various disciplines [10] [11] [12]. A point (i.e., a state vector) in the reconstructed phase space of the time series $x(n)$, $n = 1, 2, …, N$, is defined as:

$$X_i = [x(i), x(i + \tau), x(i + 2\tau), …, x(i + (m - 1)\tau)]^T \qquad (1)$$

where τ and m are the time lag and the embedding dimension, respectively, and $i = 1, 2, …, N - (m - 1)\tau$. The global recurrences of states (i.e. distance matrix) in phase space are then defined as the pairwise distances between pairs of state vectors, $D_{i,j} = \|X_i - X_j\|$. The main advantage of the distance matrix D is that, independent from the embedding dimension m (even for $m \geq 3$), it always provides a two-dimensional representation, which makes it an applicable option for visualization purposes.

Often instead of the distance matrix D, the recurrence plot (RP) is used. In the classical RP, the elements of the recurrence matrix R are defined as 0 when the pairwise distances in D are smaller than a threshold, and 1 otherwise (binarization):

$$R_{i,j} = H(\varepsilon - \|X_i - X_j\|) \qquad (2)$$

where $H(\cdot)$ is the Heaviside step function and ε is the pre-determined distance threshold. However, this approach is correct only if the time series is embedded in a minimal sufficient dimension [13]. This means that when a proper dimension is used the topological structure of the reconstructed attractor is similar to the original phase space. If this condition is not met, then a state might be projected into a neighborhood, which it is not located in the original phase space (false neighbor). Therefore, for a valid representation of the states' recurrences, the embedding dimension should be chosen by caution. In addition, the binarization process loses a large amount of information, which could be crucial for accurate processing of dynamical systems.

Due to the aforementioned limitations of the RP, in this study, we use the pairwise distances with some modification. Moreover, due to the high computational complexity, we choose $m = 2$. However, as discussed earlier such low embedding dimension makes the phase space reconstruction to be prone to the false nearest neighbor effect. Thus, we apply a threshold, to consider the small distance values to be zero so we can capture only the main structure in the distance matrix. To do so, $E_{i,j}$ element of ε-distance matrix E is defined as follows:

Table 1. The proposed CNN architecture. K, F, P, S denote the Kernel size, number of Kernels (filters), size of Pool, and Stride, respectively.

Layer	Parameters
Convolution	K 5×5, F16
MaxPooling	P 2×2, S 2×2
Convolution	K 5×5, F32
MaxPooling	P 2×2, S 2×2
Convolution	K 5×5, F64
Convolution	K 5×5, F128
FullyConnected	Neuron 100
FullyConnected	Neuron 100
Softmax	-

$$E_{i,j} = \left(1 - R_{i,j}\right) \cdot \left\| X_i - X_j \right\| \tag{3}$$

where the distance threshold ε is implicitly absorbed into this equation by $R_{i,j}$ defined in Eq. (2). It is worth pointing out that ε-distance matrix E has opposite and richer information than the recurrence matrix R in the sense that when the pairwise distance values are small the corresponding numbers in E are 0, and when they are larger than the threshold ε, the distance values are used directly. In Figure 1, four examples of ε-distance matrices of arousal and non-arousal events are illustrated for EEG and EMG signals.

2.2.   Analysis of ε-distance matrices using CNN

The properties of distance matrices are hard to grasp. The conventional solution to quantify the patterns of states distances is extracting common features in this domain, such as recurrence rate, determinism, entropy, and laminarity [14]. In this work instead of using hand-engineered features, we used CNN to automatically learn the small-scale structure in the ε-distance matrices.

The proposed CNN architecture is shown in Table 1, in which four convolution layers are followed by two fully connected layers. The extracted ε-distance matrices (as discussed in Section 2.1) are fed into the CNN as input. In each convolution layer, the constant kernel size 5×5 and the rectified linear unit (ReLU) activation function are used.

The stochastic gradient descent with momentum algorithm [15] is used to train the CNN with 256 mini-batch size, 0.2 dropout ratio, and 0.01 learning rate. These hyper-parameters are tuned empirically. In addition, due to the high imbalances between the arousal (the rare class) and non-arousal events, we balanced the data by bootstrapping (i.e., random sampling with replacement of arousal class).

3.   Results and discussion

In this work, only the three channels of C3-M2 (EEG),

Table 2. The proposed classification results (using the ε-distance and CWT methods) on the training set in 3-fold cross-validation. $AUPRC_G$ and $AUROC_G$ are the area under the precision-recall and the area under the ROC curves, respectively.

	Different CNN Inputs			
Folds	ε-distance matrices		CWT	
	$AUPRC_G$	$AUROC_G$	$AUPRC_G$	$AUROC_G$
1	18.98	78.65	6.75	50.03
2	18.72	78.93	6.99	50.04
3	19.91	78.14	7.41	50.03
Average (std)	19.20 (0.62)	78.57 (0.40)	7.05 (0.33)	50.03 (0.0058)
Test Dataset	19	-	-	-

ABD (electromyography of abdominal movement), and SaO2 (oxygen saturation) are used. Each time series is windowed into 30 seconds with 25 seconds overlap to investigate the temporal evolution of the underlying dynamic. Then, the ε-distance matrix of each time frame is reconstructed using $m = 2$ and $\tau = 37$ samples which is 185 ms (as addressed in Section 2.1). Then it is normalized and resized into 50×50 matrix. Therefore, the input size of the CNN is 50×50×3. Moreover, the threshold ε is set to the standard deviation of each time frame.

We use 3-fold cross-validation on the training data to evaluate the performance of the proposed method. In addition, for comparative evaluation of the ε-distance matrix representation of the PSG data, the results are compared with continuous wavelet transform (CWT). The results are reported in Table 2 (for more information about the scoring system refer to [8]). As can be seen in Table 2, the ε-distance matrix representation achieves significantly higher performance compared to the CWT method using the same CNN architecture. As a consequence, the ε-distance is chosen for final submission, which achieved 19% $AUPRC$ on the unseen test dataset.

In order to have a fair comparison between the performance of the ε-distance and CWT methods, we use another CNN architecture, which is specifically designed for CWT application. The second CNN architecture is presented in Table 3. The performance of the CWT and ε-distance methods using the second CNN architecture are shown in Table 4. Although the architecture of this CNN is manually optimized for CWT application, the ε-distance approach still has superior performance.

Table 3. The second CNN architecture.

Layer	Parameters
Convolution	K 9×9, F16
MaxPooling	P 2×2, S 2×2
Convolution	K 7×7, F32
MaxPooling	P 2×2, S 2×2
Convolution	K 5×5, F64
FullyConnected	Neuron 500
FullyConnected	Neuron 500
Softmax	-

Table 4. The achieved performance using the second CNN architecture

Folds	Different CNN Inputs			
	ε-distance matrices		CWT	
	$AUPRC_G$	$AUROC_G$	$AUPRC_G$	$AUROC_G$
1	18.52	79.23	16.86	78.77
2	18.40	78.41	16.92	78.18
3	19.33	77.90	17.20	78.06
Average (std)	**18.75 (0.50)**	**78.51 (0.67)**	**16.99 (0.18)**	**78.34 (0.38)**

This suggests not only ε-distance method has better performance than CWT for both architectures, but also it has less sensitivity to the architecture of the CNN such as filter size and the number of convolutional layers.

All the experiments are implemented in Matlab R2017a version. This is in accordance with the challenge organizers' strategy, which consequently prevents us from taking advantage of the recent developments in Matlab R2018a and R2017b versions such as access to various advanced CNN architectures, availability of more pre-trained models, and possibility to use more than 3 input channels. In the future, for further improvement in performance, different channel combinations and pre-trained models will be explored.

4.   Conclusions

In this study, we propose an approach for sleep arousal detection using state distance analysis in phase space representation of PSG signals. We have investigated and compared the proposed approach with the continuous wavelet transform as an alternative two-dimensional representation of 1D signals. Moreover, we developed and evaluated two deep CNN architectures.

The comparative evaluation results demonstrate the applicability and effectiveness of the proposed method for PSG signals. In addition, we conclude that using CNN for learning small-scale structures in distance matrices can provide versatile approaches and methods to analyze the nonlinear dynamics of time series effectively.

In the future, the training process will be extended by adding different PSG signals and using more advanced CNN architectures, both of which promise potential for significant performance improvements.

References

[1]   R. Berry , R. Brooks, C. Gamaldo , et al., "for the American Academy of Sleep Medicine. Darien, IL: American Academy of Sleep Medicine; 2014. AASM manual for the scoring of sleep and associated events: rules, terminology and technical specifications," 2014.

[2]   G. Matsuoka, T. Sugi, F. Kawana, M. Nakamura, "Automatic detection of apnea and EEG arousals for sleep apnea syndrome," in *ICROS-SICE International Joint Conference*, Fukuoka, Japan, 2009.

[3]   A. H. Khandoker, C. K. Karmakar, M. Palaniswami, "Interaction between sleep EEG and ECG signals during and after obstructive sleep apnea events with or without arousals," in *Computers in Cardiology*, Bologna, Italy, 2008.

[4]   T. Sugi, F. Kawana, M. Nakamura, "Automatic EEG arousal detection for sleep apnea syndrome," *Biomedical Signal Processing and Control,* vol. 4, no. 4, pp. 329-337, 2009.

[5]   J.-P. Eckmann, S. Oliffson Kamphorst, D. Ruelle, "Recurrence Plots of Dynamical Systems," *Europhysics Letters,* vol. 4, no. 9, pp. 973-977, 1987.

[6]   E. Garcia-Ceja, M. Zia Uddin, J. Torresen, "Classification of Recurrence Plots' Distance Matrices with a Convolutional Neural Network for Activity Recognition," in *The 9th International Conference on Ambient Systems, Networks and Technologies*, Porto, Portugal, 2018.

[7]   N. Hatami, Y. Gavet, J. Debayle, "Classification of Time-Series Images Using Deep Convolutional Neural Networks," *arXiv:1710.00886v2[cs.CV],* 2017.

[8]   M. Ghassemi, B. Moody, L. Lehman, C. Song, Q. Li, H. Sun, R. Mark, M. Westover, G. Clifford, "You Snooze, You Win: the PhysioNet/Computing in Cardiology Challenge 2018," in *Computing in Cardiology*, Maastricht, Netherlands, 2018.

[9]   F. Takens, "Detecting strange attractors in turbulence," *Lecture Notes in Mathematics,* vol. 898, pp. 366-381, 1981.

[10]   A. Fabretti, M. Ausloos, "Recurrence Plot and Recurrence Quantification Analysis Techniques for Detecting a Crittical Regime," *International Journal of Modern Physics C,* vol. 16, no. 5, pp. 671-706, 2005.

[11]   U. R. Acharya, S. Bhat, O. Faust, H. Adeli, E. C.-P Chua, W.J.E. Lim, J.E.W. Koha, "Nonlinear Dynamics Measures for Automated EEG-Based Sleep Stage Detection," *European Nourology,* vol. 74, no. 6, 2015.

[12]   L. Wang, P. Kim, D. McCarty, C. Frilot, A. Chesson, S. Carrubba, A. Marino, "EEG recurrence markers and sleep quality," *Journal of the Neurological Sciences,* vol. 331, no. 1, pp. 26-30, 2013.

[13]   M. B. Kennel, R. Brown, H. D. I. Abarbanel, "Determining embedding dimension for phase-space reconstruction using a geometrical construction," *Physical Review A,* vol. 45, no. 6, p. 3403–3411, 1992.

[14]   N. Marwan, J. Kurths, "Nonlinear analysis of bivariate data with cross recurrence plots," *Physics Letters A,* vol. 302, no. 5, pp. 299-307, 2002.

[15]   C. M. Bishop, Pattern Recognition and Machine Learning, New York, NY: Springer, 2006.

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