Towards Model-Independent Mode Detection and Characterisation of Very Long Biomedical Time Series

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Abstract: A novel technique, the Delay Vector Variance method, which provides model-independent characterisation of time series in terms of their predictability is introduced and applied in a biomedical context. The merits of the procedure are demonstrated in a mode segmentation context on a set of long nonstationary physiological signals, obtained from subjects undergoing different sleep and wake stages. It is shown that the features extracted remain consistent within and across subjects. Next, the presence of nonlinearity associated with the different modes is investigated. A comparison with other measures supports the obtained results, namely that the signals show a higher degree of nonlinearity during wake than during sleep stages.

Keywords: time series characterisation, mode detection, nonlinearity

Introduction

The recent progress in mathematical modelling and the increasing availability of computational resources have initiated the resolution of problems of high complexity, involving high degrees of nonlinearity and nonstationarity. Too often, overly complex models are used to address these problems, resulting in weak generalisation ability and poor training performance. For this reason, the assessment of the signal's multimodality and the nature of these modes in terms of required model order and model nonlinearity, should precede the development of data processing or prediction systems [4].

The method proposed here draws upon the 'Delay Vector Variance' (DVV) method [2]. It characterises the signal in terms of its predictability, and achieves this in a model-independent manner which is closely related to the dynamical structure of the signal. The method is computationally and conceptually appealing. Its simplicity enables an incremental calculation, allowing for on-line signal processing applications.

The application discussed in this paper is concerned with the analysis of non-stationary physiological signals recorded from subjects undergoing different sleep stages. Currently, the most successful approaches towards this problem employ Hidden Markov Models [1, 3]. Since the sleeping patterns (i.e., the transitions from one stage to another) are very similar across subjects, these approaches can achieve good results without the need to directly grasp the dynamics of the signal modes. The proposed DVV method on the other hand, is strictly data-driven and yields excellent results, without exploiting temporal information such as state transition probabilities. This is a strong indication that the features extracted are closely related to the underlying dynamics of the system.

Biomedical Time Series Used

To illustrate the method, a set of biomedical signals obtained from subjects during different wake and sleep stages is used. The set contains recordings of three successive naps for five different subjects. For each nap a manual labelling assigned by a medical expert is available. The labels segment the data into different wake and sleep classes. These data sets are publicly available[1] and have been used before in the context of mode segmentation [3]. The analyses are limited to the respiration (RES) and electro-encephalogram (EEG) signals of the first two subjects.

The Delay Vector Variance Method

A time series is first transformed into a set of delay vectors (DVs) of a given embedding dimension m, $\mathbf{x}(k) = [x_{k-m1}, \ldots, x_{k-1}]$. The next sample, x_k, is referred to as the target of the DV. The proposed DVV method examines the mean target variance of all sets Ω_k, generated by grouping the DVs that are within a certain distance to $\mathbf{x}(k)$. To make the results comparable over different embedding dimensions as well as across different dynamical ranges of the time series, the distance threshold is varied in a standardized manner. For a given embedding dimension, the proposed 'Delay Vector Variance' method can be summarised as follows [2]:

- The mean, μ_d, and standard deviation, σ_d, are computed over a discrete set of all pairwise distances between DVs, $\|\mathbf{x}(i) - \mathbf{x}(j)\|$ $(i \neq j)$;
- The sets Ω_k are generated such that $\Omega_k = \{\mathbf{x}(i) \mid \|\mathbf{x}(k) - \mathbf{x}(i)\| \leq d\}$, i.e., sets which consist of all DVs that are within a certain uniformly spaced distance d from $\mathbf{x}(k)$, taken from the interval $[\mu_d - n_d\sigma_d ; \mu_d + n_d\sigma_d]$, where n_d is a parameter controlling the span over which to perform the DVV analysis;

[1] http://www.first.gmd.de/persons/Kohlmorgen.Jens/publications.html

- For every[2] set Ω_k, the variance of the corresponding targets, σ_k^2, is computed[3]. The average over all sets Ω_k, normalised by the variance of the time series, σ_x^2, yields the measure of unpredictability, σ^{*2}:

$$\sigma^{*2} = \frac{\frac{1}{N}\sum_{k=1}^{N}\sigma_k^2}{\sigma_x^2} \tag{1}$$

An example of a typical 'DVV plot' is shown in Figure 1. Small target variances for small spans (left hand side of Figure 1) are an indication of a strong deterministic component (high predictability). For large spans, the curve smoothly converges to unity, since all DVs belong to the same universal set and therefore the variance of the corresponding targets will be equal to the variance of the time series.

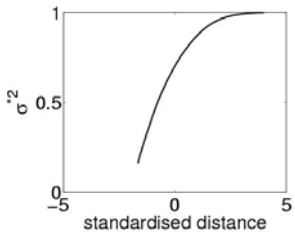

Fig. 1. Example DVV plot

To cope with nonstationarity, DVVs are calculated on short, overlapping windows that are slided over the signal one sample at a time.

Mode Segmentation

The goal of the proposed mode segmentation procedure is to identify the sleep stages, labelled by a medical expert. In the following, the analysis is limited to the three respiration signals of patients 1 and 2. Since these signals are very noisy and contain many outliers, a pre-processing step is first performed. Categories labelled as artifacts are removed and DVVs are calculated in such a way that the windows contain only a single mode. Next, the on-line version of the algorithm is used to extract DVV plots from the resulting signals[4]. Since the extracted features are high-dimensional and still contain redundancy, a dimensionality reduction using the Principal Component Analysis (PCA) is applied before proceeding to the segmentation.

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[2] To improve robustness, only sets containing at least 30 DVs are taken into consideration.

[3] The reasoning is that, for a stationary signal, similar DVs should have similar targets.

[4] A window length of 400 samples, embedding dimension 4 and a span of 3 standard deviations were used in the DVV analyses.

Table 1. Classification accuracies obtained while testing within-subject generalisation

signal		accuracy (%)	
train	test	subject 1	subject 2
1	2	86	82
1	3	93	69
2	1	76	68
2	3	87	74
3	1	79	70
3	2	92	87
mean		86	75

Using a standard multi-layer perceptron[5], the data is segmented from the extracted features into a wake and a sleep mode. A first set of analyses examines the subject-dependent generalization performance of the network. One signal of a particular subject is used to train the network that is subsequently used to segment a signal, recorded during a different nap of the same subject. To prevent the network from overfitting the data, cross-validation (early stopping) is used. Table 1 contains the classification accuracies for the three signals of both subjects. The high accuracies clearly indicate that DVV extracts features that remain consistent over different sleeps of the same subject. A subsequent analysis investigates whether these features remain consistent over different subjects as well by using all DVV plots from one subject to classify the DVV plots of the other subject. This procedure results in classification accuracies of 64 % when training on subject 1 and testing on subject 2, and 74 % when training on subject 2 and testing on subject 1. Such a high accuracy is remarkable given the fact that medical experts need different signals (EEG, EOG, etc.) to correctly identify sleep stages. In the following, the DVV method is used to further examine the nature of the signals during sleep and wake stages.

Nonlinearity Analysis

To help clarify the differences observed during sleep and wake stages, the proposed characterisation method is applied to investigate the degree of nonlinearity present in the signals. Although the different procedures explained in this section consistently indicated strong nonlinearity in the respiration signals during both wake and sleep stages, no significant differences were found between the stages. For this reason, the analyses in the remainder of this section focus on the EEG signals only. For subject 1, three EEG signals are available. In order not to introduce any artifacts or spurious correlations, the windows belong strictly to one class and do not overlap. This results in a data set containing 133 and 166 signal windows belonging to respectively the sleep and wake class.

[5] In all simulations, a network containing one hidden layer (consisting of 2 neurons) and initialised with different random seeds was used.

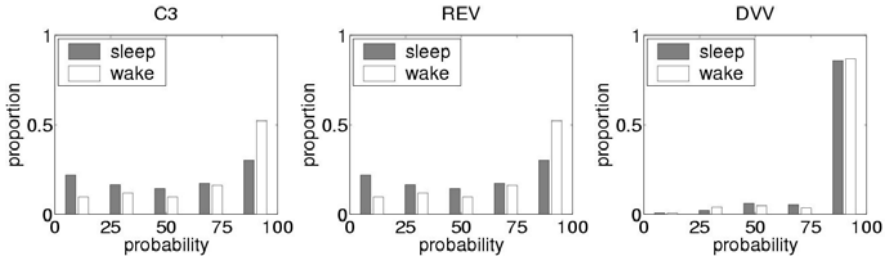

Fig. 2. Histograms of the rankings obtained with C3, REV and DVV on the sets of wake and sleep signals. All rank indices have been translated into probabilities

It is plausible to assume that a higher cognitive awareness and the larger number of processes that exert an influence on the signal during awakeness manifests itself in a higher degree of signal nonlinearity during wake than during sleep stages. This hypothesis is investigated using DVV and validated with two well-known measures of nonlinearity: the third-order autocovariance (C3) and the asymmetry due to time reversal (REV) [7]. All three measures provide a characterisation of the time series. By comparing these measures to those calculated on linearised versions, 'surrogates', of the original signals, an assessment of the degree of nonlinearity can be made [6]. A rank test is used to establish whether or not the null hypothesis of linearity can be rejected. Unlike C3 and REV, DVV provides a range of values. Single measures are obtained by computing the distances, for all surrogates and the original signal, between their respective DVV plot and an average DVV plot (averaged over all surrogates). Figure 2 contains the binned rank indices for all windows and for all three measures[6]. The larger amount of rejections on wake signals as compared to sleep signals in C3 and REV, is already a strong indication that the signals contain a higher degree of nonlinearity during wake stages. Using the DVV analysis, nearly all windows reject the null hypothesis of linearity. This result is in line with previous nonlinearity analyses, performed on EEG signals [5].

To obtain more quantitative results, a statistical test is performed on the measures themselves. The measures calculated on the original signal provide a direct indication of nonlinearity. To allow for inter-signal comparisons, these measures are first normalised by the spread of the values obtained on the surrogates. Next, a non-parametric statistical test, the Wilcoxon rank sum test, is used to investigate the null hypothesis of identical distributions. The following p-values are obtained: $4.5 \cdot 10^{-6}$ for C3, 0.025 for REV and 0.0058 for DVV. All three measures thus consistently reject the null hypothesis at the 0.05 level of significance. For this subject, the working hypothesis that the EEG signals exhibit higher nonlinearity during wake than sleep is validated.

[6] The rankings of the two-sided tests (C3 and REV) have been rearranged so that the rightmost bin represents the rejection of the null hypothesis.

Conclusions

It has been demonstrated that the proposed method for time series characterisation, the 'Delay Vector Variance' method, is able to extract features, related to the predictability of the respiration signals, that allow for a subject-independent segmentation into wake and sleep stages. In a subsequent study, these features were used to examine the difference in degree of nonlinearity of EEG signals. The results obtained (higher degree of nonlinearity during wake as opposed to sleep) are in line with those obtained using established nonlinearity measures.

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