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Comparison of Transfer Entropy Methods for the Study of Physiological Interactions

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Abstract: Transfer entropy (TE) is an approach frequently used to identify and quantify interactions between physiological systems. Different methods exist to numerically estimate TE, but there is no consensus about which one performs best in a specific application. In this study, five methods (linear, k-nearest neighbors, fixed-binning with ranking, kernel density estimation and adaptive partitioning) were assessed and compared. The comparison was made on three simulation models with different dynamics (linear, non-linear and linear + non-linear). The results from the simulations showed that the best method to quantify the different interactions was adaptive partitioning. This method was then applied to clinical data from a polysomnography (PSG) study to test the hypothesis that stronger non-linear cardio-respiratory interactions are present in deep sleep. Surrogate analysis was used to assess the significance of the interactions found for the PSG data. It was found that non-linear interactions were consistently higher for deep sleep at different time lags. It could be concluded that with an appropriate estimation method, combined with surrogate analysis, TE can be used to study the presence of linear and non-linear cardio-respiratory interactions during sleep.

Keywords: transfer entropy; surrogate data; cardio-respiratory interactions; polysomnography

1. Introduction

Physiological signals are observations of complex processes resulting from the combination of their internal dynamics, their interactions with other processes and third party effects, such as the influence of medication and treatments. These interactions might occur in a linear and/or a non-linear fashion. The development of methods to evaluate and quantify these interactions is currently an active research topic.

Several methods to identify the interactions between complex processes have been developed across different fields, and many of them have been adapted to the study of physiological data [1–10]. One of these approaches, widely used for the detection of information flow between processes, is Transfer Entropy (TE). TE is able to identify linear and non-linear interactions, depending on its implementation. It is also able to identify the directionality of the interactions [11]. TE relies on the past observations of the processes, and can be considered as a parametric or a non-parametric approach according to the assumptions made for its computation. For its numerical estimation, two factors

need to be considered. First, an embedding technique to generate vectors describing the past of the processes and, second, an entropy estimator [11–14]. There are several entropy estimators differing in assumptions, advantages and limitations, with no consensus about which one performs best [15]. For this reason, the selection of the best method to estimate TE for each specific application is still an open problem.

A first aim of this study is to compare five of the most commonly used methods for TE computation, in order to provide a framework to support the selection of the best approach to be applied in short physiological signals to identify and quantify linear and non-linear interactions. Each method uses a different entropy estimator (linear [12,16,17], k-nearest neighbors estimator [12,18], fixed-binning with ranking [13,15], kernel density estimator [13,19,20], and adaptive partitioning [13,15]). In all the implementations, an uniform embedding technique is chosen to generate the embedding vectors [11,14].

Each method is hypothesized to perform differently according to the tuning of their parameters and the characteristics of the interactions between the processes in which they are applied [21]. Considering this, three simulation models are proposed: linear [16], non-linear [13], and linear + non-linear [22]. Two analyses were conducted for each of these simulations. The goal of the first analysis was to find the best set of parameters for each method and to observe their potential to identify the correct lag at which the interactions occur. The second analysis studied the behavior of the methods when modifying the strength of the interactions between the processes. The performance was evaluated in the simulations using Transfer Entropy Excess (TEE), a new metric proposed in this study.

A second goal of this study is to use the proposed framework to select the best method and apply it on clinical data. Specifically, on polysomnography (PSG) recordings, to test the hypothesis that the linear and non-linear components of the cardio-respiratory interactions during light (NREM1) and deep (NREM3) sleep change with the sleep stage.

Previous studies have shown that the linear and non-linear dynamics in both cardiac and respiratory signals change with the sleep-wake cycle and between sleep stages [6,7,15,16], and that these changes affect both signals similarly [23–25]. This fact raised some questions regarding how these changes affect the cardio-respiratory interactions during sleep, which led to the identification of three forms of coupling, namely, respiratory sinus arrhythmia (RSA), cardio-respiratory phase synchronization (CRPS), and time delay stability (TDS) [6]. In this study, TE was used to identify and quantify the cardio-respiratory interactions during sleep stages, using the best method for its computation found with the simulation models.

To the best of the knowledge of the authors, no study exists that compares all five methods presented here for the computation of TE. Also, the way this study quantifies and identifies linear and non-linear interactions during light and deep sleep has not been found elsewhere in the literature. The results of this study could serve as a base for the selection of suitable TE methods for the analysis of linear and non-linear interaction in physiological systems.

This paper is divided as follows: Section 2 introduces the used methods and datasets. Section 3 shows the results for the TE computation on the simulation models and the clinical data. Section 4 discusses the results. Finally, Section 5 concludes this work.

2. Materials and Methods

This section describes the theory behind Transfer Entropy (TE) and the factors to be considered for its computation. Following these descriptions, the simulation models and the clinical data are explained.

2.1. Transfer Entropy

Consider the stochastic process $Y = \{y_1, y_2, y_3, ..., y_N\}$, with N the total number of observations of the process. The Shannon Entropy can be defined as the average information content of the process [11]. This can be computed as,

$$H(Y) = -\sum_{y \in Y} p(y) log(p(y)), \tag{1}$$

where $p(y)$ is the probability density function (PDF) of the observation y. The base of the logarithm determines the units of H. When using the natural logarithm (log), H is measured in *nats*.

Now, consider a second stochastic process $X = \{x_1, x_2, x_3, ..., x_N\}$, which has a joint probability distribution with Y. The joint information provided by both processes is described by the Joint Entropy, as

$$H(X, Y) = -\sum_{y \in Y} \sum_{x \in X} p(x, y) log(p(x, y)), \tag{2}$$

where $p(x, y)$ is the joint PDF of the observations x and y.

The remaining uncertainty for the observations of Y given the information of X is described by the Conditional Entropy as,

$$H(Y|X) = -\sum_{y \in Y} \sum_{x \in X} p(y) p(y|x) log(p(y|x)), \tag{3}$$

where $p(y|x)$ is the conditional PDF of the observation y given the observation x.

Transfer Entropy (TE) estimates the reduction of uncertainty of the observations of Y (target process), accounted by both the past observations of X (driver process) and the past observations of Y, compared to the reduction of uncertainty of the observations of Y accounted only by its past [26]. TE can be defined in terms of joint or conditional entropies as

$$TE_{(X \rightarrow Y)} = H(Y, Y^-) - H(Y^-) - H(Y, X^-, Y^-) + H(X^-, Y^-), \tag{4}$$

$$TE_{(X \rightarrow Y)} = H(Y|Y^-) - H(Y|X^-, Y^-), \tag{5}$$

where $H(Y, Y^-)$ is the joint entropy of Y and its past, $H(Y, X^-, Y^-)$ is the joint entropy of Y and the past of both processes, and $H(X^-, Y^-)$ is the joint entropy of the past of both processes. $H(Y|Y^-)$ is the conditional entropy of Y given its own past, and $H(Y|X^-, Y^-)$ is the conditional entropy of Y given its own past and the past of X. Given this dependency on the past observations of both processes, TE is an asymmetric measure, which constitutes an advantage when quantifying the directionality of the information transfer from one system to the other [11,27].

Considering the definition of TE, two factors are relevant for its computation: the definition of the vectors describing the past observations, or so-called embedding vectors, of the processes; and the estimation of the entropies. Depending on the estimation of entropies, TE accounts for linear and/or non-linear interactions [14].

2.2. Definition of embedding vectors

From the observations of the driver and target processes, embedding vectors can be defined to describe their past to estimate the TE [11–14,28].

The selection of the elements of the embedding vectors is important, given that they should contain the most relevant past observations of the processes. Sub-optimal selection might be problematic. Too long embedding vectors will lead to redundancy as well as increased computational requirements, and too short vectors will lead to insufficient information. In order to tackle this challenge, several embedding techniques can be used. The uniform embedding (UE) is the most common technique used in the computation of TE, because of its simplicity. For this reason, in this study this technique in combination with different entropy estimators is used.

For UE, the embedding vectors are constructed as $X_t^m = \{X_{t-\tau}, X_{t-2\tau}, \ldots, X_{t-(m-1)\tau}, X_{t-m\tau}\}$ and $Y_t^n = \{Y_{t-\tau}, Y_{t-2\tau}, \ldots, Y_{t-(n-1)\tau}, Y_{t-n\tau}\}$, where τ is the time lag, and m and n are the embedding dimensions.

2.3. Estimation of entropies

The exact estimation of the PDF is an analytical way is an open research problem. However, there is a wide range of options to estimate the PDFs, depending on the application and the characteristics of the processes to analyze [11]. In this study, five entropy estimators that are implemented in the open source tools by Montalto et al. [12] and Lee et al. [13] were considered: linear (LIN); k-nearest neighbors (KNN); fixed-binning with ranking (FBR); kernel density estimation (KDE); and adaptive partitioning (DVP).

2.3.1. Linear estimator

The linear estimator (LIN) assumes that the processes X and Y have a joint Gaussian PDF. This assumption allows working with exact expressions already derived for the entropy measures [12,16]. The entropy of a Gaussian random process Y can be expressed as,

$$H(Y) = \frac{1}{2}\log\left(2\pi e\Sigma(Y)\right), \tag{6}$$

where $\Sigma(Y)$ is the covariance of Y, and e is the Euler's constant. Now, the conditional entropy of Y given X is defined as,

$$H(Y|X) = \frac{1}{2}\log\left(2\pi e\Sigma(Y|X)\right), \tag{7}$$

where $\Sigma(Y|X)$ is the partial covariance of Y given X, which corresponds to the variance of the residuals of a linear regression of Y on X. Considering this, the conditional entropy can be rewritten as

$$H(Y|X) = \frac{1}{2}\log\left(|\Sigma(\epsilon)|\right) + \frac{1}{2}N\log\left(2\pi e\right), \tag{8}$$

where ϵ are the residuals of the linear regression [17]. Finally, the TE is computed by implementing (8) in (5). More details about this approach can be found in [17].

2.3.2. K-nearest neighbors estimator

The k-nearest neighbors (KNN) estimator approximates the PDF by calculating a local probability mass in the neighborhood of each of the observations of the process Y. The probability mass is estimated by considering a sphere whose diameter is equal to twice the expected distance to the k-th nearest neighbor of each observation.

Following the procedure presented in [18], $H(X,Y)$ can be computed as

$$H(X,Y) = -\psi(k) + \psi(N_{X,Y}) + \log\left(c_{d_X}c_{d_Y}\right) + \frac{d_X + d_Y}{N_{X,Y}}\sum_{i=1}^{N_{X,Y}}\log\left(p(\zeta(i))\right), \tag{9}$$

where ψ is the digamma function, $N_{X,Y}$ is the number of observations in the joint space $[X,Y]$, d_X and d_Y are the dimensions of X and Y, c_{d_X} and c_{d_Y} are the volumes of the d-dimensional unit sphere, and $\zeta(i)$ is twice the distance from a point (x_i, y_i) to its k-th nearest neighbor. TE is computed applying (9) to estimate the entropies in (4). More details about this method are given in [18] and [12].

2.3.3. Fixed-binning with ranking estimator

The fixed-binning estimation is one of the approaches most widely used for PDF approximations due to its simplicity. This method performs a uniform quantization of the observations of the processes

in Q bins, after normalizing the values to zero mean and unit variance. With this, the approximation of the probabilities, p, is done based on the relative frequencies of occurrence of each quantized state,

$$p(g_i) = \frac{r_i}{N}, \tag{10}$$

where g_i is the event associated to a specific bin i (X, X^-, Y^- and their combinations) and r_i is the number of observations that lie in the bin i.

The fixed-binning method faces challenges related to robustness, convergence with high dimensionality, and the selection of the number of bins to be used when quantizing the time series. To improve the robustness of this method, some modifications have been proposed [13,15]. One of them consists of an ordinal sampling, also known as ranking. For the fixed-binning with ranking (FBR) estimator, the time series of the observations of X and Y are replaced by two new series U and V, respectively. The values in U and V are integers ranging from 1 to N, representing the rank of the corresponding observations of X and Y. After the ranking, the PDFs are estimated using (10) in the space defined by U and V. Using the same number of bins in each dimension for simplicity, $H(V|U)$ is computed as

$$H(V|U) = -\frac{1}{N}\sum_{i=1}^{Q}\sum_{j=1}^{Q} r_{i,j} \log \frac{r_{i,j}}{r_j}, \tag{11}$$

where i and j indicate the indices of the bins along V and U, respectively, and $r_{i,j}$ is the number of observations that lie in the intersection of the bins i and j. TE can be computed by combining (11) and (5). More details about this method can be found in [15] and [13].

2.3.4. Kernel density estimator

In the kernel density estimator (KDE), the PDF is estimated using a preselected distribution which is centered at each observation of the processes. All the distributions are summed to obtain an overall, smooth distribution for the processes [13,19]. The shape of the distribution is defined by a kernel, which in this study corresponds to the widely used Gaussian kernel. The magnitude of this kernel decreases as the distance from the center increases. Hence, one of its main parameters is its bandwidth.

The probability density for one observation x_t, using the KDE is estimated as

$$p(x_t) = \frac{1}{N}\sum_{i=1}^{N}\frac{1}{h}K\left(\frac{x_t - x_{t,i}}{h}\right), \tag{12}$$

where K is the kernel function with bandwidth h. The Gaussian kernel is defined as

$$K(u) = \frac{1}{\sqrt{2\pi}}e^{-0.5u^2}, \tag{13}$$

where $u = (\frac{x_t - x_{t,i}}{h})$, with the bandwidth of the kernel defined as

$$h = 1.06\alpha\hat{\sigma}N^{-\frac{1}{5}}, \tag{14}$$

where α is a scaling multiplier and $\hat{\sigma}$ is the sample standard deviation.

Now, in the case of a given point (x_t, y_t) in the joint space defined by the target and driver processes, the joint probability can be estimated as

$$p(x_t, y_t) = \frac{1}{N}\sum_{i=1}^{N}\frac{1}{h_{x_t}h_{y_t}}K\left(\frac{x_t - x_{t,i}}{h_{x_t}}\right)K\left(\frac{y_t - y_{t,i}}{h_{y_t}}\right). \tag{15}$$

Using (15) to compute $H(X,Y)$ with (2), TE can be calculated with (4). More information about this method can be found in [13] and [19].

2.3.5. Adaptive partitioning estimator

When working with binning methods for the estimation of PDF, the fact of having a fixed number of bins with a defined and equal width can lead to an overestimation of the PDF. One solution to this issue is to use a non-uniform partition of the space defined by the observations of the processes [15,19]. This solution is implemented with the Darbellay-Vajda (DV) algorithm, combined with ordinal sampling [13].

For the adaptive partitioning (DVP) estimator, the ordinal sampling is performed as described for the FBR, replacing the time series of the observations of X and Y by U and V, respectively. The DV algorithm recursively partitions the three-dimensional space defined by V, U^- and V^- into cubes of different size, in order to obtain an even distribution of the data across the partitions. At first, the three-dimensional space is partitioned into eight equal cubes, of which the boundaries are at the mid-points in the three dimensions. The null hypothesis of an even distribution of the data points across the eight cubes is tested using a χ^2 statistic,

$$s_{\chi^2} = \sum_{i=1}^{8} (M_i - \mu_M)^2, \tag{16}$$

where M_i corresponds to the number of points contained in each of the eight cubes and μ_M is the total number of data points divided by the total number of cubes. If s_{χ^2} is greater than the χ^2 statistic at a 5% significance level and 7 degrees of freedom, the null hypothesis is rejected and each of the eight cubes is further partitioned into eight smaller cubes. If the null hypothesis is not rejected, the current cubes are taken as one partition.

The result of the recursion process is a finite number of cubes, L, with nonzero data points. The approximation of the probabilities for the computation of the entropies is done by counting the number of data points that are greater than or equal to the lower bounds and less than the upper bounds of each cube in each dimension, following (10). $H(V|U)$ is estimated using (11) along all the cubes L. Finally, TE is computed using (5). More information on this method can be found in [13] and [15].

2.4. Experiments

The methods used in this study have open source implementations. Two methods were taken from the MuTE Toolbox [12], and three from the functions developed by Lee et al. available on PhysioNet [13].

Given the wide range of dynamics that are present in physiological systems, it is difficult to account for confounding effects. This makes the understanding and interpretation of their interactions more complex and the selection of a method for their study more difficult. Therefore, three simulation models were used to study the previously explained methods for the computation of TE. These simulation models vary in complexity, from a simple bivariate autoregresive (AR) linear model, to a bivariate model that includes linear and non-linear components in its interactions. For each simulation model, the performance of the methods was assessed using two analyses. For the first analysis (**A1**), the parameters of the methods to compute the TE were allowed to change. The effect of the selection of the lag (τ) for the generation of the embedding vectors was also assessed in this analysis. In the second analysis (**A2**), the strength of the interactions between the time series of each model was changed. An overview of the parameters of the methods that were changed in the analyses is presented in Table 1. The range in which the parameters change is based on the values used in previous studies [12,13,16,29,30].

2.4.1. Simulation models

For all simulation models described below, the variations of TE from the driver process X to the target process Y were analyzed. The TE from Y to X is expected to be equal to zero, since no influence of Y on X was imposed. **A1** and **A2** were performed on 50 trials of the models. Each trial corresponded

Table 1. Parameters of methods for TE computation.

Method	Parameter	Range of change	Source
LIN	regression model order	[1,2,3,4,5,6,7,8,9,10]	MuTE Toolbox [12]
KNN	number of neighbors (nn)	[5,10,15]	MuTE Toolbox
FBR	quantization levels (Q)	[4,6,8,10]	Physionet [13]
KDE	multiplier of kernel bandwidth (α)	[0.5,0.75,1,1.25,1.5]	Physionet
DVP	none		Physionet

to a new pair of signals X and Y, where the noise components are allowed to change. The length of the simulated signals was set to N = 200 samples. This length was selected so that it was comparable to the length of the clinical data, which ranges from 150 to 330 points.

Linear model

The first simulation model corresponds to a linear AR bivariate Gaussian process of order 2 based on the work presented by Faes et al. [16], and defined as

$$\begin{aligned} x_n &= -0.5x_{n-2} + \varepsilon_{x_n} \\ y_n &= -0.5y_{n-2} + ax_{n-1} + \varepsilon_{y_n}, \end{aligned} \tag{17}$$

where ε_{x_n} and ε_{y_n} are independent Gaussian white noise processes with zero mean and unit variance. The effect of X on Y is modulated by the parameter a.

For **A1**, the parameter a of the model is set to 0.5 and the time delay (τ) for the generation of the embedding vectors is changed between 1 and 5 (around the value at which the interaction takes place, $\tau = 1$). For **A2**, the parameter a is allowed to vary in the range from 0 to 0.5, while $\tau = 1$.

Non-linear model

The second simulation model is a bivariate process of order 2 that includes a non-linear interaction. It is based on the work presented by Lee et al. [13], and defined as

$$\begin{aligned} x_n &= s_{x_n} + \xi_{x_n} \\ y_n &= (b\, x_{n-2})^2 + \xi_{y_n} \\ \\ s_{x_n} &\sim \mathcal{N}(10,1) \\ \xi_{x_n} &\sim \mathcal{L}(0,1),\ \xi_{y_n} \sim \mathcal{L}(0,1), \end{aligned} \tag{18}$$

where ξ_{x_n} and ξ_{y_n} correspond to noise components drawn from a Laplace distribution, and b is the coupling factor.

The parameter b is fixed at 0.4, while τ changes between 1 and 5 (around the value at which the interaction takes place, $\tau = 2$), for **A1**. For **A2**, the parameter b is allowed to change between 0 and 0.5, maintaining $\tau = 2$.

Linear + non-linear model

The third simulation model is a bivariate system including a linear and a non-linear term in Y. This model is adapted from the simulation study presented by Khadem and Hossein-Zadeh [22], and is defined as

$$\begin{aligned} x_n &= 0.3x_{n-1} + \varepsilon_{x_n} \\ y_n &= 0.3y_{n-1} + cx_{n-2} + df(x_{n-4}) + \varepsilon_{y_n} \end{aligned} \tag{19}$$

$$f(x_{n-4}) = \frac{2.4 - 0.9(x_{n-4})}{1 + \exp(-4(x_{n-4}))},$$

where ε_{x_n} and ε_{y_n} are independent Gaussian white noise processes with zero mean and unit variance, the function $f(x_{n-4})$ represents the non-linear term, and the parameters c and d regulate the strength of the linear and non-linear dynamics, respectively. $\tau_l = 2$ and $\tau_{nl} = 4$ correspond to the lags at which the linear and non-linear interactions occur, respectively.

For **A1**, c and d were fixed at 0.4 and 0.6, respectively, while τ was changed from 1 to 5 (around the values at which the interactions take place, $\tau_l = 2$ and $\tau_{nl} = 4$). For **A2**, there were two set-ups for this model. The first one was for the linear interaction, having c varying between 0 and 0.6, while d was fixed at 0.4, and $\tau = 2$. The second one was for the non-linear interaction, for which c was fixed at 0.6, d changed from 0 to 0.6 and $\tau = 4$.

2.4.2. Evaluation metrics

For **A1**, the $TE_{X \to Y}$ was expected to reach a maximum when using the lag at which the interaction between the signals occurs, and zero otherwise [31,32].

In order to evaluate the results of the methods for **A1**, a new metric named Transfer Entropy Excess (TEE) is proposed. This metric calculates the ratio between the total sum of TE for all the lags studied and the TE at the lag at which the interaction occurs. It is defined as

$$TEE = \frac{\sum_{i=1}^{T} TE_{X \to Y}(\tau_i)}{TE_{X \to Y}(\tau_{interaction})}, \tag{20}$$

where T is the total number of lags used in the analysis, $TE_{X \to Y}(\tau_i)$ refers to the TE computed with the lag τ_i, and $\tau_{interaction}$ is the τ of the interaction imposed in each simulation model. TEE can vary between 1 and infinite. The closer TEE is to 1, the better the method identifies the lag of the interaction. Higher values of TEE indicate that for other lags, the TE is higher than zero.

In **A2**, an increment in $TE_{X \to Y}$ with stronger interactions between the signals was expected. To quantify the increment of TE as a function of the coupling parameter of the model, the linear regression of the TE on the coupling factor is used.

$$TE_{X \to Y} = \beta_0 + \beta_1 \omega, \tag{21}$$

where β_0 is the intercept of the regression, β_1 is the slope of the regression, and ω is the coupling factor of each simulation model. The higher the slope, the higher the sensitivity of the method to identify changes in the interaction strength.

2.4.3. Clinical Data

In this study, 50 one-minute segments from PSG recordings of 25 subjects referred to the sleep laboratory of the University Hospitals Leuven, UZ Leuven, Belgium were used. The study was approved by the ethical committee of UZ Leuven (S53746, S60319) and all subjects signed an informed consent. The median (25th; 75th) age and BMI of the subjects was 37 (34; 47) years, and 24.98 (23;

32.19) kg/m^2. From the PSG, the ECG and respiratory signals were extracted ($fs = 500$ Hz). Segments in which the subjects did not present apnea events from NREM1 and NREM3 were selected. The annotations of the respiratory events and hypnograms were done following the AASM2012 rules [33].

The ECG signal was filtered using a zero-phase Butterworth bandpass filter with cut-off frequencies at 0.03 and 150 Hz to remove baseline and high frequency noise. Then, it was filtered with a zero-phase Butterworth stopband filter at 50 Hz to remove powerline interferences. Next, the location of the R-peaks was found using R-DECO [34]. These locations were then used to compute the time-series corresponding to time intervals between consecutive heart beats. This time series was resampled to 2 and 4 Hz to have an evenly sampled heart rate variability (HRV) representation. After that, a zero-phase Butterworth bandpass filter with cut-off frequencies at 0.03 Hz and 1 Hz was applied.

The respiratory signal ($RESP$) corresponded to the nasal airflow, recorded using a pressure sensor. This signal was first bandpass filtered using a zero-phase Butterworth filter with cut-off frequencies at 0.03 and 1 Hz. Then, it was resampled at 2 and 4 Hz. The reason to use two different sampling frequencies was to observe the effect that this has on the $TE_{RESP \rightarrow HR}$ estimation. Previous works have found that the sampling frequency might influence the estimation of cardio-respiratory interactions [35], while other studies have found an effect of filtering and downsampling electrophysiological data on the estimation of TE between different brain areas [36].

2.4.4. Significance analysis

To validate the significance of the computed $TE_{RESP \rightarrow HR}$, a surrogate data analysis was performed. Two approaches were used. The first one, known as iteratively refined surrogates (IRS), is applied to one signal at a time, and conserves the spectrum and distribution of the original data. This method guarantees that the generated surrogates of each signal maintain some of the characteristics of the original data, but that none of the interactions between them are preserved [37]. In the second approach, known as iterative multivariate surrogates (IMS), the surrogates are generated taking into account two or more signals at the same time. In this way, the distribution and spectrum of the original data and, additionally, the cross-correlation of the signals are preserved. The IMS will preserve the linear interactions of the original signals, but not the non-linear interactions [37].

According to [37], to conduct a one-sided surrogate test at a significance level of 5 %, at least 19 surrogate series are needed. Therefore, in the current work, for each segment, the $TE_{RESP \rightarrow HRV}$ of the original data was compared against all of the $TE_{RESP \rightarrow HRV}$ of 20 surrogates, generated with each approach. It is concluded that the $TE_{RESP \rightarrow HRV}$ of the segment is significant if it is higher than the values obtained from all the surrogates.

By applying this methodology, it is possible to check whether linear or non-linear interactions are present in the data. If the $TE_{RESP \rightarrow HRV}$ of a segment is significant when using IMS, it can be concluded that the interaction between the signals includes a non-linear component. On the other hand, if the $TE_{RESP \rightarrow HRV}$ is significant when using IRS the interaction between the signals could be either linear or non-linear. In this case, if the $TE_{RESP \rightarrow HRV}$ is also not significant using IMS, it can be concluded that the interaction is mostly linear. When the $TE_{RESP \rightarrow HRV}$ is significant for IRS and IMS, it could be concluded that there is a non-linear component in the interaction between the signals, but it is not possible to conclude anything about the linear component. These possible outcomes are shown in Table 2.

Table 2. Possible outcomes of the significance tests with each surrogate generation methodology.

Result Significance Test with IRS [a]	Result Significance Test with IMS [b]	Linear Interaction	Non-linear Interaction
NS [1]	NS	No	No
S [2]	NS	Yes	No
S	S	I [3]	Yes

[a] IRS = Iteratively Refined Surrogates, [b] IMS = Iterative Multivariate Surrogates
[1] NS = Not significant, [2] S = Significant, [3] I = Inconclusive

The explained framework for the analysis of TE on clinical data was applied to test the hypothesis that the linear and non-linear interactions between $RESP$ and HRV change in NREM1 and NREM3. This is done by counting the number of segments on which linear and non-linear interactions were found to be significant for NREM1 and NREM3.

3. Results

3.1. Simulation models

For all the simulations, the five methods behaved similarly. However, FBR and KDE showed a positive bias consistently for all the simulations, due to the numerical approximations done when estimating the entropies. With KNN, some values of the TE were found to be negative, also because of the numerical approximations done by this method. LIN and DVP did not present any bias.

For **A1**, all the methods identified correctly the lag at which the interaction takes place, presenting a higher $TE_{X\to Y}$ at this lag compared to the other lags. In the case of the linear model, additionally to the peak at $\tau = 1$, there were some smaller peaks at $\tau = 3$ and $\tau = 5$ for all methods. This was due to the autoregresive nature of the model, which includes the influence of more past states of the driver process into the target process. In the case of the non-linear model, there was only one peak in the TE, at $\tau = 2$, for all the methods. Finally, in the case of the linear + non-linear model, there are two peaks present in the TE, given that at $\tau = 2$ the linear interaction takes place and at $\tau = 4$ the non-linear interaction occurs.

In Figure 1, the results of two of the methods (LIN and DVP) for this analysis are shown.

The TEE was calculated for all methods, and the parameters for which it was closer to 1 were selected and fixed to continue with **A2**. The best parameters for each method are presented in Table 3.

Table 3. Best parameters of methods for TE computation.

Method	Parameter	Value
LIN	regression model order	linear model, non-linear model, and linear+non-linear model: 1
KNN	number of neighbors (nn)	linear model: $nn = 15$, non-linear model: $nn = 5$, linear+non-linear model: $nn = 15$
FBR	quantization levels (Q)	linear model, non-linear model, and linear+non-linear model: $Q = 4$
KDE	multiplier of kernel bandwidth (α)	linear model, non-linear model,and linear+non-linear model: $\alpha = 1.5$
DVP	none	

For **A2**, all methods behaved similarly, with the only difference being the slope of the TE with respect to the interaction parameter. In Figure 2 the results for **A2** are presented, only for LIN as a representative for all the methods. Only in the case of the linear + non-linear model, for the non-linear interaction, the methods did not show a clear increment in TE when the interaction parameter d increased, demonstrating a very small slope in all cases.

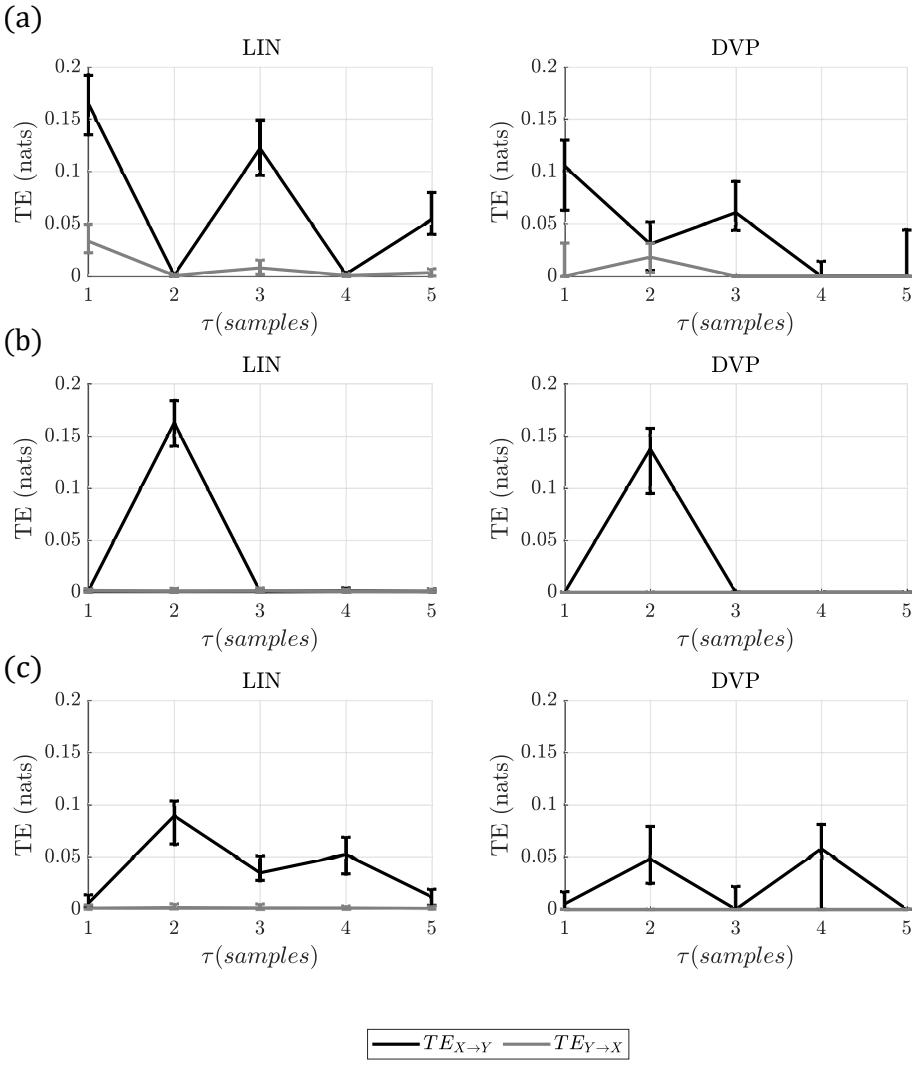

Figure 1. Results of changing the lag for the embedding vectors generation for (**a**) linear model (interaction at $\tau = 1$), (**b**) non-linear model (interaction at $\tau = 2$), and (**c**) linear + non-linear model (interaction at $\tau = 2$ and $\tau = 4$). Each plot shows the median TE vs. lag (τ) in samples. The error bars indicate the interquartile range.

A summary of the evaluation of the performance of the methods for all the simulation models is presented in Table 4. The best method corresponds to the one with the lowest TEE combined with the highest β_1.

Table 4. Scores of TEE and β_1 for the assessment of the performance of the methods for each simulation model.

	Linear model		**Non-linear model**		**Linear + Non-linear model**		
method	TEE	β_1	TEE	β_1	TEE	$\beta_1 linear$	$\beta_1 non-linear$
LIN	2.09	0.35	1.03	0.46	1.37	0.29	0.07
KNN	2.04	0.28	1.06	0.54	1.33	0.22	0.09
FBR	3.39	0.26	2.59	0.24	2.09	0.13	0.04
KDE	2.71	0.24	1.91	0.44	1.81	0.19	0.08
DVP	1.87	0.31	1	0.39	1.05	0.20	0.08

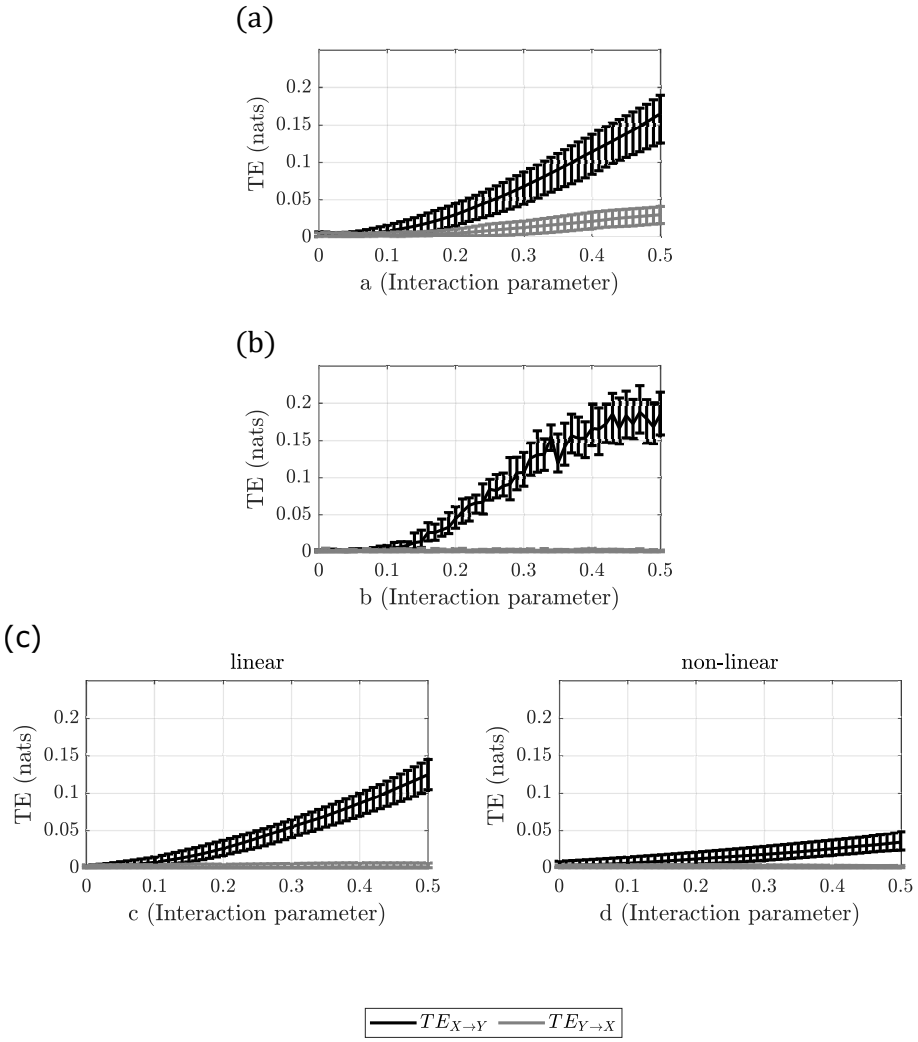

Figure 2. Results of LIN for changing the interaction strength for (**a**) linear model, (**b**) non-linear model, and (**c**) linear + non-linear model (linear interaction on the left and non-linear interaction on the right). Each plot shows the median TE vs. the interaction parameter. The error bars indicate the interquartile range.

In general, it could be seen that DVP performed better than the other methods when identifying the correct lag of the interaction for all simulation models, given that its TEE was always closer to 1. For FBR and KDE, the identification of the lag of the interaction for all the simulation models visually was similar to that of DVP. Nevertheless, their TEE values were higher, because of their intrinsic bias. LIN and KNN also presented slightly higher values of TEE compared to DVP, because for lags different from the interaction lag, the TE was not exactly zero.

When observing the β_1 values, it could be seen that LIN and KNN presented slightly higher slopes than the other methods, while FBR presented the lowest slope.

When taking all the experiments into consideration, the best performing method was DVP. Hence, it was selected for the analysis in clinical data.

3.2. Clinical data

The analysis of the clinical data focused on the linear and non-linear dynamics of the interactions between the respiration ($RESP$) and the heart rate variability (HRV) in two sleep stages, NREM1 and NREM3. Given that the delay at which the cardio-respiratory coupling occurs is not known, lags between 1 and 5 seconds were considered.

For each sleep stage, the significance of the TE was assessed using the surrogate analyses explained in Section 2.4.4. It is worth noting that if the linear interaction is found significant in a segment, it means that the only component identified by TE was the linear one. Instead, if the non-linear interaction is significant in a segment, it means that TE was able to identify a non-linear component, but there could also be a linear component not identified by the significance analyses (see Table 2).

The number of segments with a significant interaction for each lag and for each sleep stage are presented in Table 5. It can be observed that for the signals sampled at 2 Hz, there were no NREM3 segments with significant interactions. For NREM1, the number of segments with significant interactions were similar for both sampling frequencies.

Table 5. Number of segments with significant linear and non-linear interactions.

	NREM1				**NREM3**			
	2 Hz		**4 Hz**		**2 Hz**		**4 Hz**	
τ **(seconds)**	**linear**	**non-linear**	**linear**	**non-linear**	**linear**	**non-linear**	**linear**	**non-linear**
1	5	17	6	22	0	0	9	17
2	8	21	7	27	0	0	8	17
3	8	16	6	12	0	0	4	14
4	6	14	8	15	0	0	8	12
5	5	17	4	23	0	0	5	16

Given that for the sampling frequency of 2 Hz no significant interactions were detected for NREM3, the exploration of the hypothesis regarding the nature of the interactions between $RESP$ and HRV in NREM1 and NREM3 was performed only with the results obtained for 4 Hz. Figure 3 shows the $TE_{RESP \rightarrow HRV}$ for the segments with significant interactions for both sleep stages.

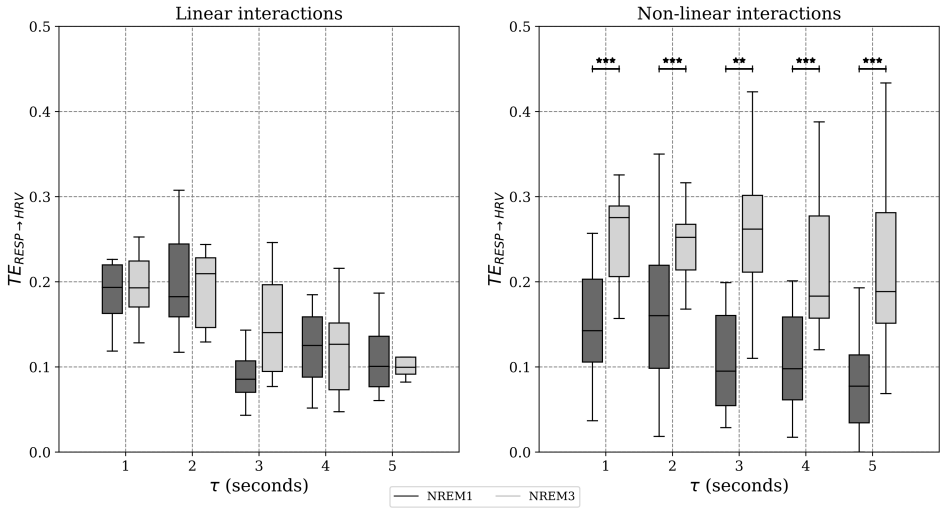

Figure 3. $TE_{RESP \rightarrow HR}$ of significant segments for each kind of interaction at 4 Hz vs. lag (τ) in seconds. Linear interactions are on the left, in which no significant differences between NREM1 and NREM3 are found. Non-linear interactions are on the right, in which for NREM3 the TE is consistently higher than for NREM1. Significant differences are depicted with star markers (** p-vale < 0.01, *** p-value < 0.001.)

When comparing the strength of the linear interactions for all lags, there was no significant difference between NREM1 and NREM3. In contrast, for the non-linear interactions, the differences between both sleep stages were always significant for all lags. It could be seen that for NREM1 at $\tau = 2$ seconds there is a maximum of the TE for the non-linear interactions, while for NREM3, this maximum occurs at $\tau = 1$ second.

4. Discussion

In this work, the application of TE for the analysis of different dynamics of interactions between time series was studied. For this purpose, five methods were applied to three simulation models with different types of interactions. It is worth noting that the simulation models used in this paper were not defined to represent the real physiological data of the cardiac and respiratory systems, but were used to illustrate the different dynamics that could be present in real physiological data.

To generate the embedding vectors for the computation of TE, UE was used because of its simplicity. This technique, however, can be redundant and arbitrary in the selection of the embedding vectors, which could cause problems such as over-fitting and detection of false influences [28]. A possible approach to prevent these issues, is to use a non-uniform embedding (NUE) technique. This approach was not covered in this study and its implementation with the entropy estimators is proposed as future work.

With TEE it was possible to select the best parameters for each method, based on the knowledge of the exact lag at which the interaction between the signals occur. However, the best parameters found for this study are not meant to be used arbitrarily, as their selection can be affected by the length of the signals, as shown in [21] for mutual information.

Out of the five methods compared in this work, only LIN was model-based, and made the assumption that the studied processes had a joint Gaussian distribution. This assumption, however, did not limit its performance when applied to non-linear processes. The results obtained in this study, in which LIN performed similarly to the other methods was contrary to the results of [12] and [30], in which LIN was outperformed by KNN. However, in [12] and [30], the signals analyzed were longer than the signals used in the current study. The limited number of points in the current study could have affected the accuracy of the estimation of the PDFs, which could explain the comparable performance of KNN and LIN. It is expected that with higher number of points, an increment in the accuracy of KNN when estimating the PDF could lead to a better performance of this method.

In [13], it was found that DVP outperformed FBR and KDE for non-linear interactions, even though KDE was more sensitive to increments in the interaction strength. In this work, the same behavior was found, considering that DVP was the best method, not only compared with FBR and KDE, but also with LIN and KNN.

K-nearest neighbors and kernel based estimators were compared in [29], showing that the kernel estimators outperformed the k-nearest neighbor estimators. However, the kernel function used in [29] is different from the one used in this study, and the effect of the selection of the kernel function was not analyzed. In the current study, it was found that KNN presented a better behavior than KDE with a Gaussian kernel function.

In general, the finding that DVP outperformed all the other methods for the simulation models is consistent with the literature. Nevertheless, many studies use k-nearest neighbors or traditional binning estimators when applying TE and other information based metrics [14,18,38,39], due to their popularity and extensive use as non-parametric estimators. The current work could constitute a base for the selection of DVP as an alternative to the popular estimators, not only because of its performance, but also because having minimal adjustable parameters can constitute an advantage when working with real data. However, as future work, it is advised to extend the comparison of the methods presented in this study, and others that were not mentioned here, with simulation models that represent real physiological data and with longer signals. Also, it is advised to explore the performance of the methods in non-stationary set-ups, relaxing the stationarity assumptions using a sliding window to obtain a continuous profile of the TE. This last approach could be useful when dealing with long and continuous measures of physiological data.

With the best method for the computation of TE identified, the cardio-respiratory interactions from segments of a PSG study were analyzed. It was decided to compute TE using lags between 1 and 5 seconds, since during sleep different forms of cardio-respiratory coupling could occur at different times [6], and the selection of the optimal embedding lag was out of the scope of this work.

In previous works, it has been suggested that the sampling frequency might influence the estimation of cardio-respiratory interactions [35], therefore two sampling frequencies were included in this analysis (2 Hz and 4 Hz). In the case of 2 Hz, there were no segments with significant interactions for NREM3 for all lags. This result does not mean that there are no interactions in this sleep stage, but it means that for this particular study, DVP was not able to capture them.

While the respiration and the HRV signals are highly regular during deep sleep for healthy subjects, the presence of sleep apneas could increase their variability. The higher variability could affect the resampling of the cardio-respiratory signals. In this case, it is possible that the information transferred from one signal to the other could not be quantified by TE. In [36] the effects of the downsampling and filtering of the driver and target signals on the computation of TE were studied, finding that the interactions were underestimated or not detected. These facts, combined with the shorter length of the signals at 2 Hz, could explain the results obtained in the current work.

The analysis of the interactions in NREM1 and NREM3 was continued only with the signals sampled at 4 Hz. It was observed that there were no differences in the strength of the linear interactions between these two sleep stages for all lags. In contrast, significant differences were found for all lags for the strength of the non-linear interactions. However, the significance for non-linear interactions only assures that at least some component of the cardio-respiratory interaction is non-linear, but a linear component could also be present. The fact that differences were found across all lags could be in line with the results of [6], about the times at which cardio-respiratory interactions are present.

5. Conclusions

In this work, the behavior of five methods to compute TE was compared based on their performance on simulated data. With this comparison, the limitations and advantages of the methods when working with different dynamics and short signals were highlighted.

It was found that the DVP method performed best for the simulations. This method identified correctly the lag at which the interaction occurred for each simulation model, presenting lower values for different lags. The other methods presented higher TE values for different lags and in the case of FBR and KDE they had a constant bias for all lags. The performance regarding the sensitivity to the strength of the interactions showed that all methods were comparable. The lack of parameters to tune when using DVP was an advantage influencing its selection to be used with the cardio-respiratory signals from a PSG study.

For the clinical data, it was found that DVP was a suitable method to quantify the linear and non-linear cardio-respiratory interactions during sleep. The results suggest that for these signals, the non-linear interactions are consistently higher for deep sleep.

The simulation study combined with the results from the clinical data could be helpful to select the best method to identify and quantify interactions between physiological signals, even when no knowledge about the nature of these interactions is available.

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