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Extraction of Stationary Components in Biosignal Discrimination

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***Abstract*— Biosignal recordings are widely used in the medical environment to support the evaluation and the diagnosis of pathologies. Nevertheless, the main difficulty lies in the non-stationary behavior of the biosignals, difficulting the obtention of patterns characterizing the changes in physiological or pathological states. Thus, the obtention of the stationary and non-stationary components of a biosignal is still an open issue. This work proposes a methodology to detect time-homogeneities based on time-frequency analysis with aim to extract the non-stationary behavior of the biosignal. Results show an increase in the stationarity and in the distance between classes of the reconstructions from the enhanced time-frequency representations. The stationary components extracted with the proposed approach can be used to solve biosignal classification problems.**

Keywords: Time-evolving Latent Variable Decomposition, Multivariate locally stationary time series.

I. Introduction

In biosignal applications, it is often of interest to be able to separate an observed time series into two or more groups with different stochastic behavior [1]. In particular, there is a need for distinguishing stationary from non-stationary components, either because its assumption is a pre-requisite for applying most of standard algorithms devoted to steady-state regimes, or because its breakdown conveys specific information in evolutive contexts, as remarked in [2], [3]. In the analysis of biomedical data, such as electroencephalography (EEG) or Heart Rate Variability (HRV), the corresponding recordings usually appear nonstationary, although there exist stationary sources, these are not discernible, since superpositions of stationary and nonstationary components can be measured.

Several techniques had been proposed for decomposition into stationary and non-stationary components, among others: Smoothing techniques based on ortogonal polynomials, time-frequency localized linear splines, time frequency representations, wavelets, empirical mode decomposition, and stationary subspace analysis [4]. Generally, extraction of stationary components from real-valued biosignal can be provided by using the following two subsequent stages: *i*) decomposition of underlying time series, by properly handling the signal model within a stochastic subspace framework, and *ii*) searching of the needed number of components to match *a priori* given stationary homogeneity constrains.

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This work is based on evolutionary time-frequency (*t-f*) analysis, for which testing of the time-homogeneity constraints of the evolutionary spectra is evaluated at different instants of time by using multivariate time series subspace representation. In this sense, a new methodology for stationarity enhancement on biosignals is introduced.

The paper is organized as follows: The section II is dedicated to the description of the methods required to perform the stationarity enhancement; in section III, the experimental setup is described and obtained results are presented. Finally, the results are properly discussed in section IV

II. Background

A. Enhanced t-f Representation

The time–frequency representation, planned to determine the energy distribution along the frequency axis at each time instant, has been proposed before to investigate the time–variant properties of the spectral parameters during either transient physiological or pathological episodes [5]. So, rather than straightforward extraction on raw data, decomposition into stationary and non-stationary components is carried out upon enhanced *t-f* representation of the input data. In particular, the short time Fourier transform is employed introducing a time localization concept by means of a tapering window function of short duration, ϕ, that is going along the underlying biosignal, $y(t)$, as follows:

$$\boldsymbol{S}_y(t,f) = \left| \int_T y(\tau)\phi(\tau - t)e^{-j2\pi f\tau} d\tau \right|^2 , \ \boldsymbol{S}_y(t,f) \in \mathbb{R}^+ \tag{1}$$

with $t, \tau \in T$, $f \in F$.

Based on introduced *spectrogram* of Eq. (1), the corresponding *t–f* representation matrix, $\boldsymbol{S}_y \in \mathbb{R}^{T\times F}$, can be described by the row vectors, $\boldsymbol{S}_y = [\boldsymbol{s}_1 \dots \boldsymbol{s}_f \dots \boldsymbol{s}_F]^\top$, with $\boldsymbol{s}_f \in \mathbb{R}^{1\times T}$, where vector $\boldsymbol{s}_f = [s(f,1) \dots s(f,t) \dots (f,T)]$, with $s(f,t) \in \mathbb{R}$, is each one of the time–variant spectral decomposition components at frequency f, and equally sampled through the time axis.

B. Measure of Stochastic Variability

Several variability analysis techniques suitable for clinical applications had been proposed, including statistical, geometric, energetic, informational, and invariant measures [6]. In this research, the amount of stochastic variability of the spectral component set is computed following the approach given in [1], that is based on time-variant decomposition estimated by adapting in time any of commonly used latent variable techniques, upon which a piecewise stationary restriction is imposed [5]. So, under the locally stationary assumption,

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consistent estimates of the time-varying spectral density matrix are obtained and consequently consistent estimates of the time-varying eigenvalues and eigenvectors may be accomplished [7]. Namely, the time–evolving principal component analysis is extended to the dynamic feature modeling by stacking the input observation matrix in the following manner:

$$\boldsymbol{\Xi}_y = \begin{bmatrix} \boldsymbol{s}_1^1 & \boldsymbol{s}_2^1 & \cdots & \boldsymbol{s}_F^1 \\ \boldsymbol{s}_1^2 & \boldsymbol{s}_2^2 & \cdots & \boldsymbol{s}_F^2 \\ \vdots & \vdots & \vdots & \vdots \\ \boldsymbol{s}_1^M & \boldsymbol{s}_2^M & \cdots & \boldsymbol{s}_F^M \end{bmatrix}, \boldsymbol{\Xi}_y \in \mathbb{R}^{M \times FT} \quad (2)$$

where vector $\boldsymbol{s}_f^i$ corresponds to f-th short–term spectral component estimated from the i-th spectrogram matrix $\boldsymbol{S}_y^i$ which is related to the i-th object, with $i \in M$, where M stands for the total number of observations. Accordingly, the amount of stochastic variability of the spectral component set is computed by the singular value decomposition calculation over observation matrix in Eq. (2). So, the following time–variant relevance measure is carried out [5]:

$$\boldsymbol{g}(\boldsymbol{\Xi}_y; \tau) = [\chi(1) \ \cdots \ \chi(\tau) \ \cdots \ \chi(FT)]^\top, \in \mathbb{R}^{FT \times 1} \quad (3)$$

being $\chi(\tau) = \boldsymbol{E}\{|\lambda_f^2 v_f(\tau)| : \forall f \in F\}$, where $\{\lambda_f\}$ is the relevance eigenvalue set of matrix $\boldsymbol{\Xi}_y$, and scalar–valued $v_f(\tau)$ is the respective element at τ moment, with $\tau = 1, \ldots, FT$ that indexes every one of the relevance values computed for the whole time–variant data set (notation $\boldsymbol{E}\{\cdot\}$ stands for the expectation operator).

To determine distinctly the relevance related to each one of the time-variant spectral components, measure vector given in Ec (3) can be arranged into a matrix, termed *relevance matrix*, as follows:

$$\boldsymbol{\Gamma}(\boldsymbol{S}_y) = [g(\boldsymbol{s}_1) \ldots g(\boldsymbol{s}_f) \ldots g(\boldsymbol{s}_F)], \quad \in \mathbb{R}^{T \times F}, \quad (4)$$

that contains stochastic variability measured for the whole spectral component set, $\{\boldsymbol{s}_f\}$. Consequently, the stationarity and non-stationarity components of a biosignal recording $i \in M$, can be derived from the amount of variablity of its spectral components.

a) Matching stochastic homogeneity constrains: For a given time series, $\boldsymbol{s}$, regarded as stochastic process, any randomness structure estimator must remain constant in time. This work proposes to take the following assumption:

$$\|\boldsymbol{E}\{g(\boldsymbol{s}_f); t\} - \boldsymbol{E}\{g(\boldsymbol{s}_f); t - \tau\}\| \to 0, \quad \forall t, \tau \in T \quad (5)$$

In practice, the extraction of non–stationary components from a random signal formally can be related as filtration task, carried out under the following assumptions [4]:

– the observed signals are linear superpositions of stationary and non-stationary sources, so, an observable given time series vector, $\boldsymbol{y}$, is separated into two unobservable components, i.e., a stationary and non–stationary, respectively;

$$\boldsymbol{y} = \boldsymbol{y}^* + \boldsymbol{\eta},$$

– the non-stationarity component, $\boldsymbol{\eta}$, is a second order measurable stochastic process.

Hence, the level of stochastic homogeneity of the random variable $\boldsymbol{s}_f^*$ is used to extract the stationary and the non-stationary component of the time series, which are constructed from weighted versions of the *t-f* representation, i.e. the stationarity components are highlighted and the non-stationary components are smoothed, and vice-versa.

Finally, the measure of the degree of non-stationarity in the time series is performed as proposed in [3]. A set of J stationary surrogate signals $\{s_j : j = 1, \ldots, J\}$ is computed from a given signal. For the test, a contrast measure has to be defined as:

$$c_n(x) := d(\boldsymbol{S}_y(t, f), \boldsymbol{E}\{\boldsymbol{S}_y(t, f) : \forall t \in T\}) \quad (6)$$

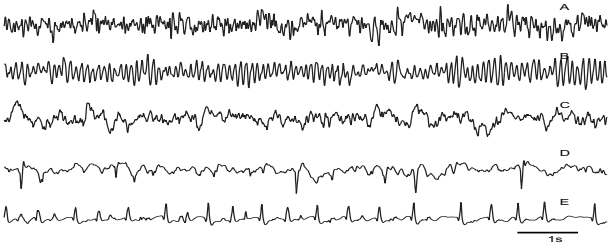
where $d \in \mathbb{R}^+$ is some suitable spectral distance, in this particular case, the Kullaback–Leibler Distance(KLD). So, the index of nonstationarity is defined as:

$$\kappa = \sqrt{\frac{\text{var}(c_n(y) : \forall t \in T)}{\boldsymbol{E}\{\text{var}(c_n(s_j) : \forall t \in T) : \forall j\}}}, \quad (7)$$

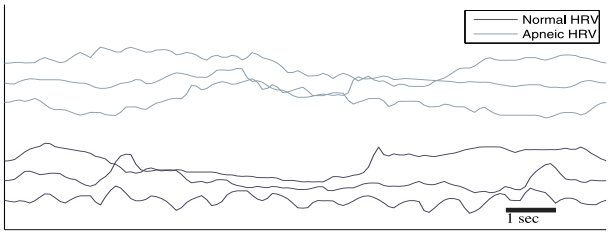
III. Experimental Set-Up

A. Database Description

The EEG Database is the PhysioNet available collection consisting of five subsets (denoted A, B, C, D, and E), each one composed of 100 single–channel EEG segments of 23.6-s duration [8]. Sets A and B have been taken from surface (extracranial) EEG recordings of five healthy volunteers with eye open and closed, respectively.



(a) EEG collection



(b) HRV collection

Fig. 1. Examples of considered biomedical recordings

Signals from sets D and C have been measured in seizure–free intervals from five subjects in the epileptic zone and from the hippocampal formation of the opposite hemisphere of the brain. Set E comprises of epileptic signals recorded during seizure (ictal) from all recording sites. Sets C–E have been recorded intracranially. All EEG signals were digitized

at 173.61 *Hz* with 12 *bit* resolution. Figure 1(a) shows exemplary of 1-*s* segments of each class.

The second database holds a collection of 1-*min* HRV segments selected from the HRV-ECG database available on Physionet. The ECG collection holds 70 electrocardiographic recordings, each one including a set of reference annotations added every minute of the recording indicating either the presence of absence of apnoea during each segment. Finally, 600 HRV segments of 1-minute length (300 apneic and 300 normal labeled) were selected from 25 training recordings to build the dataset [1]. Figure 1(b) shows 1-*min* segments for both normal and apneic recordings.

B. Time-Frequency Representations Enhancement of Estimated Time Series

In this work, based on spectral EEG and HRV signal properties, the STFT– based quadratic spectrogram is computed by sliding windows for the following set of estimation parameters:

i). For the EEG signals, a 2.9 *s* gaussian window and 512 frequency bins within a range of 0 to 83 *Hz*.

ii). For the HRV recordings, a 32.5 *ms* hamming window, 50% of overlapping, and 512 frequency bins within a range of 0 to 1 *Hz*.

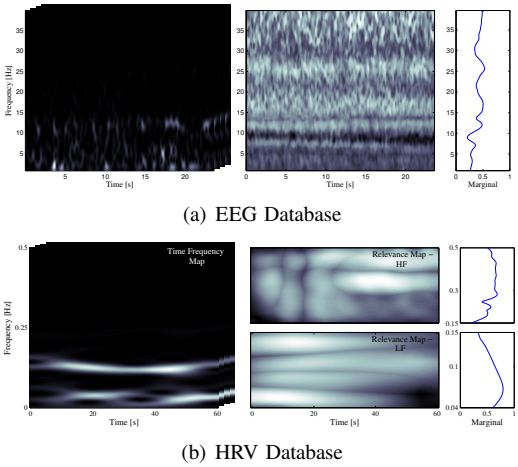
C. Split into stationary and non-stationary subspaces based on stochastic variability

The main core of this approach is to find the stationary and non-stationary components of a given signal. For this aim, a measure of the spectral component smoothness along the time, can be derived from the relevance map, which can be used as weighting function of each component, by:

$$\boldsymbol{S}^i_{y^*} = \boldsymbol{W}\boldsymbol{S}^{i\,T}_y \qquad \boldsymbol{S}^i_{\eta} = (\boldsymbol{I}-\boldsymbol{W})\boldsymbol{S}^{i\,T}_y,$$

where $\boldsymbol{W} \in \mathbb{R}^{F\times F}$ is a diagonal matrix, where each element of the diagonal $0 \leq w_{ff} \leq 1$ stands for the amount of stochastic homogeneity of the random variable $\boldsymbol{s}_f$, derived from the marginal of Eq (4), $\boldsymbol{I}$ stands for the identity matrix and $\{\cdot\}^T$ stands for the transpose operator. Thus the weighted sum of the frequency bands with soft and strong variability changes can be used to construct the stationary and non-stationary components of the signal, respectively.

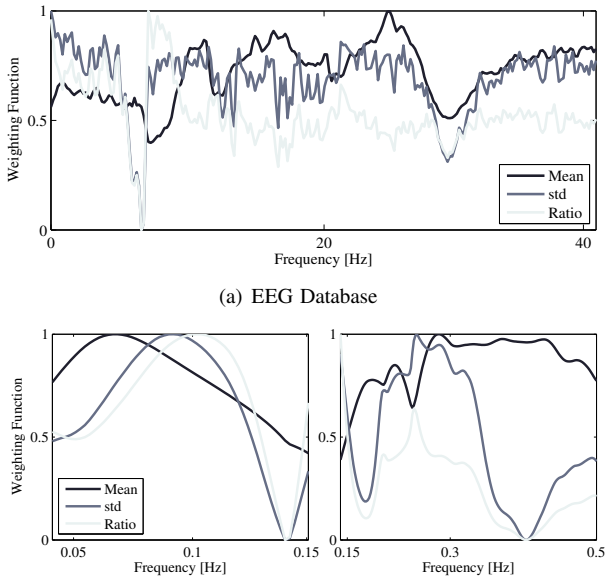
Figure 2 shows an example of the estimated time frequency representations (left), along to the obtained relevance matrices (middle) and the relevance marginal (right). In the case of EEG signals (Figure 1(a)), the time-frequency representations were computed from 0 to 40 *Hz* while for the HRV signals (Figure 1(b)) the frequency rank is split into the two bands of clinical interest, termed Low Frequency (LF) spectral band ($\boldsymbol{f} \in [0.04, 0.15]$ *Hz*) and High Frequency (HF) spectral band ($\boldsymbol{f} \in [0.04, 0.15]$*Hz*). Particulary in the present study, three different measures were used as weighting functions: *i*) the *mean* along the frequency axis of the relevance map, *ii*) the inverse of the standard deviation along the frequency axis of the relevance matrix (termed *std*), and *iii*) the ratio $mean/std$. Figure 3 shows the different weighting functions for both databases.



(a) EEG Database

(b) HRV Database

Fig. 2. Measured relevance matrixes in terms of stochastic variability.



(a) EEG Database

(b) HRV Database

Fig. 3. Evaluated marginal weighting functions.

The weighting functions are selected as follows: i) The *mean* of the relevance matrix stands for the spectral components with more information, because the relevant matrix can be interpreted as an relevance function. ii) The *std* stands for the spectral components with lower variations along the time (stationarity restriction), and iii) the ration *mean/std* to create a function that contains information of the relevance and the stationarity of each spectral component.

IV. Results and Discussion

To test the performance of the methodology, the κ index, which measure the degree of non-stationarity in a signal is used, for instance the higher the value of κ, the more non-stationary the signal in hand. Thus, the κ values are computed for each recording on the datasets and its stationary and non-stationary reconstructions obtained with the proposed approach. The results are computed as the mean of the κ

index.

In general, results on Table I show an increase in the stationarity of the reconstructions from the enhanced *t-f* representation, while the non-stationary residual shows the largest κ. Nevertheless, it can be noted that best values in each database are obtained for different weighting functions. For EEG recordings, as the *standard deviation* oscillates on a close interval ($0.8 - 1$), most of the information is given by the *mean*, obtaining values of κ such that $\kappa_{y^*} < \kappa_y < \kappa_\eta$.

	Weighting Function	$\boldsymbol{y}$	$\boldsymbol{y}^*$	$\boldsymbol{\eta}$
EEG	Mean	0.81	0.81	0.85
	Std	0.81	0.81	0.80
	Ratio	0.81	0.83	0.81
HRV	Mean	0.59	0.54	0.66
	Std	0.59	0.53	0.67
	Ratio	0.59	0.64	0.56

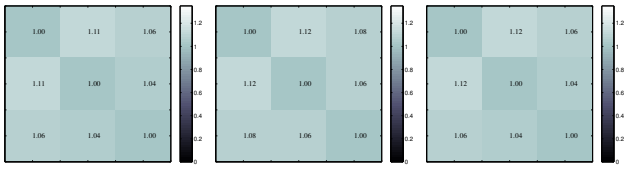
TABLE I

NORMALIZED κ INDEX FOR THE EEG AND HRV DATABASES.

Unlike the EEG database, the *standard deviation* for the HRV recordings behaves as a smooth function restricting, the level of stationarity of each spectral component, improving the κ index.

Finally, to evaluate the capability of the proposed approach in biosignal discrimination, intra and inter class distance functions are employed to measure quantitatively the influence of the stationarity and non-stationarity on the groupping of raw-signals. A Hausdorff distance scheme was employed as the distance between two sets (classes). Since such scheme requires the comparison of all possible pairs of time-variant subjects, the correlation distance is choosen as the pairwise subject comparison.

For the EEG database, for a three class classification problem, namely (AB,CD,E), the distance between each pair of classes tends to take higher values when the stationary reconstruction is used. Nevertheless, the level of separability of the (AB) class remains constant.



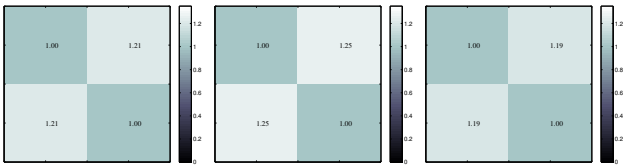
(a) $\boldsymbol{y}$ (b) $\boldsymbol{y}^*$ (c) $\boldsymbol{\eta}$

Fig. 4. Inter class distance for for EEG recordings

For the HRV database, the behavior of the distance between classes is improved, i.e. the distance is higher with the stationary part and lower with the non-stationary reconstruction, which is the ideal behavior.

V. CONCLUSIONS

A new methodology for stationarity enhancement on biosignals is presented. The performance is tested on two well known databases, which comprise non-stationary behaviors, namely, electroencephalography and heart rate variability recordings. The methodology estimates a spectral weighting function from a stochastic variability map. Such function is applied as a filter enhancing the stationary components of the signal. As measure of the non-stationarity the κ, proposed by [3] is used, as well the Hausdorff distance among classes. Results show an increase in the stationarity and the distance between classes of the reconstructions from the enhanced *t-f* representations. As future work, the use of several non-stationarity measures is proposed, as well as the use of the methodology for solving non-stationary signal discrimination issues by approaches to characterize the stationary reconstructions of the biosignal recordings.



(a) $\boldsymbol{y}$ (b) $\boldsymbol{y}^*$ (c) $\boldsymbol{\eta}$

Fig. 5. Inter class distance for HRV recordings

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