

Communications

Convolutional Blind Source Separation Algorithms Applied to the Electrocardiogram of Atrial Fibrillation: Study of Performance

Carlos Vayá*, José J. Rieta, César Sánchez, and David Moratal

Abstract—The analysis of the surface electrocardiogram (ECG) is the most extended noninvasive technique in medical diagnosis of atrial fibrillation (AF). In order to use the ECG as a tool for the analysis of AF, we need to separate the atrial activity (AA) from other cardioelectric signals. In this matter, statistical signal processing techniques, like blind source separation (BSS), are able to perform a multilead statistical analysis with the aim to obtain the AA. Linear BSS techniques can be divided in two groups depending on the mixing model: algorithms where instantaneous mixing of sources is assumed, and convolutional BSS (CBSS) algorithms. In this work, a comparison of performance between one relevant CBSS algorithm, namely Infomax, and one of the most effective independent component analysis (ICA) algorithms, namely FastICA, is developed. To carry out the study, pseudoreal AF ECGs have been synthesized by adding fibrillation activity to normal sinus rhythm. The algorithm performances are expressed by two indexes: the signal to interference ratio (SIR_{AA}) and the cross-correlation (R_{AA}) between the original and the estimated AA. Results empirically prove that the instantaneous mixing model is the one that obtains the best results in the AA extraction, given that the mean SIR_{AA} obtained by the FastICA algorithm (37.6 ± 17.0 dB) is higher than the main SIR_{AA} obtained by Infomax (28.5 ± 14.2 dB). Also the R_{AA} obtained by FastICA (0.92 ± 0.13) is higher than the one obtained by Infomax (0.78 ± 0.16).

Index Terms—Atrial fibrillation, convolutional blind source separation, ECG, independent component analysis.

I. INTRODUCTION

The prevalence of atrial fibrillation (AF) is less than 1% in people under 60 years old, but it increases significantly in those over 70, approximating to 10% in those over 80 [1]. The exhaustive analysis of AF episodes requires to separate previously the atrial activity (AA) component from other bioelectric signals that contribute to the electrocardiogram (ECG) formation [2]. Some of these signals are ventricular activity (VA), muscular activity, noise and artifacts introduced by electrodes, and the powerline interference [3].

Blind Source Separation (BSS) techniques have been successfully applied to the extraction of the AA from the ECG of AF episodes by assuming instantaneous and linear mixing of the bioelectric signals in the human body [3]. The feasibility in this matter of the FastICA algorithm, based on independent components analysis (ICA), is proved in [3] and [4]. Nonetheless, the propagation delays of the bioelectric signal in the

body and specially the movements of the heart could violate the ICA assumptions of spatial stationarity and instantaneous mixing of physical sources [3]. On the contrary, in the convolutional model, these circumstances can be considered by using convolutional BSS (CBSS) algorithms. CBSS algorithms have not been applied yet to the extraction of the AA. Our objective is to compare the performance of one relevant CBSS algorithm, namely Infomax [5], and the FastICA algorithm [6]. The main goals of this contribution are, on the one hand, to reveal whether CBSS algorithms are reliable to extract the AA from the ECG of AF episodes when the typical ECG sampling rate of 1 kHz is used and, on the other hand, to study their possible improvement in the AA estimation with respect to the instantaneous BSS algorithms.

II. BLIND SOURCE SEPARATION EXTRACTION TECHNIQUES

Time-domain-based techniques, like Average Beat Subtraction [7], have been well accepted and used in clinical applications [8] to cancel out the QRS complex and the T wave. Nonetheless, they are only applied to the leads where atrial fibrillation is more easily distinguishable, e.g., V1. This means that if we apply QRST cancellation techniques to different leads, we would obtain different atrial activities as well. Consequently, they do not make use of the information included in every lead in an unified way. On the contrary, BSS techniques make a multilead statistical analysis by exploiting the spatial diversity that multiple spatially separated electrodes introduce [3], [9]. When linear mixing of sources is considered, we talk about linear BSS techniques. Three main conditions must be fulfilled in order to apply linear BSS techniques: 1) independence of sources; 2) nongaussianity of sources; 3) linear mixing of sources [10]. Within the context of AF episodes, these three conditions are applicable. First, in AF episodes the bioelectric sources of the heart generating AA and VA can be considered to be statistically independent. This is justified because only a portion of atrial waveforms traverse the atrioventricular node and provoke ventricular depolarization [3], [4]. Furthermore, the physical origin of the atrial wavefront that has been able to produce ventricular depolarization could be very variable. This uncoordinated operation of AA and VA during an AF episode allows us to consider them as statistically independent [4]. Second, AA has a sub-Gaussian probability distribution whereas the VA is clearly super-Gaussian [3]. Finally, the mixing process of the bioelectric sources in the human body can be considered to be linear [11], [12]. Therefore, linear BSS techniques can be applied to extract the AA in AF episodes.

These are the most important linear models used in BSS:

1) *Instantaneous Linear Mixing Model*: Within the assumption of linearity, the simplest situation is the instantaneous linear model. In this case, the instantaneous mixing of the cardioelectric sources in the human body is assumed. This can be expressed as [6]

$$\mathbf{x}[k] = \mathbf{A} \cdot \mathbf{s}[k] + \mathbf{n}[k] \quad (1)$$

where \mathbf{A} is a matrix that represents the linear transformation of source mixing, $\mathbf{x}[k]$ is the column vector that contains the observations at the k th sampling time, $\mathbf{s}[k]$ contains the sources, and $\mathbf{n}[k]$ the additive noise in every source. The BSS algorithms based on the instantaneous linear mixing model try to find the matrix \mathbf{W} as the pseudoinverse of the \mathbf{A} that obtains the best estimation of the sources [6]:

$$\hat{\mathbf{s}}[k] = \mathbf{W} \cdot \mathbf{x}[k]. \quad (2)$$

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*C. Vayá is with the Department of Innovation in Bioengineering, Castilla-la Mancha University, Escuela Politécnica Superior de Cuenca, Camino del Pozuelo s/n, 16071 Cuenca, Spain (e-mail: carlos.vaya@uclm.es).

J. J. Rieta and D. Moratal are with Biomedical Synergy, Polytechnic University of Valencia, EPSG, Carretera Nazaret Oliva s/n, 46730 Gandía, Valencia, Spain.

C. Sánchez is with the Department of Innovation in Bioengineering, Castilla-la Mancha University, Escuela Politécnica Superior de Cuenca, Camino del Pozuelo s/n, 16071 Cuenca, Spain (e-mail: carlos.vaya@uclm.es).

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The global mixing-unmixing system is characterized by the matrix \mathbf{G} , so that $\mathbf{G} = \mathbf{W} \cdot \mathbf{A}$.

The FastICA algorithm [6], based on the instantaneous mixing model, has already been applied to the extraction of the AA from ECGs of AF episodes [3]. In FastICA the instantaneous mixing of the sources is assumed and quite good results in the extraction of the AA have been obtained by using this algorithm [2].

2) *Convolutional Linear Mixing Model*: In the convolutional model, a more realistic case is considered. Here, weighted and, besides, delayed contributions in the generation of the observations are taken into account [6].

The convolutional model is a more general linear mixing BSS model where coefficients of \mathbf{A} are substituted by finite-duration impulse response (FIR) filters and the product operator of (1) and (2) by the convolution operator $*$. Indeed, the previous instantaneous model could be considered as a particular case of the convolutional model where the length of the filters is one.

The performance of several CBSS algorithms has been tested, but only the results obtained by Infomax [5] are presented here. Infomax belongs to an important family of algorithms based on information theory. Mutual information (MI) is a natural measure of the dependence between random signals [6]. MI is always nonnegative, and zero if and only if the variables are statistically independent. MI can be used as a criterion for obtaining the original sources of the BSS problem [6].

The other algorithms that have been tested are the Multi-channel Blind Least-Mean Square (MBLMS) algorithm [13], the time-delayed decorrelation (TDD) algorithm [14], and the Convolutional Blind Signal Separation (CoBlISS) algorithm [15]. Results obtained by TDD are very similar to results obtained by Infomax, and results obtained by MBLMS and TDD are quite poorer. Consequently, only results of Infomax have been reported in this paper.

III. PERFORMANCE ESTIMATION AND DATABASE

A. Spectral Concentration (SC)

Considering that the typical spectral morphology for AA is characterized by a very pronounced peak in frequencies from 5 to 8 Hz, with no harmonics and insignificant amplitudes above 15 Hz [16], it is possible to define a performance extraction index capable of evaluating AA extraction quality based on the spectral concentration [9]. The SC can be defined as

$$SC = \frac{\sum_{f=0.82f_p}^{1.17f_p} P_{AA}(f)}{\sum_{f=0}^{0.5f_s} P_{AA}(f)} \quad (3)$$

where P_{AA} is the power spectral density of the AA signal, f is the frequency, f_s is the sampling rate (1 kHz), and f_p is the main frequency peak of the AA. Experimental observations prove that the AA is the estimated independent component with the highest SC when the limits of the numerator summation are those specified in (3) [8]. Therefore, the SC can be used as an indicator to select, in an automated way, the estimated source that best matches the AA. A wider distance between frequency limits introduces high frequency noise components in the calculation of the SC indicator so that the probability of discriminating correctly the AA is reduced. A shorter distance between limits reduces the AA power considered in SC so that the probability of AA discrimination is reduced too.

B. Performance Indexes

1) *Signal-to-Interference Ratio (SIR)*: Considering x_i as the one of the M observations with the highest contribution of AA and s_j as the

one of the N sources that contains the AA, the SIR of x_i expressed in decibels is defined as [17]

$$SIR_{AA}^o = 10 \log \frac{\mathbf{E}\{(h_{ij} * s_j)^2\}}{\mathbf{E}\left\{\left(\sum_{k=1, k \neq j}^N h_{ik} * s_k\right)^2\right\}} \quad (4)$$

where h_{ij} are the FIR filters of the mixing matrix \mathbf{A} , which represent the contribution of the j th source on the i th observation. \mathbf{E} stands for the mathematical expectation. In the same way, considering that \hat{s}_p is the estimated source with the highest contribution of AA (i.e. the estimated source with the highest SC), the SIR of \hat{s}_p is [17]

$$SIR_{AA}^e = 10 \log \frac{\mathbf{E}\{(g_{pj} * s_j)^2\}}{\mathbf{E}\left\{\left(\sum_{k=1, k \neq j}^N g_{pk} * s_k\right)^2\right\}} \quad (5)$$

where g_{pk} are the FIR filters of the global system matrix \mathbf{G} . Finally, the signal-to-interference ratio SIR_{AA} is defined as

$$SIR_{AA} = SIR_{AA}^e - SIR_{AA}^o. \quad (6)$$

2) *Cross-Correlation*: The cross-correlation between the original AA and the estimated AA is calculated as

$$R_{AA} = \frac{\mathbf{E}\{s_{AA} \cdot \hat{s}_{AA}\}}{\sqrt{\mathbf{E}\{s_{AA}^2\} \mathbf{E}\{\hat{s}_{AA}^2\}}} \quad (7)$$

where s_{AA} and \hat{s}_{AA} are the original and the estimated AA, respectively.

C. ECG Database

The calculation of the previously defined indexes needs the original sources and the mixing matrix to be known. Given that the sources that contribute to the generation of real ECGs are unknown, we needed to establish two environments of synthesized ECGs, so that the performance indexes could be applied.

1) *First Environment*: In the first environment, 15 pairs of separated AA and VA of AF episodes are mixed using the convolutional model. These separated AA and VA have been previously obtained from the V1 lead of real ECGs by using QRST cancellation [7]. The mixing is made by random mixing matrices \mathbf{A} . Obviously, this is not the real mixing process of the bioelectric signals in the human body. Nonetheless, it can be considered as a valid and objective way of testing and discarding those algorithms (CoBlISS and MBLMS) that were clearly useless to extract the AA. The FIR filters length of these mixing matrices (N_m) has been changed from 1 to 8. All ECGs are 12 s in length, and they all were obtained at a sampling rate of 1 kHz. In the separation process, the filter length of the separation matrix \mathbf{W} is an adjustable parameter in the CBSS algorithms (N_s). It has been changed in the tests from 2 to 32. The value of two is the lowest value allowed by all the tested CBSS algorithms. The value of 32 has been chosen so that the controlled maximum delay due to the mixing-unmixing process equals to 40 ms in duration, accordingly to the aforementioned maximum value of N_m and the sampling rate [13].

2) *Second Environment*: In the second environment, AF 12-leads ECG are synthesized by adding AA and VA of every lead. AA and VA were previously separated from real ECGs of AF episodes by using QRST cancellation [7]. Therefore, the synthesized ECGs are exactly the original real recorded signals. In this way we know their AA and VA components, so that the previously defined parameters can be applied. The convolutional mixing is assumed to be present in the generation of the real ECGs and, consequently, in the separated AA and VA. This synthesis process is depicted in Fig. 1. All resulting ECG recordings last for 8 s and are sampled at 1 KHz. This second environment comprises 20 synthesized ECGs. The maximum value of N_s has been fixed

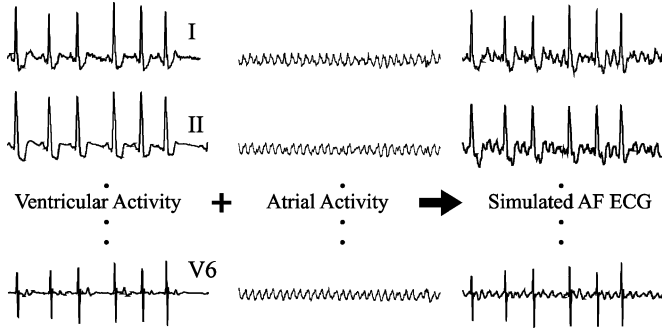


Fig. 1. Second environment synthetic ECG generation. The AF 12-leads ECGs are synthesized by adding the AA and the VA of every lead, previously separated from real ECGs of AF episodes.

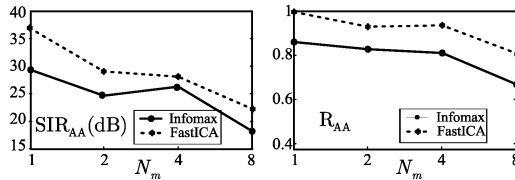


Fig. 2. SIR_{AA} and R_{AA} mean values of Infomax and FastICA algorithms in the first environment as a function of the FIR filters length of the random mixing matrices (N_m).

to 128 by considering 128 ms as a reasonable maximum propagation delay for all the bioelectric signals in the human body [11]. The respiratory induced axis-shifts of all the analyzed ECG recordings have been previously eliminated by signal filtering. All these recordings are free from ectopic beats or other nonideal characteristics. This allows us to develop an initial work focused in the performance of the CBSS algorithms when regular signals of AF are considered.

Note that the presence of previous convolution in the initial AA and VA is not an obstacle to the study of performance of CBSS algorithms. If previous convolution is present, the CBSS algorithms would try to invert the global linear system composed by the previous convolution and the additional simulated convolution. On the other hand, given that the mixing process of sources is unknown, the only way to test the performance of extraction when no direct access to the atrial activity is available (we are using surface recordings) is to define a set of synthetic signals so that we can compare the signals estimated by BSS algorithms with the original signals.

IV. RESULTS

A. First Environment Results

The global mean SIR_{AA} obtained in this environment by FastICA algorithm (37.6 ± 17.0 dB) is higher than the global mean SIR_{AA} obtained by Infomax (28.5 ± 14.2 dB). Also the R_{AA} obtained by FastICA (0.92 ± 0.13) is higher than this obtained by Infomax (0.78 ± 0.16).

The influence of N_m in the first environment is shown in Fig. 2. Both performance indexes, SIR_{AA} and R_{AA} , decrease when mixing filters length (N_m) increases. Mean values of SIR_{AA} obtained by Infomax are several decibels lower than the respective FastICA mean values, regardless of N_m . Furthermore, FastICA R_{AA} mean values are always nearer to one than those of Infomax.

Fig. 3 illustrates the influence of the separation filters length (N_s). The mean values of FastICA are included only as a reference constant

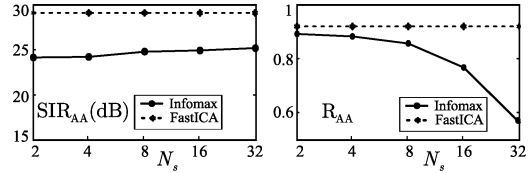


Fig. 3. SIR_{AA} and R_{AA} mean values of Infomax and FastICA algorithms in the first environment as a function of the FIR filters length of the separation matrices (N_s).

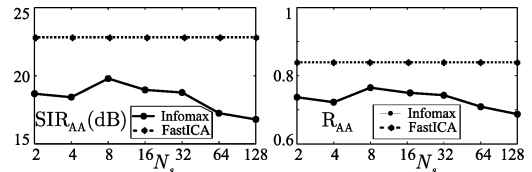


Fig. 4. SIR_{AA} and R_{AA} mean values of Infomax and FastICA algorithms in the second environment as a function of the FIR filters length of the separation matrices (N_s).

value, given that FastICA does not match the convolutive model and, therefore, the filters length parameter cannot be chosen. Mean SIR_{AA} and R_{AA} of Infomax are slightly lower than the respective indexes of FastICA. R_{AA} decreases when N_s increases. Thus, the best separation performance of Infomax is obtained when the instantaneous model is considered in this environment.

B. Second Environment Results

Also in this environment, the global mean SIR_{AA} obtained by FastICA algorithm (22.8 ± 4.8 dB) is several decibels higher than the one obtained by Infomax (18.4 ± 5.4 dB). In the same way, the global mean R_{AA} obtained by FastICA (0.84 ± 0.16) is higher than the one obtained by Infomax (0.73 ± 0.16).

The influence of N_s in the second environment is shown in Fig. 4. Note that the highest values of SIR_{AA} and R_{AA} , in the Infomax algorithm, are obtained when N_s equals to eight.

V. CONCLUSION

Infomax obtained acceptable results but poorer than those of FastICA. With regard to the N_m parameter in the first environment, FastICA always exceeds the results obtained by the Infomax algorithm in the case of instantaneous mixing ($N_m = 1$). Hence the instantaneous linear mixing model can be considered as an acceptable approximation for the bioelectric mixing in the human body. Given that the instantaneous linear mixing model is the particular case of the convolutive mixing model when N_m is equal to one, we can conclude that CBSS algorithms need an improvement to reach at least the performance of the FastICA algorithm in the case of instantaneous mixing and to obtain better results in the convolutive case.

The Infomax algorithm has been easily adapted to the standard 12-lead real ECG of the second environment, reaching its best performance when a convolutive model ($N_s = 8$) is considered. An in-depth analysis of the Infomax algorithm and its adjustment to the special features of ECG signals could obtain an appropriate algorithm for the extraction of the AA.

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Use of Genetic Algorithms to Optimize Fiber Optic Probe Design for the Extraction of Tissue Optical Properties

Gregory M. Palmer and Nirmala Ramanujam*

Abstract—This paper outlines a framework by which the optimal illumination/collection geometry can be identified for a particular biomedical application. In this paper, this framework was used to identify the optimal probe geometry for the accurate determination of tissue optical properties representative of that in the ultraviolet-visible (UV-VIS) spectral range. An optimal probe geometry was identified which consisted of a single illumination and two collection fibers, one of which is insensitive to changes in scattering properties, and the other is insensitive to changes in the attenuation coefficient. Using this probe geometry in conjunction with a neural network algorithm, the optical properties could be extracted with root-mean-square errors of 0.30 cm^{-1} for the reduced scattering coefficient (tested range of $3\text{--}40 \text{ cm}^{-1}$), and 0.41 cm^{-1} for the absorption coefficient (tested range of $0\text{--}80 \text{ cm}^{-1}$).

I. INTRODUCTION

The diffuse reflectance spectrum, which reflects the absorption and scattering properties of a turbid medium, is sensitive to a number of important physiological indicators and thus, is a useful tool for the early diagnosis of precancers and cancers. The illumination/collection geometry is a critical aspect of tissue diffuse reflectance spectroscopy in that it affects sensitivity to the absorption and scattering properties of the medium, the sensing depth and the signal-to-noise ratio. Specialized probe geometry designs have been previously shown to be useful in characterizing tissue optical properties from diffuse reflectance spectra [1], [2].

This paper outlines a framework by which the optimal illumination/collection geometry can be identified given a particular design objective. Here, the framework is used to identify the optimal probe geometry for the accurate determination of tissue optical properties representative of that in the ultraviolet-visible (UV-VIS) spectral range. The unique benefits of this approach are 1) *no a priori* information is needed about the tissue absorbers and scatterers and 2) there is no requirement for complex multiple source-detector separation fiber probe geometries.

II. METHODS

A. General Optimization Methodology

The optimization methodology proceeds in the following manner. First, a population of fiber probe geometries was randomly initialized. Next, diffuse reflectance measurements were simulated for each of these probe geometries for a wide range of tissue optical properties using Monte Carlo modeling. The *training* data set for each of the probe geometries was used to optimize a neural network algorithm to take the diffuse reflectance as an input, and output the optical properties. The optimized neural network algorithm was applied to an

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G. M. Palmer is with the Department of Radiation Oncology, Duke University, Durham, NC 27710 USA (e-mail: greg.palmer@duke.edu).

*N. Ramanujam is with the Department of Biomedical Engineering, Duke University, Durham, NC 27703 USA. (e-mail: nimmi@duke.edu).

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