An automatic method for separation and identification of Biomedical Signals from Convolutive Mixtures by Independent Component Analysis in the Frequency Domain

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Abstract: - In this study we propose an automatic method for solving convolutive mixtures separation. The independent components are extracted by frequency domain analysis, where the convolutive model can be solved by instantaneous mixing model approach. The signals are reconstructed back in the observation space resolving the ICA model ambiguities. Simulations are carried out to test the validity of the proposed method in convolutive mixtures of electrocardiographic (ECG) and electromyographic (EMG) signals. The algorithm is also tested on real ECG and EMG acquisitions derived from wearable systems.

Key-Words: – Independent component analysis, convolved mixtures, frequency domain, biomedical signals

Introduction

Traditional methods employed to recover the signals of interest in presence of artifacts includes linear and non linear filtering techniques [1], wavelets transformation [2] and adaptive filtering [3].

Other approaches take advantage from multichannel data acquisition. Blind source separation (BSS) tecnhiques are used to recover a set of source signals when only their mixtures are available and neither the sources nor the mixing process are known. Independent component analysis (ICA) [4] is a method to solve the BSS problem that starts from the hypothesis of statistical independence among the original sources originated by different physiological phenomena. This statement entails that components belonging to different physiological phenomena can be extracted from the signals detected by the sensors, even though they overlap in time and frequency.

The basic ICA model assumes an instantaneous mixing process and its applications in removing artifacts from biomedical signals have been presented in several publications [5,6,7,]

In order to take into account the effects of the different paths from the source signals to the sensors and spatio-temporal dynamics (as hypothesised for electroencephalographic data [8]), we propose a method based on blind separation of convolutive mixtures. The observed data are seen as linear mixtures of filtered source signals where neither the source signals nor the convolution and mixing processes are known.

We decided to solve this problem in the frequency domain as this allows us to use fast algorithms developed for the instantaneous mixing problem. This decomposition provides components that can be classified either as 'signal of interest' or as 'signal of no interest'. Choosing a frequency domain approach it was also possible to estimate the original sources only in the spectral bands where they overlap. To perform the artifact removal process, the components of interest are reconstructed back in the original observation space in the channel where they are significant. An approach based on the autocorrelation function of the estimated sources spectrogram is proposed to correctly locate the components in the relevant acquired channels.

A convolutive mixtures of an ECG signal and an EMG is simulated. The decomposition process is carried out to test the effectiveness of the model in practical situations. The algorithm was applied also to remove reciprocal artifacts in signals acquired by wearable systems.

1 Problem formulation

1.1 Istantaneous ICA model

The problem of blind source separation consists in recovering a set of sources $s_j(t)$ from their mixtures $x_i(t)$ when both the sources and the mixing process are unknown. Independent component analysis is a method for solving blind source separation that starts from the hypothesis of statistical independence among the sources. If we consider that mixing process does not involve any delayed version of the sources we can introduce the so called instantaneous ICA model, mathematically expressed by (1):

$$x_i(t) = a_{i1}s_1(t) + \ldots + a_{ij}s_j(t) + \ldots + a_{in}s_n(t) \quad (1)$$

with $i=1,2,...m$, $j=1,2,...,n$ and $t=1,2,...,T$ as we operate with discrete time signals.

We can drop the time index t and assume that each mixture x_j as well as each source s_k is a random variable instead of a proper time signal. Within this framework the information about their time structure is lost and the model only takes into account the statistical properties of the distributions of the variables. Thus, if we denote $x=[x_1,...,x_m]^T$ and $s=[s_1,...,s_n]^T$, we can express (1) in matrix notation:

$$x = As \quad (2)$$

where A is the mixing matrix.

The goal of ICA is to use the general hypothesis of statistical independence, to estimate a matrix W, called the unmixing matrix, such that $y=Wx$ is an estimate of the original sources s. Assuming that the number of observed mixtures is the same as the number of underlying sources ($m=n$), the mixing matrix can be inverted and we can write $W \cong A^{-1}$.

In order to estimate the original sources several methods have been proposed, like the infomax principle [9], minimization of mutual information [10] or the maximum likelihood estimation [11].

Hyvarinen [12] proposed a fixed point algorithm for computing W based on maximization of the nongaussianity of extracted components. The idea takes origin from the central limit theorem, which states that the distribution of a sum of independent random variables, under certain assumption, tends toward a Gaussian distribution. Thus, searching for the directions w_i that maximize the nongaussianity of $y=w_i^T x$, means searching the directions that maximize the statistical independence among such components. Negentropy can be employed, as a measure of non Gaussianity.

As pre-processing step, before performing ICA both a removal of the mean value and a whitening operation using PCA is performed. This operation simplifies the estimation of the unmixing matrix W that becomes orthogonal with only $n(n-1)/2$ degrees of freedom instead of n^2.

The one unit fixed-point algorithm derived by Hyvarinen for withened data, is:

$$\mathbf{w}_i \leftarrow E\{zf(\mathbf{w}_i^T x)\} - E\{f'(\mathbf{w}_i^T x)\}\mathbf{w} \quad (3)$$

where $f(\cdot)$ is a nonlinear function used in order to take into account higher order cumulants that approximate the neg-entropy of the data and can be chosen among $f(y)=tanh(y)$, $f(y)=yexp(-y^2/2)$ or $f(y)=y^3$.

1.2 Convolutive mixtures

The techniques described in the previous paragraph assume that the mixing process is instantaneous, that is each source reaches the sensors at the same time. In some applications this assumption may be too strong since the paths of the signals to each sensor may be different and the finite propagation speed in the medium may generate different time delays. Moreover, some kind of convolution of the original sources may take place, or to spatio-temporal propagations, as has been hypothesized for electroencephalographic activity [8].

Given the above, we decided to modify the basic ICA model and introduce a convolution process between the original sources $s_j(t)$ and the elements a_{ij} of the mixing matrix A, which become the coefficients of unknown FIR filters $a_{ij}(k)$.

$$x_i(t) = \sum_{j=1}^{n} \sum_{k=1}^{L} a_{ij}(k)s_j(t-k) \quad for\ i=1,...,n \quad (3)$$

The problem can be solved in the time domain by using natural gradient methods [13] or as ordinary ICA [14]. It is worth to observe that such methods are computational heavy in order to reach the convergence criteria, so that the frequency domain approach appears more appealing. Fourier transform techniques are useful in dealing with convolutive mixtures, because convolutions become products between Fourier transform in the frequency domain.

To search independent components we need a number of observations of the mixtures for each bin. So we decided to apply a Short Time Fourier Transform (STFT) to split the signal in short-time sliding windows and get the Fourier spectrum in each window, in order to obtain a time-varying spectral description. Consequently the whole separation problem is devided into N linear complex source separation problem, one for every frequency bin [15]. The one-dimensional sequence $x_i(t)$, which is a function of a single variable t, is converted into a two-dimensional function $X_i(f,t)$.

After this transformation the convolutive mixtures model can be represented by the following expression:

$$X_i(f,t) = \sum_{j=1}^{n} A_{ij}(f)S_j(f,t) \quad (4)$$

where $A_{ij}(f)$ are the discrete Fourier transforms coefficients (DFT) of the FIR filters $a_{ij}(k)$ present in the mixing matrix A.

Thus, starting from the statement that the observations are instantaneous mixtures of the original sources in each frequency bin, we can use the original instantaneous unmixing algorithms, introduced in the previous paragraph, to achieve separation of convolved mixtures. But as we are operating with complex valued data we need to reformulate these algorithms and perform two important modification. First we must convert matrix transpositions to Hermetian transpositions (conjugate transpose). Then the nonlinear

functions $f(\cdot)$ must be defined again in the complex domain. We chose to employ $f(y)=tanh(Re\{y\})+tanh(Im\{y\})i$ [15]. The centering and prewhitening operations are not altered working with complex numbers.

The computational load of the algorithm exploits the conjugate symmetry property of the DTF of a real signal. In fact, for an N discrete transform point FFT, only *N/2+1* or *(N+1)/2*, when *N* is even or odd respectively.

So we can apply the modified algorithm independently to each frequency bin obtained from the STFT of the data. The corresponding unmixing matrices can be used to obtain the estimated independent components in different frequencies.

However, in complex ICA, some extra complications occur. In instantaneous ICA it is well known that it is impossible to determine the order in which the independent components are extracted. In fact, as both the independent components and the mixing matrix are unknown, a permutation matrix *P* and its inverse can be substituted in the model *x=AP⁻¹Ps*. The elements of *Ps* are the original independent components in another order and the matrix *AP⁻¹* is just a new unmixing matrix. This permutation ambiguity becomes a serious problem. We need to align the independent components along the frequency bins so that separated components in the time domain contain frequency components from the same source signal.

Several approaches have been proposed in order to solve this permutation invariance. One method consists in smoothing separation matrices by averaging them with the adjacent frequencies one [15]. Another solution was proposed by direction of arrival (DOA) estimation methods, in which source directions are estimated and independent components can be aligned consequently [16]. In this paper we make use of an approach based on inter-frequency correlations [17]. We suppose that two spectral envelopes belonging to the same source have a higher correlation coefficient than the one they would show if they belong to different sources. If we denote the spectral envelope of the component i at frequency f as $v_i^f(t)=\left|Y_i(f,t)\right|$, we can look for neighbouring frequencies that exhibit the highest correlation coefficient. We computed correlation coefficients only for adjacent bins aligning the independent components as they are extracted.

$$corr\left(v_i^f,v_i^{f+1}\right)=\frac{\left[E\{v_i^f\cdot v_i^{f+1}\}-E\{v_i^f\}E\{v_i^{f+1}\}\right]}{\sigma_{v_i^f}\sigma_{v_i^{f+1}}} \qquad (6)$$

where $\sigma_{v_i^f}$ is the standard deviation of $v_i^f(t)=\left|Y_i(f,t)\right|$.

Since the measurements are based on separated signals, this method is precise as long as independent components are well separated by ICA.

Another drawback is that the independent component, in each frequency bin, can be estimated up to a scalar and a phase factor In fact, the model expressed in (5) does not change by multiplying any of the sources $S_j(f,t)$, by a scalar

factor, $\alpha_j\in\Re$, $\alpha_j\neq 0$, which can be cancelled by dividing the relevant column a_j of *A(f)* by α_i: $a_j S_j=(\alpha_j a_j)(\alpha_j^{-1}S_j)$. This operation does not change the statistical distribution of $X_i(f,t)$.

Similarly, there is an unknown phase ϑ_i for each S_j, because $a_j S_j=(\vartheta_j a_j)(\vartheta_j^{-1}S_j)$, with $\left|\vartheta_j\right|=1$ and $\vartheta_j\in$ C.

The phase and scalar factor ambiguities are removed when returning the separate independent components $Y_i(f,t)$ into the original space. This is achieved in the frequency domain as follows:

$$X_i Y_j\left(f,t\right)=[W_f^{-1}]_{ij}Y_j\left(f,t\right) \qquad (7)$$

where $X_iY_j(f,t)$ is the *j*-th estimated independent component observed at the *i*-th detector and $[W_f^{-1}]_{ij}$ is the *ij*-th element of the inverse of the unmixing matrix for the specified frequency bin f. Thus X_iY_j represents the contribute of Y_j in the channel X_i

After performing all this linear transformations, we can group the $X_iY_j(f,t)$ in the following way:

$$X'_i\left(f,t\right)=\sum_j X_i Y_j\left(f,t\right) \quad for\ j=1,...,m \quad (8)$$

If we move j go from *1* to *n*, extending the sum in each channel to the contribute given by all the independent components, we obtain exactly the observed signals. But in the case some independent components returned in the observation space are not significant for the information provided by the channel *j*, they can be set to zero in (8). An example in this sense is given by artifacts removal in multichannel acquisition of biomedical signals. In this case in fact, we could decide, for each channel, that some components are of interest and must be summed in (8) while others can be considered artifacts and must not take part to the sum.

After the selected independent components have been returned to the observation space in the frequency domain, an inverse short time Fourier transform (ISTFT) can be used to obtain the reconstructed signals in the temporal domain.

2 Identifying different sources

Once the independent components have been separated and the permutation problem solved with inter-frequency correlation (6), we need an automatic method to identify the biophysical origin of each time-frequency separated dataset. After this operation is performed, it is possible to select, in each channel, the components of interest that must be returned in the observations frequency space by (7) and (8). Time domain signals are obtained through an ISTFT.

In this work we present two methods to locate the correct sources in the relevant channels and set to zero the artefacts,

starting from their time-frequency representation.

The first approach allows recognizing an almost periodic signal taking advantage of periodicity of its spectrogram in every frequency bin.

A more general approach to identify each detected source in the acquired channels based on principal component analysis is under evaluation. This method requires a training step, using a dataset consisting of spectrograms belonging to m different classes of noise free biosignals, i.e. EMG, ECG, breathing patterns. Each spectrogram can be seen as a vector in R^n, where n is the number of frequency bins. The purpose is to find a transformation from R^n to R^m, with $m<n$, such that the identification of each class is simplified. Once this transformation is found, it can be applied to a new set of spectrograms, derived from the algorithm [18].

As far as the first method, we note that the periodicity observed in one original signal, is still present in the autocorrelation function of the spectrogram, at a fixed frequency bin.

Fig. 1(a) shows the spectrogram of a noise free ECG signal taken from the MIT-BIH database [19]. In fig. 1(b) the mean value of the autocorrelation function, computed over all the frequency bins, is shown. The ECG signal can be considered, with good approximation, a periodic signal, at least for a short observation window of the time signal.
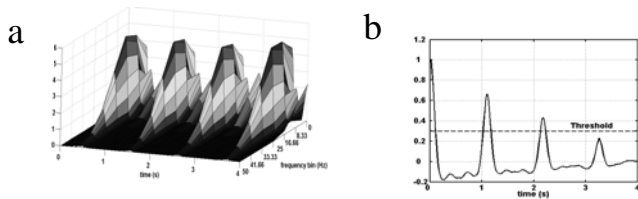

Fig. 1. (a) Spectrogram and (b) relevant autocorrelation function of a 4 seconds ECG obtain with a 120 ms Hamming window with 90% overlap

This pattern for the autocorrelation function can be used to discriminate ECG component from other non periodic components: in fact, in the spectrogram of a signal that has not important periodic components, the time over which a certain pattern is correlated is very short and settles rapidly to zero. Fixing a proper threshold, the area of the autocorrelation function of an ECG component, exceeding a prefixed threshold, will be larger than the other component ones, and this source can be identified.

This method can be useful if we are acquiring an ECG and an EMG signal, corrupting each other, and we desire to separate the original sources from the observed mixture and reconstruct them in the relevant channel. Moreover, in a multichannel acquisition of several ECG leads, we could be interested in separating and dropping all kinds of components not belonging to the ECG signals, like motion artefacts or muscle activity contaminations, which are supposed not to have a periodic evolution.

We suggest to compute the autocorrelation function after

the estimated sources have been returned in the observation space by (7), to overcome the scale indeterminacy of the components in each frequency bin. The comparison among the areas estimated from the autocorrelation function can be carried out in one channel (preferably the ECG lead): once the components have been identified, their order is preserved in other channels as explained by (7). The knowledge of what we expect to observe in each detected signal makes possible to automatically select the interesting components in (8) and set to zero the other ones.

3. Experimental validation of the model

We carried out some simulation studies to test the validity of our method and the assumptions made.

The sources vector $s(t)$ consisted of two real and noise-free signals: one ECG, $s_1(t)$, and one EMG, $s_2(t)$, taken from the MIT-BIH database which is standard for testing ECG algorithms [5]. The EMG recording is a surface registration of the activity of the chin muscles, and both the signals downloaded from the database were sampled at *250 Hz*. The mixing filters were designed to work on the signals frequency bands, which are from *0.3 Hz* to *50 Hz* for the ECG and from *10-20 Hz* and above for the EMG. Note that the generic FIR filter $a_{ij}(k)$ represent the effects produced by each source $s_j(t)$ in the detected signals $x_i(t)$. The elements of A were also chosen to take into account possible time delays that may occur from the source origins to the electrode. Thus $a_{11}(t)$ was a 20 coefficient low pass filter with cut off frequency $f_1=50Hz$ followed by ten zeros, while $a_{12}(t)$ was a shifted but attenuated version of $a_{11}(t)$. In the same way $a_{22}(t)$ was a high pass filter with cut off frequency $f_2=10Hz$ and $a_{12}(t)$ was a shifted but augmented version of $a_{22}(t)$. Fig. 2 shows (a) the original sources s, (b) the FIR filters used and (c) the convolutive mixtures x. Note that a sampling rate equal to $f=250Hz$ correspond to a sampling period $T=4ms$.
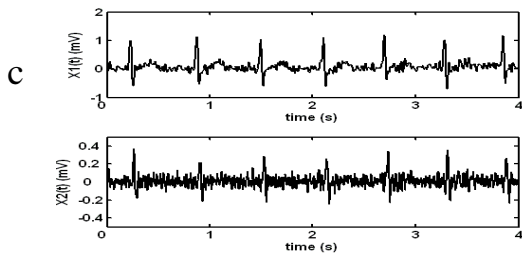
c
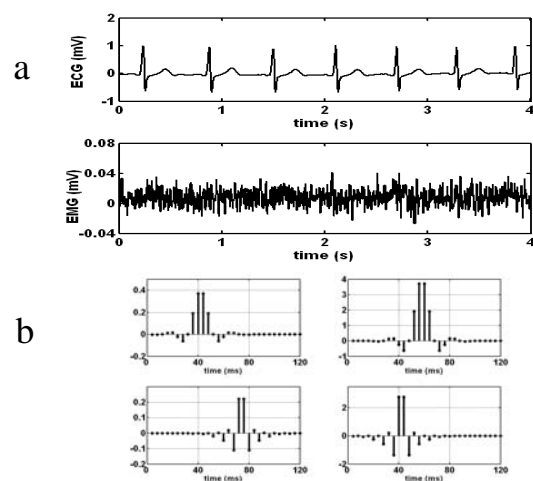
Fig. 2. (a) original sources, (b) convolutive filters, (c) convolved mixtures.

The convolved signals x were analyzed with our method. The STFT was computed with a 30 points (120 ms) Hamming window with a 90% overlap degree. After a centring and a whitening step, the sources were estimated by performing ICA only in those frequencies where the signals overlap (in this experiment between f_1 and f_2) and the frequency bins were aligned by (6).

In order to discriminate the two components we estimated the average autocorrelation function of the spectrogram returned in the observed ECG channel using (7): the autocorrelation function must be averaged only in the frequency band where the ICA is carried out. Fig. 3 shows the autocorrelations and the area exceeding a threshold level equal to 0.3.
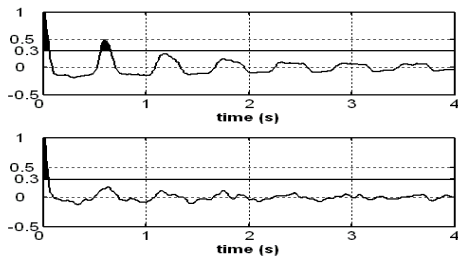

Fig. 3 Averaged autocorrelation functions of the two spectrogram

The black coloured area of the autocorrelation function in the first graph is equal to 7.67 while in the second is 2.3. Thus, the first spectrogram can be automatically associated to the ECG component and the second with the EMG. This result allows to identify the spectrogram of the component of interest for each channel and set to zero in (8) the other one. In the frequency bins, where we didn't carry out ICA, no reconstruction is required and the observations are left unchanged. An inverse short time Fourier transform can be used to obtain the reconstructed signals in the temporal domain. The result of the entire procedure is shown in Fig. 4 where we can observe the two signals without artefacts. In order to give an objective evaluation index we computed the correlation coefficient between the spectrogram of the source signals and the processed ones. The coefficient was computed fixing the frequency bin and this value was averaged between f_1 and f_2. The ECG source and the related processed spectrogram obtained a correlation equal to 0.83
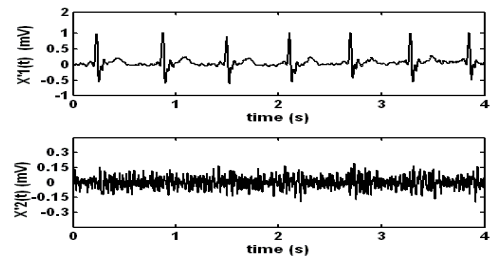
while the two EMG signals 0.75.

Fig. 4. Reconstructed components in acquired channels

4. Results

The algorithm was tested on real biomedical signals acquired by wearable systems. In these systems conductive and piezoresistive materials in form of fiber and yarn are used to realize clothes where knitted fabric sensors and electrodes are distributed and connected to an electronic portable unit.

A bipolar lead DI and an abdominal surface EMG were acquired at a sampling rate of 250 Hz, and then organized in the observation matrix x. The convolutive model analysis was carried out in the same way described in the simulation section. A 30 points Hamming window was employed for the STFT and the spectrogram autocorrelation function was used for automatically discriminating the different components. The detected signals and the ones obtained as result of our analysis are shown in Fig. 5.
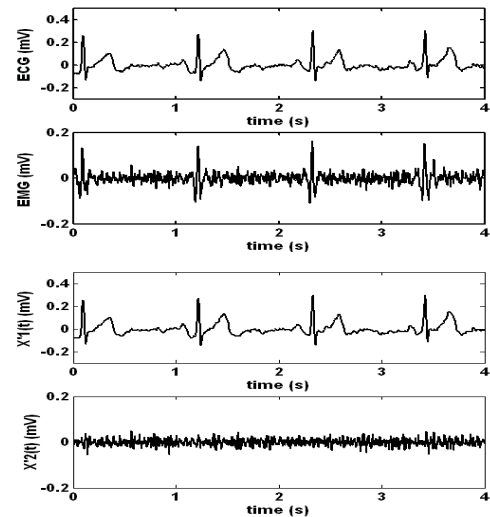

Fig. 5 Acquired and processed signals.

5. Discussion

The separation of independent components from a mixture of observed variables was applied to the multichannel acquisition of bioelectrical signals. Statistical independence has been proven to be a valuable criterion to decompose signals that originate from different physiological sources.

In this work we tested the validity of a convolutive model which is an extension of the instantaneous linear mixing model. Our model should be able to take into account a more realistic generative process of the measured signals, such as differences in propagation paths from the real sources to different sensors and spatio-temporal dynamics. A frequency domain approach to convolutive mixtures separation problem, allows to carry out an ICA analysis only in the frequency bands were the sources overlap.

The indeterminacy in the extraction order of the independent components was solved by aligning the components that showed a higher value of the correlation function computed between adjacent frequency bins. We proposed an approach based on the evaluation of the area subtended by the averaged autocorrelation function of the spectrograms to discriminate the components associated with a periodic signal from others non periodic; the first ones were assumed to exhibit a higher area subtended by the autocorrelation function exceeding a fixed level. Another method to identify different components, based on cluster analysis of sources spectrogram, is under study.

Simulation experiments showed that our algorithm can separate a convolved mixture of an ECG signal and an EMG, and reconstruct them in the relevant channels, without artifacts components. The ECG component was reconstructed more accurately than the EMG (respectively correlation coefficient higher than 0.8 for the ECG and about 0.75 for the EMG).

Our method demonstrated to be successful in artifact removal from biosignals acquired in real life condition by wearable systems. In fact the convolutive model succeeded in separating reciprocal contamination in ECG and EMG signals.

As our method is completely blind (we know nothing about the sources and the mixing process) it may be extended to a wide collection of artifacts that may contaminate biomedical signals.

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