Contents lists available at [ScienceDirect](http://www.ScienceDirect.com)

Computer Methods and Programs in Biomedicine

journal homepage: www.elsevier.com/locate/cmpb

A low-rank matrix factorization approach for joint harmonic and baseline noise suppression in biopotential signals

Miroslav Zivanovicª_'*, Maciej Niegowskiª, Pablo Lecumberri ^b, Marisol Gómez ^b

^a *Electrical Engineering Department, Public University of Navarra, Campus Arrosadía s/n, 31006 Pamplona, Spain* ^b *Mathematics Department, Public University of Navarra, 31006 Pamplona, Spain*

a r t i c l e i n f o

Article history: Received 8 June 2016 Revised 25 December 2016 Accepted 17 January 2017

Keywords: Harmonic noise Baseline noise Low-rank matrix Sparsity Non-negative matrix factorization

A B S T R A C T

Background and objectives: In this paper we propose a novel single-channel harmonic and baseline noise removal approach based on the low-rank matrix factorization theory. It aims to enhance spectrogram sparsity in order to significantly reduce the dimensionality of the underlying sources in the input data. Such a low-rank non-negative representation approach admits efficient noise removal.

Methods: The sparsity is improved by a modification of the time-frequency basis through the following signal processing steps: (1) spectrograms segmentation, (2) non-negative rank estimation, and (3) source grouping. The source waveforms are retrieved by means of non-negative matrix factorization and the overlap-add method. The proposed method was tested on real electrocardiogram and electromyogram signals for different analysis scenarios, against two state-of-the-art reference methods.

Results: Performance evaluation was carried out by means of the output signal-to-interference ratio. In the electrocardiogram analysis scenarios, for the input signal-to-interference ratio as low as −15 dB, the proposed method outperforms the reference methods by 8 dB and 17 dB respectively. Regarding electromyogram denoising, the performance improvement is about 3 dB.

Conclusions: The proposed method was shown to be very efficient in harmonic and baseline simultaneous removing from electrocardiogram and electromyogram signals. Its structure allows for a straightforward extension to other biopotential signals e.g. electroencephalograms and multichannel processing.

© 2017 Elsevier Ireland Ltd. All rights reserved.

1. Introduction

Noise removal is very often a crucial step in processing and interpreting biopotential data. The noise artifacts most commonly encountered in such signals are harmonic (a.k.a. powerline) and baseline noise. Harmonic noise is characterized by a few timevariant harmonic components centered at integer multiples of the fundamental frequency (50 Hz/60 Hz). It typically arises as a combination of several unwanted effects: capacitive coupling between the subject and power lines, differences in the electrode impedances, separation between the electrodes, measurement interconnections, to name a few $[1-4]$. Baseline noise is defined as a long-term drift (slowly-varying DC component) whose frequency range usually falls below 1 Hz $[5]$. It is mainly caused by subject's movements during the measurements, spatial-variant electrodeskin impedance and breathing $[6-8]$. Both noise sources spectrally

Corresponding author.

E-mail addresses: miro@unavarra.es (M. Zivanovic),

maciej.niegowski@unavarra.es (M. Niegowski), pablo.lecumberri@unavarra.es (P. Lecumberri), marisol@unavarra.es (M. Gómez).

cited. To the best of our knowledge, only a few approaches deal jointly with both noise sources: FIR filtering [\[26\],](#page--1-0) fractal and empirical mode decomposition [\[27\]](#page--1-0) and sinusoidal modeling [\[28\].](#page--1-0)

Herein we focus our attention on matrix sparsity and nonnegative rank, which are one of the most prominent concepts of the low-rank matrix decomposition theory [\[29,30\].](#page--1-0) Briefly, it states that a large matrix with a small number of significant non-negative

overlap with frequency bands that contain clinically relevant information. Moreover, the useful signal instantaneous amplitude is often very close to the noise level, giving rise to low signal-to-noise ratio (SNR) measurements. Accordingly, to ensure minimal signal distortion while suppressing the artifacts is a very difficult task. Related work encompasses a number of approaches where the problem of harmonic and baseline noise removal was usually treated separately. Amongst the approaches that aim at suppressing the harmonic noise the most salient are notch filtering [\[9\],](#page--1-0) adaptive filtering $[10-15]$, outlier detection $[16]$, component subtraction [\[17,18\],](#page--1-0) intrinsic mode decomposition [\[19\],](#page--1-0) wavelet analysis [\[20\].](#page--1-0) Regarding baseline removal problem, the research focus was set on high-pass filtering [\[21\],](#page--1-0) adaptive filtering [\[22\],](#page--1-0) curve fitting [\[23,24\],](#page--1-0) empirical mode decomposition [\[25\],](#page--1-0) to name the most

<http://dx.doi.org/10.1016/j.cmpb.2017.01.008> 0169-2607/© 2017 Elsevier Ireland Ltd. All rights reserved. entries can be replaced by a lower rank matrix, providing a more efficient representation of the relationship between data elements. Such a matrix brings out the most relevant components of the data while, at the same time, mitigating the effect of possible disturbances. Harmonic and baseline noise are time-variant narrow-band signals which are almost sparse in the time-frequency (TF) domain i.e. their individual spectrograms can be compactly described by non-negative vectors/matrices of a very small rank. However, in presence of a biopotential signal, this convenient description often does not hold for two reasons. On the one hand, some biopotential signals are wide-band signals (e.g. EMG) which spectrally encompass the harmonic and baseline noise. As a biopotential signal is usually the dominating source in the data, the sparsity condition of the harmonic and baseline noise might be seriously degraded. On the other hand, we cannot uniquely determine the non-negative rank of individual sources in the data if no additional information on the mixing system is available. A usual shortcut to this problem is to assign a user-defined rank to each source and then tune them up by some iterative trial-and-error input matrix decomposition procedure. Such an approach is computationally costly and is not guaranteed to converge to optimal individual ranks.

Recently there have been a few attempts which aimed at separating ECG–EMG signal mixtures by making use of sparsity and unsupervised learning algorithms based on NMF [\[31,32\].](#page--1-0) The former focused on enhancing the sparsity of the ECG spectrogram by filtering and downsampling the input signal, thus bringing out the QRS complexes against the EMG background. The latter processed input data by the wavelet transform with adequately chosen basis functions (Cauchy-type non-linearly scaled wavelets) which captured the basic ECG waveforms shapes with a relatively small number of wavelet coefficients. Both methods provided a sparse ECG TF representation which was used as the initialization for the NMF algorithms and they both achieved a very good ECG–EMG separation compared to the existing state-of-the-art techniques. However, both methods have important drawbacks, namely: (1) they do not work with data containing more than two signal sources, (2) their performance largely depends on the analysis window size used to generate TF representations, and (3) they always consider unitary rank matrix description independent of the signal source dynamics.

The present application deals with separating more than two sources from the input mixture; therefore, the above methods could not be used in the current form. Adopting the general approach based on sparsity and unsupervised learning, we propose a novel method which poses the harmonic and baseline noise removal task as a source separation problem (the preliminary re-search in the context of EMG denoising was discussed in [\[33\]\)](#page--1-0). The proposed method overcomes the aforementioned drawbacks by introducing new algorithm features, namely: unambiguous nonnegative rank estimation of individual sources in the data and phase-preserving spectrogram segmentation. Optimal non-negative rank is a key factor in any non-negative matrix decomposition because: (1) it provides a way to drastically reduce problem dimensionality without losing any relevant characteristic of the underlying source; (2) it allows for fast convergence of the NMF algorithms. However, existing algorithms for computing the nonnegative rank introduce a prohibitively high computational cost, which impedes its use in on-line applications. Herein we develop a study which (1) discusses a general relationship between standard and non-negative matrix rank, and (2) shows under which circumstances those ranks can be used interchangeably in the context of the present application. A major benefit of this study is that the estimation of the non-negative rank can be carried out by an economy-size singular value decomposition (SVD), which drastically relaxes the algorithm's overall computational cost. Furthermore, we introduce a spectrogram segmentation procedure which aim at coarse separation of underlying signal sources in the TF domain by means of a set of data-driven spectrogram shaping vectors. Such a segmentation scheme ensures that no spectral phase modification occurs; accordingly, the estimated signal component waveforms are virtually distortionless.

By combining these novel features with NMF, our algorithm achieves an unambiguous and physically meaningful signal-noise separation from the spectrogram of the input data in only a few computational iterations. Moreover, such a separation strategy was proven experimentally to be especially efficient in data acquisitions with very low SNR.

2. Methods

As we deal with matrices with non-negative entries, it is assumed that the signal to be processed $x \in \mathbb{R}^m$ is in the form of the Short-Time Fourier Transform: $STFT{x} = X \circ \Theta$, $X \in \mathbb{R}_+^{m \times n}$ and $\Theta \in \mathbb{C}^{m \times n}$, where *m* equals the number of frequency bins in [0, π) rad/sample, *n* is given by the number of overlapped short-time segments, whilst the operator '◦' stands for the Schur-Hadamard entry-wise multiplication. Thus, *X* contains the amplitudes whilst Θ encodes the phases in the form of unitary-magnitude complex exponentials. Accordingly, the squared modulus of the STFT provides a spectrogram matrix *S* = X◦X.

2.1. Spectrogram segmentation

Let us assume that the number of concurrent sources in the input record is *N*, which typically encompasses the desired biopotential source plus interferences and perturbations of either a deterministic or a random nature. Starting from *S* we seek to obtain *N* sub-spectrograms $S_i \in \mathbb{R}_+^{m \times n}$, $i = 1,...,N$ such that S_i contains most of the energy of the *i*th source plus energy-attenuated contributions from the remaining sources. If we express $S = (s_1, ..., s_n)$ with $s_k \in \mathbb{R}_+^m$, $k=1,...,n$ being column vectors, the sub-spectrograms are obtained:

$$
S_i = (s_1^{\circ}h_i, \dots, s_n^{\circ}h_i), \quad i = 1, \dots, N,
$$
\n
$$
(1)
$$

where $h_i \in \mathbb{R}^m$ are spectrogram shaping vectors. The shapes of h_i are determined under the assumption that the number and nature of the underlying sources is known. It is very important to highlight that spectrogram shaping is not equivalent to filtering. With spectrogram shaping the phase information is fully preserved, which is crucial for the final time-domain conversion step [\(Section](#page--1-0) 2.4). As an illustration, [Fig.](#page--1-0) 1 shows the vectors *hi* for an input EMG recording corrupted by baseline and harmonic noise.

Algebraically, the sub-spectrograms (being rough TF estimates of the underlying sources) are matrices where a certain number of rows (spectra) contain entries close to zero. This is especially true for the noise sub-spectrograms due to the highly selective performance of the shaping vectors. Accordingly, these matrices are almost sparse because rather than being exactly zeros, the entries are relatively small numbers. Such approximately sparse matrices admit important dimensionality reductions where optimal non-negative rank estimation plays a key role.

2.2. Non-negative rank estimation

At this point we must first differentiate between standard rank and nonnegative rank. The standard rank of a matrix, as revealed by the SVD for instance, is the size of the largest set of its columns (or rows) that are linearly independent. However, for a non-negative matrix we need to consider the non-negative rank which is defined as follows [\[34\].](#page--1-0)

Download English Version:

<https://daneshyari.com/en/article/4958190>

Download Persian Version:

<https://daneshyari.com/article/4958190>

[Daneshyari.com](https://daneshyari.com)