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Signal (Stream) synchronization with *White noise* sources, in biomedical applications

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ABSTRACT

When multiple acquisition systems are used to simultaneously acquire signals, synchronization issues may arise potentially causing errors in the determination of acquisition starting points and continuous clock offsets and shifts on each device. This paper introduces a processing method to efficiently synchronize these signals in the presence of white noise sources without the requirement of clock sharing or any other digital line exchange. The use of a signal source, such as white noise with a very wide frequency band, is of great interest for synchronization purposes, due to its aperiodic nature. This high bandwidth signal is simultaneously acquired by all the acquisition channels, on distinct systems, and, synchronized afterwards using cross-correlation methods. Two different correlation methods were tested; a global method, used when clock system frequencies are exactly known, and a local method, used when independent clocks evidence shifts over time that cumulatively account for long term acquisition errors in the synchronization process. In a computational simulation with known clock frequencies the results show a synchronization error of ≈1/10 of the time resolution, for both methods. For unknown clock frequencies, the global method achieved an error of 24/10 the time resolution, indicating a much poorer performance. In the experimental set-up, only the local method was tested. The best result shows a synchronization error of 4/10 of the time resolution. All the signal conditioning and acquisition parameters were chosen taking into account potential biomedical applications.

1. Introduction

The human body is a highly complex system which is composed by many subsystems with specific functions. The assessment of human health condition is made by visual observation or biomedical signals acquisition. These signals can be composed by multiple variables (different physical quantities) which are measured at different body locations [1]. Some examples of biomedical signals are: body temperature; bio-electric potentials; arterial blood pressure (ABP); or respiratory rate [2].

The assessment of multiple biomedical signals is a common medical situation that produces valuable information to improve clinical diagnosis. Usually, biomedical signals are acquired by different devices, each one with its own acquisition set-up. Different equipments have different sampling frequencies, resolutions, ranges, signal-to-noise-ratios (SNR) and temporal references [3].

The absence of a common temporal reference between signals occurs when multiple signals are acquired from the same patient. This situation makes the combined analysis of these signals extremely difficult. A common situation in biomedical applications is the use of different acquisition modules, from different manufacturers, each one with a specific internal clock source. The inclusion of an external clock is often very difficult or impossible. Even if the clocks are equal, an offset in the starting points of the acquisitions appears.

To overtake these issues, it is mandatory to have a time reference, of some sort, in order to guarantee the synchronization of independent data streams. This work proposes a scheme where an electronic circuitry (*white noise* generator) is used to automatically synchronize data signals acquired from different devices and setups.

This technique is based on the acquisition of a random signal (*white noise*) by all the data acquisition systems (DAS) during their normal operation. The biomedical signal must be internally synchronized with the random signal by each device. Thereafter, these random signals are processed using cross-correlation methods to determine the delay between each physiological signal and to build a common temporal reference. Cross-correlation is a widely used method for delay determination in random shifted signals [4–6], including for biomedical purposes [7].

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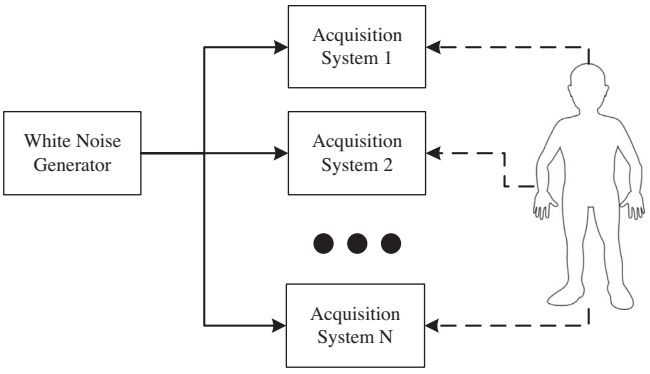

Fig. 1. Block diagram for hardware connections.

2. Methods

2.1. General approach

The proposed methodology requires an external hardware implementation that generates the synchronization signal (*white noise* generator). This signal is digitized by all the DAS (Fig. 1). At this point, one should say that this requirement is a drawback because the majority of the biomedical devices, used in clinical practice, do not allow either hardware or firmware changes. Nevertheless, in research areas that use laboratory-phase equipment, these changes are easily applied.

White noise is a random nature process with constant spectral density (Eq. (1)), *i.e.*, all the frequencies presented in the spectrum have the same power. Moreover, it presents a Gaussian probability density function (PDF) given by Eq. (2) [8].

$$|H(jw)|^2 = \text{constant} \tag{1}$$

$$p(x) = \frac{e^{-((x-\mu)^2/2\sigma^2)}}{\sigma\sqrt{2\pi}} \tag{2}$$

where $p(x)$ is the PDF, μ is the mean of the distribution and σ is the standard deviation. In the frequency domain, the *white noise* is characterized by a constant distribution, yielding a theoretical infinite bandwidth (Eq. (1)), which means that two adjacent samples are completely independent. The randomness of *white noise* makes it aperiodic, in other words, a signal with infinite period.

The autocorrelation of a periodic function ($P \in \Re$) (Eq. (3)) is itself periodic with the same period.

$$\nexists P \in \Re : f(x+P) = f(x) \tag{3}$$

A correlation is performed between two synchronization signals acquired by different DAS and delayed by a certain number of samples. The autocorrelation becomes a cross-correlation but the considerations about periodic and aperiodic signals are still valid [9,10].

To our application, the correlation can be written as Eq. (4) where the correlated signals are the same ($x[n]$) but with one of them delayed by a random number of samples (δ).

$$c_{xx}[k] = \frac{1}{N}\sum_{n=0}^{N-1} x[n]x[n+\delta+k] \tag{4}$$

where x is the synchronization signal and N represents the number of samples of the largest signal. The result from the cross-correlation is a measure of the similarity of both signals as function of the delay k.

2.2. Computational simulation

A simulation was conducted to prove the concept of *white noise* synchronization using cross-correlation. This simulation started with the generation of a random signal with a Gaussian PDF (S_{noise}), with a large sampling frequency ($f_s^0 = 1$ MHz) and 20 s length. Fig. 2 (left) shows the histogram of the S_{noise}, which is similar to a Gaussian function with a zero mean and a standard deviation equals to one. The spectrum is presented in Fig. 2 (right). Although with some fluctuations, the spectrum is constant for all the frequencies. These fluctuations occur due to the existence of a finite number of samples.

To prevent the cross-correlation to be periodic, a signal with infinite bandwidth is the perfect solution. However, the complete independence of two consecutive samples in S_{noise} cause problems after the digitalization. Fig. 3 shows two signals (S_1 and S_2), that result from the downsampling of the S_{noise}, with the same frequency and delayed by only one sample. Signals are completely different from each other.

Moreover, by the Nyquist theorem, when the signal is digitized at a specific sampling frequency (f_s), the resulting bandwidth is restricted in the range $[0, f_s/2]$. Aliasing occurs when the original data has frequencies above this limit distorting the digitized data. These limitations can be bypassed with the use of a low-pass filter.

A low-pass filter limits the bandwidth of the synchronization signal and causes samples to be dependent on past values. The cut-off frequency selection is the key point in the design of the method. To choose a correct frequency it is necessary to take into account the sampling frequencies used by all the DAS. A high cut-off frequency will lead to aliasing but a low cut-off frequency can compromise the correlation and cause a periodic output where it is difficult to compute the real delay between signals.

The selection of the digitalization sampling rate depends on the acquired physiological signals. For example, ECG sampling rate vary from 125 Hz to 1 kHz [11,12], pulse oximetry from 125 Hz to 1 kHz [13–15] and pulse waveform from 1 kHz to 20 kHz [16,17]. Only in special cases higher frequency rates are utilized [18].

According to that information, a minimum sampling rate of 2000 samples/s was considered, leading to an anti-aliasing second order (Butterworth) low-pass filter with a cut-off frequency of 1 kHz. This frequency ensures enough precision for biomedical applications and prevent the occurrence of a periodic signal. The filter transfer function is defined as:

$$|H(j\omega)| = \frac{1}{\sqrt{1+(\omega/\omega_c)^4}} \tag{5}$$

where ω_c is the cut-off angular frequency in rad/s.

Fig. 4 shows the frequency response of the applied filter (red). This response is characteristic of a second order low-pass filter with a roll-off of 40 dB/decade. The spectrum signal (blue) shows the filtered *white noise* signal spectrum. This new signal would be denominated S_{rand}. The amplitude of the spectrum decreases above 1 kHz but high frequencies are not completely extinguished.

Low order filters (first and second) are suitable for this application since the existence of some high frequencies is not a critical issue and the selection of a cut-off frequency of 1 kHz ensure sufficient precision for biomedical applications.

2.2.1. Global method

The S_{noise} was intentionally created with a large number of samples, to allowing for a simulation of the acquisition process. This simulation requires a downsampling of the signal with a fixed sampling rate and delay. Two different DAS have been simulated with sampling frequencies of 20 kHz and 2000 Hz and with a random delay between the starting points. No external noise (*e.g.*