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Selection of statistical indices in the biospeckle laser analysis regarding filtering actions

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ABSTRACT

This paper tests some traditional methods to analyze dynamic laser speckle regarding their filtering actions. Additionally, we propose two new biospeckle indices based on the binary entropy, including one that avoids filtering the original signals. The work was based on theoretical developments and was validated using a drying paint monitoring test. We proved that the dynamic laser speckle, or biospeckle, is compromised by filtering actions and that it is possible to elect an index that does not provide filtering.

1. Introduction

The dynamic laser speckle phenomenon is a source information in an illuminated material, and its ability to monitor activity started to be used not far from when the first laser was built. Additionally, as long as the phenomenon presented a reliable alternative to monitor the multitude of changes originated in biological samples, it was also named as biospeckle laser [1].

In order to viabilize the biospeckle laser phenomenon as a feasible sensor, many approaches have been made to suggest experimental configurations and, particularly, signal processing strategies. The autocorrelation of the speckle pattern in time was one of the alternatives presented [2,3] using the space–time speckle [2,4] or the whole matrix in time [3] to measure the memory of a signal and from that to extract a number which we call as an index. In turn, the space–time speckle, also known as time history of the speckle pattern [5], was likely used in second order statistics procedures such as the Inertia Moment (IM) method [5] or in its derivative the Absolute Value of the Differences (AVD) method [6]. All these methods are known as numerical methods and they are applied in homogeneous regions of interest (ROIs). In other hand, beyond the numerical methods, there are many approaches that create maps of activity from the pattern's collections using the same principle adopted in the numerical outcomes, i.e., the subtraction of consecutive patterns [7–9].

Therefore, since we are working with signal in time, some operations represent the filtering of frequencies that could be useful to associate the outcome of biospeckle laser to the biological phenomena under monitoring. Frequency analysis associated to biospeckle laser proved that the signal can be split and that some components are linked to different sources of the biological activity [10,11].

Our hypothesis is that most of the known methods damp the signal in a way that compromise the correlations of the biospeckle indices with the biological activity. Thus, the aim of this work was to prove that some methods can damp frequency components of the biospeckle laser signal, additionally presenting an alternative index free from damping.

2. Entropy and standard deviation

To get a signal interpretation perspective, from point of view the statistic and the information theory, it is important to know some operations very implemented in these fields; thus, we have the standard deviation and the entropy. These operations have been proved, in the literature, as important tools to describe the temporal behavior of the signals. In the next sections we describe the characteristics of these operations with more details.

2.1. Entropy of a digital signal

The (binary) entropy [12,13] $H_b(X)$ of a random variable X that represents a digital signal $X(k)$ is defined by Eq. (1):

$$H_b(X) = -\sum_{i=0}^{M-1} \Pr(X = x_i)\log_2(\Pr(X = x_i)); \tag{1}$$

where $\Pr(X = x_i)$ is the probability of an arbitrary value of the random variable X be equal to $\{x_0, x_1, \ldots, x_{M-1}\}$, where M is the number of quantization levels of $X(k)$.

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The entropy $H_b(X)$ represents the amount of bits that are necessary as minimum to transmit the information contained in each sample of $X(k)$. Thus, if we choose M different quantization levels to map the value of each sample of $X(k)$ and we code these with $\log_2(M)$ bits per sample, after the calculus of entropy, we note that the information contained in each sample of the signal $X(K)$ can be compressed to $H_b(X)$ bits, and consequently exist a codification method that only would need $2^{H_b(X)}$ quantization levels. So that

$$H_b(X) \leq \log_2(M). \tag{2}$$

The entropy $H_b(X)$ measures the information produced by a randomness level in the amplitude values of each sample of a random variable X, not considering the temporal position (frequency of signal) or amplitude values (signal power) of samples. For example, given a digital signal $X(k)$; if we define the digital signal $X_f(k)$, as a temporal reordering of the samples of $X(k)$ in increasing order of amplitude, and the digital signal $X_p(k) = 10X(k)$; then we can assure that $H_b(X) = H_b(X_f) = H_b(X_p)$.

2.1.1. Normalized entropy

Usually we want to compare the quantity of information of X (this is $H_b(X)$) in relation to the quantity of bits by sample, $\log_2(M)$, used in your codification, and thus to know if the randomness of X justify the use of this bits quantity. Therefore, the entropy can be normalized to have a maximum value of 1.0 and here we define the normalized entropy of X in Eq. (3):

$$H_N(X) \equiv \frac{H_b(X)}{\log_2(M)} \tag{3}$$

so that $0 \leq H_N(X) \leq 1$.

2.2. Relation between the standard deviation and the mean deviation

If we have a random variable X with a Gaussian distribution (mean μ_X and standard deviation σ_X), that represents a signal $X(k)$ with L samples; then, for a very large number L of samples ($L \to \infty$), we can get experimentally the next values,

$$\mu_X \equiv \sum_{l=0}^{L-1} X(l), \tag{4}$$

$$\sigma_X^2 \equiv \sum_{l=0}^{L-1} |X(l) - \mu_X|^2; \tag{5}$$

thus, the relation [14] between the mean value μ_X, the standard deviation σ_X and the mean absolute deviation d_X, can be expressed by Eqs. (6) and (7)

$$d_X \equiv \sum_{l=0}^{L-1} |X(l) - \mu_X|, \tag{6}$$

$$\frac{d_X}{\sigma_X} \overset{L\to\infty}{=} \sqrt{\frac{2}{\pi}} \tag{7}$$

3. Biospeckle indices

3.1. Initial concepts

In relation to biospeckle analysis, there are many types of indices (biospeckle indices) that use light intensity returned from samples as speckle patterns (biospeckle signal), to measure indirectly the activity level of a biological material (biological activity). These biospeckle indices show some characteristics of the biospeckle signal; so that, additional studies must be responsible to set the relation between these characteristics with the biological activity, see Fig. 1; in this sense, here we encourage to use the term biospeckle index instead of "activity index" or even "biospeckle activity" [3] because it is necessary to establish whether there is a linear, nonlinear, direct or inverse relation between the biological activity and the biospeckle index.

Thus, to understand all this process it is necessary to have a clear definition of biological activity, biospeckle signal and biospeckle index, among others.

3.1.1. What is the biological activity?

Mosby's Dictionary of Medicine [15] defines biological activity as: "the inherent capacity of a substance, such as a drug or toxin, to alter one or more chemical or physiological functions of a cell, tissue, organ, or organism". Knowing this, it is easy to see that the biological activity is related to many parameters, so that the measured biospeckle signal has the information of a mixture of all these parameters, and additionally the information of the sample setup; for example, the laser light power, incidence angle of beam, frequency sampling, etc.

3.1.2. What is the biospeckle signal?

Given that the analysis of biospeckle phenomenon is based on processing the information of a pixel set, it is better to define the biospeckle signal in terms of a light intensity, $I(k)$, of a generic pixel in the instant k; being $I(k)$ a digital function with a range of values, traditionally, between $0 \leq I(k) \leq 255$. Thus, we define biospeckle signal as the set of samples obtained of the function $I(k)$ when we evaluate each value of k, $\forall\ 0 \leq k \leq L-1$, being L the number of samples of signal.

3.1.3. What is the biospeckle index?

A biospeckle index is a number, returned after performing a digital signal processing, and it represents or describes one or more characteristics of the biospeckle signal. The relation between the biospeckle index and these characteristics can be linear or not, but it is desirable that they have a biunivocal correspondence.

Many biospeckle indices were designed to describe the behavior of a specific characteristic of a biospeckle signal $I(k)$. These analyses were made focusing in statistical or frequency behavior, among others. In the next subsections it is shown some types of signal processing and biospeckle indices seen in the literature.

3.1.4. Time history speckle pattern

The time history speckle pattern (*THSP*) is a matrix that is created performing a digital processing over the biospeckle signal, and it is used to group samples of light intensities in a set of φ pixels $\{I_0, I_1, I_2, \ldots, I_{\varphi-1}\}$, so that each line of this matrix contains L samples of one pixel separated by columns. Eq. (8) represents the k-th column of the *THSP* matrix,

$$THSP(:,k) = \begin{pmatrix} I_0(k) \\ I_1(k) \\ I_2(k) \\ \vdots \\ I_{\varphi-1}(k) \end{pmatrix}, \tag{8}$$

by other side, a line is represented by Eq. (9)

$$THSP(m,:) = (I_m(0) \ \ldots \ I_m(k) \ \ldots \ I_m(L-1)) \tag{9}$$

meaning all samples of m-th pixel, so that $I_m(k) \equiv THSP(m,k)$.

3.1.5. Normalized co-occurrence matrix

The normalized co-occurrence matrix (*NCOM*) [16,5] is represented by the variable N and it can be extracted from the *THSP* matrix, showing the probability of a pixel $I(k)$, or set of pixels in the *THSP*, to have a light intensity jump from a value $I(k) = i$ to a value $I(k+1) = j$ at any instant k. Thus, the element $N(i,j)$ of the matrix N represents

$$N(i,j) \equiv \Pr(i \to j). \tag{10}$$

Given that, the measured light intensity level, i and j, in a pixel is