An Automatic Sequential Smoothing Method for Processing Biomechanical Kinematic Signals

F.J. ALONSO*, F. ROMERO, D.R. SALGADO
Department of Mechanical, Energetic and Material Engineering
University of Extremadura
Escuela de Ingenierías Industriales, Avda. de Elvas s/n, 06006, Badajoz
SPAIN
fjas@unex.es http://www.unex.es/investigacion/grupos/dedalo

Abstract: - The combined application of Singular Spectrum Analysis (SSA) and Cluster Analysis to the automatic smoothing of raw kinematic signals is an alternative to the use of traditional digital filtering and spline based methods. SSA is a non parametric technique that decomposes original time series into a number of additive time series each of which can be easily identified as being part of the noise present in the acquired signal. Nevertheless, the smoothing automation is not a trivial task. This work presents a heuristic automatic smoothing procedure for processing kinematic biomechanical signals based in sequential SSA. Cluster analysis is used to group the SSA decomposition in order to obtain several independent components in the frequency domain. The procedure eliminates iteratively the noise present in the signal in a simple and intuitive way. The new method is applied to several signals to demonstrate its performance.

Key-Words: - Signal processing, Smoothing, Noise removal, Singular Spectrum Analysis, Signal differentiation, Automatic smoothing, Cluster analysis.

1 Introduction

Motion capture systems used in biomechanical analysis introduce introduce systematic and random measurement errors that appear in the form of high-frequency noise in the recorded displacement signals. Raw displacement signals must be filtered or smoothed prior to differentiation to avoid noise amplification due to the ill-posed derivative estimation process [1-3].

The filtering of displacement signals to obtain noiseless velocities and accelerations has been extensively treated in the literature. Traditional filtering techniques include Digital Butterworth filters, splines, and filters based on spectral analysis [1-5]. In order to filter non-stationary signals, advanced filtering techniques like Discrete Wavelet Transforms [6], the Wigner Function [7-8], non-stationary Butterworth filter [9] and Singular Spectrum Analysis (SSA) [10] have been used. Nonetheless, the drawback in these cases is the complexity of devising an automatic and systematic procedure. A mother wavelet function must be selected when using Discrete Wavelet Transforms, the filtering function parameters must be chosen when using the Wigner Function, window length and grouping strategy must be selected when using SSA [10].

The goal of this paper is to demonstrate the advantages of automatic smoothing methods based on sequential Singular Spectrum Analysis (SSA) and cluster analysis techniques.

SSA is a non-parametric technique that decomposes original time series into a number of additive time series each of which can be easily identified as being part of the noise present in the acquired signal.

This work presents a heuristic automatic smoothing procedure for processing kinematic biomechanical signals based on sequential SSA. Cluster analysis is used to group the SSA decomposition in order to obtain several independent components in the frequency domain. The procedure then applies sequential SSA to eliminate iteratively the noise present in the signal in a simple and intuitive way.

2 Singular Spectrum Analysis

Singular spectrum analysis is a novel nonparametric technique of time series analysis based on principles of multivariate statistics. It decomposes a given time series into an additive set of independent time series. The set of series resulting from the decomposition can be interpreted as consisting of a trend representing the signal mean at each instant, a set of periodic series, and an aperiodic noise [11].

The original application of SSA was to extract trends from climatic and geophysical time

series and to identify periodic motion in complex dynamical systems.

The SSA method builds a Hankel matrix, called the trajectory matrix, from the original time series in a process called embedding. This matrix consists of vectors obtained by means of a sliding window that traverses the series. The trajectory matrix is then subjected to a singular value decomposition (SVD).

The SVD decomposes the trajectory matrix into a sum of unit-rank matrices known as elementary matrices. Each of these matrices can be transformed into a reconstructed time series. Elementary matrices are no longer Hankel matrices, but an approximate time series may be recovered by taking the average of the diagonals (diagonal averaging). The resulting time series are called principal components [11]. The sum of all the principal components is equal to the original time series.

The objective is to obtain a frequency decomposition of the original signal in which the latent low-frequency signal can be detected in a simple fashion. The SSA decomposition algorithm will be described in the following. A more detailed explanation may be found in Golyandina et al. [11]. The above description of SSA may be expressed in formal terms as follows:

Step 1. Embedding

Let $\mathbf{F} = (f_0, f_1, ..., f_{N-1})$ be the length N time series representing the original signal. Let L be the window length, with $1 < L < N$ and L an integer. Each column $\mathbf{X}_j$ of the Hankel matrix corresponds to the "snapshot" taken by the sliding window: $\mathbf{X}_j = (f_{j-1}, f_j, \ldots, f_{j+L-2})^T$, $j = 1, 2, \ldots, K$ where $K = N - L + 1$ is the number of columns, i.e., the number of different possible positions of the said window. The matrix $\mathbf{X} = (\mathbf{X}_1, \mathbf{X}_2, \ldots, \mathbf{X}_K)$ is a Hankel matrix since all elements on the diagonal $i + j = c$ are equal. This matrix is sometimes referred to as the trajectory matrix. The form of this matrix is:

$$\mathbf{X} = \begin{pmatrix} f_0 & f_1 & \cdots & \cdots & f_{N-L} \\ f_1 & f_2 & \cdots & \cdots & f_{N-L+1} \\ \vdots & \vdots & \ddots & \iddots & \vdots \\ f_{L-2} & f_{L-3} & \iddots & \ddots & f_{N-1} \\ f_{L-1} & f_{L-2} & \cdots & \cdots & f_N \end{pmatrix} \quad (1)$$

Step 2. Singular value decomposition (SVD) of the trajectory matrix.

It can be proven that the trajectory matrix (or any matrix, for that matter) may be expressed as the summation of d rank-one elementary matrices $\mathbf{X} = \mathbf{E}_1 + \mathbf{E}_2 + \ldots + \mathbf{E}_d$, where d is the number of non-zero eigenvalues of the $L \times L$ matrix $\mathbf{S} = \mathbf{X} \cdot \mathbf{X}^{\mathbf{T}}$. The elementary matrices are given by $\mathbf{E}_i = \sqrt{\lambda_i}\,\mathbf{U}_i \cdot \mathbf{V}_i^{\mathbf{T}}$, $i = 1, 2, \ldots, d$, where $\lambda_1, \lambda_2, \ldots, \lambda_d$ are the non-zero eigenvalues of $\mathbf{S} = \mathbf{X} \cdot \mathbf{X}^{\mathbf{T}}$ in decreasing order, $\mathbf{U}_1, \mathbf{U}_2, \ldots, \mathbf{U}_d$ are the corresponding eigenvectors, and the vectors $\mathbf{V}_i$ are obtained from $\mathbf{V}_i = \mathbf{X}^{\mathbf{T}} \cdot \mathbf{U}_i / \sqrt{\lambda_i}$.

The norm of elementary matrix $\mathbf{E}_i$ equals $\sqrt{\lambda_i}$, so that, the contribution of the first matrices to the norm of $\mathbf{X}$ is much higher than the contribution of the last matrices. Therefore, it is likely that these last matrices represent noise in the signal. The plot of the eigenvalues in decreasing order is called the singular spectrum, and gives the method its name.

Reconstruction (diagonal averaging)

At this step, each elementary matrix $\mathbf{E}_i$ is transformed into a principal component of length N by applying a linear transformation known as diagonal averaging or Hankelization. The elementary matrices are not themselves Hankel matrices, so that to reconstruct each principal component one calculates the average along the diagonals $i + j = c$. The diagonal averaging algorithm [11] is as follows:

Let $\mathbf{Y}$ be any of the elementary matrices $\mathbf{E}_i$ of dimension $L \times K$, the elements of which are y_{ij}, $1 \le i \le L, 1 \le j \le K$. The time series $\mathbf{G} = g_0, g_1, \ldots, g_{N-1}$ (the principal component) corresponding to this elementary matrix is given by:

$$g_k = \begin{cases} \dfrac{1}{k+1} \displaystyle\sum_{m=1}^{k+1} y_{m,k-m+2} & \text{for } 0 \le k < L^* - 1 \\ \dfrac{1}{L^*} \displaystyle\sum_{m=1}^{L^*} y_{m,k-m+2} & \text{for } L^* - 1 \le k < K^* \\ \dfrac{1}{N-k} \displaystyle\sum_{m=k-K^*+2}^{N-K^*+1} y_{m,k-m+2} & \text{for } K^* \le k < N \end{cases} \quad (2)$$

Where $L^* = \min(L, K)$, $K^* = \max(L, K)$, and the length $N = L + K - 1$. It can be shown that the squared norm of each elementary matrix equals the

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corresponding eigenvalue, and that the squared norm of the trajectory matrix is the sum of the squared norms of the elementary matrices [11]. Thus the ratio:

$$\lambda_i / \sum_{i=1}^{d} \lambda_i \tag{3}$$

represents the contribution of the elementary matrix $\mathbf{E}_i$ in the expansion of the trajectory matrix $\mathbf{X} = \mathbf{E}_1 + \mathbf{E}_2 + \ldots + \mathbf{E}_d$.

The largest eigenvalues in the singular spectrum represent the large amplitude components in the decomposition. Contrariwise, the low-amplitude components of the signal are represented in the singular spectrum by the smallest eigenvalues.

2.1 Separability

The obtained SSA decomposition is a function of the window length choice. This choice therefore conditions whether the components obtained will be correlated to a greater or lesser degree in the frequency domain. To study whether these components are mutually independent, one defines the following necessary (but not sufficient) separability condition [11]:

Two principal components $\mathbf{F}_1$ and $\mathbf{F}_2$ obtained from the elementary matrices $\mathbf{E}_1$ and $\mathbf{E}_2$ are separable (w-orthogonal) if the inner product of series $\mathbf{F}_1$ and $\mathbf{F}_2$ is null, i.e.:

$$\left(\mathbf{F}_1, \mathbf{F}_2\right)_w = \sum_{i=0}^{N-1} w_i f_1(i) f_2(i) = 0 \tag{4}$$

where the weights w_i are defined by

$$w_i = \begin{cases} i+1 & for\ 0 \le i \le L^* - 1 \\ L^* & for\ L^* \le i < K^* \\ N-i & for\ K^* \le i \le N-1 \end{cases} \tag{5}$$

and $L^* = \min(L, K)$, and $K^* = \max(L, K)$

If the original series $\mathbf{F}$ is decomposed using SSA into a sum of separable components $\mathbf{F}_1, \mathbf{F}_2, \ldots, \mathbf{F}_L$ that match equation (4) then this sum can be interpreted as an expansion of the original signal $\mathbf{F}$ with respect to a certain w-orthogonal basis generated by the original series itself [11]. The weights in the inner product have the form of a trapezium and reduce the influence of data close to the end-points of the components with respect to the central terms in the series, particularly for large window lengths. Real-life signals do not match equation (4). In practice, one speaks only about approximate separability. To quantify the quality of separation between two components, one defines the weighted correlation or w-correlation of two components $\mathbf{F}_1$ and $\mathbf{F}_2$:

$$\rho_{12}^{w} = \frac{\left(\mathbf{F}_1, \mathbf{F}_2\right)_w}{\left\|\mathbf{F}_1\right\|_w \left\|\mathbf{F}_2\right\|_w} = \frac{\sum_{i=0}^{N-1} w_i f_1(i) f_2(i)}{\sqrt{\sum_{i=0}^{N-1} w_i f_1(i) f_1(i)} \sqrt{\sum_{i=0}^{N-1} w_i f_2(i) f_2(i)}} \tag{6}$$

This coefficient is a measure of the deviation of two series, $\mathbf{F}_1$ and $\mathbf{F}_2$, from w-orthogonality. If the absolute value of the w-correlation is near zero, then the two series are separable. If it is large (near 1), the two components are badly separable.

It is desirable to obtain a decomposition such that the principal components are mutually independent in order to extract the noise present in the displacement signal.

Figure 1 shows the SSA decomposition of a displacement signal (described in the results section) using a window length $L = 10$. Figure 1 shows the decomposition obtained together with the original signal (see figure caption for details). Figure 1(b) shows a graphical representation of the w-correlation matrix corresponding to the decomposition obtained. Cell ij represents the correlation between components i and j, gray-scale coded from black for $\rho_{ij}^{w} = 0$ to white for $\rho_{ij}^{w} = 1$

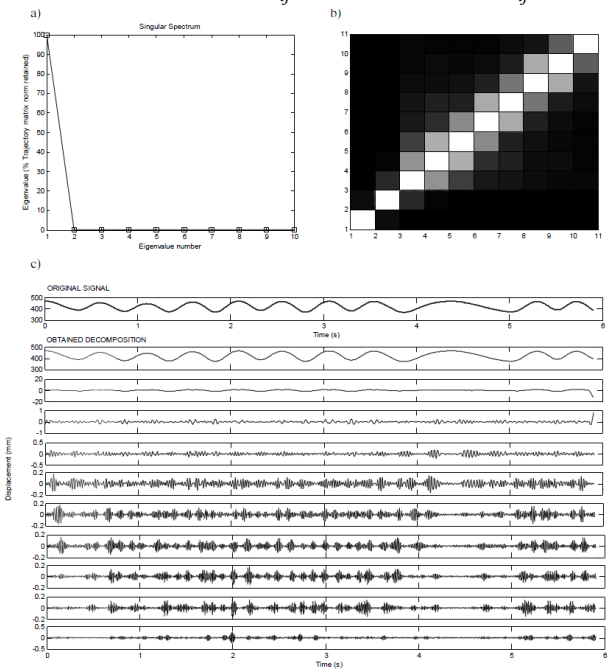

Fig. 1. (a) Singular spectrum. (b) w-correlation matrix. (c) Original time series and principal components obtained in the time domain.

3 Cluster Analysis

As was discussed above, the statistical independence of the principal components depends on the size of the window length chosen. With large values $(L \geq 15)$ while the separation is good, the number of principal components obtained for the representation of the trend signal is impractically large. In order to reduce the number of principal components with which to extract the trend signal and ensure their statistical independence, we apply a cluster analysis procedure.

Namely, we perform K-means clustering on the w-correlation matrix in order to obtain K groups of independent components. The K-means algorithm classifies a given data set through a certain number K of clusters fixed a priori [12]. The main idea is to define K centroids, one for each cluster. Since different locations of these centroids cause different results, the best choice is to place them as far as possible from each other.

The next step is to take each point belonging to a given data set and associate it to the nearest centroid. When no point is left, the first step is completed and a putative grouping is made. At this point, one needs to recalculate K new centroids as barycenters of the clusters resulting from the previous step.

After one has these K new centroids, a new binding procedure has to be carried out between the same data set points and the nearest new centroid. A loop has thus been generated. As a result of this loop, the K centroids change their location step by step until no more changes are made, i.e., the centroids do not move any more. Finally, the algorithm aims at minimizing an objective function, in this case the following squared error function:

$$J = \sum_{j=1}^{k} \sum_{i=1}^{n} \left\| x_i^{(j)} - c_j \right\|^2 \tag{7}$$

Where $\left\| x_i^{(j)} - c_j \right\|^2$, a distance measure between a data point $x_i^{(j)}$ and the cluster centre c_j, is an indicator of the distance of the n data points from their respective cluster centers.

This simple version of the K-means procedure can be viewed as a greedy algorithm for partitioning the n samples into K clusters so as to minimize the sum of the squared distances to the cluster centers. Unfortunately there is no general theoretical solution to find the optimal number of clusters for any given data set. A simple and systematic heuristic approach to obtain an optimal number of clusters is to compare the obtained error function (Equation 7) of multiples runs with different K classes and chose the number of clusters that minimize this function.

4 Smoothing Automation

The SSA smoothing procedure presented in Alonso et al. [10] is based on the fact that raw-displacement acquired signals present a very large signal-to-noise ratio. In this situation, the contribution of the first matrices to the norm of $\mathbf{X}$ is much higher than the contribution of the last matrices, that represent noise. To eliminate the noise present in the displacement signal it is sufficient to choose the leading eigenvalues that represent a large percentage of the entire singular spectrum.

As it has been pointed out [10-11], one of the drawbacks of SSA application is the lack of general rules for selecting the values of the parameters L and r that arise in the SSA algorithm. Moreover, certain window lengths and grouping strategy choices produce a poor separation between signal trend and noise. In other words, trend components would be mixed with noise components in the reconstruction of the signal.

A way to overcome the uncertainty in the choice of the truncation value r is to apply sequential SSA. This means that we extract some components of the initial series by the standard SSA and then extract the components of interest by applying SSA smoothing to an already smoothed record. Such a recursive SSA application produces a gradual elimination of the noise present in the signal. To ensure that any significant part of the noise is eliminated, the number of eigenvalues $L-r$ to eliminate in each iteration was chosen to satisfy the following criteria:

$$\log \frac{\lambda_r}{\lambda_{r-1}} < \frac{1}{L} \log \frac{\lambda_1}{\lambda_L} \tag{8}$$

This criterion ensures that the eigenvalues whose logarithmic difference $\log \frac{\lambda_r}{\lambda_{r-1}}$ is lower than the average logarithmic range of the entire singular spectrum: $\frac{1}{L} \log \frac{\lambda_1}{\lambda_L}$ are eliminated. This criterion ensures that we eliminate eigenvalues in a zone where the singular spectrum has sufficient flatness.

The convergence of the sequential procedure may be measured by means of the percentage root mean square (RMS) difference between the current and previous acceleration signals obtained in each iteration. The algorithm stops when this difference

is sufficiently small, namely the stop criterion at iteration i is:

$$E = \frac{RMS(\ddot{\mathbf{G}}_i - \ddot{\mathbf{G}}_{i-1})}{RMS(\ddot{\mathbf{G}}_i)} \cdot 100 < \varepsilon = 1 \quad (9)$$

Where $\ddot{\mathbf{G}}_i$ is the smoothed acceleration reconstructed at iteration i.

The automatic filtering procedure is summarized in the following way:

• Choose an arbitrary window length L.
• Perform 4-means clustering on the w-correlation matrix in order to obtain 3 groups of independent components and extract the trend signal.
• Apply sequential SSA to the extracted trend signal (truncation value r is fixed to account for the grouping criterion, Equation 8).
• Calculate the acceleration signal numerically in each iteration.
• Stop the procedure according to the stop criterion (Equation 9).

5 Results

In order to study the performance of the filtering procedure three signals were tested. Two reference acceleration signals were taken from the literature. A double differentiation is performed on each signal in order to quantify the effect of smoothing. First order central finite differences are used to calculate the higher derivatives. The sequential SSA algorithm stops when the percentage difference between the current and previous values of the RMS acceleration is smaller than 1% in order to prevent excessive smoothing.

The first signal is the motion of a vertical slider moved by hand to obtain a non-stationary mono-dimensional motion of biomechanical origin. A subject was asked to move the slider randomly with fast upward and downward movements. The vertical position (Figure 2) was acquired with the use of a marker attached to the slider and the Qualisys camera system (Qualisys Medical AB). The second derivative of this record, or of the record obtained after smoothing, is compared to the acceleration obtained directly from an accelerometer attached to the slider. Displacement and acceleration were sampled at 200 Hz during 5.90 seconds, obtaining records of 1182 elements each.

SSA decomposition was attained using a window length $L = 10$ (see Figure 1). Various window lengths were tested in order to study the influence of this parameter on the obtained decomposition.

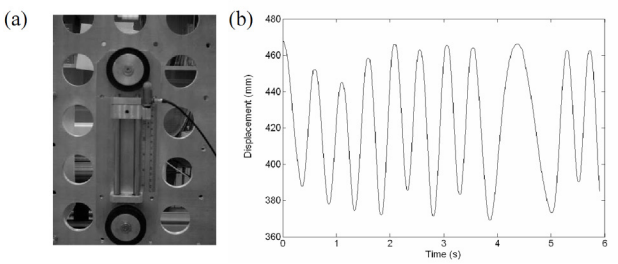

Fig. 2. (a) Experimental layout. (b). Noisy vertical displacement signal acquired.

Figure 3 shows the w-correlation matrices obtained using $L = 5$, $L = 20$, $L = 50$ and $L = 100$. It is clear from Figure 3 that the smaller window lengths do not adequately separate the high and low frequency components. The greater window lengths, however, yield a good separation of the high and low frequencies.

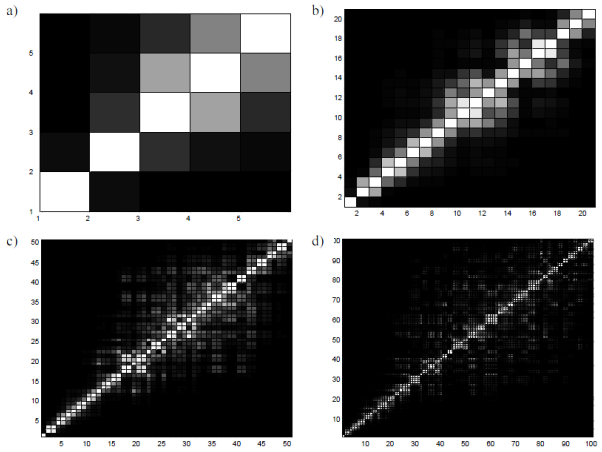

Fig. 3. w-correlation matrices. (a) $L = 5$. (b) $L = 20$. (c) $L = 50$. (d) $L = 100$.

After the SSA decomposition, a 4-means cluster analysis was performed in order to obtain four frequency independent components for each vibration signal. The principal components forming the low-frequency signal are $\mathbf{I} = [1,2,3]^T$. It is important to stress that four components would also have obtained using a window length of $L = 4$ in a SSA decomposition of the original series, but without performing the cluster analysis, these four components would not, however, have been independent in frequency, which is the fundamental point of this smoothing method.

In order to eliminate the noise present in the obtained reconstruction sequential SSA-cluster analysis was applied. Such a recursive SSA application produces a gradual elimination of the

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noise present in the reconstructed signal. Figure 4 shows the results obtained for two iterations of the method using $L = 10$. Figure 4 (top) shows the acceleration calculated from original raw displacement data (dotted line) and acceleration measured by the accelerometer (continuous line). Figure 4 (middle) shows the acceleration calculated after having been passed through a 4 Hz cut-off frequency Butterworth filter (dotted line) and acceleration measured by the accelerometer (continuous line). This figure shows the large end-point errors associated to the usage of this filter. Finally, Figure 4 (bottom) represents the acceleration calculated after smoothing the raw displacement signal using sequential SSA-cluster analysis ($L = 10$) and acceleration measured by the accelerometer (continuous line).

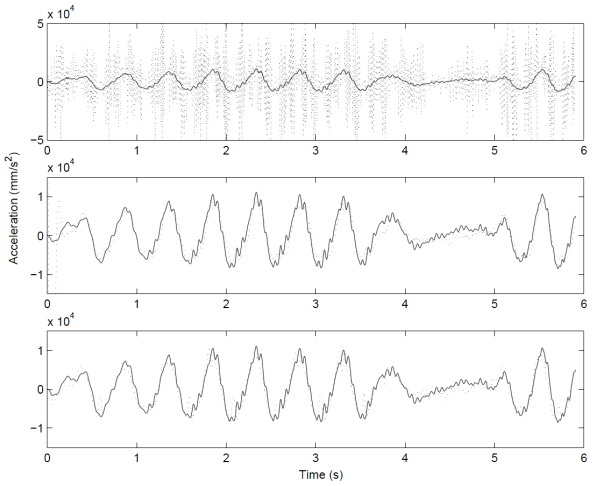

Fig. 4. Signal 1 results. See descriptions in the text.

Figure 5 shows the singular spectrum evolution in each of the two iterations required to achieve the convergence criterion. It is clear from the figure that the proposed procedure sequentially reduces the noise amplitude in each iteration.

Comparison with traditional and advanced filtering techniques is quantified by taking the root mean square of the error signal (RMSE) of the acceleration. The error signal is the difference between the measured reference signal (accelerometer) and the signal obtained after filtering and differentiating the raw data. The errors in terms of RMSE are $29.54\, m/s^2$ for the Butterworth filter and $1.82\, m/s^2$ using SSA-cluster analysis respectively.

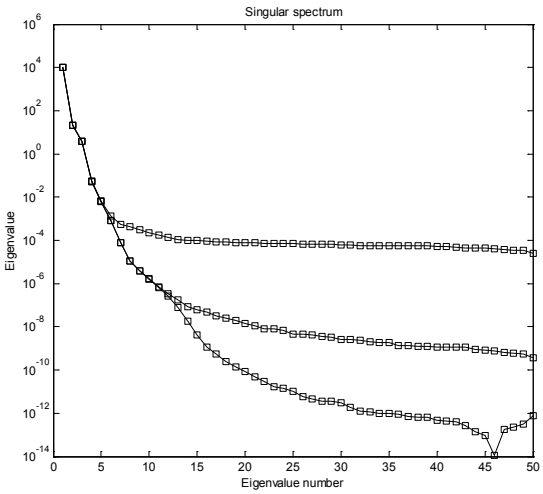

Fig. 5. Singular Spectrum evolution for the first signal

Table 1 summarizes the results obtained using several window lengths. It can be concluded that the results are robust to variations of the window length L and number of clusters.

L	RMSE	N. iterations
10	1.82	2
50	1.51	3
100	1.52	2

Table 1. Summary of the results for several window lengths.

The second signal corresponds to the 'woman' file from GAITLAB (Vaughan et al., 1992). The signal measures the lateral displacement of a marker attached on the right tibial tubercle. Data was acquired for 0.94 seconds using a sampling frequency of 50 Hz. The reference signal is taken as that obtained after filtering the raw data at 6.25 Hz, but different amplitude white noises are added in order to test smoothing methods. An amplitude 1, time generated, white noise was used for comparisons, see Giakas and Baltzopulos, 1997 [5].

For signal 2, using $L = 20$ the automatic procedure achieved $RMSE = 298.87\, mm/s^2$ versus $RMSE = 400\, mm/s^2$ obtained by Giakas and Baltzopoulos, [5] using Power Spectrum Assessment (PSA) and $RMSE = 256.89\, mm/s^2$ using a SSA non-automatic approach. The accuracy of the obtained acceleration may also be appreciated in Figure 6 (bottom), where the acceleration obtained from the reference signal is plotted along with the

acceleration calculated from SSA–smoothed displacement data.

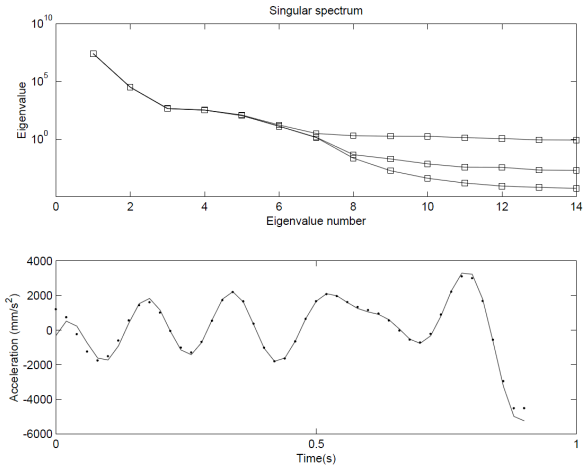

Fig. 6. (Top) Singular Spectrum evolution. (Bottom) Acceleration obtained from reference signal 2 (continuous line) and acceleration calculated from SSA-smoothed displacement data (dotted line).

The third signal is a measure of the angular coordinate of a pendulum impacting against a compliant wall [4]. The angular acceleration obtained from the motion capture system is compared to that obtained directly (after dividing by pendulum length) from accelerometers. Three accelerometers were used in order to average their measurements to reduce noise. The average signal, logged at a sampling rate of 512 Hz is used as the acceleration reference signal.

The same procedure was performed on the third signal. Using $L = 50$ the automatic procedure achieved $RMSE = 24.37\ rad/s^2$ (Figure 7). The result is similar to the value $RMSE = 23.60\ rad/s^2$ obtained by Giakas et al. [8] with the help of the Wigner distribution. The slight loss of accuracy in the SSA method is compensated by the ease with which the method is applied and the fact that one must not extend the ends of the record in order to eliminate end–point errors. Moreover, the automatic filtering procedure obtain similar results for a reasonable range of window lengths.

6 Conclusions

The present work has studied the applicability of the sequential SSA method and cluster analysis to automatic smoothing of biomechanical kinematic signals.

The SSA algorithm decomposes the original signal into independent additive components of decreasing weight. This fact allows the method to successfully extract the latent trend in the signal from the random noise inherent to the motion capture system. An automatic heuristic procedure based in sequential SSA and cluster analysis to extract the trend signal has been presented.

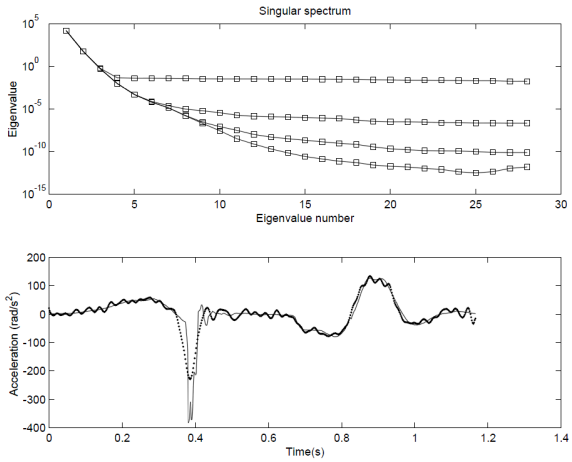

Fig. 7. (Top) Singular Spectrum evolution. (Bottom) Acceleration obtained from reference signal 3 (continuous line) and acceleration calculated from SSA-smoothed displacement data (dotted line).

The method does not use any information from the reference acceleration signal (which is not available in practice) to perform the smoothing. One of the main advantages to the method is the fact that the algorithm requires the selection of just one parameter. Namely, the window length L, moreover, the results are robust to variations of the window length. In conclusion, we believe that this new automatic smoothing technique, that has proven its effectiveness with complex signals, will help to improve the accuracy of raw kinematic data processing in biomechanical analysis.

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