A GENETIC ALGORITHM FOR CLUSTERING TEMPORAL DATA
Application to the Detection of Stress from ECG Signals

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Abstract: Electrocardiography signals are typically analyzed for medical diagnosis of pathologies and are relatively unexplored as physiological behavioral manifestations. In this work we propose to analyze these signals with the intent of assessing the existence of significant changes of their features related to stress occurring in the performance of a computer-based cognitive task.

Given the exploratory nature of this analysis, usage of unsupervised learning techniques is naturally adequate for our purposes. We propose a work methodology based on unsupervised automatic methods, namely clustering algorithms and clustering ensemble methods, as well as on evolutionary algorithms.

The implemented automatic methods are the result of the adaptation of existing clustering techniques, including evolutionary computation, with the goal of detecting patterns by analysis of data with continuous temporal evolution. We propose a genetic algorithm for the specific task of assessing the continuous evolution and the separability of the stress states.

The obtained results show the existence of differentiated states in the data sets that represent the ECG signals, thus confirming the adequacy and validity of the proposed methodology in the context of the exploration of these electrophysiological signals for emotional states detection.

1 INTRODUCTION

Of the existing pattern recognition methods, unsupervised learning is especially appealing to organize data which has little or no labeling information associated to it. A clustering algorithm organizes the patterns into k groups or clusters, based on the similarity or dissimilarity values between pairs of objects such that objects in the same cluster are more similar than objects of different clusters (Xu and Wunsch, 2005) (Jain et al, 1999). The adopted similarity might be statistical or geometrical, such as a proximity measure based on a distance metric in the d-dimensional representation space of the d features that characterize the data. The result will be a partition of the analyzed data set.

The work presented here is centered on the analysis of temporal series of electrophysiological signals from an unsupervised learning perspective to assess in particular the existence of differentiated emotional states. Given that typically the signal is characterized by a continuous temporal evolution, this means that the values of the features that represent it will also change gradually with time and that will possibly reflect transient emotional states present in the structure of the signal. In the clustering context, the fact that such transient states occur means that it is difficult to assign signal samples to clusters such that each cluster corresponds to a differentiated state. This represents a challenge in the implementation of clustering methods to analyze temporal series like the aforementioned electrophysiological signals because the clusters are not well separated, which in turn introduces ambiguities in the observation of differentiated emotional states.

In order to assess and evaluate the existence of these emotional states, we propose an analysis methodology based on a genetic algorithm combined with state of the art clustering techniques. The goal of this work methodology is to eliminate transient

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states in order to clarify the existence of well separated clusters, each corresponding to differentiated states present in the temporal series of data.

This methodology may be applied to temporal series of electrophysiological signals acquired during the performance of cognitive tasks, such as electrocardiography signals (ECG) or electroencephalography signals (EEG). In this paper we specifically address the identification of stress from ECG signals.

2 APPLICATION DOMAIN: DETECTION OF STRESS FROM ECG SIGNALS

The temporal series analyzed correspond to electrocardiography, or ECG, signals. These signals are part of a more vast experience of multi-modal acquisition of physiological signals - the HiMotion project. The ECG signals were acquired from a group of 24 subjects performing a stress inducing cognitive task, illustrated in Figure 1. This task is a concentration test that consists of the identification and annotation of pairs of numbers that add to 10, by examination of the lines of a matrix of 20 lines per 40 columns of numbers (Gamboa, 2008). The population of subjects is comprised of 18 males and 9 females, being their mean ages 23.4 years. For each one of these subjects, a montage with two electrodes called V_2 bipolar single lead electrocardiogram was used to collect signals from the heart (Gamboa, 2008).

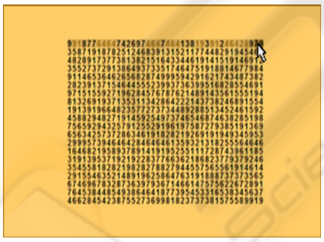


Figure 1: Concentration task - examination of a matrix with 800 numbers.

Given that this concentration task is stress inducing, the following methodology is applied to the ECG signals in order to assess the existence of stress states.

3 PROPOSED METHODOLOGY

We propose a methodology for analysis of temporal data series, represented in Figure 2. It is based on unsupervised learning techniques in order to unveil similarity relations between the temporal patterns that represent the data, and also to detect differentiated states in the temporal sequences that represent the data by applying a genetic algorithm specifically conceived for this purpose. After the acquisition and preprocessing of electrophysiological signals, these are represented by a set of j samples. Each sample corresponds to a given segment of the signal, therefore being associated to a time stamp, and is characterized by a d-dimensional feature vector, $f = \{f_1 \ldots f_d\}$.

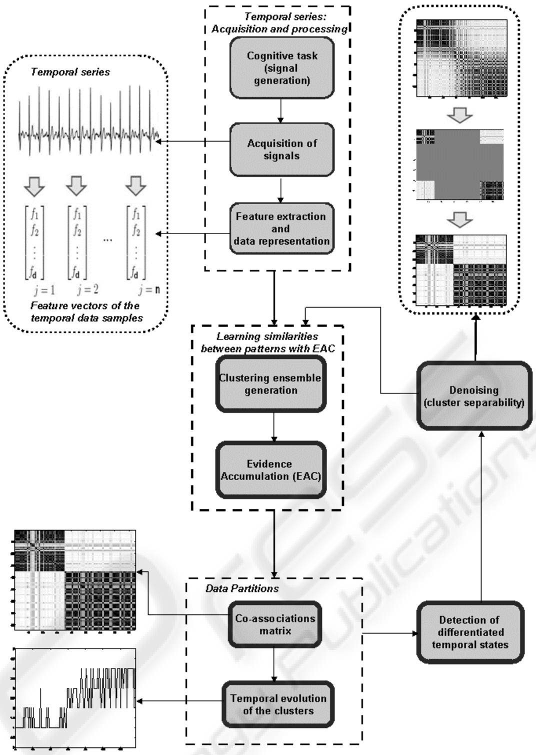

Temporal series
f_1
f_2
$\vdots$
f_d
...
$j=1$
$j=2$
$j=n$
Feature vectors of the temporal data samples
Temporal series: Acquisition and processing
Cognitive task (signal generation)
Acquisition of signals
Feature extraction and data representation
Learning similarities between patterns with EAC
Clustering ensemble generation
Evidence Accumulation (EAC)
Denoising (cluster separability)
Data Partitions
Co-associations matrix
Temporal evolution of the clusters
Detection of differentiated temporal states

Figure 2: Proposed work methodology for analysis of temporal series. The time series illustrated corresponds to ECG signals.

The proposed methodology encompasses steps of learning similarities between temporal patterns and the detection of states from these. These two main steps are described in the following subsections. The overall process consists of refining the state detection by means of a genetic algorithm that uses the output of these clustering and state detection procedures. The proposed genetic algorithm is described in detail in Section 4.

3.1 Learning Similarities with Evidence Accumulation

Different clustering algorithms lead in general to different clustering results. A recent approach in unsupervised learning consists of producing more robust clustering results by combining the results of different data clusterings. Groups of partitions of a data set are called clustering ensembles and can be generated by choice of clustering algorithms or algorithmic parameters, as described in (Fred and Jain,2005). Evidence Accumulation (EAC) is a clustering ensemble method that deals with partitions with different number of clusters by employing a voting mechanism to combine the clustering results, leading to a new measure of similarity between patterns represented by a co-association matrix. The underlying assumption is that patterns belonging to a ”natural” cluster are very likely to be assigned in the same cluster in different partitions. Taking the co-occurrences of pairs of patterns in the same cluster as votes for their association, the N data partitions of n patterns are mapped into a $n \times n$ co-association matrix:

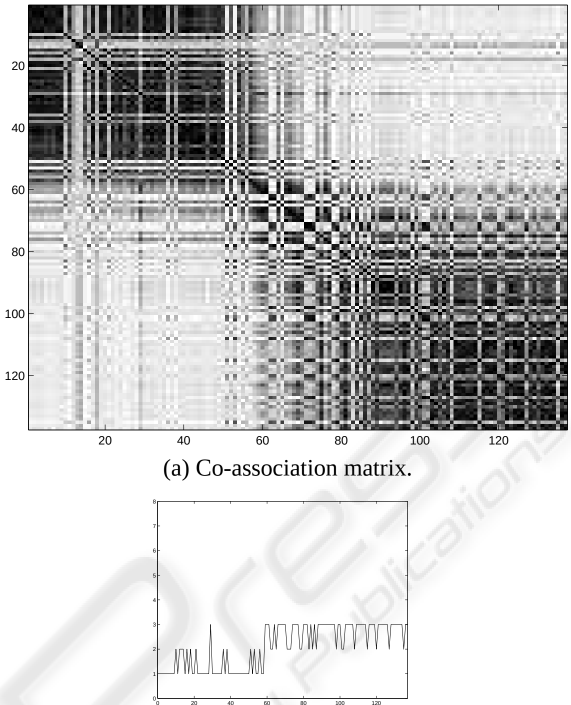
$$C(i,j) = \frac{n_{ij}}{N} \tag{1}$$

where n_{ij} is the number of times the pattern pair (i,j) is assigned to the same cluster among the N partitions. The final partition is then extracted from the learned similarity matrix (co-association matrix) by employing, for instance, a hierarchical clustering method.

Graphically, the clusters can be visualized in the representation of the co-association matrix: if contiguous patterns belong to the same cluster, then quadrangular shapes will be present in this representation that correspond to neighboring patterns that are assigned to the same cluster in different partitions of the data (Lourenço and Fred, 2008). A co-association matrix is illustrated in Figure 3(a). The chosen color scheme ranges from black to white (grayscale), corresponding to the gradient of similarity. Pure black corresponds to the highest similarity. Given that our major goal is to test that the temporal evolution of emotional states corresponds to a temporal evolution of the analyzed signal, the graphical representation of the co-association matrix is a powerful tool to assess the relationships of signal samples ordered by instant of occurrence.

The final partition can be extracted from the co-association matrix by applying a hierarchical clustering method. For the work here described, five agglomerative hierarchical methods were used: Single Link (SL), Complete Link (CL), Average Link (AL), Ward’s Link (WL) and Centroid’s Link (CenL). Detailed descriptions and studies of these algorithms may be found in (Jain and Dubes, 1988).

An example of an extracted partition for a set of temporal series samples is depicted in Figure 3(b), where the relationship between the temporally sequenced samples (x-axis) and the cluster to which they are assigned (y-axis), is emphasized. It is possible to observe that cluster transitions generally occur between adjacent clusters: cluster 1 evolves to cluster 2, cluster 2 evolves between clusters 2 and 3, etc. This is a meaningful result for the testing of the hypothesis of temporal evolution of emotional states.



(a) Co-association matrix.

(b) Cluster evolution over time.

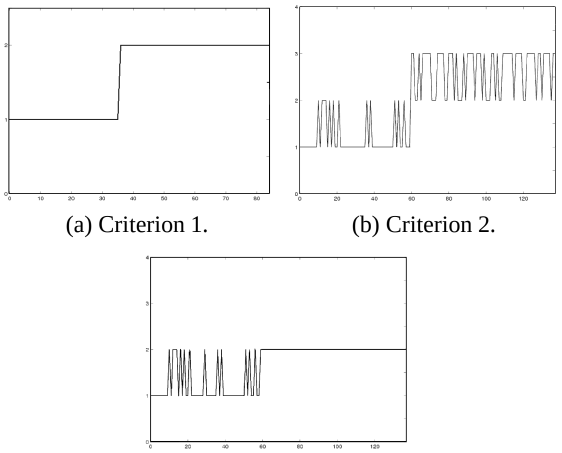
Figure 3: Subject 6 - Graphical representation examples.

3.2 Detection of Temporal States

The detection of temporal states is performed by comparing and examining the temporal evolution of clusters of all the partitions produced from the learned similarity matrix, by different hierarchical methods, and for several extraction criteria. The goal of this analysis is the assessment of underlying structures that might correspond to the temporal evolution of differentiated states. The proposed criteria for this assessment are illustrated in Figure 4. Each criterion considers sample segments of the temporal evolution of the clusters. Differentiated states are detected if:

1. There are segments such that all the samples of each segment belong to a single cluster (Figure 4(a));

2. Each segment is comprised of samples belonging to different clusters, such that each of those



(a) Criterion 1.

(b) Criterion 2.

(c) Criterion 3.

Figure 4: Visualization of the proposed state detection criteria.

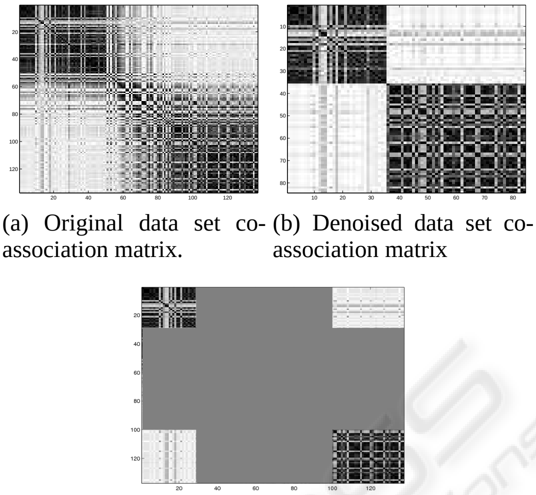
segments corresponds to a unique combination of clusters (Figure 4(b));

3. There are segments that correspond either to a single cluster or to a unique combination of clusters (Figure 4(c)).

4 GENETIC ALGORITHM FOR DENOISING OF THE DATA

To assert the existence of stress states with continuous temporal evolution, one of the hypothesis to be tested is that each stress state corresponds to a single group, or possibly to an unique combination of two or more groups. On the other hand, the occurrence of several transient states may induce ambiguities in the observations of the graphical representations of the clusters evolution, and obscure the structure of the data. These transient states correspond to an intermediate group of samples of the temporal series which represents the analyzed signal. It is expected that, after removing this subset of samples from the original data set and performing EAC on the clustering ensemble based on the new reduced data set, a structure of separate states might emerge from the respective co-association matrix.

Figure 5 illustrates the testing of the existence of at least two well separated stress states, each corresponding to a single cluster, by denoising. Figure 5(a) represents the co-associations matrix that corresponds to the original data set of subject 6; Figure 5(c) illustrates the group of samples to be removed in order to obtain two completely separated quadrangular blocks, with no transient structures between them; finally Figure 5(b) illustrates the co-association matrix obtained from the new data set.



(a) Original data set co-association matrix.

(b) Denoised data set co-association matrix

(c) Intermediate subset of samples to be removed.

Figure 5: Example of the application of denoising.

The intermediate groups of samples to be removed are determined by applying a task-specific genetic algorithm (GA), specifically conceived and implemented for this purpose. Several operators and procedures must be declared in order to define a particular GA (Sumathi et al, 2008). These operators were defined for the denoising GA as follows and the GA is summarized in Table 1.

Representation. Each individual is a set of samples, generated after one or more subsets of intermediate samples are removed from the original data set. The first pattern of the removed subset is called minimum limit, (l_{min}), and the last pattern is referred to as maximum limit, (l_{max}).

Fitness Function. The evaluation of the fitness value of each individual is comprised of two stages, each concerning a partial fitness value function.

1. Determine if two or more of the m partitions that are associated to the individual are consistent, or similar. Two partitions are said to be similar if the same samples are assigned by different hierarchical methods to the same clusters. The partial fitness value, F_1, is incremented for every consistent partition extracted by two or more hierarchical methods:

$$F_1 = \sum P_{Consistent} \qquad (2)$$

2. Determine, for each of the m partitions associated to the individual, the degree of cluster separability. Given that we want to assess the existence

Table 1: Proposed GA for denoising of the data sets.

1. Generate randomly a population of M individuals.

2. Produce a clustering ensemble for each of the individuals of the current population, G_i. Apply EAC and extract from each of the resulting co-association matrices m final partitions with m hierarchical methods according to the lifetime criterion. Each individual has m associated partitions.

3. Evaluate the fitness of each individual.

4. If a termination criterion is satisfied, then terminate the algorithm.

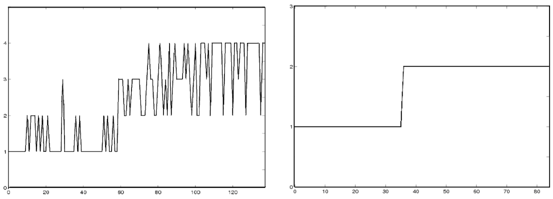
5. Initialize an empty new population, G_{i+1}. Add individuals to it according to the following procedure:
5.1 Select a pair of individuals from G_i.
5.2 Recombine the selected individuals. This operation has a probability of occurrence of p_R.
5.3 Randomly mutate the new individuals. This operation has a probability of occurrence of p_M.
5.4 Insert the new individuals in G_{i+1}.

6. Return to step 2.

of completely separated states and given that the data samples are temporally ordered, the separability criterion is based on temporal separability.

Giving as an example the removal of a single intermediate subset, the individual can be said to be comprised of two smaller sets: one corresponding to the samples of lower temporal index than the index of l_{min}, and another set corresponding to the samples of higher temporal index than the index of l_{max}. Two clusters are completely separated if the samples assigned to the first cluster belong to the first temporal segment, and the samples of the second cluster belong to to the final temporal segment. This means that the evaluated partition corresponds to a structure of two completely separated states, thus removing any ambiguities for the observation of partitions and state detection. This procedure is generalized to more that one subset of intermediate samples.

Figure 6 illustrates the given example: a partition of the original data set is represented in Figure 6(a), where one can observe that different temporal segments of samples correspond to different clusters or combinations of clusters. However, it is not possible to draw conclusions about the number of these states or how many samples correspond to each of them. Figure 6(b) represents the partition obtained after denoising of the original data set by employing the proposed denoising GA. This partition consists of two separated clusters and we can conclude that at least two different emotional states are present in the data: an initial state comprised of the first 35 ECG samples and a final state comprised of the final 50 ECG samples.



(a) Original data set. (b) Denoised data set.

Figure 6: Subject 6 - Partitions obtained for the original and denoised data sets. The x-axis represents the temporally ordered ECG samples and the y-axis the clusters to which they are assigned.

Samples that are assigned to clusters that do not correspond to their temporal segment are said to be outliers. The partial fitness function, F_2, takes the number of these outliers, $n_{outliers}$, and subtracts it from the total number of analyzed samples, $n_{samples}$. Given that each individual has m associated partitions, then:

$$F_2 = \frac{1}{m}\sum_{m}\frac{n_{samples} - n_{outliers}}{n_{samples}} \qquad (3)$$

The final fitness value, F_{total}, for each individual is

$$F_{total} = \alpha F_1 + (1-\alpha)F_2 \qquad (4)$$

Selection. Two individuals are selected for recombination based on the fitness values associated, by applying deterministic tournament selection.

Recombination. This operation consists on the recombination of the minimum and maximum limits of the selected individuals, in order to generate a new individual; the new minimum and maximum limit values are chosen randomly as intermediate values of the selected individuals' minimum and maximum limits, respectively.

Mutation. This operation consists on modifying the minimum and maximum limits by adding or subtracting a randomly chosen number, n_{mut}, to or from the limits values. Addition and subtraction have the same probability of occurrence.

Termination Criteria. The GA terminates either if the fitness of an individual reaches a certain threshold, or if a maximum value of G is reached, whatever happens first. In either case, the solution is given by the individual with the highest fitness at termination.

5 APPLICATION TO ECG TEMPORAL DATA

5.1 ECG Processing and Feature Extraction

An ECG signal is a recording of the electrical activity of the heart that consists of sequences of heart beats. Each heart beat has a typical morphology which consists of five waves (P, Q, R, S, T), schematically represented in Figure 7.

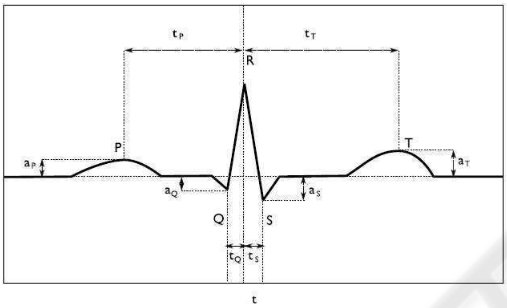


Figure 7: PQRST wave.

From the acquired time series corresponding to the ECG signal, signal processing techniques were applied for signal segmentation (Gamboa, 2008) and a mean wave form was calculated based on 10 consecutive heart beats, to remove some spurious noise. All the waves were aligned with respect to the R wave. The recorded signal for each subject is then summarized in a temporal sequence of 137 mean waves, each wave represented by a feature vector (Gamboa, 2008).

The representation of the ECG signals is based on the P, Q, S, T waves. The R wave is used for time alignment, setting the initial instant of the beat $(t_(R) = 0)$. The following rules are used to locate the position of each of the P, Q, S, T waves and to extract the eight main features of each mean wave (Gamboa, 2008), as depicted in Figure 7:

1. t_P - the first maximum before the R wave;
2. a_P - the amplitude of the P wave;
3. t_Q - the first minimum before the R wave;
4. a_Q - the amplitude of the Q wave;
5. t_S - the first minimum after the R wave;
6. a_S - the amplitude of the S wave;
7. t_T - the first maximum after the R wave;
8. a_T - the amplitude of the T wave.

Each mean wave is represented by a 53-dimensional feature vector: the aforementioned 8 features, plus the amplitudes of the signal at 45 points of the signal obtained by re-sampling of the mean wave (Gamboa,2008). Thus, for each of the 24 subjects, there is a group of 137 temporally sequenced samples or patterns, corresponding each sample to a vector of 53 features.

5.2 Algorithmic Parameters and Experiments

Two spectral clustering algorithms are used to produce two clustering ensembles for each of the 24 data sets. These algorithms were originally proposed by (Ng et al, 2002) and (Shi and Malik, 2000). Each partition of the clustering ensemble is generated such that it corresponds to a combination of possible values of the spectral algorithm's parameters. These parameters consist in the number of clusters of the partition, k, and a scaling parameter, s. The ranges of values used for partition generation are as follows: each partition corresponds to a combination of $k \in [2,6]$ and $s \in [0.3, 0.4, ..., 2.9, 3.0]$. The co-association matrix generated for each data set by EAC corresponds to the accumulation of information from the two clustering ensembles, which corresponds to 280 partitions of the data, being that the five hierarchical methods referenced in Section 3.1 are used for combined partition extraction.

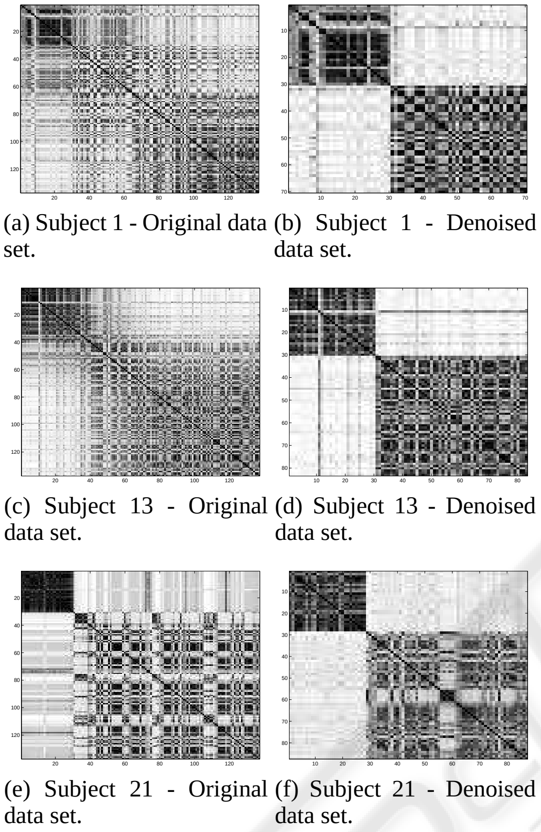
The results of two experiments concerning the ECG data sets are described and compared in this paper: (1) state detection in the partitions obtained for the original data sets and (2) state detection in the partitions obtained for the denoised data sets by the proposed GA.

The parameter values chosen for implementation of the denoising GA are the following:

- Number of individuals: $M = 20$;
- Number of partitions associated to each individual: $m = 5$;
- Number of populations generated (termination criterion): $G = 20$;
- Threshold of fitness value (termination criterion): 0.95;
- Probability of recombination: $p_R = 0.9$;
- Probability of mutation: $p_M = 0.1$;
- Range of mutation values: $n_{mut} \in [0,5]$;
- Weight of partial fitness value: $\alpha = 0.1$;

5.3 Results and Discussion

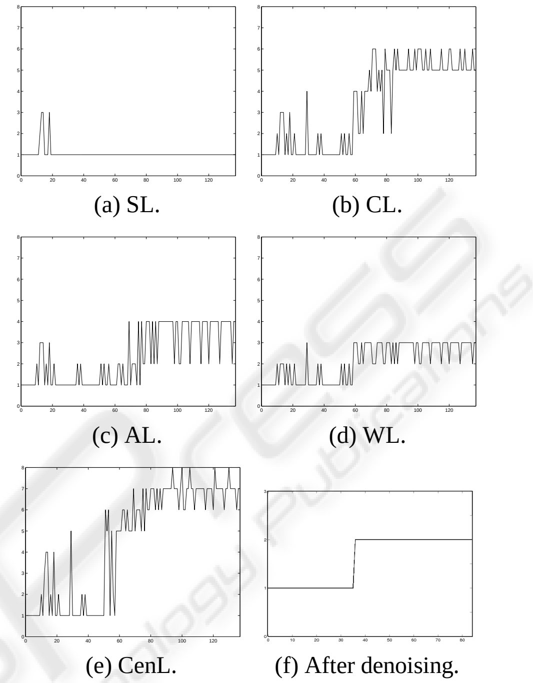
Figure 8 represents co-association matrices obtained for the original data set and for the denoised data set of subjects 1, 13 and 21, which show different levels of separability of the evolution into stress states. By comparing the representations of both co-association matrices for the same subject, it is possible to observe that denoising of the original data sets, such that the eliminated subsets of samples correspond to zones of transition of the temporal evolution, will lead to the revelation of the structure of states in the temporal ECG series. Similarity relationships between contiguous samples are thus emphasized, which means that the clusters are separated such that a structure of two differentiated states emerges, with no ambiguities in the observation and detection of these states.



(a) Subject 1 - Original data set.
(b) Subject 1 - Denoised data set.
(c) Subject 13 - Original data set.
(d) Subject 13 - Denoised data set.
(e) Subject 21 - Original data set.
(f) Subject 21 - Denoised data set.

Figure 8: Subjects 1, 13 and 21 - Co-association matrices.

This better separability of emotional states by the proposed GA-based method is further evaluated by observing the temporal evolution of clustering results produced from the learned similarities. Figures 9(a)-9(f) illustrate the temporal evolution of clusters obtained for the original data set of subject 6, while Figure 9(e) pertains to the corresponding denoised data set. Each partition corresponds to one of the five hierarchical methods used for combined partition extraction.

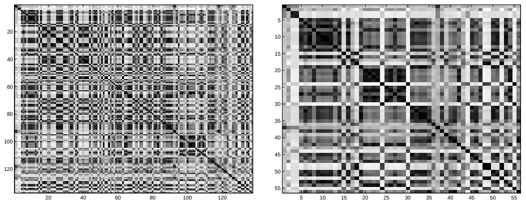


(a) SL.
(b) CL.
(c) AL.
(d) WL.
(e) CenL.
(f) After denoising.

Figure 9: Subject 6 - Figures (a) to (e): Original data set partitions. Figure (f): Denoised data set partition (the same partition was extracted by the five hierarchical methods). The x-axis represents the temporally ordered ECG samples and the y-axis the clusters to which they are assigned.

By inspection of Figure 9, it is possible to observe that the five hierarchical methods extract different partitions, in terms of number of clusters and samples assigned to each cluster. Though a structure of the data appears to be present, the transitions between clusters induce ambiguities in the observation of differentiated states. After applying the proposed genetic algorithm to determine which subsets of samples must be removed in order to eliminate these ambiguities, it is possible to observe in Figure 9(e) that the five methods extract the same partition of the data, and that these partitions reveal two completely separated clusters each corresponding to a different emotional state. Thus, these results validate the observations of the original data set and it is possible to conclude that emotional states are observable in the ECG temporal series of subject 6.

It is worth emphasizing that the proposed methodology does not impose structure on the data, but rather enhances the underlying structure. As an illustrative example, Figure 10 shows the co-association matri-



(a) Original data set. (b) Denoised data set.

Figure 10: Subject 5 - Co-association matrices.

ces of one subject that exhibits no differentiated states during the execution of the concentration task. In this case, no states were detected for the original data set or the denoised data set.

Overall, by visual inspection of co-association matrices and clusters evolution associated to the original data sets, it is possible to infer the existence of emotional states with temporal evolution for 12 of the 24 subjects. After applying the proposed genetic algorithm, these states are differentiated and in a few cases completely separated for 8 of those 12 subjects, and also for two other subjects for whose temporal series is not possible to obtain a state structure using just the original data sets. For these 10 subjects, a maximum of 59% samples and a minimum of 31% are removed in order to evidentiate the temporal separation of the clusters.

The fact the number of subjects for whom differentiated states are detected is greater for the original data sets than for the subsets obtained with denoising is related with the fitness function proposed for evaluation of each possible subset. The criteria chosen to implement it are strict, given that we want to evidence completely separated states, using for each evaluation different partitions obtained by each hierarchical method. It is possible that one or more of these methods, for instance Single Link, may be inadequate for the analysis of the temporal series, thus degrading the fitness values

6 CONCLUSIONS

The proposed methodology of analysis is based on unsupervised learning techniques, namely representative clustering algorithms and a state of the art clustering ensemble method, and also on a proposed genetic algorithm for assessment of the existence of differentiated states in temporal series of signals by denoising of the data sets, as well as for validation of the results obtained for the original data sets. Results show that the use of denoising techniques as a means of pre-processing the data and validation of the state observations for the original data sets reinforces the assumption that at least two different states are present in the data set, each corresponding to a single cluster or combination of clusters. Thus, it is possible to infer the existence of emotional states in the temporal series analyzed by employing unsupervised learning methods and an evolutionary computation technique.

Ongoing work consists on a further extensive validation of the proposed methodology in the herein presented application domain, as well as extrapolation to the automatic analysis of other time series, such as EEG data.

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