Temporal Assessment Model for Monitoring Critical Patients

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Abstract: This paper gives an integrated view of developing a model for an assessment systems and monitoring tasks of critical patients. This model was designed according to the Temporal Abstraction dimensions and state interpretation levels, particularly the monitored physiological state. Monitoring arrhythmias was used as reference case for models development. A model based on the algorithm Smith-Waterman with the matrix substitution modified, was developed for the assessment state interpretation model, for this application. The modification was oriented to give more influence to the principal state for the temporal pattern represented. The assessment state space model, allow to obtain additional temporal information about a possible evolution, not previously available in classic monitors.

1. Introduction

One of the aims in the development of intelligent systems for monitoring clinical patients is to improve the common performance of traditional monitors by integrating multiple sources of observations and medical knowledge in the diagnosis process and patients´ evolution. The assessment of critical patients requires a continuous representation of temporal features of the processes being monitored, which is derived from a great amount of data. This leads to the need of automatic mechanisms for the representation process, so that it can be more easily interpreted by users, improving the decision-making process speed and reliability and thus providing better assistance to patients. There are three main tasks in the intelligent assessment of patients: data acquisition, data processing (producing reduced descriptions of collected signals) and diagnosis. The objective of this last task is to detect potential pathological states, as early as possible, and to characterize the situation by offering explanations based on passages from previous states [1].

One of the ways of characterizing the inference methods used for the diagnosis task is to analyze how they operate in data and temporal dimensions. The level of data or interpretation is related to the data type used by the inference method, whereas the temporal abstraction dimension indicates if such method interprets individual data points or sequences of data points ordered in time. Figure 1 shows these dimensions and the corresponding inference methods [2].

![Figure 1. Dimensions and inference methods](image)

On the one extreme of the interpretation spectrum, there are inference methods which interpret individual parameters values. In this level, if the system just considers points of isolated data, the inference operation is...
called classification, and it typically consists of a transformation of numbers into symbols. If the system interprets sequences of data, the inference method can be referred to as based on trends detection. The following level of abstraction in the data dimension is based on states. The inference methods that operate at this level synthesize interpretations of physiological and physio-pathological states from the interpretation of parameter values. If they are extended to the degree of temporal state sequences, they reach the degree of trajectory in the state space. This level allows modeling the sequence of states followed by pathological cases. The last level of abstraction in the interpretation dimension is that of disorders, which can be defined as a collection of physio-pathological states at a given time or as a trajectory of vectors in the state space over time. Traditional diagnosis Expert Systems operate at this level, but they suggest some limitations. For instance, a system that reasons in the three levels will be more robust, since it will be able to synthesize the physiological interpretations of parameter values and physiological states into interpretations of pathologies and complications [2].

In order to model the temporal patterns from the data in the different levels of interpretation, a desirable representation of the time series is first required [3]. As previously mentioned, a convenient methodology to obtain an appropriate and meaningful compact representation of temporal data is related to the construction of Temporal Abstractions (TAs) [4]. TA is a methodology of Artificial Intelligence characterized by leading a quantitative representation of the temporary data to an intervals-based qualitative representation. In each interval, a specific pattern is observed in the data. This pattern represents a summary of the original data and can be used to derive traits that characterize the dynamics of the system under observation. The algorithms that take a time series as input, generating a series of intervals, which correspond to periods in which a specific pattern is present in the input, are referred to as AT mechanisms [5-7]. In this work, they will be related to the cardiac arrhythmias problem. The cardiac arrhythmias could be detected from electrocardiogram (ECG). This signal represents the sequence of polarization (negative and positive) of atrias and ventricles. The electrical stimulus in a healthy heart is born in the nodule sinus atrial (a small muscular tissue in the right atria) and gives origin to a depolarization wave on both auricles (P wave). When this wave arrives at the site where right atrial and right ventricle join, it must go through another specialized structure: the atrioventricular nodule. This nodule has an electrical conduction speed that is slower than that of the other conduction tissue, causing a delay of the wave and a flat line on the electrocardiographic record.

In the atrioventricular nodule, the His beam (a muscular fiber beam with greater conductivity than other muscular fibers) extends through the wall that connects both ventricles and ends in fiber ramifications (Purkinje fibers) connected to the rest of the ventricular tissue. During the conduction period of the electrical impulse, from the His beam to the last cells of the ventricular myocardium, the so-called QRS wave is registered. Then, ventricles remain in an idle state (segment ST), after which they are re-polarized, which is reflected in the presence of the T wave. Besides the aforementioned waves, there is usually an additional wave called U wave, whose origin is not clearly known. When a fault in the heart rate occurs, regularity, the generation or conduction of the electrical impulses and/or the sequence of events do not follow the normal pattern previously described, and thus the arrhythmia occurs, which is very common in critical patients [8]. Among the arrhythmias caused by the abnormal generation of the cardiac impulse, there are those that occur by an increase in automaticity (for example sinusal tachycardia, bradycardia sinusal, auricular tachycardia, etc.) or by the firing activity (syndrome of long QT, toxicity by digoxina, etc.). Conduction disorders of impulse include atrioventricular tachycardia or atrioventricular-nodules, atrial fluttering, atrial fibrillation, ventricular tachycardia, ventricular fibrillation, blockade atrioventricular and sinus atrial and branch blockade. It is possible to group these arrhythmias according to the degree of risk they represent for patients’ lives. A first group comprises tachycardia and ventricular fibrillation, which jeopardize patients’ lives and require immediate action by the personnel to revert the state. On the other hand, there is a set of other arrhythmias, which even though they do not represent an imminent threat of death for patients, they might require therapy to avoid further problems [9].

One of the main reasons for which patients with myocardium infarct are admitted in intensive care units (or coronary care unit) is the possibility of monitoring them permanently and thus preventing malignant arrhythmias like ventricular fibrilation. In addition to the need for an intelligent supervision system that detects
indicators of this type of arrhythmias, it is also interesting, that the intelligent system, to inform users of the presence of the second type of arrhythmias, which in some cases offer early indications of a possible malignant arrhythmia. For example, premature ventricular contractions (PVC) are often warning signals of the possible occurrence of malignant arrhythmias. Although PVC in ECGs of normal patients can be registered, several events per minute are considered pathological. A high rate of PVC may be due, among other causes, to poor coronary irrigation, specific medication effects and deficit of sanguineous oxygenation. This must be detected, especially in patients with infarcts [9].

To reach a level of representation that allow for the search of temporal patterns, as the sequence of PVCs, it is first necessary to address the task of identifying V beats. These beats are normally mixed with normal heartbeats, which from the point of view of a classification model pose a problem with unbalanced classes. This imbalance between data sets for each class usually presents more "normal" examples than "abnormal". This problem becomes more serious when trying to make a multiple classification, because the classes containing fewer examples are disadvantaged by more than one class with more examples. All approaches improve the classification rate to the original classification problems analyzed in each work, which coincides with the findings presented in [10], which suggest similar effects on classification rates. On the other hand [11] questioned the incidence of examples imbalance in the degradation of the classification rate, arguing similar degradations in non-imbalanced problems.

In the temporal sequence dimension, this problem is reflected in the fact that pathological states are temporarily mingled with sequences of normal states with different lengths. This leads to the need of distinguishing the importance beat classes over the time sequence.

This paper will specifically address the time representation and modeling of the second type of arrhythmia, which offer early warning, representing states trajectory. For the representation of the trajectory in the space of arrhythmia states, a representation of the PVC time pattern is exemplified. It was previously described according to the application domain data through the Smith-Waterman algorithm with its substitution matrix being adjusted to the requirements of this application.

Database overview Section describes the signals and data being used. State-Space Assessment Model Section discusses the proposed model, based on the considerations made for the level of interpretation of the physiological status. Finally, we present the results and conclusions on the data used for the model application.

2. Database overview

2.1. Temporal Abstraction for Arrhythmia analysis

In the context of beats rate detection, temporal abstraction was conducted at three levels: at first, basic abstractions, and at the other two levels, complex abstractions were carried out. Figure 2 shows a diagram of these tasks.

The first level consists of the features-extracting module, which processes ECG samples to obtain a set of features that characterize a segment of the signal. The aim of the abstraction made by the features-extracting module is to facilitate the task of the classifying module. Even though it is possible to build a classifier using ECG samples, better results will be usually obtained using a number of features that is smaller than the number of samples in that interval [12]. It is also possible to use the outcome of the first abstraction to perform other diagnostic tasks such as detecting periods of ischemia in patients.

The second level of TA is performed by classifier I. This module uses the set of features of each segment given by the basic abstractions obtained in the previous stage to extract information regarding the type of heartbeat, either normal or arrhythmic, introduced by a patient.

The final level consists of classifying module II performing an abstraction based on sequences of beat types to extract information as regards temporal patterns at a higher level scale, which may provide evidence of poor oxygenation and malignant arrhythmias.
2.2. Signal database

ECG signals used in this work are part of the database of arrhythmia MIT-BIH [13]. This database contains 48 registers of 2 electrocardiographic derivations of 30 minutes each. These signals were filtered between 0.1 and 100 Hz before being digitized at 360 Hz, with a resolution of 11 bits and a range of ± 5 mV.

This database consists of two sets of records: those ranging from 100 to 124 inclusive, which contain a set of representative samples of morphologies of both the waves and usual artifacts in clinical practice routines. The second set includes records ranging from 200 to 234 and were chosen to represent complex and unusual cases, such as juncture ventricular and complex supraventricular arrhythmias, as well as conduction abnormalities, which are generally more difficult to be distinguished either by the human experts or by automatic detectors.

In addition, each record has a file of annotations for the type of beat that is manually labelled by cardiologists. This information is vital to the classifying module because it works in a supervised fashion. Among the entries, there are 15 types of different beats. In this paper, they are grouped into 5 classes according to AAMI recommendations (AAMI, 1998): N class: normal beats; S class: supraventricular ectopic beats; V class: ventricular ectopic beats; F class: fusion between normal beats and ventricular ectopic beats; Q class: other types of beats, including odd ones.

DS comprises the following records: 109_A, 112_A, 115_A, 118_A, 121_A, 122_A, 124_A, 212_A, 220_A, 230_A, 233_A, 100_A, 103_A, 108_A, 111_A, 113_A, 114_B, 116_A, 117_A, 123_A, 231_A, 234_A.

3. State-Space Assessment Model

One way to characterize a sequence of states (in this case beats) is the search for similar sequences in databases as well as additional available data to contextualize them (age, sex, etc.).

When there are patterns of beats sequences, arrhythmias are interspersed among normal beats. Its quantities vary according to the patient, which means that there are variations to be considered during the search for similar patterns. With this in mind and with the intention of finding significant similarities in the sequence of beats that include some form of arrhythmia, a classification or scoring model is used during the process of seeking similarities. For this, the Smith-Waterman algorithm (based on dynamic programming) was used for local alignments of nucleotide sequences [14], with the substitution matrix adjusted for this application.
Taking into account the importance of the V beats for PVCs, defined qualify, with one higher magnitude order than other beats, the V-beat coincidence. The lowest positive value was assigned to the coincidence of normal heartbeats, given that this condition varies greatly according to each patient and has no clinical importance for this type of problem. Negative classifications are associated with non-matching types of beats and act as a penalty. As previously mentioned, this is implemented in a substitution matrix, which is used during the search process for similar sequences. In addition, “spaces” are incorporated in the sequence during comparison. These spaces allow a better alignment of sequences to find similarities, thus enabling a variable number of normal beats between arrhythmias.

The idea of the search process is to align complete sequences through optimal linear alignments according to an additional global score. This results from considering the qualifications of the substitution matrix and from penalization of incorporating spaces during the search. Partial qualifications of the alignment are stored in matrix F according to the following definition:

\[
F(i, j) = \begin{cases} 
0, \\
F(i - 1, j - 1) + s(x_i, y_j), \\
F(i - 1, j) - d, \\
F(i, j - 1) - d, 
\end{cases}
\]

where d is the penalty for the included spaces, "x" and "y" are the sequences that are being compared, F (0,0) = 0, and s is the substitution matrix. Then, the maximum value of matrix F is sought in the last row and column, and from this element of the matrix the alignment is recovered seeking the previous maximum score in the previous row and column.

For instance, let us suppose that the following sequence of beats must be compared: \( x = \text{NNVNNVNP} \) and \( y = \text{NVNNPNNVNNNP} \). By applying the algorithm, the following alignment is obtained:

\[
\begin{align*}
\text{NNVNN} & \quad \text{--} \quad \text{VNNP} - \\
- & \quad \text{NNP} \quad \text{NNV} \quad \text{NNNP}
\end{align*}
\]

It can be seen that some spaces have been introduced in the alignment (represented with dashes), giving priority to the coincidence of beat V, which has the highest rating by coincidence in the substitution matrix. It is also intended to align heartbeat P, but since it has less weight, it admits some difference in the sequence. The above example is intended to show the effects of the algorithm application to the comparison of two sequences. However, in a more realistic situation, it might be of clinical interest to find a sequence in particular within another longer one. To illustrate this, sequence x previously presented with sequence y extended in both directions by normal beats (e):

\[
ye = \text{NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
4. Results

State-Space Assessment Model

Based on classifiers for normal beats, V-beats and other pathological beats, it is possible to compare a sequence x that is being monitored. To give greater importance to PVCs, the model put to the fullest qualification matches of the V beats in the temporal pattern. For this, a stretch (2.5 minutes) of a sequence (109_A record) is taken from the Database and compared with other nine full sequences through the Smith-Waterman algorithm.

Table 1. Results of sequence comparison.

| Patient | Score (normalized) | Age | Sex     |
|---------|--------------------|-----|---------|
| 109_A   | Current case       | 87  | Female  |
| 112_A   | 1                  | 64  | Male    |
| 115_A   | 0.8758             | 54  | Male    |
| 118_A   | 0.9876             | -   | Male    |
| 121_A   | 0.8758             | 39  | Female  |
| 124_A   | 0.9123             | 69  | Male    |
| 212_A   | 0.8758             | 51  | Male    |
| 220_A   | 0.9441             | 77  | Male    |
| 230_A   | 0.8758             | 87  | Female  |
Sequence comparison to the monitored case
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
Conclusions

The approach proposed in this paper allows a disaggregated analysis by granularities information provided by a monitor in a critical care unit, allowing higher quality information that facilitates the task of forecasting the evolution of patients. As for the states space trajectory assessment model, this provides a vision in perspective about the evolution from a search considering temporal and non-temporal aspects. A greater availability of previously monitored cases would improve the quality of the database used to obtain conclusions. The posed contextualisation through a clustering algorithm allows for selecting the most similar case, including information on non-temporal aspects, which are relevant to set a forecast in the area of critical care. This model form the basis of the operation logic for a system to support decision-making in the clinical setting, aimed at the representation of temporal patterns associated with early warning signs of critical issues, and enhancing the quality of the available information for decision making. The temporal abstraction approach used for the development and implementation of monitoring models can be extended to other aspects of monitoring, including information on invasive blood pressure, oxygen saturation, heart rate and breathing, leading to the analysis of the changing stable / unstable and intermediate states. For this, is necessary to generate an indicator of stability from the available data, and then analyze the existing patterns during monitoring.

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