A Fuzzy Constraint Satisfaction Approach to Identify and Characterize Apnea Episodes

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***Abstract*—This paper presents an algorithm that permits the identification of apneas – cessations in the sleeping patient's respiratory flow – in the respiratory airflow signal and relates them to the drops in blood oxyhemoglobin saturation that they produce. The structural nature of the algorithm allows us to perform a detailed characterization of the identified events and to easily modify the morphological detection criteria. This proposal is based on the fuzzy set theory for the representation and manipulation of the vagueness of the medical knowledge on which it is based, and on the constraint satisfaction problem formalism to provide a computable support to medical knowledge.**

***Index Terms*—Sleep Apnea Syndrome, Biosignal Processing, Structural Pattern Recognition, Fuzzy Constraints.**

I. Introduction

Sleep Apnea Syndrome (SAS) is a very frequent sleep-breathing disorder. Its prevalence is especially high in adult males with obesity problems and is recognized as an important public health issue [1]. This disorder is characterized by interruptions of the respiratory airflow whilst the patient is sleeping – apneas – caused by obstructions of the upper airway. As a consequence, they produce a drop in blood oxyhemoglobin saturation (SpO2) and cause micro-awakens (arousals) that fracture the patients' sleep. The global result is a decrease in the refreshing effects of sleep and a consequent diurnal somnolence and cognitive deficit that increases the risk of accidents.

Polysomnography is a fundamental test for the diagnosis of SAS. It is performed in a hospital Sleep Unit and consists of the registration of a wide range of physiological parameters whilst the patient is asleep. An algorithm is presented in this paper that permits the identification and characterization of apneas and the desaturations that these cause, using two of these parameters: the respiratory airflow and the SpO2. The algorithm is based on the Multivariable Fuzzy Temporal Profile model (MFTP) [6], a structural model that permits the projection onto a computable representation of a signal pattern made up by a set of morphologies defined over the temporal evolution of the physiological parameters of a patient and a series of relationships between these morphologies. The pattern is obtained directly from a human expert by means of a graphic tool developed for this purpose [5].

In the following section, the MFTP model is presented and how it can be used to represent an apnea and the corresponding desaturation is also shown. In Section III, the algorithm that permits the identification and characterization of both events is shown and Section IV includes a validation of the aforementioned algorithm. In Section VI the results obtained are discussed and, finally, a series of conclusions on the paper are given and possible lines of extension are commented.

II. Apnea representation

An apnea is defined as a decrease in the respiratory airflow of a patient to at least 10% of its basal value, maintained for at least 10 seconds. This hypoventilation usually produces a drop in the SpO2. The standard polysomnographic criteria consider a drop in the SpO2 to be relevant only when this drop is of 4% or higher. The drop in the SpO2 begins approximately from 10 to 30 seconds after the start of apnea. Shortly after the hypoventilation ceases, the SpO2 should begin to recover (see Fig. 1). In this section, how to represent this pattern using the MFTP model is shown.

A. The MFTP model

The MFTP model [6] makes it possible to represent signal patterns, comprising a set of morphologies defined over the evolution of a set of physiological variables and temporal and magnitude relations between these morphologies. The MFTP model is based on the constraint satisfaction problem formalism [3] and on fuzzy set theory. An MFTP allows a pattern to be represented by means of a network of fuzzy constraints between a set of significant points.

We shall introduce some basic concepts of the fuzzy set theory on which the MFTP model is based. Given as discourse universe the set of real numbers $\mathbb{R}$, a *fuzzy number* C is a normal ($\exists\, v \in \mathbb{R}, \mu^C(v) = 1$) and convex ($\forall v, v', v'' \in \mathbb{R}, v' \in [v, v''], \mu^C(v') \geq \min\{\mu^C(v), \mu^C(v'')\}$) fuzzy subset of $\mathbb{R}$. We obtain a fuzzy number C from a flexible constraint given by a possibility distribution π^C, which defines a mapping from $\mathbb{R}$ to the real interval $[0, 1]$. Given a precise number $v \in \mathbb{R}$, $\pi^C(v) \in [0, 1]$ represents the possibility of C being precisely v. By means of π^C we define a fuzzy subset C of $\mathbb{R}$, which contains the possible values of C.

We shall represent possibility distributions by means of a trapezoidal representation. In this way, $C = (\alpha, \beta, \gamma, \delta)$, $\alpha \leq \beta \leq \gamma \leq \delta$, where $[\beta, \gamma]$ represents the core, $core(C) = \{v \in$

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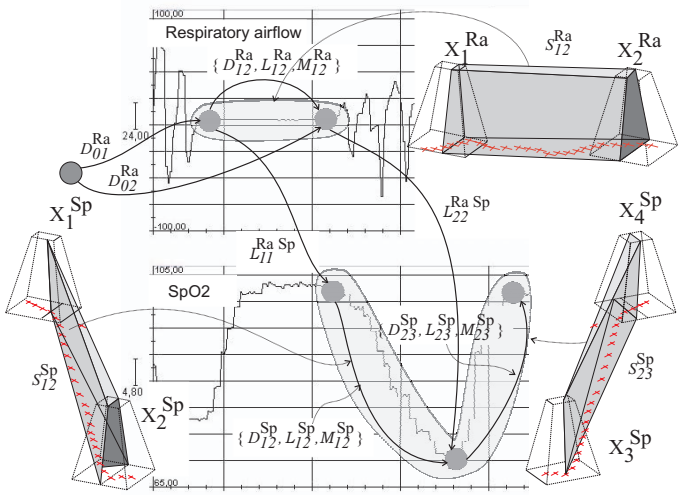

Fig. 1. Graph of the apnea MFTP drawn over a real apnea occurrence.

$\mathbb{R}|\ \pi^C(v) = 1\}$, and $]\alpha, \delta[$ represents the support, $supp(C) = \{v \in \mathbb{R} | \pi^C(v) > 0\}$. We have opted for this representation on the basis of its computational efficiency and the intuitiveness of its semantics for the medical users.

We shall consider time as being projected onto a one-dimensional discrete axis $\tau = \{t_0, t_1, ..., t_s, ...\}$, where t_s represents a *precise* instant and for every $i \in \mathbb{N}$, $t_{s+1} - t_s = \Delta t$. We will denote as $\mathcal{P} = \{P^1, ..., P^m\}$ the set of physiological variables obtained from the monitoring of a patient. In this case $\mathcal{P} = \{P^{Ra}, P^{SpO2}\}$ where P^{Ra} is the respiratory airflow and P^{SpO2} the SpO2. Each of the physiological variables $P^p \in \mathcal{P}$ is obtained by a signal sampling process, in the form of a temporal series $P^p = \{(v^p_{[s]}, t^p_{[s]});\ s \in \mathbb{N}\}$, where $v^p_{[s]}$ is the value of P^p at the instant $t^p_{[s]}$.

We define *significant point* on a physiological parameter P^p, X^p_i, as the pair formed by a variable from the domain V^p_i and a temporal variable T^p_i. A significant point $X^p_i = \{V^p_i, T^p_i\}$ represents an unknown value for P^p at an unknown temporal instant. In the absence of constraints, V^p_i and T^p_i may take any precise value v^p_i and t^p_i, respectively, where $(v^p_i, t^p_i) \in P^p$. By A^p_i we denote the assignment of precise values from the evolution P^p to the variables of X^p_i; i.e., $A^p_i = (v^p_i, t^p_i)$.

A *constraint* L^{pq}_{ij} between two significant points X^p_i and X^q_j is defined by means of a normal, convex possibility distribution $\mu^{L^{pq}_{ij}}(X^p_i, X^q_j) = \pi^{L^{pq}_{ij}}(h)$, $h \in \tau$, which represents the possibility of the *fuzzy temporal extension* between X^p_i and X^q_j being h. The assignments $T^p_i = t^p_i$ and $T^q_j = t^q_j$ are possible if $\pi^{L^{pq}_{ij}}(t^q_j - t^p_i) > 0$. In Fig. 1 L^{Ra}_{12} models the linguistic description "*more than approximately 10 seconds*".

A *constraint* D^{pq}_{ij} between a pair of significant points X^p_i and X^q_j is defined by means of a normal and convex possibility distribution $\mu^{D^{pq}_{ij}}(X^p_i, X^q_j) = \pi^{D^{pq}_{ij}}(d)$, $d \in \mathbb{R}$, which represents the possibility of the *fuzzy increase* between X^p_i and X^q_j being d. The assignments $V^p_i = v^p_i$ and $V^q_j = v^q_j$ are possible if $\pi^{D^{pq}_{ij}}(v^q_j - v^p_i) > 0$. In Fig. 1 D^{Sp}_{12} models the description "*decrease of 4% or more*".

Following the bibliography on constraint networks [3], and with the aim of obtaining a more compact notation, we define the *origin significant point* $X^p_0 = < V^p_0, T^p_0 >$ which will make it possible to represent value constraints (e.g. "*approximately 20 units*") as increase constraints relating to the origin significant point. Any arbitrary value can be assigned to X^p_0, although it is habitually assigned the value $V^p_0 = basal(P^p)$, $T^p_0 = 0$ where $basal(P^p)$ represents the value of the parameter P^p under normal conditions. In Fig. 1 D^{Ra}_{01} and D^{Ra}_{02} model the linguistic description "*less than approximately 10% of the basal value*".

A *constraint* M^p_{ij} between a pair of significant points X^p_i and X^p_j, defined over the same parameter P^p, is defined by means of a normal and convex possibility distribution $\mu^{M^p_{ij}}(X^p_i, X^p_j) = \pi^{M^p_{ij}}(m)$, $m \in \mathbb{R}$, which represents the possibility of the *fuzzy slope* between X^p_i and X^p_j being m. The assignments $V^p_i = v^p_i$, $V^p_j = v^p_j$, $T^p_i = t^p_i$ and $T^p_j = t^p_j$ are possible if $\pi^{M^p_{ij}}(m^p_{ji}) > 0$, where $m^p_{ji} = (v^p_j - v^p_i)/(t^p_j - t^p_i)$. In Fig. 1 $\mathcal{M}^{Ra}_{12}$ models the description "*...sustained...*", where "*sustained*" is modelled by means of an approximately zero slope value.

We define a *Multivariable Fuzzy Temporal Profile* (MFTP) $\mathcal{M} =< \mathcal{W}^{\mathcal{M}}, \mathcal{X}^{\mathcal{M}}, \mathcal{R}^{\mathcal{M}} >$ as a finite set of MFTPs $\mathcal{W}^{\mathcal{M}} = \{\mathcal{M}^{\mathcal{M}}_1, ..., \mathcal{M}^{\mathcal{M}}_s\}$, a finite set of significant points $\mathcal{X}^{\mathcal{M}} = \{X^{p_1}_{i_1}, X^{p_2}_{i_2}, ..., X^{p_g}_{i_g}\}$ and a finite set of constraints $\mathcal{R}^{\mathcal{M}} = \{R_1, ..., R_f\}$ amongst the points of $\mathcal{W}^{\mathcal{M}}$ and $\mathcal{X}^{\mathcal{M}}$.

The recursive structure of the MFTP model is based in the way that humans define patterns; a complex pattern is often made up of a set of findings and a set of relations between them. Each of the findings of the pattern may also be a pattern, and may comprise a set of findings and relations between them, and so on, successively.

An MFTP can be represented by a graph in which nodes correspond to significant points, and arcs correspond to constraints (see Fig. 1). The MFTP model also enables us to restrict the evolution of a parameter P^p between each pair of significant points X^p_i and X^p_j by means of a constraint $\mathcal{S}^p_{ij}$ represented by a membership function $\mu^{\mathcal{S}^p_{ij}}(\mathcal{A}^p_i, \mathcal{A}^p_j)$ which defines a fuzzy course (see Fig. 1) within which the temporal evolution of the parameter must remain in order to satisfy the constraint [6].

B. Apnea pattern modelling

A decrease in the respiratory airflow corresponding to an apnea is projected in an MFTP that represents a straight section with an almost constant value. The magnitude of the significant points that delimit the extremes, X^{Ra}_1 and X^{Ra}_2, should be less than approximately 10% of the basal value of the respiratory airflow (i.e. $D^{Ra}_{01} = D^{Ra}_{02}$="*less than approximately 10% of the basal value*"). The temporal relationship between both points should be L^{Ra}_{12}="*at least approximately 10 seconds*", the variation in magnitude D^{Ra}_{12}="*approximately zero*" and, consequently, the slope between them should be M^{Ra}_{12}="*approximately zero*". The magnitude of the samples of the signal section between both points should also be lower

than approximately 10% of the basal value. Therefore, the section samples should satisfy the constraint $\mathcal{S}_{12}^{Ra}$ defined as:

$$\mathcal{S}_{12}^{Ra}(A_1^{Ra}, A_2^{Ra}) = \min_{(v_{[s]}^{Ra}, t_{[s]}^{Ra}); t_1^{Ra} \leq t_{[s]}^{Ra} \leq t_2^{Ra}} \pi^{D_{12}^{Ra}}(v_{[s]}^{Ra}),$$

where $A_1^{Ra} = (v_1^{Ra}, t_1^{Ra})$ and $A_2^{Ra} = (v_2^{Ra}, t_2^{Ra})$ are the assignments performed to X_1^{Ra} and X_2^{Ra}. Therefore, the MFTP that represents an apnea would be: $\mathcal{M}_{Ra}^{Ap} =< \varnothing, \{X_0^{Ra}, X_1^{Ra}, X_2^{Ra}\}, \{D_{01}^{Ra}, D_{02}^{Ra}, L_{12}^{Ra}, D_{12}^{Ra}, M_{12}^{Ra}, S_{12}^{Ra}\} >$.

Similarly, the drop in the SpO2 produced by the apnea could be represented by $\mathcal{M}_{Sp}^{Ap} =< \varnothing, \{X_1^{Sp}, X_2^{Sp}, X_3^{Sp}\}, \{L_{12}^{Sp}, D_{12}^{Sp}, M_{12}^{Sp}, S_{12}^{Sp}, L_{23}^{Sp}, D_{23}^{Sp}, M_{23}^{Sp}, S_{23}^{Sp}\} >$ where the constraints between X_1^{Sp} and X_2^{Sp} forces a drop of at least 4% between them, and the constraints between X_2^{Sp} and X_3^{Sp} model the recovery of the parameter value. In this case, the samples of each section should verify a determined change rate: those between A_1^{Sp} and A_2^{Sp} should show compatibility with M_{12}^{Sp} taking assignment A_1^{Sp} as a reference (see Fig. 1); and those between A_2^{Sp} and A_3^{Sp} should show compatibility with M_{23}^{Sp} taking assignment a A_2^{Sp} as reference (see Fig. 1). Therefore, S_{12}^{Sp} would be given by:

$$S_{12}^{Sp}(A_1^{Sp}, A_2^{Sp}) = \min_{(v_{[s]}^{Sp}, t_{[s]}^{Sp}); t_1^{Sp} \leq t_{[s]}^{Sp} \leq t_2^{Sp}} \max_u \{\mu_{(v_{[s]}^{Sp} - v_1^{Sp}) \cap M_{12}^{Sp} \otimes (t_{[s]}^{Sp} - t_1^{Sp})}(u)\},$$

where $\otimes$ represents the fuzzy product. S_{23}^{Sp} is given by an analogous expression.

Given that we want to associate each apnea with its corresponding desaturation, we consider that both events form a part of the pattern to be identified. The temporal relationship between the beginning of the apnea and the beginning of the drop in SpO2 is $L_{11}^{Ra\ Sp}$ ="*approximately between 10 and 30 seconds afterwards*", and the recovery in the SpO2 should be subsequent to the end of the apnea (i.e. $L_{22}^{Ra\ Sp}$ ="*afterwards*"). Therefore, the pattern that models an apnea and its corresponding desaturation, which we denote by $\mathcal{M}^{Ap}$, would be: $\mathcal{M}^{Ap} =< \{\mathcal{M}_{Ra}^{Ap}, \mathcal{M}_{Sp}^{Ap}\}, \varnothing, \{L_{11}^{Ra\ Sp}, L_{22}^{Ra\ Sp}\} >$.

III. Apnea Recognition and Characterization

The MFTP definition allows the matching task to be structured hierarchically, where a pattern $\mathcal{M}$ constitutes a processing level that incorporates a set of findings detected in the previous processing level. Identifying the pattern $\mathcal{M}^{Ap}$ over $\mathcal{P} = \{P^{Ra}, P^{SpO2}\}$ is equivalent to finding a solution to the fuzzy constraint network defined by $\mathcal{M}^{Ap}$ [3]. A network solution is built by means of the assignment of a sample of the evolution of $\mathcal{P}$ to each significant point of $\mathcal{M}^{Ap}$. A solution $\mathcal{A}^{Ap}$ to the MFTP $\mathcal{M}^{Ap}$ is defined as a set of assignments $\mathcal{A}^{Ap} = \{A_1^{Ra}, A_2^{Ra}, A_1^{Sp}, A_2^{Sp}, A_3^{Sp}\}$ that satisfy the set of constraints that make up $\mathcal{M}$, with a degree higher than zero.

In order to match $\mathcal{M}^{Ap}$ we start by searching for occurrences of the two findings that make it up. In order to calculate the degree of compatibility of $\mathcal{M}_{Ra}^{Ap}$ with $\mathcal{A}^{\mathcal{M}_{Ra}^{Ap}} = \{A_1^{Ra}, A_2^{Ra}\}$ the following expression is used:

$$\pi^{\mathcal{M}_{Ra}^{Ap}}(\mathcal{A}^{\mathcal{M}_{Ra}^{Ap}}) = min\{\pi^{D_{01}^{Ra}}(v_1^{Ra}), \pi^{D_{02}^{Ra}}(v_2^{Ra}), \pi^{L_{12}^{Ra}}(t_2^{Ra} - t_1^{Ra}), \pi^{D_{12}^{Ra}}(v_2^{Ra} - v_1^{Ra}), \pi^{M_{12}^{Ra}}(m_{21}^{Ra}), \mathcal{S}_{12}^{Ra}(A_1^{Ra}, A_2^{Ra})\},$$

where the assignments A_1^{Ra} and A_2^{Ra} are taken from the values registered for the respiratory airflow and $m_{21}^{Ra} = (v_2^{Ra} - v_1^{Ra})/(t_2^{Ra} - t_1^{Ra})$. A similar expression applies for $\mathcal{M}_{Sp}^{Ap}$. Solutions are then searched for $\mathcal{M}^{Ap}$ over the previously found occurrences for $\mathcal{M}_{Ra}^{Ap}$ and $\mathcal{M}_{Sp}^{Ap}$. The degree of compatibility of $\mathcal{M}^{Ap}$ with $\mathcal{A}^{Ap} = \{\mathcal{A}_{Ra}^{Ap}, \mathcal{A}_{Sp}^{Ap}\}$ is given by:

$$\pi^{\mathcal{M}^{Ap}}(\mathcal{A}^{Ap}) = min\{\pi^{\mathcal{M}_{Ra}^{Ap}}(\mathcal{A}_{Ra}^{Ap}), \pi^{\mathcal{M}_{Sp}^{Ap}}(\mathcal{A}_{Sp}^{Ap}), \pi^{L_{11}^{Ra\ Sp}}(t_1^{Sp} - t_1^{Ra}), \pi^{L_{22}^{Ra\ Sp}}(t_2^{Sp} - t_2^{Ra})\}.$$

After it has been identified, the pattern is characterized using the structural information contained in $\mathcal{M}^{Ap}$. From $\mathcal{A}^{Ap}$ it is possible to calculate the duration of the apnea ($t_2^{Ra} - t_1^{Ra}$); the duration and slope of the drop section ($t_2^{Sp} - t_1^{Sp}$ and m_{21}^{Sp}, respectively) and of the recovery section ($t_3^{Sp} - t_2^{Sp}$ and m_{32}^{Sp}, respectively) of the desaturation; the time elapsed from the beginning of the apnea to the beginning of the drop in SpO2 ($t_1^{Sp} - t_1^{Ra}$); and the time elapsed from the end of the apnea until the SpO2 begins to recover ($t_2^{Sp} - t_2^{Ra}$) and until it has fully recovered ($t_3^{Sp} - t_2^{Ra}$). Also, the energy of the respiratory airflow signal is calculated for the interval of apnea, normalized by the number of samples of this interval, and the maximum, minimum and average values of the SpO2 during the desaturation episode.

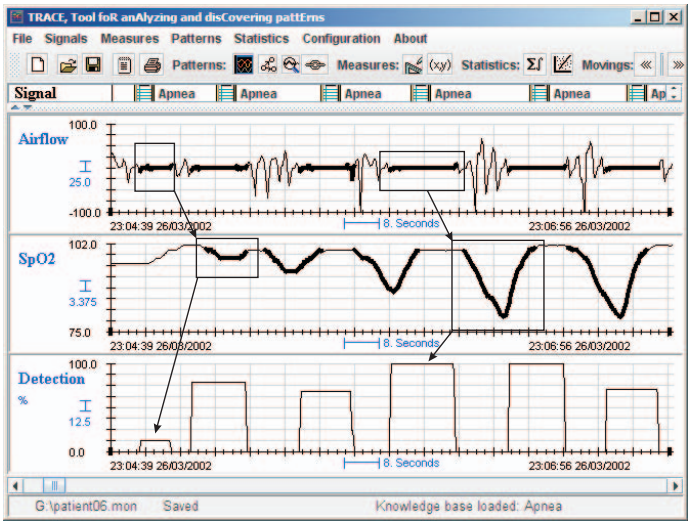

Fig. 2. TRACE showing the detection for the apnea and desaturation pattern.

IV. Experimental Results

Based on the MFTP model we have constructed the Tool foR anAlyzing and disCovering pattErns, TRACE, a tool for creating, editing and validating MFTPs [5]. The tool makes use of the very graph that represents the MFTP, whose shape

resembles the pattern it represents, as a visual metaphor to assist in editing knowledge relating to signal patterns. This editing can be carried out in an entirely visual manner, using only a mouse. The tool also allows the matching procedures for the MFTP model to be executed, and its results viewed. Each detection emphasizes the fragments of each physiological parameter that has demonstrated compatibility with the morphology defined over it, and adds a signal to the environment called detection, which represents the compatibility of the global pattern (see Fig. 2).

Using TRACE, 28 hours of polysomnographic registers from 5 different patients subjected to a sleep study were processed. Of the 787 apneas present in the registers, 741 apneas were correctly identified (94%), 46 false negatives (5.8%) and 11 false positives (1.5%) were produced.

V. Discussion

The results of the preliminary evaluation presented here allow us to be optimistic with regard to the potential of our proposal as a support to the diagnosis of SAS. The very low number of false positives (1.5%), obtained as a result of the integration of information from two different parameters (respiratory airflow and SpO2) in the detection process, should be noted. This high specificity increases the value of the characterization of the apnea episodes, as the presentation of a high rate of false positives could contaminate the characterization information and so decrease its value.

On the other hand, during the validation process, the metaphors employed by TRACE to show the results of the detection process have demonstrated that they are sufficiently intuitive for the pneumologist to understand the detection results without assistance, which endorses the viability of employing TRACE in the clinical routine.

In the bibliography there are several proposals which provide a diagnostic test to determine automatically whether or not a patient suffers from SAS [7]. However, there are very few proposals that include algorithms capable of individually identifying each apnea [2], [4] and, to the best of our knowledge, none propose mechanisms for their characterization.

The set of descriptors that our algorithms employ to characterize the apneas were selected with the collaboration of a medical team. Their purpose is to serve as a basis for carrying out a detailed study of the physiopathological processes that are subjacent in SAS and, thereby achieve a more profound knowledge of this disorder. Thus, for example, the sections between the end of the apnea and the beginning and ending of the recovery in the SpO2, together with the slope of this recuperation, reflect the capacity of the patient to recover from the hypoxia. It is well known that patients with chronic obstructive pulmonary disease who suffer SAS recover more slowly from the hypoxia, due to their problems of ventilation. However, there are no detailed studies on how the capacity for recovery reflects the different degrees of the seriousness of the illness or if this should have some impact on the therapy.

The structural character of the algorithm, together with the availability of a graphical tool -TRACE- that permits edition of the morphological criteria of the apnea pattern, supplies support for analyzing polysomnographic registers using criteria different to the standard ones. For example, the medical team with which we work believes that flow limitations of only five or six seconds can have repercussions on the architecture of the patients' sleep although, if standard polysomnographic criteria were employed, these would not be considered as apneas.

VI. Conclusion and future work

This paper presents an algorithm of a structural character that permits the identification of apneas and relates them to the drops in the SpO2 that these produce. The algorithm takes, as a starting point, medical knowledge of the morphology of these manifestations and is based on the fuzzy set theory for the representation and manipulation of the vagueness characteristic of this knowledge. Using a graphic tool, TRACE, the clinical staff can edit the morphological criteria of the pattern to be identified, which provides support for the employment of customized criteria in the analysis of a polysomnographic register.

The algorithm calculates a set of descriptors that permit the characterization of the apnea, the desaturation and the temporal relationships between them. This characterization can serve as a basis for obtaining a more profound knowledge of the subjacent physiopathological processes in SAS. One of our future lines of research is directed towards this end: we hope to process a database of polysomnographic registers with the algorithm and apply data-mining techniques to the information that is generated to discover new medical knowledge. We also hope to develop algorithms based on the MFTP model to identify other events that are registered during a polysomnography and that are relevant for cardiopulmonary sleep disorders.

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