# Variability Analysis of the Respiratory Volume Based on Nonlinear Prediction Methods

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*Abstract – This work proposes a method to automatically classify respiratory volume signals as high (HV) or low (LV) variability by means of the nonlinear analysis of the respiratory volume. The analysis uses volume signals generated by the respiratory system in order to construct a model of its dynamics and to estimate the quality of the predictions made with the model. Different methods of prediction evaluation, prediction horizons, and embedding dimensions have also been analysed. Assessment of the method is made using a database that contains 40 respiratory volume signals classified using clinical criteria into two classes: low (CLV) or high (CHV) variability. The results obtained using the method of surrogate data have presented evidence of nonlinear determinism in the respiratory volume signals. A discriminant analysis carried out using nonlinear prediction variables has been able to classify the respiratory volume signals with an out-of-sample accuracy of 95%.*

**Key words –** *Respiratory pattern variability, nonlinear prediction methods, pressure support ventilation.*

## 1 Introduction

The possible causes of breath-to-breath variability in the pattern of breathing have been discussed (BRUCE, 1996a; BRUCE, 1996b; KHOO, 2000). Stochastic processes or dynamical behaviours of the Autonomic Nervous System (ANS) can produce this variability (MODARRESZADEH ET AL, 1990; JUBRAN ET AL, 1997; BRACK ET AL, 2002). The analysis of respiratory variability provides a new tool to study the action of the chemoreflexes without application of external stimuli (VAN DEN AARDWEG and KAREMAKER, 2002). The determination of the variability of the respiratory volume also enables to know the ability of the patients to control the mean tidal volume in response to alterations in respiratory demand (WRIGGE ET AL., 1999). Recently, it has been described that the respiratory variability was reduced in patients with restrictive lung disease when compared with healthy subjects (BRACK ET AL., 2002). One of the most challenging problems in intensive care (TOBIN, 2001) is the process of discontinuing mechanical ventilation, termed weaning. It was also hypothesized that the variability of the respiratory volume could be a convenient weaning criteria to reduce the number of patients not successfully weaned (DEL ROSARIO ET AL., 1997).

The traditional techniques of data analysis in the time and frequency domains are often not sufficient to characterise the complex dynamics of respiration. Various attempts have been reported to apply the concept of nonlinear dynamics to the analysis of complex physiological systems (RIGNEY ET AL., 1992; TURCOTT, 1996; ACHERMANN, 1994) and to distinguish between variations that are random and those that are deterministic. The nonlinear behaviour and the time delays of the respiratory mechanisms of the ANS together with the muscle activity and the lung can introduce non-stochastic variability in the respiratory system. In this way, several studies have evidenced the nonlinear dynamical behaviour of the respiratory system. Several methods describing the nonlinear deterministic variability of physiological time series have been proposed: Correlation dimension, Lyapunov exponents, Kolmogorov-Sinai entropy, etc. (BRUCE and DAUBENSPECK, 1995;

SMALL ET AL.,1999; AKAY ET AL., 2002). SCHREIBER and SCHMITZ (1997) showed that nonlinear prediction is an excellent method for detecting nonlinearity in signals where determinism has not been established previously. Other approaches may present limitations according to the fractal nature of the time series (SAMMON ET AL., 1993; WESSEL ET AL., 1998; TAPANAINEN, 1999) or even can lead to misinterpretations of the data (SMALL ET AL.,1999). Cardiorespiratory synchronisation in humans and nonlinear analysis of heart rate and respiratory dynamics have also been analysed using a prediction framework (HOYER ET AL., 1998; HOYER ET AL., 2002; CENSI ET AL., 2000).

In this work, nonlinear prediction methods have been applied in order to find a set of indices that effectively characterise the variability of the respiratory volume. Since respiratory volume can be measured non-invasively, these indices may be advantageous in future automatic diagnostic of patients.

## 2 Material and methods

### *2.1 Analysed data*

A group of 20 patients on weaning trials from mechanical ventilation has been studied in the Department of Intensive Care Medicine at Santa Creu i Sant Pau Hospital. According to a protocol approved by the local ethic committee and with an informed consent obtained, the patients were each placed under two different levels of pressure support ventilation (PSV), classified as low PSV ($5 \pm 2$ cm $H_2O$) and high PSV ($12 \pm 2$ cm $H_2O$). In this way, the database contains respiratory volume signals with different variability, mainly due to the fact that changes in pressure support are often associated with changes in variability. The respiratory volume signals were obtained by means of a respiratory inductive plethysmograph. Respiratory volume at each PSV level was recorded during 30

minutes with a sampling frequency of 250 Hz and resampled at 10 Hz for this study. The 40 recordings of 30 minutes were classified by the medical doctors into two classes, low (CLV) or high (CHV) variability, using clinical criteria based on respiratory rate, minute ventilation and rapid shallow breathing index. (CAPDEVILA, 1998).

This work proposes a method to automatically classify the volume signals in high (HV) or low (LV) variability which does not necessarily match to low and high PSV level. For out-of-sample evaluation, the 40 volume recordings were organised into two sets: a training set and a testing set. A training set has been selected that includes patients presenting both CLV and CHV levels when changing the PSV (9 patients and 18 volume recordings). A volume recording is considered correctly classified when the automatic classification coincides with the classification done by the medical doctor considered as gold standard.

*2.2 Nonlinear prediction*

Figure 1 shows CLV and CHV signals. The CHV signal in this case is at a slower frequency and, qualitatively displays greater irregularity both in the waveform of a single cycle and the spacing of cycles. The amplitude range of the signals is approximately the same. We sought to quantify this irregularity by measuring the auto-regressive predictability of the signal. The time series is used to construct a model of the dynamics; the model is then used to predict other signal segments. The resulting prediction error quantifies irregularity.

There are different ways to construct dynamical models from data. Since all of the state variables of the systems are not directly measured or even known, we used the lag embedding technique to represent the system's state variables. By embedding the scalar time series $D_t$, the following vector sequence is created:

$$\mathbf{D}_t = (D_t,\ D_{t-1},\ \ldots\ D_{t-(m-1)})$$

where *m* is the embedding dimension. Each $\mathbf{D}_t$ is a point in the m–dimensional embedding space, and the embedded time series can be regarded as a sequence of points, one point at each time *t.* Each point represents the state of the system at that time.

A deterministic data set sampled at discrete times can be described by a discrete-time map

$$\mathbf{D}_{t+1} = \mathbf{F}(\mathbf{D}_t)$$

which is, however, immediately applicable only if the mapping **F** is known. With **F** unknown some assumptions about its properties have to be made. With the minimal assumption that the mapping **F** is continuous the following prediction scheme can be constructed (KANTZ and SCHREIBER, 2000). This method implements a nonlinear regression model by stitching smoothly together a large number of locally linear models. The method works as follows: In order to predict the future state $\mathbf{D}_{t+1}$ given the present one $\mathbf{D}_t$, the state that is closest to $\mathbf{D}_t$ with respect to some norm is searched. Let's say that this closest point has time index *a*. The definition of determinism is that future events are set causally by the past events. $\mathbf{D}_t$ describes the past events to $D_{t+1}$. Similarly $\mathbf{D}_a$ describes the past events to the measurement $D_{a+1}$. If $\mathbf{D}_t$ is close to $\mathbf{D}_a$, and if the system is deterministic, then it is expected that $D_{a+1}$ will also be close to $D_{t+1}$. In the same way $D_{a+h}$ will be used as a predictor of $D_{t+h}$ and it will be called $P_{t+h}$.

Every measurement of a continuous quantity is only valid up to some finite resolution and this fact has to be taken into account. The finite resolution implies that looking for the single closest state is no longer the best can be done since interpoint distances are contaminated with an uncertainty. All points within a close region in phase space have to be considered to be equally good predictions a priori. Then the proposed prediction algorithm to be used forms a neighbourhood $U(\mathbf{D}_t)$ around the point $\mathbf{D}_t$. For all points $\mathbf{D}_{a_i} \in U(\mathbf{D}_t)$, that is, all points close to $\mathbf{D}_t$ look up the individual predictions $\mathbf{D}_{a_i+h}$. Then the matrix **H** of the application $\{ \mathbf{D}_{a_i+h} \} = \mathbf{H} \{ \mathbf{D}_{a_i} \}$ is obtained, that transforms the points of the neighbourhood $U(\mathbf{D}_t)$ into their predictions. Finally, the prediction $\boldsymbol{P}_{t+h}$ is obtained

applying the matrix **H** to the vector $\mathbf{D}_t$. Two ways have been considered in order to define the neighbourhood: i) the neighbours inside an hypersphere of radius $\varepsilon$ around the point $\mathbf{D}_t$; ii) the $K$ neighbours closest to the point $\mathbf{D}_t$.

Given a method for making a prediction $P_{t+h}$, an actual measurement of $D_{t+h}$ is needed in order to decide if the prediction is good or bad. The difference between $P_{t+h}$ and $D_{t+h}$ is the prediction error, which informs about the quality of the prediction. As a single prediction might be good or bad just by chance, in order to give a more meaningful indication of the determinism in the data an average of many prediction errors should be taken.

Two different ways have been considered in order to define this indication of determinism: i) Cross-prediction; ii) Leave-one-out auto-prediction. In the cross-prediction approach the time series is broken into M segments. For each of the M segments, one at a time, the model is fit and then residuals are calculated on each of the other segments. The residuals are summarized by one number, the mean absolute value. The result is a M-by-M matrix of cross-predictabilities. In this study the respiratory volume data set at each PSV level that contains 18000 samples has been divided in M = 3 segments of 6000 samples. In this case the 3-by-3 matrix has 6 entries (the diagonal elements that correspond to self prediction are not computed) and their mean value is computed in each patient for each PSV level.

In the leave-one-out auto-prediction the time series of length N is modelled N different times: for each model, a single data point is left out when fitting the model and the residual for the model is computed only for the left-out data point. The result is a set of residuals one for each point, that provide an estimate of the prediction error of a model. In this study the respiratory volume data set at each PSV level has been divided in 9 subsets of N = 2000 samples. In this way the mean prediction error related to each patient for each PSV level corresponds to the mean absolute value of the prediction errors in the nine subsets.

A preprocessing step has been applied to each respiratory volume data set in order to improve the analysis of the results. Each respiratory volume signal has been normalized by substracting by its mean value and dividing by its standard deviation. Figures 2a and 2b shows the actual measurements and predictions for the respiratory volume of a patient with clinically labelled low and high variabilities (CLV and CHV), respectively. The different quality of the prediction is shown comparing CLV and CHV.

*2.3 Parameter setting*

The first analysis related with the nonlinear prediction was done in order to select between auto-prediction or cross-prediction methodologies. Three patients (CRR, MMX and SAT) that clinically present two different variability levels (CLV and CHV) when changing the PSV were randomly selected for the analysis. An embedding dimension $m = 2$ was considered. Two kinds of neighbourhoods were analysed: the neighbours inside an hypersphere of radius $\varepsilon = 0.2$ and the $K = 20$ closest neighbours. Tables I and II present as an example the values obtained in patient CRR using the neighbours inside an hypersphere and the $K$ closest neighbours, respectively. In the three analysed patients the auto-prediction methodology presented the best statistical significant differences ($p$-value) when comparing CLV and CHV signals. Then this methodology has been selected for the next steps.

In order to decide the best kind of neighbourhood to discriminate the different irregularity of the respiratory volume, in low and high variabilities, the following neighbourhoods were considered: the neighbours inside hyperspheres of radius $\varepsilon = 0.1, 0.2, 0.3$ and the $K = 20$ closest neighbours. The same three patients were analysed and an embedding dimension $m = 2$ was considered. Table III presents as an example the values obtained in patient CRR. In the three analysed patients the statistical significance ($p$-value) obtained when comparing CLV and CHV signal were found not dependent of the different neighbourhood methodology. Then, as the radius of the hyperspheres could

be dependent of the embedding dimension, the *K* closest neighbours methodology has been selected for the next steps.

The next analysis has been done to select the best prediction horizon $h$. For each patient and for each PSV level the mean respiratory period has been calculated. This mean respiratory period translated to sample units is called $h_{Ttot}$. Three prediction horizons have been considered: $0.5\,h_{Ttot}$, $h_{Ttot}$ and $2\,h_{Ttot}$. The three patients were analysed and the embedding dimension $m = 2$ was considered. Table IV presents as an example the values obtained in patient CRR using the different prediction horizons. In the three analysed patients the statistical significance (*p*-value) obtained when comparing CLV and CHV signals were found not dependent of the considered $h$ value. A prediction horizon of $h_{Ttot}$ has been selected for the next steps.

*2.4 Nonlinear determinism in the respiratory volume signal*

The typically slower frequency of the CHV signals suggests that a frequency domain analysis using, e.g., power spectrum analysis, might be effective at performing the discrimination. In order to assess to what extent our nonlinear prediction method processes information not accessible to linear method, we used the method of surrogate data (THEILER ET AL, 1992; SHREIBER and SCHMITZ, 1996). This method involves generating synthetic volume signals, called surrogate data, with the same Fourier spectra, mean, standard deviation, and other percentiles as the original data. All of the information that could be accessed by a linear power spectrum analysis, whatever form that analysis might take, is contained in the surrogate data. The algorithm to generate this surrogate data is based on the null hypothesis that the data comes from a stationary linear process with gaussian white noise inputs.

A set of surrogate data is generated for each volume signal tested. For all the signals (original data and surrogate data) a nonlinear index is computed. Then, a statistical test is applied between the set of surrogate data and the original data.

If the null hypothesis is rejected, this suggests that the original data are due to a nonlinear deterministic process and/or non-Gaussian inputs or nonstationarity. In the case of the signals analysed in this study, ten series of surrogate data have been generated for each of the volume signals of the three patients CRR, MMX and SAT. The nonlinear index selected has been the mean prediction error.

*2.5 Discriminant analysis*

A discriminant analysis has been applied in order to get a discriminant function that enables to automatically classify the volume signals in high (HV) and low (LV) variability. In order to know the best variables to be introduced in the discriminant analysis, a previous non parametric analysis of variance test (Mann-Whitney) has been used to analyse statistically the differences between the respiratory volume signals with CLV and CHV. Different variables from the classical time-domain analysis and from the described nonlinear prediction analysis have been considered.

In the classical time-domain analysis of the respiratory volume signal, for each patient and for each PSV level the following time series have been obtained: Breath duration ($T_{tot}$), inspiration time ($T_i$) and tidal volume ($V_t$), related to the respiratory cycles of each 30-minutes recording. From these time series the mean values of $T_{tot}$, $T_i$ and $V_t$ were obtained ($\overline{T_{tot}}$, $\overline{T_i}$ and $\overline{V_t}$).

From the respiratory volume signals training set different discriminant functions have been obtained and subsequently validated with the testing set. The validation has been done comparing the results obtained with the discriminant functions and the classification done by medical doctors.

## 3 Results

Time-domain analysis of the respiratory volume signal has been previously done. Table V shows the results obtained with the mean values of $T_{tot}$, $T_i$ and $V_t$ when comparing low and high variability levels, defined using clinical criteria, in all the 20 patients. $\overline{T_{tot}}$ and $\overline{T_i}$ variables present statistically significant differences ($p < 0.0005$ and p = 0.03, respectively). This change in $\overline{T_{tot}}$ reflects the slow frequency of the CHV signals and the differences between the populations of signals. However, since the populations overlap substantially, classification of individual signals will not be very accurate.

Table VI shows the results obtained when surrogate data method was applied to the respiratory volume signals of CLV and CHV in the 3 selected patients CRR, MMX and SAT who had both CLV and CHV recordings. The mean prediction error (*mpe*) of the original signal ($Q_D$), and the mean value $\pm$ standard deviation of the *mpe* of the surrogate data ($\mu_H \pm \sigma_H$) are presented. For both low and high variability recordings of the 3 patients the respiratory volume signals of the patients analysed have significant differences with respect to surrogate data generated, and so the null hypothesis can be rejected.

In order to analyse the level of irregularity in the respiratory volume signals related to high variability in comparison with the low variability, Table VII shows the mean prediction errors (*mpe*) obtained for $m = 2$ when considering all the patients. The results show a statistically significant difference ($p < 0.0005$) between both groups (Mann-Whitney test).

The role of the embedding dimension *m* on the prediction errors has been analysed in all the patients for each one of the PSV levels. Figure 3 shows as an example the relation between the mean prediction error and the embedding dimension for the patient CRR. Line labelled as CRR20 belongs to the CHV signal and CRR06 to the CLV signal.

Another way to characterize predictability involves finding embedding dimension needed to model the dynamics of the patients with a low prediction error. For example in patient CRR (Figure 3) an embedding dimension $m = 8$ is needed to get a mean prediction error below 0.4 when analysing the CHV signal, while a $m = 2$ is enough to get the same prediction error for the CLV signal. The values of the embedding dimension ($m$) needed to model the dynamics of the signals with a prediction error ($e$) of 0.35, 0.40, 0.45 (*me35*, *me40* and *me45*, respectively) have been calculated. Table VII shows the values of the *me35*, *me40* and *me45* when analysing all the patients. The embedding dimension needed to model the dynamics of the patients with a low prediction error show a statistical significant difference ($p < 0.0005$) between both low and high variability signals (Mann-Whitney test).

The aim of the last part of this study has been to obtain discriminant functions able to discriminate low and high respiratory pattern variability. From the respiratory volume signals of the training set different discriminant functions have been constructed using each single variable presented in Table VII (mpe, me35, me40, me45), as well as $\overline{T_i}$ and $\overline{T_{tot}}$ variables. Table VIII shows the critical threshold of the discriminant functions, related to each one of the considered single variables, and the results achieved during the evaluation process with the 22 respiratory volume signals of the testing set. In this process a signal is considered False HV when the discriminant function classifies it as high variability (HV) when it was considered by the medical doctor as low variability (CLV), and a signal is considered as False LV when the discriminant function classifies it as low variability (LV) when it was considered by the medical doctor as high variability (CHV). Accuracy is the percentage of volume signals correctly classified. The variables obtained with the nonlinear prediction methodology present better discriminant results than the best variable proposed from the time-domain analysis. Table IX shows the results obtained using discriminant functions of two variables. The mean prediction error (*mpe*) and the *mpe* combined with the embedding dimension needed to get a *mpe* of 0.40 or 0.45 achieve an accuracy of 95%.

## 4 Discussion and conclusions

To analyse the respiratory pattern variability in respiratory volume signals nonlinear prediction methods have been applied. The volume time series have been used to construct a model of the respiratory system dynamics and the accuracy of the predictions made from the model have been analysed. Two different ways have been considered in order to define the indication of determinism: cross-prediction and leave-one-out auto-prediction. The auto-prediction methodology has been selected because it presented the best statistical significant differences when comparing CLV and CHV signals. Two kinds of neighbourhoods have been analysed: the neighbours inside an hypersphere of radius $\varepsilon$ and the $K$ neighbours closed to a point in the phase space. The $K$ closest neighbours methodology has been selected because it got the same statistical significance level than the neighbours inside an hypersphere, and this last method presented the inconvenience that the radius of the hyperspheres could be dependent of the embedding dimension. The incidence of different prediction horizons $h$ has also been considered. As the results were found not dependent of the considered $h$ value, the mean respiratory period has been selected as the prediction horizon.

Highly statistically significant differences have been obtained when comparing the mean prediction error (mpe) of the volume signals clinically classified as low variability $(0.35 \pm 0.09)$ in relation with high variability signals $(0.63 \pm 0.08)$, $p < 0.0005$. The embedding dimension needed to model the dynamics of the system with a low prediction error is also a good parameter to discriminate different respiratory patterns.

The results obtained using the method of surrogate data means that the nonlinear prediction method is detecting signs of nonlinearity, nonstationarity or non-gaussianity in the signals. But note that the prediction errors for the surrogate data in the different classes of CHV and CLV signals follow roughly the same pattern of variability as for the original data. That is, there is lower nonlinear prediction error for surrogates from CLV signals than for surrogates from CHV signals. Since the

surrogate data has, by construction, no statistically identifiable nonlinear, nonstationary, or nongaussian components, this suggests that it might be possible to find some linear analysis method that can perform a discrimination between CLV and CHV similar to the one using nonlinear prediction. This does not necessarily mean, however, that the physiological mechanisms generating the linear structures are themselves linear. The hypotheses on the physiological mechanisms governing the respiratory volume variability are based on the nonlinear dynamic interactions between various components of the respiratory control system, such as the lung vagal afferents and the respiratory pattern generator, or through the propagation of stochastic disturbances around the chemoreflex loops (BRUCE, 1996a; KHOO, 2000).

The discriminant analysis carried out with the training set, when using the mean prediction error, obtained discriminant functions able to classify with an accuracy of 95% the testing respiratory volume signals, while the discriminant analysis using classical time-domain variables present lower accuracy (77%). These results indicate that nonlinear prediction is a promising methodology to study the respiratory pattern variability. It should be validated by a larger number of patients, especially to check out the discriminant functions.

The clinical relevance of such a method to discriminate respiratory volume variability is related with the study of the action of chemoreflexes without application of external stimuli, and the analysis of the ability of patients to control the mean tidal volume in response to alterations in respiratory demand. Furthermore, this method could be a convenient weaning criteria to reduce the number of patients not successfully weaned.

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respiratory work of patients with chronic obstructive pulmonary disease", *Intensive Care Med.*, **25**, n. 8, pp. 790-798.

TABLE I

| | CLV | CHV | *p*-value |
|---|---|---|---|
| Leave-one-out auto-prediction | $0.41 \pm 0.06$ | $0.82 \pm 0.11$ | 0.008 |
| Cross-prediction | $0.45 \pm 0.04$ | $0.90 \pm 0.06$ | 0.028 |

Mean ± standard deviation for the mean prediction error of the patient CRR with $m = 2$, $\varepsilon = 0.20$, when considering leave-one-out auto-prediction and cross-prediction. Statistical significance (p-value) when comparing low and high variability levels.

TABLE II

| | CLV | CHV | *p*-value |
|---|---|---|---|
| Leave-one-out auto-prediction | $0.36 \pm 0.05$ | $0.76 \pm 0.09$ | 0.008 |
| Cross-prediction | $0.43 \pm 0.03$ | $0.88 \pm 0.06$ | 0.027 |

Mean ± standard deviation for the mean prediction error of the patient CRR with $m = 2$, $K = 20$, when considering leave-one-out auto-prediction and cross-prediction.

TABLE III

| | CLV | CHV | *p*-value |
|---|---|---|---|
| $\varepsilon = 0.1$ | $0.41 \pm 0.05$ | $0.81 \pm 0.09$ | 0.008 |
| $\varepsilon = 0.2$ | $0.41 \pm 0.06$ | $0.82 \pm 0.11$ | 0.008 |
| $\varepsilon = 0.3$ | $0.38 \pm 0.06$ | $0.81 \pm 0.11$ | 0.008 |
| $K$ neighbours | $0.36 \pm 0.05$ | $0.76 \pm 0.09$ | 0.008 |

Mean ± standard deviation for the mean prediction error of the patient CRR with $m = 2$ when considering different radius $\varepsilon$ of the hyperspheres and the $K = 20$ closest neighbours.

TABLE IV

| | CLV | CHV | *p*-value |
|---|---|---|---|
| $0.5\,h_{Ttot}$ | $0.34 \pm 0.07$ | $0.67 \pm 0.09$ | 0.008 |
| $h_{Ttot}$ | $0.36 \pm 0.05$ | $0.76 \pm 0.09$ | 0.008 |
| $2\,h_{Ttot}$ | $0.55 \pm 0.07$ | $0.81 \pm 0.09$ | 0.008 |

Mean ± standard deviation for the mean prediction error of the patient CRR with $m$ = 2 when considering different prediction horizons $h$.

TABLE V

| | CLV | CHV | *p*-value |
|---|---|---|---|
| $\overline{T_{tot}}$ | $2.48 \pm 0.65$ | $3.63 \pm 1.04$ | $< 0.0005$ |
| $\overline{T_i}$ | $0.88 \pm 0.12$ | $1.04 \pm 0.30$ | 0.030 |
| $\overline{V_t}$ | $466 \pm 195$ | $601 \pm 265$ | ns |

Mean ± standard deviation for classical time-domain analysis variables when comparing low and high variability levels in all the 20 patients.

TABLE VI

| | $Q_D$ | $\mu_H \pm \sigma_H$ | $p$-value |
|---|---|---|---|
| CRR-CLV | 0.36 | $0.49 \pm 0.01$ | $< 0.0005$ |
| CRR-CHV | 0.72 | $0.75 \pm 0.01$ | $< 0.0005$ |
| MMX-CLV | 0.24 | $0.31 \pm 0.01$ | $< 0.0005$ |
| MMX-CHV | 0.33 | $0.39 \pm 0.01$ | $< 0.0005$ |
| SAT-CLV | 0.31 | $0.40 \pm 0.01$ | $< 0.0005$ |
| SAT-CHV | 0.70 | $0.79 \pm 0.01$ | $< 0.0005$ |

Values of mean prediction error for volume signals and surrogate data with statistical significance

TABLE VII

| | CLV | CHV | *p*-value |
|---|---|---|---|
| *mpe* | 0.35 ± 0.09 | 0.63 ± 0.08 | < 0.0005 |
| *me35* | 3.3 ± 2.0 | 6.8 ± 1.7 | < 0.0005 |
| *me40* | 2.4 ± 0.7 | 5.9 ± 1.5 | < 0.0005 |
| *me45* | 2.1 ± 0.3 | 5.1 ± 1.4 | < 0.0005 |

Mean ± standard deviation of the mean prediction errors (*mpe*) and the embedding dimensions (*m*) needed to model the dynamics of the patients with a reduced mean prediction error (*e*) of 0.35, 0.40 and 0.45 (*me35, me40 and me45, respectively*).

TABLE VIII

| | Critical threshold | False HV | False LV | Accuracy |
|---|---|---|---|---|
| $\overline{T_{tot}}$ | 2.86 | 4 | 1 | 77% |
| $\overline{T_i}$ | 0.97 | 4 | 3 | 68% |
| *mpe* | 0.50 | 1 | 0 | 95% |
| *me35* | 5.3 | 0 | 2 | 91% |
| *me40* | 4.4 | 1 | 1 | 91% |
| *me45* | 3.9 | 3 | 1 | 82% |

Validation, using the testing set, of the discriminant functions of single variables obtained from the training set

TABLE IX

| | False HV | False LV | Accuracy |
|---|---|---|---|
| *mpe* and *me35* | 2 | 1 | 86% |
| *mpe* and *me40* | 0 | 1 | 95% |
| *mpe* and *me45* | 0 | 1 | 95% |

Validation, using the testing set, of the discriminant functions of two variables obtained from the training set

Figure 1. Respiratory volume recordings classified by the medical doctors as low variability (CLV) and high variability (CHV).

Figure 2. Actual measurement and prediction of the respiratory volume of a patient with clinically labelled low (a) and high (b) variabilities. The mean respiratory period has been selected as the prediction horizon.

Figure 3. Prediction errors (*mpe*) obtained as a function of the embedding dimension *m* for the patient CRR. The lines labelled as CRR20 and CRR06 belong to the CHV and CLV signals, respectively.