Analysis of Respiratory Flow Signals to Identify Success of Patients on Weaning Trials

H. González[1], C. Arizmendi[2], B.F. Giraldo[3]

[1] Autonomous University of Bucaramanga, Colombia
[2] Autonomous University of Bucaramanga, Colombia
[3] Universitat Politècnica de Catalunya, Spain

Abstract. Statistical analysis is used to analyze seven temporal series obtained from respiratory flow signals of 66 patients on weaning trials. In which, 33 patients belong to successful group (SG), and 33 patients belong to failure group (FG), i.e. failed to maintain spontaneous breathing during trial. Patients were then classified with a pattern recognition neural network, obtaining 78.78 % of accuracy in the classification.

Index Terms. Mechanical Ventilation, Mann–Whitney U test, Genetic Algorithm, Artificial Neural Networks.

1 Introduction

Mechanical ventilators are used to artificially ventilate the lungs of patients who are unable to naturally breathe from the atmosphere. There are two main divisions of mechanical ventilation: invasive ventilation and non-invasive ventilation. There are two main modes of mechanical ventilation within the two divisions: positive pressure ventilation, where air (or another gas mix) is pushed into the trachea, and negative pressure ventilation, where air is essentially sucked into the lungs [1].

Discontinuation of mechanical ventilation, also called weaning or extubation, should be performed as soon as autonomous respiration can be sustained. It is one of the most challenging problems in intensive care units. Despite advances in mechanical ventilation and respiratory support, the science of determining if the patient is ready for extubation is still very imprecise. A failed weaning trial is discomforting for the patient and may induce significant cardiopulmonary distress. When mechanical ventilation is discontinued, up to 25 percent of patients have respiratory distress severe enough to necessitate reinstitution of ventilatory support. Hence the need for a more accurate prediction of the optimal disconnection time, which is extended to the whole weaning process [2-3]. The variability of breathing pattern is not random and can be explained by central neural mechanisms or instability of the feedback loops [4]. This variability was analyzed previously in [5-8].

As in many real situations, the suitable variables that describe the problem are partially unknown. When irrelevant variables are present, there may be many different models able to fit the data. But only some of them (those that do not use irrelevant variables) will lead to good generalization performance on unseen examples. However, in general it is not possible to control that irrelevant variables are not used during the training phase to learn the training set. The Neural network is a technique capable of modeling this type of problem.

The aim of this study is to analyze respiratory pattern variability in a specific process, the weaning process, by applying neural networks, in order to find possible differences between patients who can maintain spontaneous breathing and patients who cannot. The input parameters to the neural network are determined by a genetic algorithm. This same problem has been worked on papers like [9], in which it used a neural network as classifier and backward selection for selection of inputs to neural network. In [10] it used a cluster analysis and neural network. In [11], applying a feature selection procedure based on the use of the support vector machine with a leave-one-out cross-validation. In [12], statistical analysis, power spectral density, and Lempel Ziv complexity, are used in a multi-parameter approach to analyze four temporal series obtained from the Electrocardiographic and Respiratory Flow signals. In [13] each patient was characterized using 7 time series from respiratory signals, and for each serie was evaluated the discrete Wavelet transform; it trains a neural network for discriminating between patients from the two groups.

2 Patients data

In this study, respiratory flow signals were measured in 66 patients under mechanical ventilation and extubation process (database WEANDB). The patients were recorded in the Departments of Intensive Care Units at Santa Creu i Sant Pau Hospital, Barcelona, Spain and Getafe Hospital, Getafe, Spain, according to the protocols approved by the local ethics committees. The patients were submitted under T-tube test, disconnected from the ventilator and maintained spontaneous breathing through an endotraqueal tube during 30 min. According to the clinical criteria, the patients were classified into two groups: successful group (SG), 33 patients whose T-tube test was overcome successfully, and failure group (FG), 33 patients who failed the test and therefore could not be extubated.

The respiratory flow was obtained with a pneumotachograph (Datex-Ohmeda monitor with variable reluctance transducer) connected to an endotracheal tube. The signals were recorded at a sampling frequency of 250 Hz during 30 minutes. The respiratory pattern can be characterized by the following time series: inspiratory time (TI), expiratory time (TE), breathing cycle duration ($TTot$), tidal volume (VT), inspiratory fraction ($TI\ /TTot$), mean inspiratory flow (VT/TI) and rapid shallow breathing (f/VT), were f is respiratory rate. The figure 1 shows a respiratory signal and the respective parameters.

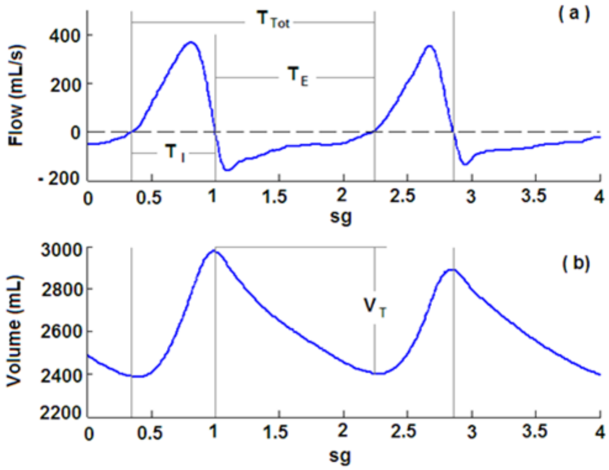

Fig. 1: (a) Respiratory flow signal and their time series: inspiratory time (TI), expiratory time (TE) and breathing cycle duration (TTot). (b) Respiratory volume signal and tidal volume (VT).

3 Methodology

For each one of the time series was evaluated eight statistics data: arithmetic mean, standard deviation, mode, variance, median, interquartile range, kurtosis and skewness.

- *Arithmetic mean.* It is the central tendency of a collection of numbers taken as the sum of the numbers divided by the size of the collection.

- *Standard deviation.* It shows how much variation or dispersion exists from the average. A low standard deviation indicates that the data points tend to be very close to the mean; high standard deviation indicates that the data points are spread out over a large range of values.

- *The mode.* It is the value that appears most often in a set of data.

- *The variance.* It measures how far a set of numbers is spread out. A small variance indicates that the data points tend to be very close to the mean (expected value) and hence to each other, while a high variance indicates that the data points are very spread out from the mean and from each other.

- *The median.* It is the numerical value separating the higher half of a data sample, a population, or a probability distribution, from the lower half. The median of a finite list of numbers can be found by arranging all the observations from lowest value to highest value and picking the middle one.

- *Interquartile range.* It is equal to the difference between the upper and lower quartiles.

- *Kurtosis.* It is a measure of whether the data are peaked or flat relative to a normal distribution. That is, data sets with high kurtosis tend to have a distinct peak near the mean, decline rather rapidly, and have heavy tails. Data sets with low kurtosis tend to have a flat top near the mean rather than a sharp peak.

- *Skewness.* It is a measure of the extent to which a probability distribution of a real-valued random variable leans to one side of the mean. For a unimodal distribution, negative skew indicates that the tail on the left side of the probability density function is longer or fatter than the right side. Conversely, positive skew indicates that the tail on the right side is longer or fatter than the left side. In cases where one tail is long but the other tail is fat, skewness does not obey a simple rule. For example, a zero value indicates that the tails on both sides of the mean balance out, which is the case both for a symmetric distribution, and for asymmetric distributions where the asymmetries even out, such as one tail being long but thin, and the other being short but fat.

3.1 The Mann–Whitney U test

The Mann-Whitney U test is a non-parametric test that can be used in place of an unpaired t-test. It is used to test the null hypothesis that two samples come from the same population (i.e. have the same median) or, alternatively, whether observations in one sample tend to be larger than observations in the other. Although it is a non-parametric test it does assume that the two distributions are similar in shape [14].

In order to reduce the problem dimensionality, a Mann Whitney Test was initially applied to eight statistics data computed in the seven time series, in order to identify the most significant variables. Test result, it was determined that the variables inspiratory time (TI), expiratory time (TE), tidal volume (VT), inspiratory fraction ($TI\ /TTot$) and rapid shallow breathing (f/VT), do not allow differentiation of patients between both SG and FG groups. Table I summarizes the p-values for each feature when compared both SG and FG groups of the variables breathing cycle duration ($TTot$), mean inspiratory flow (VT/TI) inspiratory fraction ($TI\ /TTot$); 11 parameters had a p-value less than 0.05.

Table 1: *p-Value* for each parameter of temporal series obtained from respiratory flow signals

Feature	Time Series		
	TTOT	***TI/TTot***	***VT/TI***
Arithmetic mean	0.0035	0.0138	0.0025
Standard deviation	x	x	x
Mode	0.0170	0.0255	x
Variance	x	x	x
Median	0.0028	0.0232	0.0032
Interquartile range	0.0071	0.0383	0.0041
Kurtosis	x	x	x
Skewness	x	x	x

x: $p > 0.05$

3.2 Genetic algorithm.

Genetic Algorithms (GA) are direct, parallel, stochastic method for global search and optimization, which imitates the evolution of the living beings, described by Charles Darwin. GA is part of the group of Evolutionary Algorithms. The evolutionary algorithms use the three main principles of the natural evolution: reproduction, natural selection and diversity of the species, maintained by the differences of each generation with the previous. GA works with a set of individuals, representing possible solutions of the task. The selection principle is applied by using a criterion, giving an evaluation for the individual with respect to the desired solution. The best-suited individuals create the next generation [15].

3.3 Artificial Neural networks

Classification is one of the most frequently encountered decision making tasks of human activity. A classification problem occurs when an object needs to be assigned into a predefined group of class based on a number of observed attributes related to that object. Traditional statistical classification procedures such as discriminant analysis are built on the Bayesian decision theory. In these procedures, an underlying probability model must be assumed in order to calculate the posterior probability upon which the classification decision is made. One major limitation of the statistical models is that they work well only when the underlying assumptions are satisfied. The effectiveness of these methods depends to a large extent on the various assumptions or conditions under which the models are developed. Users must have a good knowledge of both data properties and model capabilities before the models can be successfully applied.

The artificial neural networks (ANN) have emerged as an important tool for classification. The recent vast research activities in neural classification have established that neural networks are a promising alternative to various conventional classification methods. The advantage of ANNs lies in the following theoretical aspects. First, ANN are data driven self-adaptive methods in that they can adjust themselves to the data without any explicit specification of functional or distributional form for the underlying model. Second, they are universal functional approximators in that ANN can approximate any function with arbitrary accuracy. Third, ANN are nonlinear models, which make them flexible in modeling real world complex relationships. Finally, ANN are able to estimate the posterior probabilities, which provide the basis for establishing classification rule and performing statistical analysis [16].

3.4 Classification

The 11 variables selected in Table 1 are the inputs of a ANN for its classification, the architecture was a feed-forward with 11 inputs in the first layer, two hidden layers with hyperbolic tangent sigmoid transfer function and one output layer of one neuron with hyperbolic tangent sigmoid transfer function. Data from the SG group were labeled with a value of 1, and the FG group with a value of -1, for training.

The number of neurons in the two hidden layers was determined for a GA. The algorithm generates two random integers, corresponding to the number of neurons the two hidden layers. The ANN was trained with Levenberg-Marquardt backpropagation method; 60%, 20% and 20 % of data were used to train, to validate and to test, respectively. For each training, the following numbers were computed: the patients classified correctly, that is, who meet the condition to belong to SG or FG; and the patients who do not comply the condition. The ANN is trained ten times and the results are averaged. Classification rate is calculated as the number of patients classified correctly divided by the total number of patients; this is the value to optimize by the GA. The algorithms were implemented based on the neural network toolbox and the genetic algorithms toolbox of Matlab. The table II summarizes the configuration parameters of ANN and GA.

Table 2: Configuration parameters of ANN and GA

Parameter	Value
Artificial Neural Network	
Maximum number of epochs to train	200
Performance goal	10^{-7}
Minimum performance gradient	10^{-7}
Value initial of learning rate	0.01
Ratio to increase of learning rate	0.1
Ratio to decrease of learning rate	10
Value maximum of learning rate	10^{-10}
Genetic algorithm	
Generations	30
Size of the population	2
Type of population	Integer
Elite population	1

Executed the GA was determined that the number of neurons appropriate for the two hidden layers are 15 and 40 neurons, respectively; with these values the accuracy was $70.8\,\% \pm 0.09$.

3.5 Dimensionality reduction

The term dimensionality reduction is applied to the task of selecting those features that are most useful to a particular classification problem from all those available. The main purpose of feature subset selection is to reduce the number of features used in classification while maintaining acceptable classification accuracy. Less discriminatory features are eliminated, leaving a subset of the original features which retains sufficient information to discriminate well among classes. For classical pattern recognition techniques, the patterns are generally represented as a vector of feature values. The selection of features can have a considerable impact on the effectiveness of the resulting classification algorithm. Consider a feature set, information to discriminate well among classes, $F = \{f_1, f_2, \ldots, f_n\}$. If f_1 and f_2 are dependent, that is they always move together, then one of these could be discarded and the classifier has no less information to work with. This has the benefit that computational complexity is reduced as there is smaller number of inputs. Often, a secondary benefit found is that the accuracy of the classifier increases. This implies that the removed features were not adding any useful information but they were also actively hindering the recognition process. Feature selection can be seen as a case of feature weighting, where the numerical weights for each of the features have been replaced by binary values. A value of 1 could mean the inclusion of the corresponding feature into the subset, while a value of 0 could mean its absence. In a domain where objects are described by d features, there are 2^d possible feature subsets. Obviously, searching exhaustively for the best subset (using any criteria to measure the quality) is difficult. For this reason, the GA has been identified as the best tools to explore such search space, and produce pseudo-optimal solutions that are sufficient to produce acceptable results [17-18]. The features selection using GA has been studied and proven effective in conjunction with various classifiers, including k-nearest-neighbours, and neural networks [19-20].

With the aim to increase the accuracy of the classifier was programmed a GA to select the inputs of ANN. The ANN architecture was a feed-forward with N inputs in the first layer, two hidden layers with hyperbolic tangent sigmoid transfer function with 15 and 40 neurons, respectively, and one output layer with hyperbolic tangent sigmoid transfer function (1 neuron). The GA generates a 11-bits binary code, in which a value of one indicates that one of eleven characteristics, defined in Table I, is selected as input to the ANN. The ANN is trained 10 times and the end of each training is calculated the classification rate, defined as the number of patients classified correctly divided by the total number of patients; this is the value to optimize by the GA. The configuration parameters for the NN are the same of Table II; the Table III summarizes the configuration parameters of GA.

Table 3:. Configuration parameters of ga

Parameter	Value
Generations	30
Size of the population	11
Type of population	Bit string
Elite Population	2
Selection Function	Roulette
Crossover Function	Scattered
Mutation function	Uniform
Crossover rate	0.7
Mutation rate	0.01

Executed GA was determined that the most relevant variables for the system are arithmetic mean TTOT, mode TI/TTOT, median TI/TTOT and interquartile range VT/TI; with accuracy of

78.78 % $\pm$ 0.07. The figure 2 showed the behavior of the data of the two groups with respect to the mean value for the four variables.

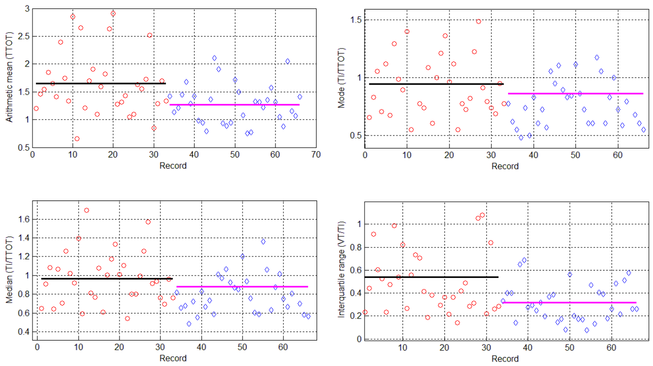

Fig. 2: Selected parameters for GA (33 SG, 33 FG). Mean values for each group are marked with lines.

4 Conclusion

A methodology based on GA and ANN has been applied for determine the moment of disconnection of patients of the mechanical ventilation, analyzing the respiratory pattern. GA are a good technique to reduce dimensionality in classification problems, improvement in 8% the accuracy.

Four variables for successful outcomes from mechanical ventilation have been identified, arithmetic mean TTOT, mode TI/TTOT, median TI/TTOT and interquartile range VT/TI, but there are not specific and reproducible criteria clearly established of the relationship of these variables with the process of weaning.

Acknowledgment

The authors would like to thank to CREB (Centre de Recerca en Enginyería Biomédica) of Polytechnic University of Catalonia (UPC), by provide the database for the development of this research.

References

1. N. Patroniti. Mechanical ventilation: skills and techniques. European society of intensive care medicine, 2011.
2. M. Meade, G. Guyatt, D. Cook, L. Griffith, Predicting success in weaning from mechanical ventilation, Chest, 120, 6, 2001.
3. M.J. Tobin, Advances in mechanical ventilation, N. Engl. J. Med., Vol. 344, N. 26, pp. 1986-1996, 2001.

4. G. Benchetrit, Breathing pattern in humans: diversity and individuality, Respiration Physiology, 122, pp. 123-129, 2000.
5. P. Caminal, L. Domingo, B.F. Giraldo, M. Vallverdú, S. Benito, G.Vázquez, D. Kaplan, Variability analysis of the respiratory volume based on nonlinear prediction methods, Medical & Biological Engineering & Computing, 42, pp. 86-91, 2004.
6. M.J. Tobin, M.J. Mador, S.M. Guenter, R.F. Lodato, M.A. Sackner, Variability of resting respiratory center drive and timing in healthy subjects, J. Appl. Physiol., 65, pp. 309-317, 1988.
7. E.N. Bruce, Measures of respiratory pattern variability, in Bioengineering approaches to pulmonary physiology and medicine, Plenum Press, pp. 149–160, 1996.
8. M.C. Khoo, Determinants of ventilatory instability and variability, Respiratory Physiology, 122, pp. 167–182, 2000.
9. B. Giraldo, C. Arizmendi, E. Romero, R. Alquezar, P. Caminal, S. Benito, D. Ballesteros, Patients on weaning trials from mechanical ventilation classified with neural networks and feature selection. Proceedings of the 28th IEEE EMBS Annual International Conference New York City, USA, 2006
10. C.A. Arizmendi, E. Romero, R. Alquezar, P. Caminal, I. Díaz, S. Benito, B.F. Giraldo, Data mining of patients on weaning trials from mechanical ventilation using cluster analysis and neural networks. Engineering in Medicine and Biology Society, 2009. EMBC 2009. Annual International Conference of the IEEE.
11. B. Giraldo, A. Garde, C. Arizmendi, R. Jané, S. Benito, I. Díaz, D. Ballesteros, Support vector machine classification applied on weaning trials patients. Proceedings of the 28th IEEE EMBS Annual International Conference New York City, USA, 2006
12. L.S. Correa, E. Laciar, B.F. Giraldo, A. Torres. Multi-paameter Analysis of ECG and Respiratory Flow Signals to Identify Success of Patients on Weaning Trials. 32nd Annual International Conference of the IEEE EMBS, Buenos Aires, Argentina, August 31 - September 4, 2010.
13. H. González, H. Acevedo, C. Arizmendi, B.F. Giraldo. Methodology for determine the Moment of Disconnection of Patients of the Mechanical Ventilation using Discrete Wavelet Transform. Procceding of 2013 ICME International Conference on Complex Medical Engineering, May 25-28, Beijing, China.
14. Gibbons, J.D., Chakraborti, S. Comparisons of the Mann Whitney, Student′s t, and alternate t tests for means of normal distributions. Journal of Experimental Education. 1991
15. R.L. Haupt, S.E. Haupt. Practical genetic algorithms. Second edition. A Wiley Interscience Publication. 2004
16. P.Z. Guoquiang. Neural networks for classification: a survey. IEEE Transactions on Systems, MAN and Cybernetics—part C: Applications and reviews, vol. 30, no. 4, November 2000.
17. K.M Faraoun, A. Rabhi. Data dimensionality reduction based on genetic selection of feature subsets. INFOCOMP Journal of Computer Science, vol. 6, no. 3, pp.36-46, 2007.
18. M.L. Raymer, W.F. Punch, E.D. Goodman, L.A. Kuhn, A.K. Jain. Dimensionality reduction using genetic algorithms. IEEE Transactions on Evolutionary Computation, vol. 4, no. 2, July 2000.
19. F. Brill, D. Brown, and W. Martin, Fast Genetic Selection of Features for Neural Network Classifiers. IEEE Transactions on Neural Networks, 1992.
20. S. Ho, C. Liu, and S. Liu, Design of an Optimal Nearest Neighbours Classifier using an Intelligent Genetic Algorithm. Pattern Recognition Letter, 2002.