



## A Parametric Model Measuring Time- Varying Respiratory Mechanics

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**Abstract:** A model is a precise representation of a system's dynamics used to answer the questions via analysis. The work present here is to provide a method for identification of the changes in human respiratory system in order to allow for an instantaneous diagnosis. The present work provides a methodology for auto regressive exogenous (ARX) modelling of human respiratory system. The proper model structure and model parameters are determine for the human respiratory system. Estimated model parameters will reflect the dynamic changes in respiratory system so the differences between normal and disease person can be detected using this model. The results are promising and models obtained for physiological system are able to describe the difference between the normal patient and disease patent by the diagnosis of change in the model parameters.

**Keywords:** Respiratory system; system identification; ARX models; Mathematical modelling of biomedical parameters.

### I. Introduction:

During the last two decades, extensive research has been carried out on the modelling and analysis of dynamic changes in the respiratory mechanics, to assist in diagnosis and clinical studies. System identification techniques [1] have been extensively applied to model the dynamic respiratory mechanism and are broadly classified as:

1. Parametric approaches (mainly based on time domain modelling and analysis [2] [3] [4].
2. Non-parametric approach (further classified as frequency domain and cross correlation analysis) [5] [6] [7].

Non-parametric approaches provide important first insight about the system. However, they do not directly estimate any model parameters and provide limited information about the system. As a comparison between the above mentioned two approaches of modelling and analysis, parametric time domain approaches [8][9] based on auto regressive exogenous (ARX) structure have been found particularly suitable for modelling dynamic respiratory system. The main advantages of ARX modelling are as follows:

1. Shorter length of input and output data can be used to build the ARX model as Compared to frequency response modelling.
2. The ARX model is less sensitive to the presence of noise in the data.

### II. Materials and methods:

ARX modelling involves two steps:

1. Model order determination [2] [10].
2. Estimation of parameters [9] [11] [12].

The model order in most of the cases is determined by trial and error method which is called as black box modelling, to identify black-box models we estimate simple polynomial models for a range of orders and compare the performance of these models. In which various type of model having different stretchers and order are used to feed with the data available from the data variation curve so the proper model which represent the given variation in the data curve and which is having least order can be obtain, the model having least order is taken so that linear response can be obtain and to reduce the complexity of the system so the speed of response can be increased , the parameters variation of the best fitted model Obtain shows the difference in the response of the respiratory system for the normal and disease patient which provides Medical applications of computer modelling [13][14].

The various model used for estimation are given as:

#### ARX Models

For a single-input/single-output system (SISO), the ARX model structure is:

$$Y(t) + a_1y(t-1) + \dots + a_ny(t-n_a) = b_1u(t-n_k) + \dots + b_nu(t-n_k-n_b+1) + e(t).$$

$Y(t)$  represents the output at time  $t$ ,  $u(t)$  represents the input at time  $t$ ,  $n_a$  is the number of poles,  $n_b$  is the number of zeros plus 1,  $n_k$  is the input delay.

**arxqs** — Fourth-order autoregressive (ARX) model using the arx algorithm here  $n_a=n_b=4$ , and  $n_k$  is estimated from the step response model imp.

**IMP** — Step response over a period of time using the impulse algorithm

**arx 692**—sixth-order autoregressive (ARX) model using the arx algorithm here  $n_a=6, n_b=9$  and  $n_k=2$ .

**arx 223**— second-order autoregressive (ARX) model using the arx algorithm here  $n_a=n_b=2$ , and  $n_k=3$ .

**State-Space Models**

The general state-space model structure

$$X(t+1) = Ax(t) + Bu(t) + ke(t)$$

$$Y(t) = Cx(t) + Du(t) + e(t)$$

$Y(t)$  = output at time  $t$ ,

$u(t)$  = input at time  $t$ ,

$X$  =state vector,

$e(t)$  = white-noise disturbance

The System Identification Toolbox estimates the state-space matrices A, B, C, D, and K from the data.

The state-space model structure is a good choice for quick estimation because it requires that you specify only two parameters to get started:  $n$  is the number of poles (the size of the A matrix) and  $n_k$  is the delay.

Type of state space model used

1. **n4s2** having second order.
2. **n4s3** having third order.

**III. ARMAX Models**

For a single-input/single-output system (SISO), the ARMAX model structure is:

$$Y(t) + a_1y(t-1) + \dots + a_{n_a}y(t-n_a) = b_1u(t-n_k) + \dots + b_{n_b}u(t-n_k-n_b+1) + e(t) + c_1e(t-1) + \dots + c_{n_c}e(t-n_c).$$

$Y(t)$  represents the output at time  $t$ ,  $u(t)$  represents the input at time  $t$ ,  $n_a$  is the number of poles for the dynamic model,  $n_b$  is the number of zeros plus 1,  $n_c$  is the number of poles for the disturbance model,  $n_k$  is the number of samples before the input affects output of the system (called the delay or dead time of the model), and  $e(t)$  is the white-noise disturbance.

Types of armax model used

amx2222  $n_a=2, n_b=2, n_c=2$  (is the number of poles for the disturbance model)

$n_k=2$ .

amx3322

$n_a=3, n_b=3, n_c=2$  (is the number of poles for the disturbance model)

$n_k=2$ .

**Model structure and model parameter determination:**

Model structure is defined by  $n_a$  = number of poles,  $n_b$  = number of zeros plus 1,  $n_k$  = pure time delay (dead time).

The data curve taken for diagnosis is the volume variation curve which is shown in the Fig.1a for the normal patient and after feeding the data of the normal patient in system identification system the estimate of the best fit model is obtain which is shown in Fig.1b:

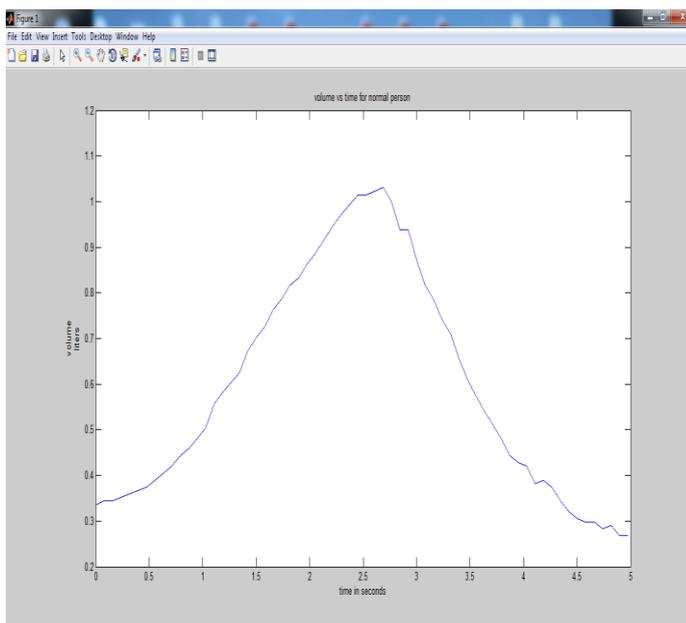


Fig.1a

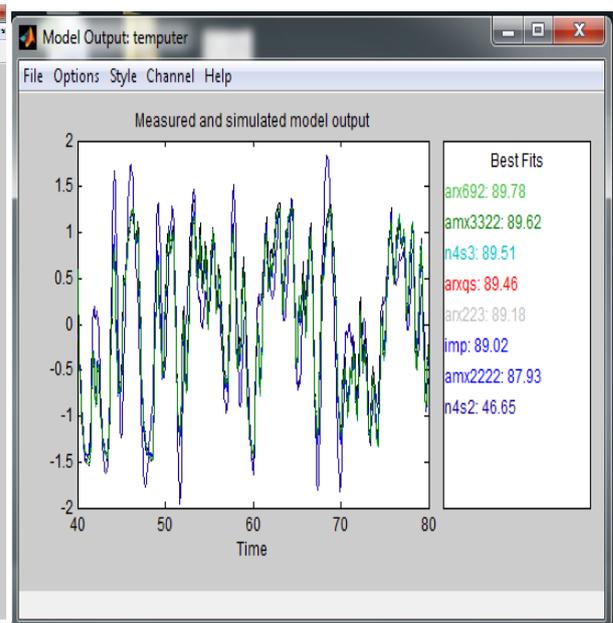


Fig.1b

A volume variation curve for the abnormal patient is shown in Fig.2a and after feeding the data of the abnormal patient in system identification system the estimate of the best fit model is obtain which is shown in Fig.2b:

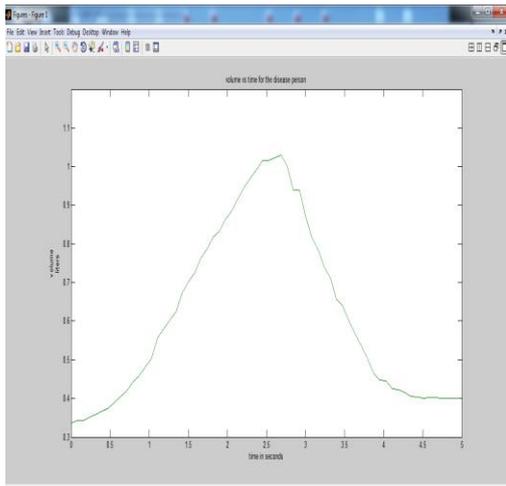


Fig. 2a

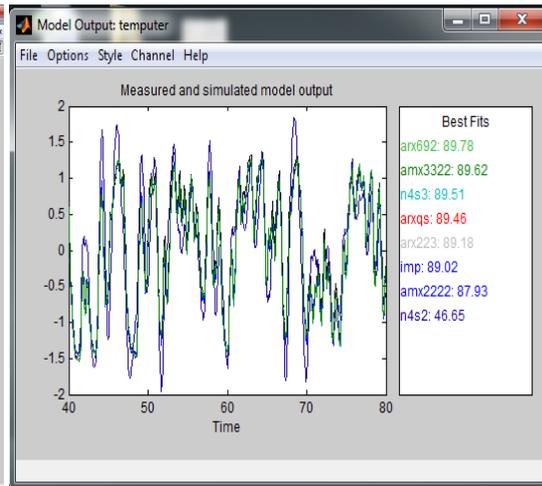


Fig. 2b

Although in both cases the best fitted model according to model fitting plot is ARX 692 but since the lower order similar model ARX 223 gives the similar fitting hence used as best fit model for the given data curve. The coefficient variation of these models for the two cases will give the difference in the respiration process.

#### IV. RESULTS AND DISCUSSION:

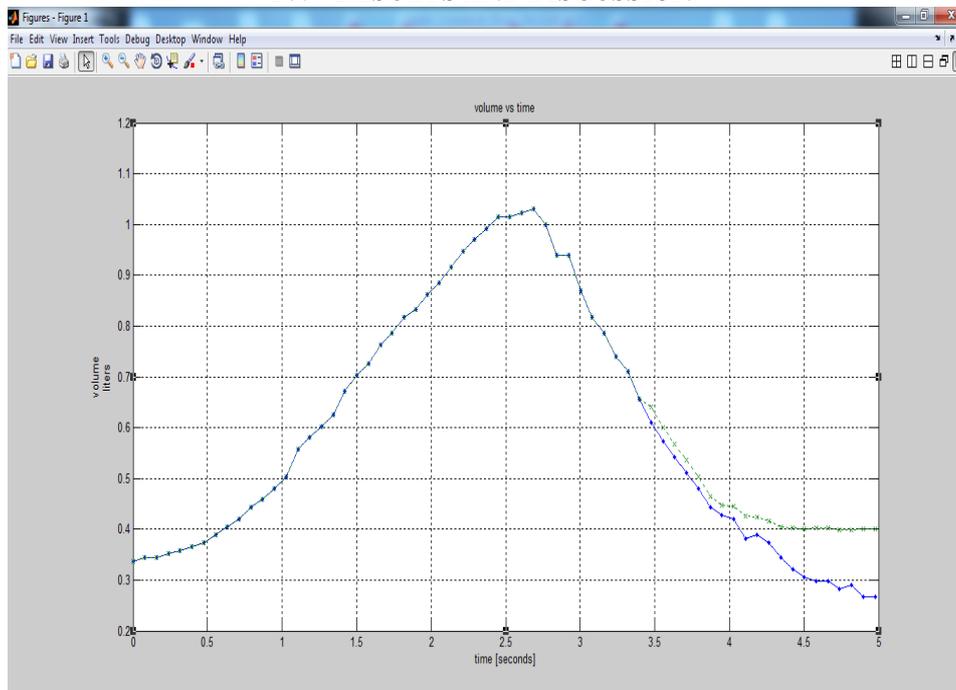


Fig.3: Volume variation curves comparison the blue line shows the response for the normal patient and the green line shows the response for the disease patient

According to the System identification Model Fitting plot the best fitted model for normal patient volume variation curve is ARX 223 with structure

$$A(q) Y(t) = B(q) U(t) + E(t)$$

ARX model with the transfer function as given in above equation has the coefficient A (q) given as:

$$A(q) = 1 - 1.278U(t-1) + 0.3973U(t-2) \text{ ----- (a)}$$

According to the System identification Model Fitting plot the best fitted model for abnormal patient volume variation curve is also ARX 223 with structure

$$A(q) Y(t) = B(q) U(t) + E(t)$$

$$A(q) = 1 - 1.15U(t-1) + 0.310U(t-2); \text{ ----- (b)}$$

The difference in the variation in the volume curve for the normal and disease patient can be identified by the coefficient variation as shown by the equations a and b also can be verified by the fig.3.

Step and impulse response analysis have been used by different research groups as standard methods to analyse the models. A faster speed of response and less settling time in step response shows normal activity of respiratory mechanism. The impulse response has also been estimated by different researchers for analysing the characteristics (behaviour) of the modelled system.

**Step response comparison of volume curves:-**

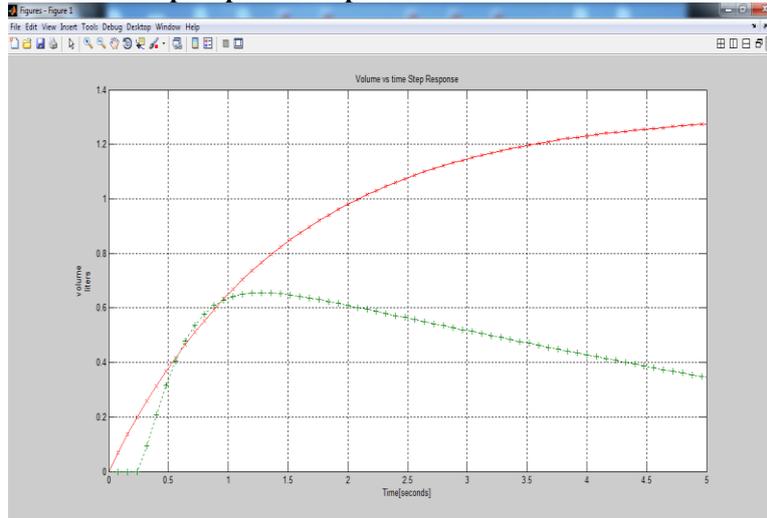


Fig.4: Step response comparison for volume variation curves the red line shows the step response for the normal patient and the green line shows the step response for the disease patient.

The step response comparison of the ARX model for the disease and the normal patient shows that the person having abnormality in its respiratory system is giving very slow response. it can be easily observe from the step response variation that the final settling value of the step response is obtain very slowly for the abnormal patient hence breathing period is longer than the normal.

**Impulse response comparison of volume curves:-**

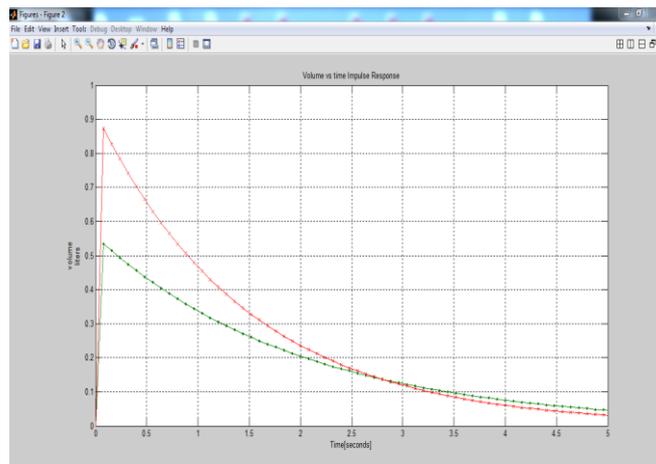


Fig.5: Impulse response comparison for volume variation curves the red line shows the impulse response for the normal patient and the green line shows the step response for the disease patient

The ARX 223 model impulse response comparison for the two cases normal and disease are shown in the figure, now from the figure it can be seen that the impulse response for the disease patient has not reached the maximum amplitude as in the case of the normal patient as shown above in the form of the impulse response variation.

**V. CONCLUSION**

The Mathematical modelling of various physiological systems empowered their study. Among them the respiratory system modelling led to solutions that covered, in a way, the gap between theory and practice. The mathematical models that were developed in accordance to the existing mathematical equations could be implemented in a computer program and presented by the most dynamic way to the public Now from the comparison of the volume curves in both condition it can be seen that the amount of air expire will get decrease in case of person having abnormality this is identified by the change in the coefficients of the model and the step, impulse response comparison of the model generated for the parameter variation curve of the human respiratory system.

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