

# ANFIS MODEL FOR THE SIMULATOR OF THE DYNAMIC BEHAVIOR OF A FED BATCH BIOREACTOR BUILT FROM THE PROPOSED MODEL TO OBSERVE THE OSCILLATING BEHAVIOR OF THE ZYMOMONAS MOBILIS

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**Abstract:** This paper explains the simulator of dynamic behavior of a Fed Batch bioreactor modeled with anfis networks. The simulator was built from the proposed model to observe the oscillatory behavior of the *Zymomonas mobilis* (*Z.m*). The model uses the anfis networks created in Matlab to simulate the system response. The commands `genfis1` and `genfis2` were used to generate the structure of the fuzzy inference system without using data grouping and with data grouping respectively. The predictions of the Anfis network are shown in the results for the output system variables: the biomass concentration, the substrate concentration, the product concentration and the biomass growth speed.

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**Keywords:** binary distillation, *Zymomonas mobilis*, substance concentration, input-output flow, biomass concentration, substrate concentration, the product concentration, biomass growth speed.

## 1. INTRODUCTION

The search for renewable energy sources such as the energy obtained from biomass is important nowadays due to the increase of the world-wide population and because of the limited reserves of the traditional and nonrenewable power plants, like fossil fuels. The emphasis on the conversion of biomass to ethanol has been increased, since the ethanol is considered the cleanest alternative liquid fuel. Consequently significant advances have been made towards the technology of ethanol fermentation. The mix of renewable energies in the future can be compound of different classes of energy, like the solar power, wind power, or even some complementary ones, but it is important to stress, that one of the most important and immediate applications energy systems is indeed the ethanol production from biomass fermentation *Quintero et al.*, (2008).

Currently the main biological process used to produce liquids that transport energy, are the

fermentations for the ethanol production, and to obtain a mixture of acetone, butanol and ethanol (ABE) *Rogers et al.*, (2007). The bacterium *Zymomonas mobilis* is a very promising ethanol producer from the point of view of its productivity in comparison with the traditional ones. It reaches ethanol performances near the stoichiometric value of 0,51 g ethanol/g glucose. These performances are often the highest reported in the literature (*Roger et al*, 2007). In addition, the fermentation of *Zymomonas mobilis* requires an optimum temperature higher than the one of *saccharomyces cerevisiae*, this reduces the cooling cost during the fermentation. The industrial interest in the use of the *Zymomonas mobilis*, is its capacity to produce ethanol and sorbitol *Oliveira et al.*, (2005). For the production industry, this is a fundamental requirement, in the search for more competitive microorganisms that generate ethanol.

The ethanol is one of the great potential fuels that could be produced and commercialized in

Latin America. The *Zymomonas mobilis* (Z.m) is a microorganism that has high resistance to adverse conditions and high ethanol productivities. For this reasons, the alcoholic fermentation from Z.m is attractive in order to obtain ethanol. However, the process of fermentation with Z.m has complex dynamic representation and is also highly nonlinear. These characteristics of the fermentations with Z.m, require strict control and monitoring of the variables involved in the process *Quintero et al.*, (2008).

This paper explains a network anfis used to simulate the evolution and dynamic behavior of the alcoholic fermentation obtained from *Zymomonas mobilis*. The model is evaluated using an adaptive neuro-fuzzy inference system, which is trained with traditional strategies of neural network training methods such as the decreasing gradient and the minimum square error, made through the program MATLAB. For the simulator design an existent model was used (Bravo et al, 2000). The concentration of biomass, substrate concentration, product concentration and the change in the volume of the bioreactor were took into account as the variables of the plant. A pulse train signal was used as input to the simulator. The Genfis1 function was used to generate the structure of a fuzzy inference system without the use of data grouping. On the other side the genfis2 function was used to generate the structure of a fuzzy inference system using data grouping.

This paper is organized as follows: Section 2 briefly describes the bioprocess model, explaining mainly the dynamic. Section 3 presents the simulator using the ANFIS network, then the results obtained by using the commands genfis1 and genfis2 are detailed. Finally the conclusions are exposed.

## 2. DESCRIPTION OF THE BIOPROCESS MODEL

The dynamic model used to describe the time evolution of a semi-batch cultivation is represented by differential equations of the variables involved. The equations are obtained from the matter and energy balance. *Quintero et al.*,(2008) :

Biomass Concentration

$$\frac{dX}{dt} = \left( \mu - \frac{F}{V} \right) X \quad (1)$$

Substrate concentration

$$\frac{dS}{dt} = -\frac{\mu X}{Y_{X/S}} - mX + \frac{F}{V} (S_f - S) \quad (2)$$

Product Concentration (ethanol)

$$\frac{dP}{dt} = Q_P - \frac{F}{V} P \quad (3)$$

Change of the bioreactor volume

$$\frac{dV}{dt} = F \quad (4)$$

Where the own dynamic variables of the microorganism are used in two different scenes, calls scenes 1 and 2:

Microorganism growth speed

$$\mu_1 = 0.99 \left( \frac{S}{36.11+S} \right) \left( 1 - \frac{P}{34.67} \right) \left( \frac{S}{2.33+S} \right) \quad (5)$$

$$\mu_2 = 0.25 \left( \frac{S}{30+S} \right) \left( 1 - \frac{P}{70} \right) \left( \frac{S}{3.0+S} \right)$$

Microorganism productivity rate

$$Q_{P_1} = 8.68 \mu X + 0.0 X \quad (6)$$

$$Q_{P_2} = 4.26 \mu X + 2.6 X$$

Yield Biomass substrate

$$Y_{X/S1} = 0.032 \quad (7)$$

$$Y_{X/S2} = 0.235$$

And the weighed constants of the concentration of microorganisms in the change of the concentration of substrate of the reactor

$$m_1 = 0 \quad (8)$$

$$m_2 = 4.42$$

$F$  corresponds to the bioreactor input flux and  $S_f$  is the concentration of substrate in the influent flow..

The simulator uses like input the variable called SIN, which is a pulse train signal of amplitude 100 g/l. The outputs of the plant obtained from the simulator are shown in fig 1.2.3.4 and 5.

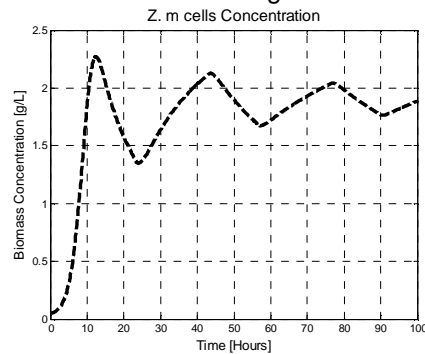


Figure 1. Zm cells concentration.

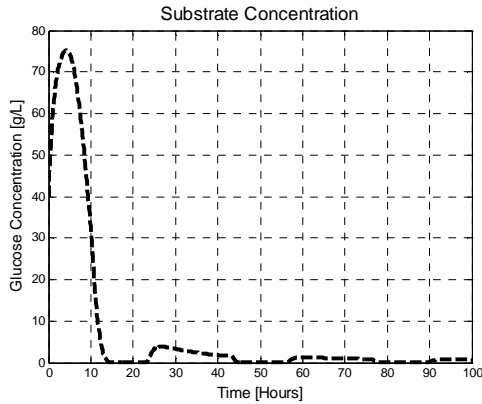


Figure 2. Substrate concentration

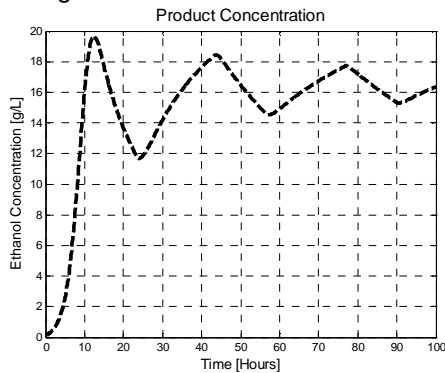


Figure 3. Ethanol concentration

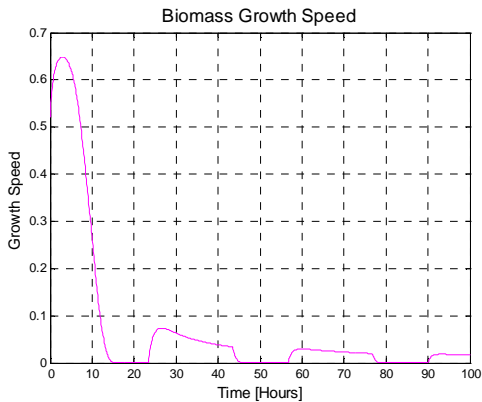


Figure 4. Biomass Growth Speed

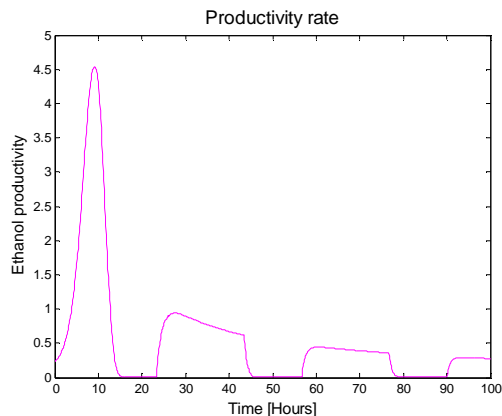


Figure 5. Ethanol Productivity Rate

### 3. ANFIS NETWORK FOR THE BIOPROCESS SIMULATOR

A neural network is a numerical tool composed of an adjustment of neurons interconnected in layers that work in parallel. A neuron is a mathematical organization that receives an input which is modified in agreement with a transfer function and some considering factors, or weights. All the weights are calculated during the training in order that the network approximates the desired output. The network architecture represents the form in which the layers and neurons are organized. The backpropagation networks are defined by the number of neurons in each layer and the type of transfer function, for instance 12 tansig - 8 tansig - 1 represents a network composed of 12 neurons with a tansig transfer function in the input layer, 8 neurons with a tansig transfer function in the intermediate layer and a neuron with a linear transfer function in the output layer. An anfis network is a training routine for neuro-fuzzy inference systems of sugeno type *Jhyshing et al., (2008)*. This network applies a combination of the minimum square method and the descending gradient method for the training of back propagation networks *Cortes et al., (2002)*.

The basic structure of the fuzzy inference that is commonly used is a model that relates the input characteristics to input membership functions, these functions with rules, rules with a set of output characteristics which are related as well to output membership functions, and these functions with a single output value or a decision associated with the output. It is generally considered only fixed membership functions that are chosen arbitrarily. Fuzzy inference systems to this point are only used for modeling systems whose rule structure is determined by the personal interpretation of the characteristics of the variables in the model.

The use of the ANFIS function applies fuzzy inference techniques to model systems. As shown in fuzzy inference systems, the shape of membership functions depends on parameters, these parameters change and it changes the shape of the functions. Instead of observing the data and choosing the parameters of the property functions, the command ANFIS allows to choose these parameters automatically.

If you are supposed to be implementing a system of fuzzy inference to a system which has a collection of input and output data that are required for the system modeling, and which does not have necessarily a pre-determined structure based in the characteristics of the system variables. In this case it is not possible to

discern the shape of membership functions by simply observing the data. So instead of choosing the parameters associated with a given membership function arbitrarily, these parameters can be chosen so as to take into account variations in the types of data. In these cases, the neuro-adaptive training techniques incorporated in ANFIS are very helpful.

The neuro-adaptive training method works in a similar way that the neural networks. The techniques of this type of training provide a method for the fuzzy modeling procedure to learn information from a data set. In certain form ANFIS calculates the parameters of membership functions that help the fuzzy inference system to adjust to the input and output data in the best way.

The acronym ANFIS derives adaptive neuro-fuzzy inference system. Using a set of input and output data the function ANFIS constructs a fuzzy inference system whose membership function parameters are adjusted using a backpropagation algorithm alone or in combination with a method of least squares. This setting allows the fuzzy systems to learn from the data that are shaping (The MathWorks, 2007).

### 3.1 Training Data

This paper uses ANFIS to predict the dynamic behavior of a bioreactor in Fed Batch. The simulator is built from the model proposed to observe the oscillatory behavior of the *Zymomonas mobilis* (ZM) as described in Section 2. It uses a simulation time of 100 hours with a sampling time of 0.1 hours. Therefore the input training data for the ANFIS model is a vector of 1001 elements. The outputs correspond to the variables: the biomass concentration X, substrate concentration S, the concentration of product P, the growth speed U and biomass ethanol production rate Qp. Therefore the input and output training set is a structure whose first component is the time T and the output is X, S, P, U, QP, respectively. There are 1001 values of input / output for each training.

### 3.2 Training of the ANFIS system using genfis1

In order to begin the training a FIS structure is needed first. The FIS structure specifies the parameters of the FIS system for learning. Genfis1 function meets these requirements because it generates the structure of a fuzzy inference system without using the data grouping. In this case, it was specified a number of five types of membership functions gbellmf (Gaussian distribution) for the input. The

generated FIS structure contains 5 fuzzy rules with 25 parameters, 10 of them are linear and 15 are nonlinear. It is important that the number of training data is much greater than the parameters to be determined. In this case the ratio between data and parameters is very high, about (1001/25).

The function genfis1 generates initial membership functions that are equally spaced and cover the full range of inputs as shown in figure 6.

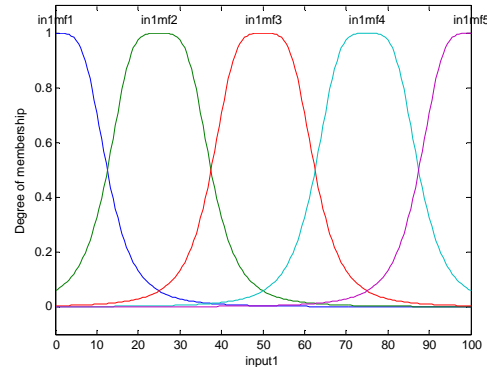


Figure 6. Initial membership functions that are equally spaced and cover the full range of inputs

The fig. 7-11 show the FIS system outputs using ANFIS and the genfis1 command to generate the initial FIS structure. It can be noted that after comparing the graphs obtained from the ANFIS estimation with the original training data, the difference is very small but noticeable. This is because of the input of a pulse train signal which makes the system to become less stable. In the case of the production rate can be observed a big difference in the initial peak due to this reason. However, it is necessary to emphasize that the training is conducted only for 20 epochs. If a longer training is applied then better results can be obtained

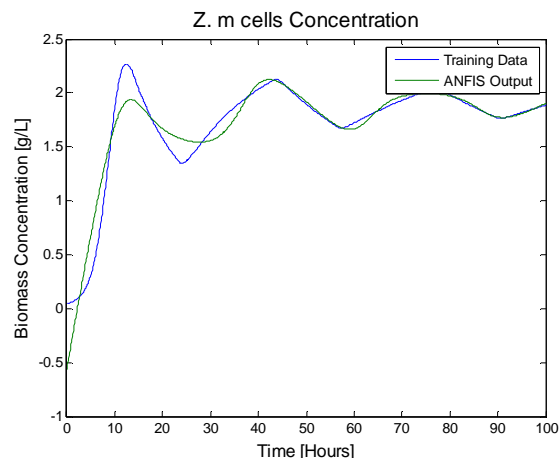


Figure 7. ANFIS prediction for the Zm cells concentration. Using genfis 1.

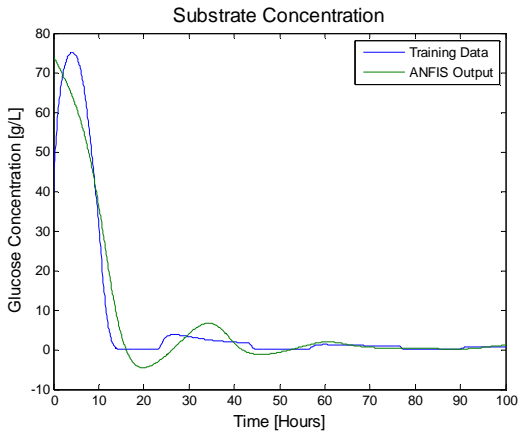


Figure 8. ANFIS prediction for the Substrate concentration. Using genfis 1.

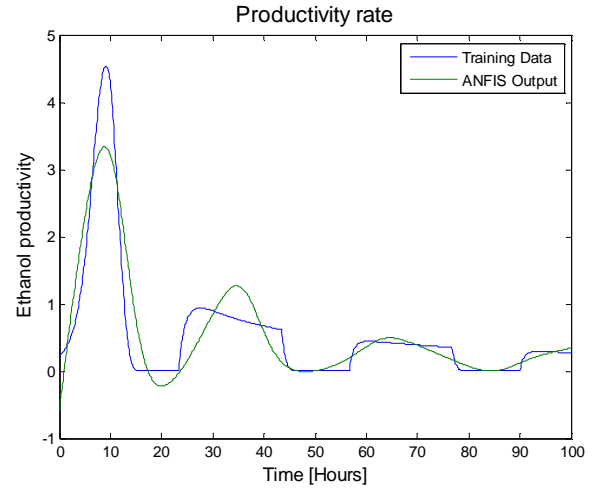


Figure 11. ANFIS prediction for the Productivity rate. Using genfis 1.

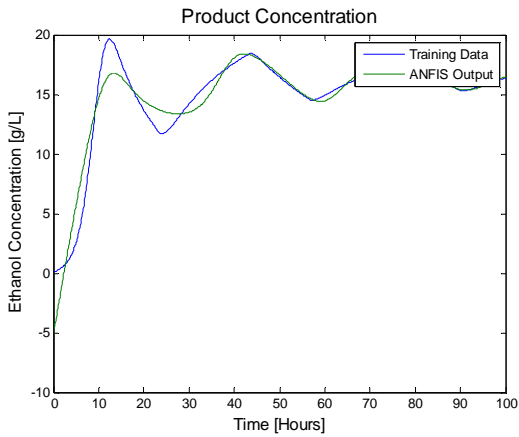


Figure 9. ANFIS prediction for the Product Concentration. Using genfis 1.

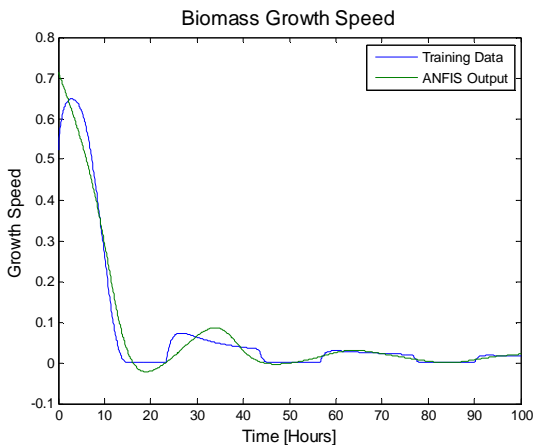


Figure 10. ANFIS prediction for the Biomass Growth Speed. Using genfis 1.

### 3.3 Training of the ANFIS system using genfis1

If there are separate input and output sets genfis2 generates a FIS structure using fuzzy Subtractive clustering. In the case of this simulator when there is only one exit, genfis2 can be used to generate an initial FIS for ANFIS training to implement first subtractive clustering in the data. Genfis2 achieves this by extracting a set of rules that model the behavior of data. The rules extraction method uses first the subclust function to determine the number of rules and membership functions and then uses the least squares estimation to determine the equations of each rule. This function returns a FIS structure that contains a set of fuzzy rules to cover the space of outputs. The generated FIS structure contains 3 fuzzy rules with 12 parameters, 6 of them are linear and 6 are nonlinear. It is important that the number of training data is much greater than the parameters to be determined. In this case the ratio between data and parameters is very high, around 100 (1001/12).

The fig. 12-16 show the outputs of the FIS system using ANFIS and the genfis2 command to generate the initial FIS structure. After comparing the graphs obtained from the anfis estimation with the original training data, the difference is much larger than when the using the function genfis1. It can be hardly noticed that the anfis estimation follows the desired trajectory.

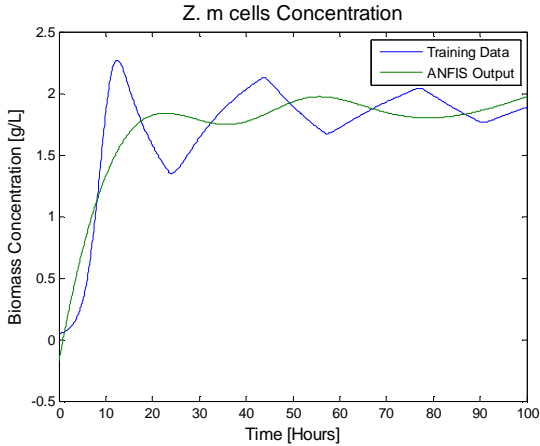


Figure 12. ANFIS prediction for the Zm cells concentration. Using genfis 2.

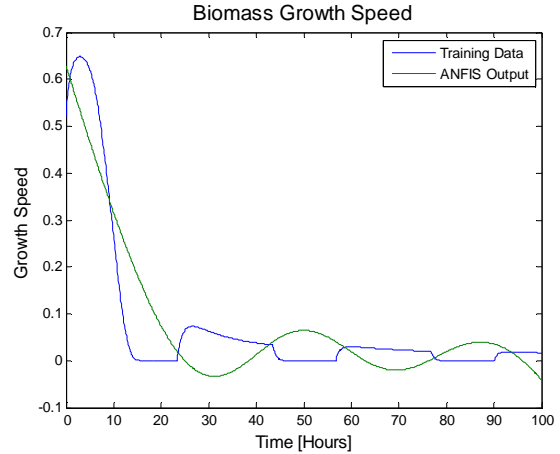


Figure 15. ANFIS prediction for the Biomass Growth Speed. Using genfis 2.

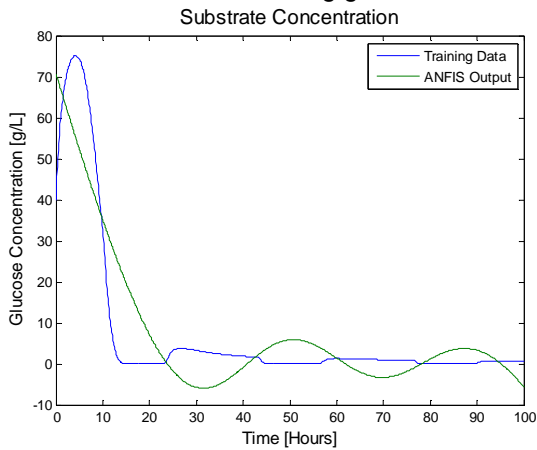


Figure 13. ANFIS prediction for the Substrate concentration. Using genfis 2.

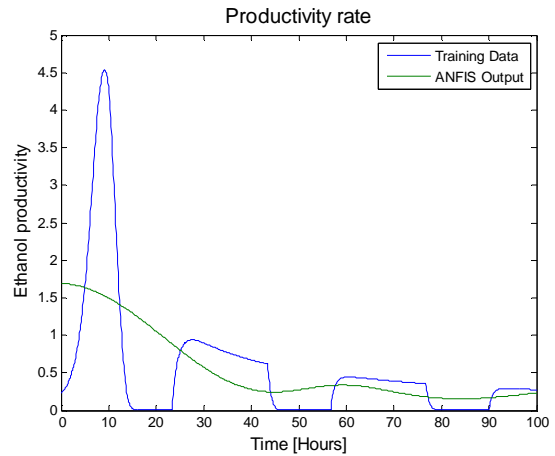


Figure 16. ANFIS prediction for the Productivity rate. Using genfis 2.

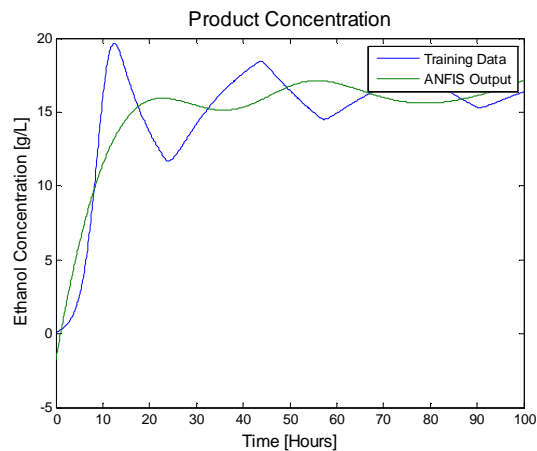


Figure 14. ANFIS prediction for the Product Concentration. Using genfis 2.

#### 4. CONCLUSIONS

The neuro-adaptive training method works in a similar way that the neural networks. The techniques of this type of training provide a method for the fuzzy modeling procedure to learn information from a data set. In certain form ANFIS calculates the parameters of membership functions that help the fuzzy inference system to adjust to the input and output data in the best way. In order to begin the training a FIS structure is needed first. The FIS structure specifies the parameters of the FIS system for learning. After comparing the graphs obtained from the ANFIS estimation with the original training data when genfis1 is used, the difference is very small but noticeable. This is because of the input of a pulse train signal which makes the system to become less stable. However, it is necessary to emphasize that the training is conducted only for 20 epochs. If a longer training is applied then better results can be obtained. After comparing the graphs obtained from the anfis estimation

with the original training data, the difference is much larger than when using the function *genfis1*. It can be hardly noticed that the *anfis* estimation follows the desired trajectory.

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