MODELING OF TAPIOCA STARCH HYDROLYSIS USING NEURAL NETWORKS

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ABSTRACT

This paper considers the use of neural network models to represent the dynamic behavior of glucoamylase-starch system. The model studied in this research is multilayered feed-forward structure with time delay. In this paper we give preliminary results on the modeling adequacy of the neural network models. Data for the training were obtained from Bioprocess Laboratory, UTM. It was found that, the model was successfully developed using multilayered structure of neural network and the model exhibited satisfactory results. It is concluded that neural network technique is a feasible tool for model development of tapioca starch hydrolysis. Further modification of the structure such as increasing the time delay is also recommended for encouraging results.

INTRODUCTION

Starch hydrolysis in the production of glucose is a two step process: liquefaction and saccharification. Both processes use different type of enzymes to break down the starch. Many studies have focused on starch hydrolysis (Swanson et al. (1986). Paolucci-Jeanjean et al. (2000), and Bryjak et al. (2000)). However, not much data is available for tapioca starch hydrolysis since many researchers did their experiment for the hydrolysis using starch source from potato, corn or whey. Thus, the aim of our research is to develop a database of tapioca starch hydrolysis and to model the process using neural network approach.

Models of starch hydrolysis have been investigated by many researchers using semi empirical or theoretical approach for example Akerberg et al.(2000), Gonzalez-Tello et al. (1996) and Fujii et al. (1988). However, the previously mentioned techniques have some limitations because of the complexity of the biochemical reaction. At any time of the process, many simultaneous reactions are involved, each with different rate. Therefore, detail kinetics of the reaction is extremely difficult to obtain. Without the kinetics, the use of a conventional modeling technique is often insufficient to describe the reaction curve faithfully. Taking into account of these problems, neural network was applied to model the reaction. This technique is possible for predicting a reaction curve without a detail kinetic model. It also has an ability to handle noisy data or inconsistent data. Consequently, the numbers of experiments to be repeated are reduced. This led to saving in development time and cost. Many Bioprocess engineering problems have been studied using artificial neural networks (Baughman & Liu, 1995). Petrova et al.,(1998) proposed a neural network model on the growth of a strain *Saccharomyces cerevisiae*. Chaudhuri and Modak (1998) utilized neural networks for optimization of fed-batch bioreactor. Yang and Linkens (1994) applied neural networks for controlling stirred tank bioreactor. Syu and Chang (1999) successfully used neural networks to adaptively control *Penicillin acylase* fermentation.

This study has emphasizes on neural network modeling, as opposed to conventional modeling technique. It would thus be of interest to learn how neural network technique works on modeling of tapioca starch hydrolysis. This paper reports on the results obtained from neural network training.

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NEURAL NETWORK MODEL

Training data were obtained from Bioprocess Laboratory, Universiti Teknologi Malaysia. Three sets of training data, varied in enzyme dosage and initial dry solid concentration, were used for the learning process focusing on one specific topology-feed forward network with time delay. For tuning the network parameters, several versions of backpropagation (BP) algorithms were utilized. The NN model predicted the value of the glucose concentration at the next instant using the information for the present values of the glucose concentration, enzyme dosage and initial dry solid concentration.

Starch hydrolysis was classified as belonging to non-linear problems and therefore the moving window method was applied. The structural parameters to be optimized were: numbers of hidden layers, number of nodes in the hidden layers, types of activation functions, number of epochs and types of BP algorithms. The training matrix contained wide ranges of enzyme dosage, initial dry solid concentration and glucose (product) concentration. The neural network model employed in this study consisted of 4 input nodes corresponding to enzyme dosage *En(t)*, initial dry concentration *Ds(t)*, present glucose concentration *G(t)* and past values *G(t-1)*. There was one output node representing prediction values of glucose concentration *G(t+1)*. Hyperbolic tangent sigmoid activation functions were applied in all nodes in the hidden layers and linear activation function was utilized in the output layer.

SIMULATION RESULTS AND DISCUSSIONS

Two types of NN models (model A and model B) were proposed. Model A is a one hidden layer NN while model B is a two hidden layer NN as shown in figure 1. Both models consist of bias, four inputs, hidden layers and one output node. Under these conditions, the effect of increasing the number of hidden nodes on the performance of the neural network models was explored. Models were trained to predict the glucose concentration profile. The performance function for the networks is mean square error (MSE). The network was trained until a mean square error performance (0.001) was met.

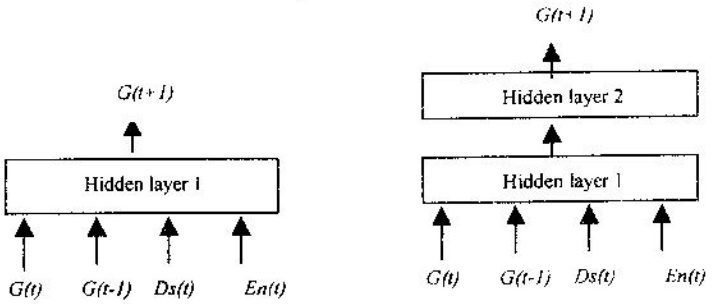

Figure 1. Feed forward neural networks architecture

The number of hidden nodes in model A was initially set as 4-5-1 (4 inputs, 5 hidden nodes and 1 output) and model B was initially set as 4-5-7-1 which were modified later. The learning rate was set as 0.01. The input variables were present values of glucose concentration *G(t)*, previous values of glucose concentration *G(t-1)*, initial dry solid concentration *Ds(t)* and enzyme dosage *En(t)*.

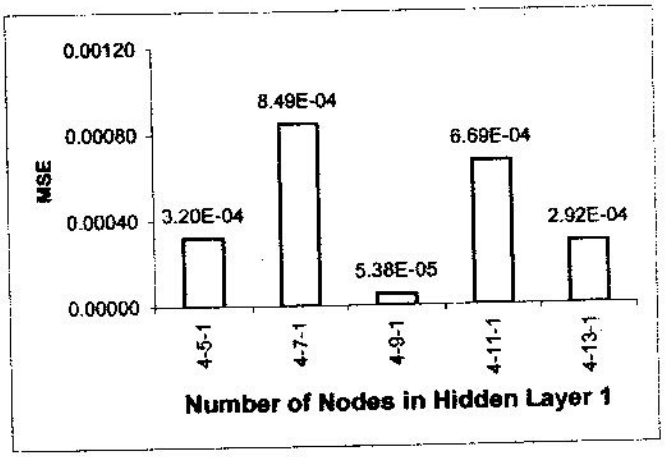

Figure 2. Neural networks performance of model A

Figure 2 shows the neural networks performance of model A. It was found that the best topology of model A was 4-9-1. The network performance was better for Model B as demonstrates in figure 3 since the highest mean square errors calculated was only 0.06%. Larger numbers of nodes in hidden layer 1 than in the second hidden layer were also investigated as shown in figure 4. In this case, a topology of 4-7-5-1 provided the best mapping of the reaction. However, the best structure among all was 4-7-12-1 as shown in figure 3. It gave the lowest values of mean square error.

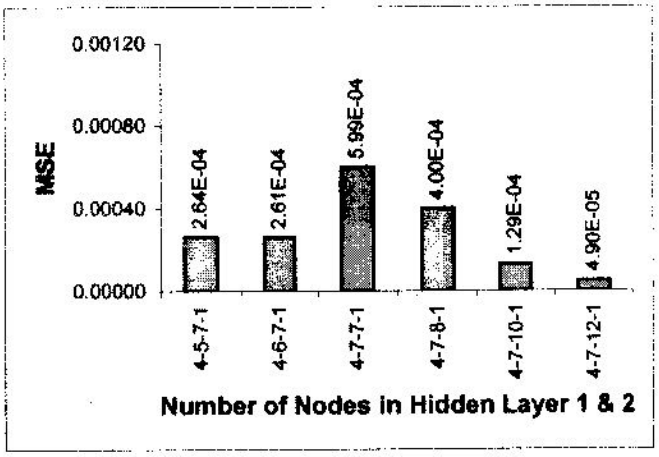

Figure 3. Neural networks performance of Model B

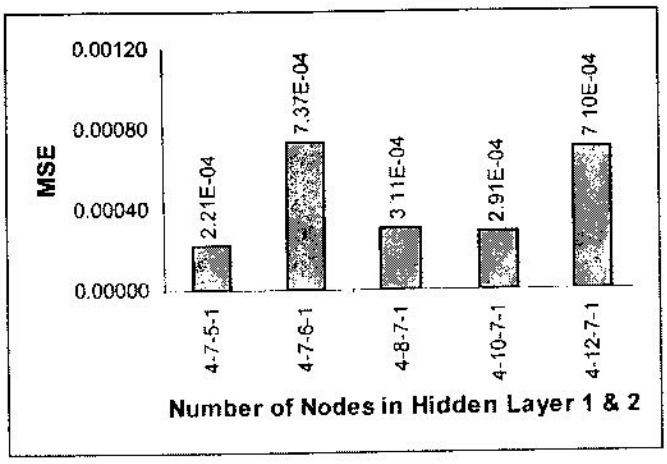

Figure 4. Neural networks performance of Model B: Larger numbers of nodes in the first layer.

Figure 5 shows the comparison of experimental and model prediction results of model structure 4 -7-12-1. The solid line represents the predicted values while points denote the experimental data. The lower graph of figure 5 shows the difference or error between the experimental data and the NN outputs. It can be observed that the estimates produced by the neural network model are in good agreement with the experimental data. Increasing the number of the hidden layers improved the quality of the process description.

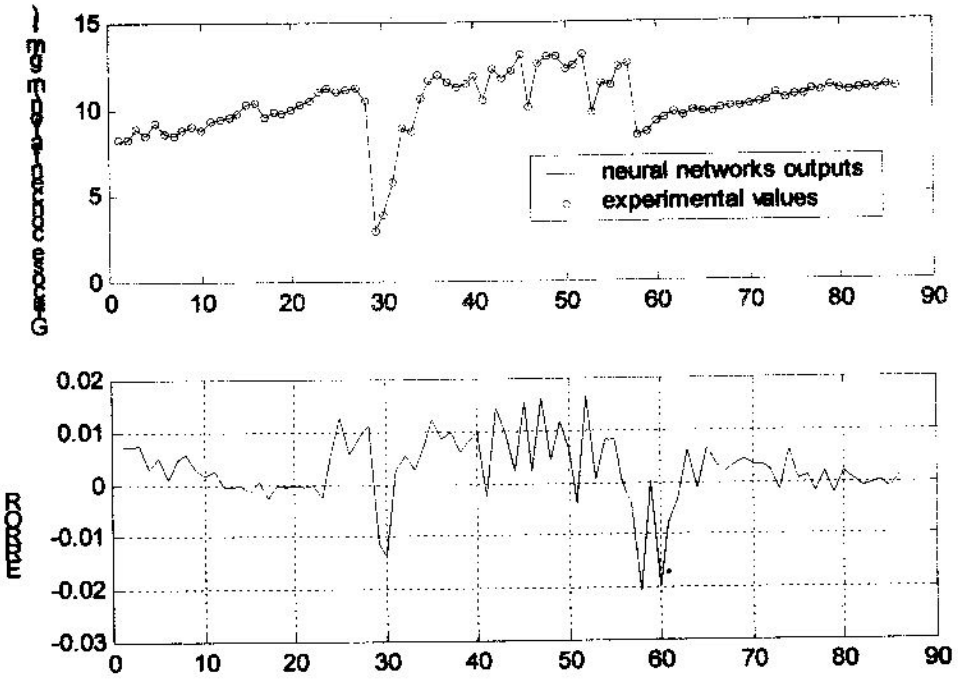

Figure 5. Glucose concentration prediction

CONCLUSIONS

Preliminary results of training the neural networks are presented in this paper. Two types of neural network models were compared. This neural network model predicted the value of glucose concentration at the next time instant using the information for the present value of enzyme dosage, initial dry solid concentration, glucose concentration and glucose concentration at time lag 1. The results clearly show that the neural network model used here is able to represent adequately the dynamics behavior of the system. In conclusion, this study shows the feasibility of NN approach in modeling the system without knowing details of the kinetics.

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