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APPLICATION OF ARTIFICIAL NEURAL NETWORK ON THE PREDICTION OF MICROBIAL POPULATION AND SPECIES DURING SPONTANEOUS FERMENTATION OF GARCINIA MANGOSTANA PERICARP

Mohd Fikri Hakim Abdullah¹ and Mohamad Sufian So'aib²

¹*Faculty of Chemical Engineering, Universiti Teknologi MARA Pulau Pinang, 13500 Permatang Pauh, Pulau Pinang Malaysia*

²*Faculty of Chemical Engineering, Universiti Teknologi MARA Pulau Pinang, 13500 Permatang Pauh, Pulau Pinang Malaysia*

sufian5129@ uitm.edu.my

Abstract:

In this study, an artificial neural network (ANN) was used to predict microbial population dynamics and species during the spontaneous fermentation of *Garcinia mangostana* pericarp. The study was conducted by collecting the experimental data from analysis of fermented *Garcinia mangostana* pericarp and train the data by using neural network in MATLAB system. The model was developed based on trial and error at different neural network architecture, transfer function, and training algorithm. The input parameter consists of days of fermentation (0-100 days) and volume of fermenters (5 and 50 liters). The data set were trained by the artificial neural network using hyperbolic tangent sigmoid (tansig) transfer function and Levenberg-Marquardt (trainlm) training algorithm. Based on the results, the best neural network architecture for prediction of the microbial population were 2-7-7-3 (bacteria) and 2-7-6-1 (yeast), while for the microbial species was 2-5-4. The correlation coefficient (R-value) for the training performance for prediction of bacteria and yeast population showed R-value were 0.99299 and 0.9703 respectively, while for the bacteria species was 0.94244. Performance of neural network design was evaluated based on mean square error (MSE) and relative error. The result shown the MSE for the training performance for prediction of microbial population were 0.009557 (bacteria) and 0.01358 (yeast), while for microbial species was 0.1077. The average relative error for microbial population for bacteria and yeast was evaluated to make sure the accuracy of the predicted data. The relative error means the percentage of incorrect predicted data. Hence, the least value of the average relative error will be good for the neural network model that indicate the accuracy between experimental data and predicted data.

Keywords:

Artificial Neural Network, Fermentation, Garcinia Mangostana Pericarp, Population, Species

Objectives:

- To develop Artificial Neural Network Model (ANN) for prediction of microbial population and species during spontaneous fermentation of *Garcinia Mangostana* pericarp.
- To compare the statistical performance of different ANN architecture for prediction of microbial population and species during spontaneous fermentation of *Garcinia Mangostana* pericarp.

Methodology:

In this experiment, population dynamics and species of the microbial were the output neurons of the network model. The input neurons were the number of days and volumes of the fermenters which are 5 and 50 litres. To determine the population dynamics and species of the microbial, the network model was run separately. The first model was to predict the population dynamics of the microbial and the second model was to determine species microbial during the spontaneous fermentation of the *Garcinia mangostana* pericarp.

In this simulation, the number of hidden layers was limited with single layer and double hidden layer to evaluate the output data of the model. Levenberg Marquadt (trainlm) was applied as fix training function in this neural network model. The hyperbolic tangent sigmoid (tansig) transfer function was set in this neural network design. The different number of neurons in hidden layer was designed in different neural network architecture. To get the optimum model, trial and error method was the good approach with changes the number of neurons. Specific neural network code was introduced in the neural network training to optimize the data set and run the prediction model. The code was generated into MATLAB script with the input and output data include in the code. Prediction of species microbial procedure was same as microbial population. The species of the microbial will group with their genus. The species of the microbial will define in numerical terms that represent the type of microbial species. The number tabulated in the table represent the present of the microbial species. The number '0' represent absent or no specific microbial on that day. The result from the simulation can be evaluate from the output data and the plotted graph from the network design.

Relative error (RE) need to calculate in this experiment because RE is a type of error that relates to the size of the item or variable being measured or put in another way. Relative error also indicates the value that tells us the accuracy of a measure compared to the true value.

$$\text{Relative error} = \frac{\text{predicted data} - \text{actual data}}{\text{Actual}}$$

R-value, Correlation coefficient and R², coefficient determination can also evaluate to determine the level of the neural network performance during prediction of the microbial population and species.

Results:

1. Microbial Population Dynamics

- **Bacteria**

Table 1: Training performance of different network architecture for prediction of bacteria population.

Neural Network Architecture	MSE	R ²
2-5-7-3	0.04469	0.92488
2-7-7-3	0.013235	0.98277
2-9-7-3	0.01454	0.9751

2-11-7-3	0.1877	0.70382
2-13-7-3	0.2093	0.57123
2-15-7-3	0.46865	0.4632

- Yeast

Table 2: Training performance of different network architecture for prediction of yeast population.

Neural Network Architecture	MSE	R ²
2-5-6-1	0.05306	0.80863
2-6-6-1	0.04886	0.82735
2-7-6-1	0.01509	0.9469
2-8-6-1	0.1566	0.9325
2-9-6-1	0.2093	0.9322
2-10-6-1	0.3135	0.98624

2. Species

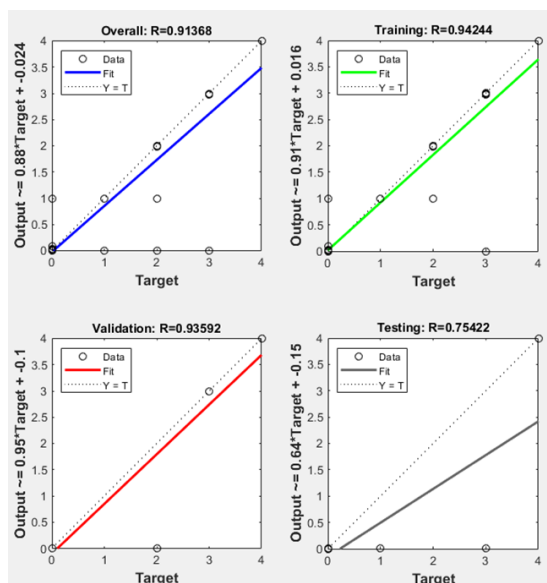


Figure 1: Neural network regression for prediction of microbial species

Conclusion:

Artificial network was successfully developed to predict the microbial population dynamics and species during spontaneous fermentation for *garcinia mangostana* pericarp. The network model found to be good with experimental data with double hidden layer was applied on prediction of microbial population with both hidden layers have 7 neurons respectively and single hidden layer with 5 neurons for prediction of microbial species. The distribution of data points for neural network model almost similar and close to the actual experimental data with correlation coefficient (R) in range in range of 0.9 - 1.0. This indicated the developed neural network model is capable of making the prediction with reasonable accuracy. The calculated relative error also proved least average relative error for the neural network model have accurate prediction on the experimental data.