International Journal of Innovative Computing, Information and Control
Volume **8**, Number **7(A)**, July **2012**

ICIC International ©2012 ISSN 1349-4198
pp. 4565–4577

NEURAL FUZZY NETWORK MODEL WITH EVOLUTIONARY LEARNING ALGORITHM FOR MYCOLOGICAL STUDY OF FOODBORNE FUNGI

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Received April 2011; revised August 2011

Abstract. *This study developed a neural fuzzy network (NFN) model with evolutionary learning algorithm for use in the field of food mycology for predicting growth in foodborne fungi. The evolutionary learning algorithm in the proposed model is a hybrid Taguchi-genetic algorithm (HTGA) that simultaneously finds the optimal antecedent and consequent parameters by directly minimizing root-mean-squared error (RMSE), which is a key performance criterion. The minimum RMSE is then used to optimize the number of fuzzy rules for the NFN. Experimental results show that the proposed HTGA-based NFN model with eight fuzzy rules outperforms recently reported neural networks in terms of accuracy in predicting the maximum specific growth rate of foodborne Monascus ruber.*

Keywords: Fungal growth, Food mycology, Neural fuzzy network, Genetic algorithm

1. **Introduction.** Advances in prediction modeling now enable rapid and cost-effective assessment of microbial growth. In the food manufacturing industry, many applications of microbial growth prediction models include product development, risk assessment of food-borne illness, and education [1]. Recently, these models have been used to assess shelf life in food products by forecasting the growth of micro-organisms that cause spoilage. Fungal spoilage of food commodities causes significant economic losses. Although industrial standards have greatly improved in recent years, food spoilage by fungi remains a major concern for both food producers and regulatory agencies. In recent years, newly developed food manufacturing, processing and packaging techniques have increased the importance of characterizing foodborne fungi [2]. Fungi can adversely affect the organoleptic value of food commodities due to the appearance of visible mycelium and off-flavour development. In addition to diminishing the nutritional value of many foods, they are a public health risk because they can produce toxic metabolites that are potentially carcinogenic [3]. Improving food quality and safety requires appropriate tools for predicting fungal growth. In recent years, many studies in predictive microbiology have analyzed foodborne pathogens, but few have developed predictive models of growth in filamentous fungi [4]. The few reported predictive models for food mycology include those developed