

Copyright © 2016 American Scientific Publishers All rights reserved Printed in the United States of America Advanced Science Letters Vol. 4, 400–407, 2016

## Co-Evolving Ensemble of Genetic Algorithm Classifier for Cancer Microarray Data Classification

Supoj Hengpraprohm<sup>1,3</sup>, Kairung Hengpraprohm<sup>1,3</sup>, Dech Thammasiri<sup>2,3</sup>, Suvimol Mukviboonchai<sup>1</sup>

<sup>1</sup>Faculty of Science and Technology, Nakhon Pathom Rajabhat University, Nakhon Pathom 73000, Thailand <sup>2</sup>Faculty of Management Science, Nakhon Pathom Rajabhat University, Nakhon Pathom 73000, Thailand <sup>3</sup>Machine Intelligence Research Unit, Nakhon Pathom Rajabhat University, Nakhon Pathom 73000, Thailand

Ensemble is the method that improves the efficiency of the classification task. In the traditional way, classifiers were built separately n times and combine to the ensemble with size n. It takes a lot of time especially in the Genetic Algorithm (GA) methodology. This paper presents the method to build the ensemble of GA classifier that processed by GA technique. The experimental results showed that the proposed method gave better classification accuracy with less time consumed in processing comparing with the traditional one.

Keywords: Ensemble Method, Data Classification, Genetic Algorithm.

## 1. INTRODUCTION

Microarray is the popular technique in studying the living process in molecular level. This technique provides us to investigate on the patterns of thousands genes simultaneously. Nowadays, it has been implemented widely and influenced the increasing of microarray datasets. The study relating to cancer is another topic which microarray techniques have been implemented to learn the patterns of gene expression in order to cure effectively. Statistics and computer processing, especially data mining and machine learning techniques are the powerful tools used to create the automatically-assisted diagnosis model.

Ensemble technique has been one of a popular data classification methods and it has been accepted in terms of significantly classification efficiency. Ensemble technique has been widely developed, for example, decision tree with bagging technique<sup>1,2</sup>, the varieties of the ensemble of classifiers and feature selections<sup>3</sup>, and the ensemble of the Genetic Programming (GP) classifier<sup>4</sup>. It

has been found that the ensemble classifiers yield better efficiency in cancer microarray classification<sup>5</sup>.

The crucial parts of the ensemble efficiency are controlling the diversities and the quality of each classifier. Generally, each classifier should be separately built, then, combined them together to the ensemble. This requires huge computation time especially the evolutionary computation technique which has been popular in building efficiently classifiers.

This work presents the co-evolving method to build the ensemble of GA classifier that can improve the classification accuracy and reduce the time consumed of the learning process.

The paper is organized as follows. In section 2, the details of the Genetic Algorithm (GA) are presented. In section 3, the GA classifier used in the research are described. In section 4, the co-evolving ensemble design is given. Section 5, the experimental settings are showed. The experimental results are presented in section 6. Finally, discussions and conclusions are summarized in the last section.