The Minimum Relevant Genes Selected from Gene Expression Data Using Two-Stage Adaptive Genetic Algorithms

Chien-Pang Lee
Yungho Leu
Department of Information Management, National Taiwan University of Science and technology, Taipei, R.O.C

Wen-Shin Lin
Bo-Jein Kuo
Biometry division, Department of Agronomy, National Chung Hsing University, Taichung, R.O.C

Because of the growing of bioinformatics technologies, the genes of species have been decoded gradually. Microarray is one of the popular technologies which have been employed in this field. The useful information of genes may be discovered by the statistical methods or data mining skill. However, the traditional statistical methods or data mining skill performed inefficient. The objective of this study is to use the two-stage adaptive genetic algorithms (AGA) to select the minimum relevant genes more efficient. Different mutation rates were assigned to the genes (or chromosomes) based on the evolution process in each generation to reach the survival-of -the-fittest principle. In addition, the extinction and immigration strategies were employed to avoid jumping into the local solution. Finally, the remained minimum relevant genes were tested by the chi-square test. The results demonstrated that two-stage AGA may select the minimum relevant genes more efficient and powerful than the other genetic algorithms methods.

[Bo-Jein Kuo, No.250, Kuo Kuang Rd., South District, Taichung City 402, Taiwan (R.O.C.); bjkuo@nchu.edu.tw]