Abstract

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Fully Automated Adaptive Shape Segmentation Method for Noisy Complementatory DNA Microarray Images

Due to the vast success of bioengineering techniques, a series of large scale analysis tools has been developed to discover the functional organization of cells. Among them, cDNA microarray has emerged as a powerful technology that enables biologists to study thousands of genes simultaneously within an entire organism, and thus obtain a better understanding of the gene interaction and regulation mechanisms involved. The analysis of DNA microarray image consists of several steps gridding, segmentation, and quantification that can significantly deteriorate the quality of gene expression information, and hence decrease our confidence in any derived research results. Thus, microarray data processing steps become critical for performing optimal microarray data analysis and deriving meaningful biological information from microarray images. Segmentation is the process, by which each individual cell in the grid must be Selected to determine the spot signal and to estimate the background hybridization. In this paper, a proposed segmentation method is explored “Adaptive Shape Segmentation”. By inspecting the results, it was found that the proposed segmentation method can segment noisy microarray images correctly, gives high accuracy results and minimal processing time, and can be applied to various types of noisy microarray images.