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Automatic Microarray Image Segmentation Based on Watershed Transformation

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Abstract

Microarrays are miniature arrays of gene fragments attached to glass chips. Microarrays allow the detection of subtle differences in genome sequences so that they can be used to detect and classify genetic diseases very accurately. Microarray experiments generate large amounts of data, because they allow thousands of genes to be processed in a single experiment. To obtain meaningful information from the massive microarray experimental results, it is needed to develop a fully automatic subgrid and spot segmentation algorithm which can measure the expression levels of each gene and the relative ratios of the genes in different situations without additional information or user intervention. In this paper, we used watershed transformation to get basic features of microarray images. Then, a graph model was used for subgrid gridding and spot segmentation based on the watershed transformation results. To verify the efficiency of our algorithm, we compared its performance with that of two previous methods: Profile and MKNN(Modified K Nearest Neighbor) algorithm. The result demonstrated the accuracy and robustness of the proposed algorithm in subgrid and spot segmentation.

1. Introduction

Microarray is the robotic placement of thousands of cDNAs on a glass microscope slide. It is capable of profiling gene expression patterns of tens of thousands of genes simultaneously. Microarrays containing sequence representatives of all human genes may soon permit the gene expression analysis of the entire human genome in a single experiment, and this will provide unprecedented access to key areas of human health, including disease prognosis and diagnosis, drug discovery, toxicology, aging, and mental illness. Thus, microarray technology is rapidly become a standard platform for functional genomics.

A microarray image consists of arrays of spots arranged in the form of a grid. All of the grids contain the same number of rows and columns of spots. These grids, called subgrids, are arranged so as to maintain a relatively equal distance from each other and together they form a complete array[1]. Figure 1 shows an example of subgrid and spot in a microarray image.

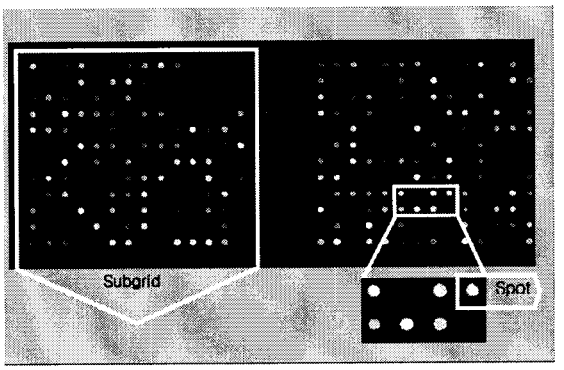

Figure 1. An example of subgrid and spot

Subgrid gridding and spot segmentation are the most important steps in microarray image processing. These steps are necessary in order to map each spot to its gene information and to determine the preliminary location of the spots before a precise segmentation and subsequent intensity measurement are performed. Since various noises exist in microarray images, a full automatic analysis of microarray image is so difficult to perform that most of microarray image analysis systems need additional information and user interaction about subgrids and spots as input parameters: the number of spots in each direction, the distances between spots and the diameter of spots[2-6]. The weakness of these systems is that it is difficult to quantify normalized spot intensities in the massive amount of microarray image data, because in most cases the user interactions require a lot of time and efforts and tend to involve subjective judgment. To solve this problem, we propose a fully automated spot segmentation algorithm which combines watershed transformation and graph algorithm.

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