Abstract

DNA Microarray is an innovative tool for gene studies in biomedical research, and its applications can vary from cancer diagnosis to human identification. It is capable of testing and extracting the expression of large number of genes in parallel. The gene expression process is divided into three basic steps: gridding, segmentation, and quantification. Automatic gridding; which is to assign coordinates to every element of the spot array, is considered the most challenging phase of microarrays image processing. For processing of microarray images, a new, automatic, fast and accurate approach is proposed for gridding noisy cDNA microarray images. In the real world, microarray image doesn’t reflect measures of the fluorescence intensities for the dye of interest only, as different kinds of noise and artifacts can be observed. In this paper, a novel gridding method based on projection is developed accompanied by a pre-processing, post-processing, and refinement steps for noisy microarray images. Results revealed that the proposed method is used with high accuracy and minimal processing time and can be applied to various types of noisy microarray images.
A New Method to Grid Noisy cDNA Microarray Images Utilizing Denoising Techniques

References

- Stanford Microarray Database (SMD; http://smd.stanford.edu/)
- Y. Wang, F. Y. Shih, and M. Ma. 2005. Precise gridding of microarray images by detecting and correcting rotations in sub-arrays. In proceedings of Sixth Inter. Conf. on Computer Vision, Pattern Recognition and Image Processing, Salt Lake City, UT.
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Keywords

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