

An Overview of Microarray Image Analysis

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Abstract

Gene expression analysis of large collections of genes has recently become a possibility, through the use of microarray technology. In brief this technology utilizes the ability of nucleic acid to specifically hybridize to complementary sequence. Very small deposits of sequence complementary to specific gene transcripts are fixed in an array on a flat solid surface, allowing fluorescent labeled samples to be quantified based on its hybridization to these. Typically a confocal scanner is used to acquire two tiff images of the array, one for each of two samples that are co-hybridized on the array. Often the array is contaminated with dust and salt precipitates etc. and the features can be irregular in shape, size, intensity and location. Traditional analysis of the image involves overlaying the two images, identifying and locating the features of the array (gridding), segmentation of the pixels into feature and background segments. Finally an intensity value for the feature and background are estimated. The presentation is meant as a state of the art presentation and inspiration for discussion of future work.