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Geometric Filters for Microarray Assays

Technology Reference

R244

Keywords

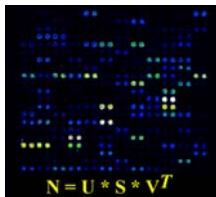
Research Tool
Diagnostic Tool

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Field

Molecular Biophysics and
Physiology

Patent Status

US Patent Pending

Cross Reference

This invention relates to
discoveries R029, R031,
R033

AREAS OF APPLICATION

The reliable identification and classification of spots corresponding to up and down regulated genes or proteins in microarray assays

- Gene expression profiling
- Protein expression profiling
- Nucleic acid sequence profiling

ADVANTAGES

- Applicable to "dye-swapping" and similar microarray protocols that produce four or more replicate data arrays
- Improves the sensitivity and specificity of the detection of up and down regulated spots relative to previous methods
- Identifies low to moderate expression spots in noisy array data with a high degree of confidence

THE TECHNOLOGY

This invention utilizes the four data sets produced by "dye swapping" or similar assay methods. For each experimental/reference array pair in such an assay, the captured array spot intensity data is background corrected and the ratios of the intensities of the experimental spots to the corresponding reference spots are computed and expressed in $\log_2(\text{ratio})$ format. The two resulting sets of ratioed data are then rank ordered according to spot intensity and "plotted" in a prescribed manner to produce a 3-dimensional response surface. This response surface is then segmented into square areas comprising approximately 100 spots and a standard deviation or similar noise-sensitive metric is computed for each area. Limiting upper and lower response surfaces are then constructed by applying these noise metrics to the initial response surface. Spots having intensity ratios that fall outside of the volume defined by the upper and lower response surfaces are accepted as representing provisionally meaningful data. A "consistency" filter then applies a series of selection rules to these provisionally accepted data to identify those spots that represent true differences between the experimental and reference samples.

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