

## Methods for Reducing False Positive Results in Genetic Analytical Assays

This novel invention provides mathematical analysis and modeling of false data in the gene microarray experimental system, and describe formulas that allow separation of false positive data to a high degree of confidence. The methodology discovers genetic expression classes in gliomas and new putative oncogenes and tumor suppressor genes in glial tumors. The technology defines analytical methods that provide a high degree of confidence that the genes it identifies are differentially expressed.

### AREAS OF APPLICATION

Bioinformatics software:

- For analysis of gene micro-arrays in the genome-wide scale.
- Accurate detection of molecular expression in the pharmaceutical and food industries.
- Gene profiling experiments.
- Discovery of molecular expression patterns associated with human disease.
- Linking expressed sequence tags (ESTs) to cellular functions.
- Analysis and modeling of false data in any experimental system.

### ADVANTAGES

- Discovery of genetic expression patterns associated with biological phenotype or human disease.
- Methods that provide results for gene profiling experiments that are known to be true positive.
- Elimination of false data and the need for repeating the test which is more efficient.

### THE TECHNOLOGY

The completion of the first stage of the Human Genome Project has created the possibility of studying changes in gene expression of the complete genetic repertoire in any disease affected tissue. However, microarray expression data and genome-wide screening are still hampered by the preponderance of false positive data in the gene microarray experimental system. Such false positive data significantly impair assessing which genes are significantly expressed in a cell, and what significant changes to such expressions are occurring as cell conditions are varied. Although a large number of expressed sequence tags (ESTs) are known, many of the ESTs have no known function, have a falsely understood function, have a true known function but may have additional unknown functions, or may have known functions that are limited to certain conditions or cell types, but not known under other conditions or in other cell types. Therefore there is a need for formulas that provide true positive results for gene profiling experiments. It is highly desirable to have a high degree of confidence that genes identified by the analytical method are differentially expressed and not false positive.

### PATENT

U.S. Utility Patent application, "Method and System for Reducing Noise in Analytical Assays"  
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