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by

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Whole Genome Microarray Analysis reveals Epigenetically regulated genes in Malignant Glioma

ABSTRACT

Microarray technology enables to measure the expression levels of tens of thousands of genes simultaneously, have evolved into indispensable tools for scientists in biology and medicine. There are multiple sources of variation, of which biological sources are of interest, and a wide range of different methods for normalization, filtering and analysis have been developed for the analysis of microarray data. Choosing right methods is challenging which is dependent on the goal of the experiments and the environment.

We have used Applied Biosystems 1700 Chemiluminescent Microarray Analyzer to understand the epigenetic regulation of gene expression in malignant glioma. The platform uses whole genome microarray consisting of 33,000 probes representing 29,098 genes and chemiluminescence technology to identify and measure gene expression levels.

The microarray data was analyzed with various analysis methods such as loess normalization, quantile normalization, t-test, SAM and false discover rate. The result of these analyses along with relevant issues will be discussed in this talk.