Integrated Analysis of genome-wide data using microarray technologies in cancer research

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After solved a mystery of *Homo sapiens* genome sequences, it provides most promise information that it bring greatest opportunities in biomedical community. Several genome-wide studies have been indicated by the development of powerful genomic analysis method and tools that allow the use genome-wide information to find prospective clues on solved biomedical questions and discovery new biological facts. One of them is widely accepted and an accessible technology is DNA microarray technology.

By using high-throughput technology, whole genome microarrays allow assessment of the profile of gene expressed under particular experiment conditions and internal changes brought about by deleting or over-expressing a gene. Gene expression microarrays have become almost as widely used as measurement tools in biological research as western or northern blots. Recently, array-based Comparative Genomic Hybridization (array CGH) with high-resolution has developed its value for analyzing DNA copy number variation. With CGH, differentially labeled test (i.e. tumor) and reference (i.e. normal individual) genomic DNA are co-hybridized to normal metaphase chromosomes, and fluorescence ratios along the length of chromosomes provide a cytogenetic representation of the relative DNA copy-number variation. Chromosomal CGH resolution is limited to 10-20 Mb therefore, anything smaller than will be not be detected.

In this presentation, the application of genome-wide gene expression profiling data will be discussed with the integration of array CGH which can be studies with expression DNA microarrays. As in many gnome-scale methodologies, data analysis and interpretation constitutes a well-known bottleneck. specifically related to data processing in array-CGH can be circumscribed. addition, various tools are introduced that an integrated web-based pipeline for the analysis of genome-wide data in cancer research.