"Integrative Functional Genomics to Decode Human Cancer Signatures"

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The majority of gene expression profiling studies using DNA-microarray platforms in human cancers has focused on identifying genes whose expression is associated with clinicopathological features of cancer patients. So far, this approach has only limited success due to many confounding factors embedded in gene expression profile data and the difficulty in identifying the key regulatory elements in gene expression profiles. Cross-comparison of gene expression data from human tumor samples with well-defined gene expression patterns from *in vitro* and *in vivo* models will allow the definition of gene expression signatures that are associated with clinicopathological conditions. In the presentation, I will describe the novel approaches of gene expression data analysis by integrating multiple data sets from human and animal models as well as array CGH data and genome sequences.