

## **Functional Analysis of OMICs Data in Breast Cancer**

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High-throughput assays become a mainstream in experimental studies of complex human diseases, particularly cancers. It also now clear that statistical analysis alone is insufficient for meaningful deciphering of the “genome-wide” results of these assays in search of biomarkers and novel therapeutic targets. Recently, a number of functional analysis methods were developed and applied for the analysis of SNP array, expression analysis by “third-generation sequencing” approaches, exon re-sequencing data, proteomics and microRNA profiles. I will describe the basic techniques of pathway, network and interactome data analysis developed and implemented by GeneGo and summarize the results of collaborative studies on breast cancer we were involved in over the last three years. The projects included analysis of breast cancer stem cells based on SAGE and microarray gene expression profiling, comparison of gene methylation (epigenetics) and expression profiles in different breast cancer cell lines, comparative analysis of somatic mutations and amplicons in breast cancer and analysis of sense/antisense expression profiles in primary breast tumors based on “third-generation” sequencing data.