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Gene expression analysis and patient stratification: Prioritization of genes relevant in BrCa.

Abstract:

The great promise of gene expression profiling and other genomic technologies like proteomics and metabolomics is patient stratification. By monitoring the expression of all genes and proteins in a patient population during clinical trials we will be able to identify groups among patients that are a priori more likely to respond to a given therapy. Tissue samples are collected from the patients pre-treatment and once the response to therapy is known, data analysis can identify correlations of expression profiles with the response profiles. The ultimate goal of gene expression profiling and computational analysis is identification of a small panel of biomarkers that could be applied clinically to predict which patient population is most likely to benefit from a therapy. However, this is often a challenging task, since the number of samples available for analysis is much smaller than the number of genes on gene chips. In my talk I will describe an approach to the analysis of breast cancer gene expression profiles, that uses gene expression profiles from in-house generated data and publicly available data sets. We identify several novel drug targets for breast cancer.