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Abstract

Integration of mRNA and gene copy number measurements for elucidation of drug resistance mechanisms

Johan Winquist

Acquired cellular resistance to cytotoxic drugs is a major problem in modern cancer treatment. This project aimed to find a high throughput approach to identify candidate genes responsible for resistance, by the means of large-scale molecular analysis and data mining. These genes could be used as targets in future attempts to resensitize cancer cells to drugs or in diagnostics of resistance. Values of in vitro resistance for 39 drugs were collected with FMCA (fluorometric microculture cytotoxicity assay), gene copy number and gene expression for 11246 genes with microarrays. Integration of the three characters by pairwise Pearson correlation studies (univariate and quasi-bivariate) identified new interesting gene transcripts as well as ones already known to be involved in resistance mechanisms. The approach proved to be robust and useful in this type of analysis.

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