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Prediction of multiple drug resistance phenotype in cancer cell lines using gene expression profiles

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When microarray gene expression data are used to predict multiple drug resistance (MDR) phenotypes for anticancer drugs, the normalization strategy and the quality of the selected signature genes are usually the main causes of inconsistency among different experiments. A stable statistical drug response prediction model is urgently required in oncology. In this study, the microarray gene expression data of multiple cancer cell lines with MDR was analyzed. For each probe-set, the expression value was defined as present/absent (1/0) and was classified into a gene set defined with protein domain organization (PDO). After employing the gene content method of phylogenetic analysis, a phylogenetic model (cell tree) for MDR phenotype prediction was built at the PDO gene set level. The results indicate that classification of cancer cell lines is predominantly affected by both the histopathological features and the MDR phenotype (paclitaxel and vinblastine). When applying this model to predict the MDR phenotype of independent samples, the phylogenetic model performs better than signature gene models. Although the utility of our procedure is limited due to sample heterogeneity, it still has potential application in MDR research, especially for hematological tumors or established cell lines.

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