

*Analysis of Gene Expression Profiles and Drug Activity Patterns for the Molecular Pharmacology of Cancer (Data Set 2)*

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High-throughput genomic analysis requires the ability to extract useful information from huge biological data. In this paper, we analyze gene expression profiles and drug activity patterns on the NCI60 cell lines data in two aspects, clustering the cell lines and the discovery of correlations among genes and drugs. K-means clustering with dimensionality reduction is applied and the experimental results show that the cell lines can be clustered according to their tissue of origin. Bayesian network learning is applied to the analysis of correlations among gene expressions and drug activities. The correlations discovered by Bayesian network learning are coincident with known causal relationships among gene expressions and drug activities.