Determination of Common Cancer-Related Genes Using Microarray Data
運用微陣列數據資料探討癌症之共同基因

Lillian Y. Chen, Yen-Chen Chen, Yuan-Chii G. Lee, Hung-Wen Chiu,
陳宇瑄、陳彥臣、李元綺、邱泓文

Graduate Institute of Medical Informatics, Taipei Medical University
臺北醫學大學醫學資訊研究所

Abstract

As cancer has drawn much of the attention worldwide these days, development of effective drugs using microarray data analytical results has become a popular method to search for drug targets. In order to determine common cancer-related genes for prostate adenocarcinomas, kidney carcinoma, hepatocellular carcinoma, ovarian adenocarcinomas, pancreatic adenocarcinomas and lung carcinomas, microarray datasets were analyzed via GeneSpring Version 6.1 based on their gene expressions. After having obtained 240 common cancer-related genes among six cancer types, a further analysis on the relationship of gene and biological pathway would be performed. MAPK signaling pathway and cytokine-cytokine receptor interaction have been found to have most genes involved in terms of the biological signaling process.

Keywords: cancer, microarray, gene expression, MAPK signaling pathway, Cytokine-Cytokine receptor interaction