# 分析公開微陣列資料庫中癌症相關基因的基因表現

# Gene Expression Analysis for Cancer-Related Genes Using Public Microarray Databases


## 中文摘要

背景：

癌症是現今世界共通的疾病，發展有效治療癌症的藥物是當下醫藥學界主要致力的目標。微陣列技術的應用已成為近幾年生醫研究的主流，許多研究利用微陣列技術來觀測人類癌症細胞株或器官組織的基因表現，藉此有效率得找出癌症相關基因。

材料和方法：

我們從 OMIM 資料庫中做資料探勘癌症相關的基因，整理得到一個癌症相關基因名單。另一方面從 GEO 和 SMD 資料庫中蒐集人類癌症相關的微陣列數據資料，並根據不同種類型癌症做分類，再利用統計原理篩選出可能的基因名單。分析這些基因名單的生化反應路徑，和比較不同資料庫來源





所得到結果的差異。

結果與討論：

我們將由 OMIM 所得到十種不同癌症的基因名單做交集，得到三個共通的癌症相關基因，分別為 APC、CDKN2A 和 PTEN。針對乳房、前列腺、肝、肺、胰臟、胃等六種器官的癌症組織相關基因名單做交集，觀察到 APC、CDKN2、APTEN、TP53 和 BRAF 是共通的癌症相關基因。另外，利用微陣列資料庫中所得到的癌症相關基因名單做交集，寡核柑酸微陣列的資料中我們得到九個基因，分別是 FOXM1、HNRPDL、BIN1、BUB3、CCNI、PMS1、PRKCBP1、PURA 和 RPA3。在 cDNA 微陣列部分，得到六個共通的癌症相關基因，分別為 ARGBP2、CD53、FCGBP、JUN、MME 和 VBP1。在這些我們所觀察到的癌症共通基因都在 Wnt signaling pathway.中扮演重要的角色。

結論：

將 OMIM 十種主要的癌症基因名單作交集，我們得到 3 個共通的癌症相關基因。另外再交集六種癌症基因名單得到五個共通的癌症相關基因，並比較這些基因在微陣列中的表現是否有所差異。結論是在 OMIM 中找到的癌症相關基因與微陣列實驗數據的結果不一定會相符合。



## 英文摘要

Introduction:

As cancer has drawn much of the attention worldwide these days, development

of effective drugs is definitely the focus in today’s medical research field.
Since microarray technologies have become a biological research trend over the last few years, using the microarray data to monitor gene expression in human cell lines and tissues is certainly the most efficient way to identify cancer-related genes.

Materials and Methods:

The cancer-related gene lists were obtained by reviewing literatures on the OMIM database. The microarray expression datasets were downloaded from the GEO and SMD websites. After having collected the cancer-related genes and microarray expression data, we would classify them according to each datum’s specific cancer-causing nature.

Results and Discussion:

When having intersected ten OMIM cancer-related gene lists, APC, CDKN2A



and PTEN were resulted as the three common cancer-related genes; when having performed the intersection of breast, prostate, liver, lung, pancreatic and stomach tissues, APC, CDKN2A, PTEN TP53 and BRAF were obtained.
Based on microarray gene expressions, intersections of cancer-related genes among oligonucleotide arrays have found nine common genes, which are the FOXM1, HNRPDL, BIN1, BUB3, CCNI, PMS1, PRKCBP1, PURA and RPA3.
Intersections of cancer-related genes among cDNA arrays have got six common genes, which are the