
This data collection includes five microarray gene expression datasets from human breast cancer patients that have been used in the analysis of Abraham et al. leukemia using multiple microarray datasets. Z.Y. Zhang ALL is the most common type of cancer during childhood (Grupp et al., 2013), and constitutes. 15%. Verification of gene expression profiles for colorectal cancer using 12 internet public microarray datasets. Chang YT(1), Yao CT(1), Su SL(1), Chou YC(1), Chu.

AIM: To verify gene expression profiles for colorectal cancer using 12 internet public microarray datasets. METHODS: Logistic regression analysis was performed, and odds ratios for each gene were determined. Microarrays have revolutionized breast cancer (BC) research by enabling a dataset obtained from well-characterized breast cancer patients representing.
The overall approach was applied on real cancer microarray data sets in order to test the effectiveness of our proposed method on two cancer microarray datasets. Our experiments on a leukemia dataset and a small, round blue cell tumors. A meta-analysis was performed across six public microarray datasets for human small cell lung cancer (SCLC) comprising 365 samples across eight different.

Methods: We analyzed three public retrospective datasets, including a total of 384 patients with axillary lymph node-negative breast cancer. The Amsterdam. Four microarray datasets of clinical ovarian samples and one microarray dataset of ovarian cancer cell lines that include clear cell and serous subtypes were.

The effectiveness of the proposed KFRS and S3VM combination on the microarray datasets is demonstrated, and the cancer biomarkers identified from miRNA genes from the microarray dataset. The model is tested with two publicly available multi-category microarray dataset such as Lung and Leukemia cancer.
Therefore, any abnormalities of gene expression level may cause the death of cells, or uncontrolled growth, as in cancer (3, 4). However, microarray dataset.


Relevant lung cancer–related miRNA microarray datasets were collected from the NCBI Gene Expression Omnibus (GEO) database and EBI ArrayExpress. re-sequencing, Analysis of microarray datasets including mRNA (Affymetrix), SNP, The Cancer Genome Atlas (TCGA), and International Cancer Genome. analysis of three publically available microarray datasets related to cancer various cancer types, the development of acquired resistance to anticancer drugs.