**[Lung Cancer](http://levis.tongji.edu.cn/gzli/data/lungcancer.zip)** [4.73 MBytes]

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| ¤ **Publication:** | ["Translation of Microarray Data into Clinically Relevant Cancer Diagnostic Tests Using Gege Expression Ratios in Lung Cancer And Mesothelioma".](http://cancerres.aacrjournals.org/content/vol62/issue17/" \l "CLINICAL_INVESTIGATIONS" \t "_blank)*[Cancer Research](http://cancerres.aacrjournals.org/content/vol62/issue17/" \l "CLINICAL_INVESTIGATIONS" \t "_blank)*[, 62:4963-4967, 2002](http://cancerres.aacrjournals.org/content/vol62/issue17/" \l "CLINICAL_INVESTIGATIONS" \t "_blank) |
| ¤ **Number of Instances:** | 32 training v.s. 149 testing |
| ¤ **Number of Attributes:** | 12533 (all numeric) |
| ¤ **Number of Classes:** | 2 (MPM v.s. ADCA) |
| ¤ **Data Source:** | [http://www.chestsurg.org/](http://www.chestsurg.org/" \t "_blank) |
| ¤ **Description:** | Classification between malignant pleural mesothelioma (MPM) and adenocarcinoma (ADCA) of the lung. There are 181 tissue samples (31 MPM and 150 ADCA). The training set contains 32 of them, 16 MPM and 16 ADCA. The rest 149 samples are used for testing. Each sample is described by 12533 genes. |