

# Package ‘cancerdata’

November 19, 2024

**Type** Package

**Version** 1.44.0

**Date** 2011-10-26

**Title** Development and validation of diagnostic tests from  
high-dimensional molecular data: Datasets

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**Description** Dataset for the R package cancerclass

**Depends** R (>= 2.10.1), Biobase

**License** GPL (>= 2)

**biocViews** CancerData, MicroarrayData

**git\_url** <https://git.bioconductor.org/packages/cancerdata>

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**Repository** Bioconductor 3.20

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cancerdata-package      *Development and validation of diagnostic tests from high-dimensional molecular data: Datasets*

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### Description

This package contains dataset for the R package cancerclass.

### Details

Package: cancerdata  
Type: Package  
Version: 1.1.0  
Date: 2010-10-26  
License: GPL (>=2)

### Author(s)

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### References

[1] Michiels S, Koscielny S, Hill C (2005), *Prediction of cancer outcome with microarrays: a multiple random validation strategy*, Lancet 365:488-492.

### See Also

[VEER1](#)

### Examples

```
### see: help(VEER1);
```

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VEER      *Breast cancer gene expression data (van't Veer)*

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### Description

Gene expression data from the breast cancer microarray study of van't Veer et al. [1]. The data set VEER includes gene expression values of 24481 genes in 78 tumor samples. The data set VEER1 is a filtered version [2] of VEER including gene expression values of 4948 genes in 78 tumor samples).

### Usage

```
data(VEER)  
data(VEER1)
```

**Value**

Data and annotations are organized in a `ExpressionSet` of the package `Biobase`.

VEER `ExpressionSet`

VEER1 `ExpressionSet`

**References**

[1] van 't Veer LJ et al. (2002), *Gene expression profiling predicts clinical outcome of breast cancer*, *Nature* 415:530-536.

[2] Michiels S, Koscielny S, Hill C (2005), *Prediction of cancer outcome with microarrays: a multiple random validation strategy*, *Lancet* 365:488-492.

**Examples**

```
### see: help(GOLUB);
```

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VIJVER	<i>Breast cancer gene expression data (Vijver)</i>
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**Description**

Gene expression data from the breast cancer microarray study of Vijver et al. [1]. The data set `VIJVER` includes expression values of 24481 genes in 295 tumor samples. The data set `VIJVER1` is a filtered version of `VIJVER` [2] including expression values of 4948 genes in 295 tumor samples.

**Usage**

```
data(VIJVER)
```

```
data(VIJVER1)
```

**Value**

Data and annotations are organized in a `ExpressionSet` of the package `Biobase`.

VIJVER `ExpressionSet`

VIJVER1 `ExpressionSet`

**References**

[1] van de Vijver MJ, He YD, van't Veer LJ, et al. (2002): *A gene-expression signature as a predictor of survival in breast cancer*. *N Engl J Med*, 347:1999-2009.

[2] Michiels S, Koscielny S, Hill C (2005), *Prediction of cancer outcome with microarrays: a multiple random validation strategy*, *Lancet* 365:488-493.

**Examples**

```
### see: help(GOLUB);
```

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YOUNG

*Breast cancer gene expression data (van't Veer, young patients)*

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### Description

Gene expression data from the breast cancer microarray study of van't Veer et al. [1]. The data set VEER includes gene expression values of 24481 genes in 19 tumor samples. The data set VEER1 is a filtered version [2] of VEER including gene expression values of 4948 genes in 19 tumor samples).

### Usage

```
data(YOUNG)
data(YOUNG1)
```

### Value

Data and annotations are organized in a ExpressionSet of the package Biobase.

YOUNG	ExpressionSet
YOUNG1	ExpressionSet

### References

- [1] van 't Veer LJ et al (2002), *Gene expression profiling predicts clinical outcome of breast cancer*, Nature 415:530-56.
- [2] Michiels S, Koscielny S, Hill C (2005), *Prediction of cancer outcome with microarrays: a multiple random validation strategy*, Lancet 365:488-492.

### Examples

```
### see: help(GOLUB);
```

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