# Package ‘cancerdata’

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**Type** Package

**Version** 1.49.0

**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 3.24

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## Contents

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

### 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);
```

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

### 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 ExtressenSet 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` *Breast cancer gene expression data (Vijver)*

## 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 ExtressenSet 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 ExtressenSet 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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