

Package ‘cancerdata’

November 26, 2024

Type Package

Version 1.44.0

Date 2011-10-26

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

Author Jan Budczies, Daniel Kosztyla

Maintainer Daniel Kosztyla <danielkossi@hotmail.com>

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>

git_branch RELEASE_3_20

git_last_commit 42ceff3

git_last_commit_date 2024-10-29

Repository Bioconductor 3.20

Date/Publication 2024-11-26

Contents

cancerdata-package	2
VEER	2
VIJVER	3
YOUNG	4
Index	5

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)

Jan Budczies <jan.budczies@charite.de>, Daniel Kosztyla <danielkossi@hotmail.com>

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 `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);
```

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

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);
```

YOUNG

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

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);
```

Index

* datasets

VEER, [2](#)

VIJVER, [3](#)

YOUNG, [4](#)

* package

cancerdata-package, [2](#)

cancerdata (cancerdata-package), [2](#)

cancerdata-package, [2](#)

VEER, [2](#)

VEER1, [2](#)

VEER1 (VEER), [2](#)

VIJVER, [3](#)

VIJVER1 (VIJVER), [3](#)

YOUNG, [4](#)

YOUNG1 (YOUNG), [4](#)