Package 'seventyGeneData'

March 19, 2026

Type Package

Title ExpressionSets from the van't Veer and Van de Vijver breast
cancer studies

Version 1.47.0

Date 2013-05-25

Description Gene expression data for the two breast cancer cohorts published
by van't Veer and Van de Vijver in 2002.

biocViews ExperimentData, CancerData, BreastCancerData, MicroarrayData

Depends R (>= 2.13.0)

Suggests Biobase, limma, breastCancerNKI, knitr, rmarkdown, readxl,
BiocStyle

License Artistic-2.0

URL https:
//bioconductor.org/packages/release/data/experiment/html/seventyGeneData.html

LazyLoad yes

Encoding UTF-8

Roxygen list(markdown = TRUE)

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VignetteBuilder knitr

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seventyGeneData-package

> *Gene expression, annotations and clinical information for the van't Veer and Van de Vijver cohorts*

Description

This package contains the two ExpressionSet instances corresponding to the breast cancer patients' cohorts published by van de Vijver and colleagues in NEJM (2002), and by van't Veer and collleagues in Nature (2002).

Usage

```
data(vantVeer)
data(vantDeVijver)
```

Format

The vantVeer ExpressionSet contains 24481 microarray features and 117 samples, while vanDeVijver ExpressionSet contains 24496 microarray features and 295 samples.

Details

Package:	seventyGenesData
Type:	Package
Version:	0.99.4
Date:	2013-03-25
License:	Artistic-2.0

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Source

<http://www.ncbi.nlm.nih.gov/pubmed/?term=11823860> <http://www.ncbi.nlm.nih.gov/pubmed/?term=12490681>

References

Laura J. van't Veer et al., "Gene expression profiling predicts clinical outcome of breast cancer", *Nature*, 2002, **415**:530-536

M. J. van de Vijver et al., "A Gene Expression Signature as a Predictor of Survival in Breast Cancer", *New England Journal of Medicine*, 2002, **347**(25):1999-2009

See Also

See ExpressionSet

Examples

```
### load Biobase package
library(Biobase)

### load the vantVeer dataset
data(vantVeer)
### load the vanDeVijver datasets
data(vanDeVijver)

### show the class of the vantVeer dataset
class(vantVeer)
### show the class of the vanDeVijver dataset
class(vanDeVijver)

### show the dimentions of the vantVeer dataset
dim(vantVeer)
### show the dimentions of the vanDeVijver dataset
dim(vanDeVijver)

### show the first 10 rows of the vantVeer phenotype data
head(pData(vantVeer), n=10)

### show the first 10 rows of the vanDeVijver phenotype data
head(pData(vanDeVijver), n=10)

### show the first 10 features of the vantVeer phenotype data
head(featureNames(vantVeer), n=10)

### show the first 10 features of the vanDeVijver phenotype data
head(featureNames(vanDeVijver), n=10)

### show the PubMed identifier and the abstract
pubMedIds(vanDeVijver)
```

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vanDeVijver   *Gene expression, annotations and clinical information for the Van de*
                               Vijver cohort

Description

This package contains the `ExpressionSet` instance for the gene expression data set published by
Van de Vijver and colleagues.

Usage

```
data(vanDeVijver)
```

Format

The `vanDeVijver` `ExpressionSet` contains 24481 microarray features and 117 samples. The fol-
lowing components were included:

- `pData(vanDeVijver)`: an `AnnotatedDataFrame` for the breast cancer patients clinical infor-
  mation.
- `featureData(vanDeVijver)`: an `AnnotatedDataFrame` containing the microarray annota-
  tions.
- `experimentalData(vanDeVijver)`: a `MIAME` instance storing the data set and experiment
  information.
- `exprs(vanDeVijver)`: the gene expression matrix accounting for the log10 ratio between
  each sample and the reference RNA used in the experiment.
- `assayData(vanDeVijver)$intensity`: the matrix contaning the geometrical mean intensity
  for both the Cy3 and the Cy5.
- `assayData(vanDeVijver)$exprsError`: the matrix containing the log10 ratio error.
- `assayData(vanDeVijver)$pValue`: the matrix accounting for the confidence level that a
  gene's mean ratio is significanctly different from 1.

Details

This dataset corresponds to the breast cancer patients' cohort published by van de Vijver and col-
leagues in NEJM (2002).

Source

http://www.ncbi.nlm.nih.gov/pubmed/?term=12490681

References

M. J. van de Vijver et al., "A Gene Expression Signature as a Predictor of Survival in Breast Cancer",
New England Journal of Medicine, 2002, **347**(25):1999-2009

See Also

See `ExpressionSet`, `AnnotatedDataFrame` and `MIAME`

Examples

```
### load Biobase package
library(Biobase)

### load the vanDeVijver dataset
data(vanDeVijver)

### show the class of the vanDeVijver dataset
class(vanDeVijver)

### show the dimentions of the vanDeVijver dataset
dim(vanDeVijver)

### show the first 10 rows of the vanDeVijver phenotype data
head(pData(vanDeVijver), n=10)

### show the first 10 features of the vanDeVijver phenotype data
head(featureNames(vanDeVijver), n=10)

### show the PubMed identifier and the abstract
pubMedIds(vanDeVijver)
```

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vantVeer	*Gene expression, annotations and clinical information for the van't Veer cohort*

Description

This package contains the `ExpressionSet` instance for the gene expression data set published by van't Veer and colleagues.

Usage

```
data(vantVeer)
```

Format

The `vantVeer ExpressionSet` contains 24481 microarray features and 117 samples. The following components were included:

- `pData(vantVeer)`: an `AnnotatedDataFrame` for the breast cancer patients clinical information.
- `featureData(vantVeer)`: an `AnnotatedDataFrame` containing the microarray annotations.

- experimentalData(vantVeer): a MIAME instance storing the data set and experiment information.
- exprs(vantVeer): the gene expression matrix accounting for the log10 ratio between each sample and the reference RNA used in the experiment.
- assayData(vantVeer)$intensity: the matrix contaning the geometrical mean intensity for both the Cy3 and the Cy5.
- assayData(vantVeer)$pValue: the matrix accounting for the confidence level that a gene's mean ratio is significanctly different from 1.

Details

This dataset corresponds to the breast cancer patients' cohort published by van't Veer and colleagues in Nature (2002).

Source

http://www.ncbi.nlm.nih.gov/pubmed/?term=11823860

References

Laura J. van't Veer et al., "Gene expression profiling predicts clinical outcome of breast cancer", *Nature*, 2002, **415**:530-536

See Also

See ExpressionSet, AnnotatedDataFrame and MIAME

Examples

```
### load Biobase package
library(Biobase)

### load the vantVeer dataset
data(vantVeer)

### show the class of the vantVeer dataset
class(vantVeer)

### show the dimentions of the vantVeer dataset
dim(vantVeer)

### show the first 10 rows of the vantVeer phenotype data
head(pData(vantVeer), n=10)

### show the first 10 features of the vantVeer phenotype data
head(featureNames(vantVeer), n=10)

### show the PubMed identifier and the abstract
pubMedIds(vantVeer)
```

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