Package ‘seventyGeneData’

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Type Package

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

Version 1.0.0

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, Cancer, RNAExpressionData

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Depends R (>= 2.13.0)

Suggests Biobase, gdata, limma, breastCancerNKI

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URL `http://luigimarchionni.org/breastTSP.html`

LazyLoad yes

R topics documented:

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seventyGeneData-package

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

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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

Author(s)

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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)
```

`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 following components were included:

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

`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 coll-leagues 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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