Package ‘mammaPrintData’

March 23, 2017

Type Package

Title RGLists from the Glas and Buyse breast cancer studies

Version 1.10.0

Date 2013-05-13

Description Gene expression data for the two breast cancer cohorts published by Glas and Buyse in 2006

biocViews ExperimentData, ExpressionData, CancerData,
BreastCancerData, MicroarrayData, TwoChannelData

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Depends R (>= 2.13.0)

Suggests Biobase, gdata, limma

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

LazyLoad yes

NeedsCompilation no

R topics documented:

mammaPrintData-package ................................................. 2
buyseRGcy3 .......................................................... 3
buyseRGcy5 .......................................................... 5
glasRGcy3 ........................................................... 6
glasRGcy5 ........................................................... 8

Index 10
mammaPrintData-package

Gene expression, annotations and clinical information for the Glas and Buse cohorts

Description

This package contains the two RGList-class instances corresponding to the breast cancer patients’ cohorts published by Glas and colleagues in BMC Genomics (2006), and by Buyse and colleagues in JNCI (2006). Since in both studies a two-colors dye swap design was applied, this package contains two distinct RGList-class instances for each data set, one for each dye-swap set of hybridizations. This package contains unprocessed data, as obtained from the original raw data files available from the ArrayExpress repository.

Usage

data(glasRG)
data(buyseRGa)

Format

The RGList-class instances contained in this package (glasRGcy5, glasRGcy5, buyseRGcy5, and buyseRGcy5, accounts for 1900 microarray features and 162 and 307 samples respectively.

Details

Package: mammaPrintData
Type: Package
Version: 0.99.5.
Date: 2013-03-25
License: Artistic-2.0

Author(s)

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Source


References


Marc Buyse et al., "Validation and clinical utility of a 70-gene prognostic signature for women with node-negative breast cancer", *JNCI*, 2006, 98(17):1183-1192
See Also

See `RGList-class`

Examples

```r
### load limma package
library(limma)

### load the glasRG dataset: two different dye-swap sets:
### glasRGcy5: information provided for RNA labeled with Cy5
### glasRGcy3: information provided for RNA labeled with Cy3
data(glasRG)

### load the buyseRG dataset: two different dye-swap sets:
### buyseRGcy5: reference RNA was labeled with Cy5
### buyseRGcy3: reference RNA was labeled with Cy3
data(buyseRG)

### show the class of the glasRGcy3 dataset
class(glasRGcy3)

### show the class of the buyseRGcy3 dataset
class(buyseRGcy3)

### show the dimentions of the glasRGcy3 dataset
dim(glasRGcy3)

### show the dimentions of the buyseRGcy3 dataset
dim(buyseRGcy3)

### show the first 10 rows of the glasRGcy3 phenotype data
head(glasRGcy3$targets, n=10)

### show the first 10 rows of the buyseRGcy5 phenotype data
head(buyseRGcy5$targets, n=10)

### show the first 10 features of the glasRGcy5 phenotype data
head(glasRGcy5$genes, n=10)

### show the first 10 features of the buyseRGcy3 phenotype data
head(buyseRGcy3$genes, n=10)
```

---

**buyseRGcy3**

*Gene expression, annotations and clinical information for the Buyse cohort: set of dye-swap hybridizations in which the reference RNA was labeled with Cy3*

---

**Description**

This package contains the `RGList-class` instance (see `limma`) for the gene expression data set published by Buyse and colleagues. This object contains the set of dye-swap hybridizations in which the reference RNA was labeled with Cy3.
Usage

data(buyseRG)

Format

The `buyseRGcy3` `RGList`-class contains 1900 microarray features and 307 samples. The following components were included:

- `buyseRGcy3$targets`: a `data.frame` for the breast cancer patients clinical information;
- `buyseRGcy3$genes`: a `data.frame` containing the microarray annotations;
- `buyseRGcy3$R`: the raw median gene expression foreground intensities from the Red channel;
- `buyseRGcy3$Rb`: the raw median gene expression background intensities from the Red channel;
- `buyseRGcy3$G`: the raw median gene expression foreground intensities from the Green channel;
- `buyseRGcy3$Gb`: the raw median gene expression background intensities from the Green channel;
- `buyseRGcy3$logRatio`: the Log ratio between Red and Green channel, as available from the raw data files;
- `buyseRGcy3$logRatioError`: the Log ratio Error associated with the Log Ratio between Red and Green channel, as available from the raw data files;
- `buyseRGcy3$ID`: the microarray features identifiers, as available from the raw data files;

Details

This dataset corresponds to the breast cancer patients’ cohort published by Buyse and colleagues in JNCI (2006).

Source


References

Marc Buyse et al., "Validation and clinical utility of a 70-gene prognostic signature for women with node-negative breast cancer", *JNCI*, 2006, 98(17):1183-1192

See Also

See `RGList-class`

Examples

```r
### load limma package
library(limma)

### load the `buyseRGcy3` dataset: dye-swap set in which the reference RNA was labeled with Cy3 (from the Glas cohort)
data(buyseRG)

### show the class of the `buyseRGcy3` dataset
class(buyseRGcy3)
```
### show the dimensions of the buyseRGcy3 dataset

```r
dim(buyseRGcy3)
```

### show the first 10 rows of the buyseRGcy3 phenotype data

```r
head(buyseRGcy3$targets, n=10)
```

### show the first 10 features of the buyseRGcy3 phenotype data

```r
head(buyseRGcy3$genes, n=10)
```

---

**buyseRGcy5**

*Gene expression, annotations and clinical information for the Buyse cohort: set of dye-swap hybridizations in which the reference RNA was labeled with Cy5*

---

**Description**

This package contains the RGList-class instance (see limma) for the gene expression data set published by Buyse and colleagues. This object contains the set of dye-swap hybridizations in which the reference RNA was labeled with Cy5.

**Usage**

```r
data(buyseRG)
```

**Format**

The `buyseRGcy5` RGList-class contains 1900 microarray features and 307 samples. The following components were included:

- `buyseRGcy5$targets`: a data.frame for the breast cancer patients clinical information;
- `buyseRGcy5$genes`: a data.frame containing the microarray annotations;
- `buyseRGcy5$R`: the raw median gene expression foreground intensities from the Red channel;
- `buyseRGcy5$Rb`: the raw median gene expression background intensities from the Red channel;
- `buyseRGcy5$G`: the raw median gene expression foreground intensities from the Green channel;
- `buyseRGcy5$Gb`: the raw median gene expression background intensities from the Green channel;
- `buyseRGcy5$logRatio`: the Log ratio between Red and Green channel, as available from the raw data files;
- `buyseRGcy5$logRatioError`: the Log ratio Error associated with the Log Ratio between Red and Green channel, as available from the raw data files;
- `buyseRGcy5$ID`: the microarray features identifiers, as available from the raw data files;

**Details**

This dataset corresponds to the breast cancer patients’ cohort published by Buyse and colleagues in JNCI (2006).
Source


References

Marc Buyse et al., "Validation and clinical utility of a 70-gene prognostic signature for women with node-negative breast cancer", JNCI, 2006, 98(17):1183-1192

See Also

See RGList-class

Examples

```r
### load limma package
library(limma)

### load the buyseRGcy5 dataset: dye-swap set in which the reference
### RNA was labeled with Cy3 (from the Glas cohort)
data(buyseRG)

### show the class of the buyseRGcy5 dataset
class(buyseRGcy5)

### show the dimensions of the buyseRGcy5 dataset
dim(buyseRGcy5)

### show the first 10 rows of the buyseRGcy5 phenotype data
head(buyseRGcy5$targets, n=10)

### show the first 10 features of the buyseRGcy5 phenotype data
head(buyseRGcy5$genes, n=10)
```

---

glasRGcy3

_Gene expression, annotations and clinical information for the Glas cohort: set of dye-swap hybridizations in which the information was associated with RNA samples labeled with Cy3_

Description

This package contains the RGList-class instance (see limma) for the gene expression data set published by Glas and colleagues. This object contains the set of dye-swap hybridizations in which the information provided in the ArrayExpress SDRF table was associated with the RNA samples labeled with Cy3.

Usage

data(glasRG)
The glasRGcy3 RList-class contains 1900 microarray features and 307 samples. The following components were included:

- `glasRGcy3$targets`: a data.frame for the breast cancer patients clinical information;
- `glasRGcy3$genes`: a data.frame containing the microarray annotations;
- `glasRGcy3$R`: the raw median gene expression foreground intensities from the Red channel;
- `glasRGcy3$Rb`: the raw median gene expression background intensities from the Red channel;
- `glasRGcy3$G`: the raw median gene expression foreground intensities from the Green channel;
- `glasRGcy3$Gb`: the raw median gene expression background intensities from the Green channel;
- `glasRGcy3$logRatio`: the Log ratio between Red and Green channel, as available from the raw data files;
- `glasRGcy3$logRatioError`: the Log ratio Error associated with the Log Ratio between Red and Green channel, as available from the raw data files;
- `glasRGcy3$ID`: the microarray features identifiers, as available from the raw data files;

Details

This dataset corresponds to the breast cancer patients' cohort published by Glas and colleagues in BMC Genomics (2006).

Source


References


See Also

See RGList-class

Examples

```r
### load limma package
library(limma)

### load the glasRGcy3 dataset: dye-swap set in which the information provided
### in the SDRF table was associated with the samples labeled with Cy3
data(glasRG)

data(glasRGcy3)

class(glasRGcy3)

dim(glasRGcy3)

### show the first 10 rows of the glasRGcy3 phenotype data
head(glasRGcy3$targets, n=10)
```
### show the first 10 features of the glasRGcy3 phenotype data

```r
head(glasRGcy3$genes, n=10)
```

#### glasRGcy5

*Gene expression, annotations and clinical information for the Glas cohort: set of dye-swap hybridizations in which the information was associated with RNA samples labeled with Cy5*

---

**Description**

This package contains the RGLList-class instance (see limma) for the gene expression data set published by Glas and colleagues. This object contains the set of dye-swap hybridizations in which the information provided in the ArrayExpress SDRF table was associated with the RNA samples labeled with Cy5.

**Usage**

```r
data(glasRG)
```

**Format**

The glasRGcy5 RGLList-class contains 1900 microarray features and 307 samples. The following components were included:

- `glasRGcy5$targets`: a data.frame for the breast cancer patients clinical information;
- `glasRGcy5$genes`: a data.frame containing the microarray annotations;
- `glasRGcy5$R`: the raw median gene expression foreground intensities from the Red channel;
- `glasRGcy5$Rb`: the raw median gene expression background intensities from the Red channel;
- `glasRGcy5$G`: the raw median gene expression foreground intensities from the Green channel;
- `glasRGcy5$Gb`: the raw median gene expression background intensities from the Green channel;
- `glasRGcy5$logRatio`: the Log ratio between Red and Green channel, as available from the raw data files;
- `glasRGcy5$logRatioError`: the Log ratio Error associated with the Log Ratio between Red and Green channel, as available from the raw data files;
- `glasRGcy5$ID`: the microarray features identifiers, as available from the raw data files;

**Details**

This dataset corresponds to the breast cancer patients’ cohort published by Glas and colleagues in BMC Genomics (2006).

**Source**


**References**

### load limma package
library(limma)

### load the glasRGcy3 dataset: dye-swap set in which the information provided
### in the SDRF table was associated with the samples labeled with Cy5
### show the class of the glasRGcy5 dataset
class(glasRGcy5)

### show the dimentions of the glasRGcy5 dataset
dim(glasRGcy5)

### show the first 10 rows of the glasRGcy5 phenotype data
head(glasRGcy5$targets, n=10)

### show the first 10 features of the glasRGcy5 phenotype data
head(glasRGcy5$genes, n=10)
Index

«Topic datasets
  buyseRGcy3, 3
  buyseRGcy5, 5
  glasRGcy3, 6
  glasRGcy5, 8
  mammaPrintData-package, 2

buyseRGcy3, 3
buyseRGcy5, 5

glasRGcy3, 6
glasRGcy5, 8

mammaPrintData
  (mammaPrintData-package), 2
mammaPrintData-package, 2