Package 'mammaPrintData'

April 8, 2015

Type Package

Title RGLists from the Glas and Buyse breast cancer studies

Version 1.1.1

Date 2013-05-13

Description

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

biocViews ExperimentData, Cancer, RNAExpressionData

Author Luigi Marchionni <marchion@jhu.edu>

Maintainer Luigi Marchionni <marchion@jhu.edu>

Depends R (>= 2.13.0)

Suggests Biobase, gdata, limma

License Artistic-2.0

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

LazyLoad yes

R topics documented:

1

---

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 collleagues 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)

Luigi Marchionni <marchion@gmail.com>

Source

<http://www.ncbi.nlm.nih.gov/pubmed/?term=17074082> <http://www.ncbi.nlm.nih.gov/pubmed/?term=16954471>

References

Annuska M Glas et al., "Converting a breast cancer microarray signature into a high-throughput diagnostic test", *BMC Genomics*, 2006, **7**:278-288

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

```
### 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(glasRGcy5)

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

### show the dimentions of the glasRGcy3 dataset
dim(glasRGcy5)

### 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 collleagues
in JNCI (2006).

Source

<http://www.ncbi.nlm.nih.gov/pubmed/?term=16954471>

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

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

### show the first 10 rows of the buyseRGcy3 phenotype data
head(buyseRGcy3$targets, n=10)

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

```
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 collleagues in JNCI (2006).

Source

<http://www.ncbi.nlm.nih.gov/pubmed/?term=16954471>

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

```
### 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 dimentions 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)
```

Format

The `glasRGcy3` `RGList-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 collleagues in BMC Genomics (2006).

Source

<http://www.ncbi.nlm.nih.gov/pubmed/?term=17074082>

References

Annuska M Glas et al., "Converting a breast cancer microarray signature into a high-throughput diagnostic test", *BMC Genomics*, 2006, **7**:278-288

See Also

See `RGList-class`

Examples

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

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

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

### show the dimentions of the glasRGcy3 dataset
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
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 `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 Cy5.

Usage

```
data(glasRG)
```

Format

The `glasRGcy5` RGList-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 collleagues in BMC Genomics (2006).

Source

<http://www.ncbi.nlm.nih.gov/pubmed/?term=17074082>

References

Annuska M Glas et al., "Converting a breast cancer microarray signature into a high-throughput diagnostic test", *BMC Genomics*, 2006, **7**:278-288

See Also

See `RGList-class`

Examples

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

### load the glasRGcy3 dataset: dye-swap set in which the information provided
###inthe SDRF table was associated with the samples labeled with Cy5
data(glasRG)
```

```
### 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