Package ‘mammaPrintData’

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Type Package

Title RGLists from the Glas and Buyse breast cancer studies

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Description Gene expression data for the two breast cancer cohorts published by Glas and Buyse in 2006. This cohorts were used to implement and validate the mammaPrint breast cancer test.

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

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License Artistic-2.0

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

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Contents

`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
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Version:	0.99.5.
Date:	2013-03-25
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Author(s)

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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)
```

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