# Package ‘mammaPrintData’

**April 9, 2024**

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<tr>
<th>Type</th>
<th>Package</th>
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<tbody>
<tr>
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<td>RGLists from the Glas and Buyse breast cancer studies</td>
</tr>
<tr>
<td>Version</td>
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<tr>
<td>Date</td>
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<tr>
<td>Description</td>
<td>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.</td>
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<tr>
<td>biocViews</td>
<td>ExperimentData, ExpressionData, CancerData, BreastCancerData, MicroarrayData, TwoChannelData</td>
</tr>
<tr>
<td>Author</td>
<td>Luigi Marchionni <a href="mailto:marchion@jhu.edu">marchion@jhu.edu</a></td>
</tr>
<tr>
<td>Maintainer</td>
<td>Luigi Marchionni <a href="mailto:marchion@jhu.edu">marchion@jhu.edu</a></td>
</tr>
<tr>
<td>Depends</td>
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<tr>
<td>Suggests</td>
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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

```r
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

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
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)
```

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)
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;

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
```r
dim(buyseRGcy5)
```

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

### show the first 10 features of the buyseRGcy5 phenotype data
```r
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**

```r
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 colleagues in BMC Genomics (2006).

Source


References


See Also

See RGList-class

Examples

### 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)

### 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 RList-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


See Also

See RGList-class

Examples

### 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
data(glasRG)
### show the class of the glasRGcy5 dataset

```r
class(glasRGcy5)
```

### show the dimensions of the glasRGcy5 dataset

```r
dim(glasRGcy5)
```

### show the first 10 rows of the glasRGcy5 phenotype data

```r
head(glasRGcy5$targets, n=10)
```

### show the first 10 features of the glasRGcy5 phenotype data

```r
head(glasRGcy5$genes, n=10)
```
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