Package 'mammaPrintData'

March 6, 2025

Type Package Title RGLists from the Glas and Buyse breast cancer studies **Version** 1.43.0 Date 2013-05-13 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 Author Luigi Marchionni <marchion@jhu.edu> Maintainer Luigi Marchionni <marchion@jhu.edu> **Depends** R (>= 2.13.0) Suggests Biobase, readxl, limma License Artistic-2.0 URL http://luigimarchionni.org/breastTSP.html LazyLoad yes git_url https://git.bioconductor.org/packages/mammaPrintData git_branch devel git_last_commit 5b1eb96 git_last_commit_date 2024-10-29 **Repository** Bioconductor 3.21 Date/Publication 2025-03-06

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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

```
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

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

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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 colleagues in JNCI (2006).

Source

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

buyseRGcy5

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 colleagues 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)
```

glasRGcy3Gene 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 colleagues 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.

glasRGcy5

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 colleagues 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)
```

glasRGcy5

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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