Package 'ccTutorial'

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Type Package

Title Data package for ChIP-chip tutorial

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Depends R (>= 2.10), Ringo(>= 1.9.8), affy(>= 1.23.4), topGO(>= 1.13.1)

Imports Biobase

Suggests biomaRt, Biobase(>= 2.5.5), xtable

Description This is a data package that accompanies a ChIP-chip tutorial, which has been published in PLoS Computational Biology. The data and source code in this package allow the reader to completely reproduce the steps in the tutorial.

References Joern Toedling and Wolfgang Huber (2008) Analyzing ChIP-chip Data Using Bioconductor. PLoS Computational Biology, 4(11):e1000227.

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biocViews ExperimentData, Mus_musculus_Data, MicroarrayData, ChipOnChipData

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R topics documented:

1

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ccTutorial-package   *What the package does (short line)*

Description

Data package for a Bioconductor ChIP-chip tutorial

Details

Package:	ccTutorial
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Version:	1.0
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Author(s)

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arrayGenesToProbeSets   *Mapping of Ensembl mm9 genes to Affymetrix Mouse 430v2 probe sets*

Description

This is a mapping of Ensembl mm9 genes to Affymetrix Mouse 430v2 probe sets. Onyl Ensembl mm9 genes that mapped at least one probe set on the array are included in the list. This mapping was created using biomaRt on 27 May 2008. Users can create this list themselves and the supplement contains the source code for doing this. For convenience sake, this object is given as a data object.

Usage

```
data(arrayGenesToProbeSets)
```

Format

a list with 14643 entries.

Details

created using biomaRt package in May 2008

Examples

```
data(arrayGenesToProbeSets)
head(arrayGenesToProbeSets)
table(listLen(arrayGenesToProbeSets))
```

barreraExpressionX   *Barrera expression data*

Description

Preprocessed expression data for five M. musculus tissues. Samples were hybridized to Affymetrix's mouse430v2 array platform, preprocessed using the MAS5 method, as implemented in Bioconductor's package affy.

Usage

```
data(barreraExpressionX)
```

Format

Preprocessed expression data as an ExpressionSet with 45101 features, 5 samples.

Details

see the supplement for the code chunk that was used to read in the CEL files that are in the expression directory of the package and to preprocess them.

See Also

[ExpressionSet](), [mas5]()

Examples

```
data(barreraExpressionX)
show(barreraExpressionX)
## the raw data is here:
dir(system.file("expression", package="ccTutorial"))
```

chersX   *List of found ChIP-enriched regions*

Description

This is the list of found ChIP-enriched regions. The package contains all the data to recreate the list and this list is merely given for convenience sake.

Usage

```
data(chersX)
```

Format

A `cherList`, a list of cher objects.

See Also

cher-class

Examples

```
data(chersX)
head(chersX)
```

---

mm9.g2p   *Mapping of Ensembl mm9 genes and reporter match positions*

Description

a list holding for each mm9 gene annotated in the Ensembl database, which reporter - if any - have been mapped into its upstream or transcribed region. Users can create this list themselves and the manuscript contains the source code for doing this. For convenience sake, this list is also given as a data object.

Usage

```
data(mm9.g2p)
```

Format

a list with 27434 entries.

See Also

features2Probes

Examples

```
data(mm9.g2p)
head(mm9.g2p)
## how many reporters are mapped per gene:
if (interactive())
 hist(listLen(mm9.g2p))
```

---

mm9.gene2GO   *GO annotation of Ensembl mm9 genes*

Description

a list holding the GO terms annotated for each mm9 gene annotated in Ensembl, as retrieved using biomaRt. Users can create this list themselves and the supplement contains the source code for doing this. For convenience sake, this is also given as a data object.

Usage

```
data(mm9.gene2GO)
```

Format

a list with 10526 entries.

Details

created using biomaRt package in March 2008

Examples

```
data(mm9.gene2GO)
head(mm9.gene2GO)
## how many genes are annotated per GO term:
mean(listLen(mm9.gene2GO))
table(listLen(mm9.gene2GO))
```

---

mm9genes   *data frame of mm9 genes in Ensembl*

Description

~~ A concise (1-5 lines) description of the dataset. ~~

Usage

```
data(mm9genes)
```

Format

A data frame with 27434 observations on the following 8 variables.

name a character vector

chr a character vector

strand a numeric vector

start a numeric vector

end a numeric vector

symbol a character vector

description a character vector

feature a character vector

Details

created using biomaRt package in March 2008

Source

~~ reference to a publication or URL from which the data were obtained ~~

References

~~ possibly secondary sources and usages ~~

Examples

```
data(mm9genes)
## maybe str(mm9genes) ; plot(mm9genes) ...
```

---

probeAnno   *probeAnno object holding mapping of reporters to genomic positions*

Description

This object of class probeAnno holds the mapping of the reporters on the tiling microarrays to positions in the mouse genome (assembly: mm9).

Usage

```
data(probeAnno)
```

Format

The format is: Formal class 'probeAnno' [package "Ringo"]

Details

The package's supplementary vignette shows how this object is constructed from the output of the alignment tool Exonerate. For sake of speed and for computers with small amounts of RAM, we also provide it as a data object here.

See Also

probeAnno-class

Examples

```
## Not run:
data("probeAnno")
show(probeAnno)
chromosomeNames(probeAnno)

## End(Not run)
```

X	*ExpressionSet containing ChIP-chip data*

Description

Preprocessed ChIP-chexpression data from *M. musculus* brain and heart cells. H3K4me3 ChIP and input samples were hybridized to a set of four custom NimbleGen microarrays with non-overlapping sets of 390k reporters each. The results were preprocessed per array type and the result fold changes were combinded via `rbind` afterwards, resulting in this ExpressionSet with 1.5m reporters.

Usage

```
data(X)
```

Format

Preprocessed ChIP-chip data as an `ExpressionSet` with 1495582 features, 2 samples.

Details

This ExpressionSet is created in the vignette, but for purposes of speed and for computers with small RAM, we provide it as a data object here as well.

See Also

[ExpressionSet](#), [preprocess](#)

Examples

```
data("X")
show(X)
pData(X)
```

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