Package ‘ccTutorial’

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Type Package
Title Data package for ChIP-chip tutorial
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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.
License Artistic-2.0
biocViews ExperimentData, Mus_musculus_Data, MicroarrayData, ChipOnChipData
NeedsCompilation no

R topics documented:

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**Description**

Data package for a Bioconductor ChIP-chip tutorial

**Details**

- **Package:** ccTutorial
- **Type:** Package
- **Version:** 1.0
- **Date:** 2008-04-29
- **License:** Artistic License 2.0

**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. Only 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.
mm9.gene2GO

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)
mm9genes

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**

```r
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**

```r
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**

```r
## Not run:
data("probeAnno")
show(probeAnno)
cromosomeNames(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 combined 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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