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.
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biocViews ExperimentData, Mus_musculus_Data, MicroarrayData, ChipOnChipData
NeedsCompilation no

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### ccTutorial-package

#### What the package does (short line)

Data package for a Bioconductor ChIP-chip tutorial

#### Details

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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

```r
data(arrayGenesToProbeSets)
```

#### Format

a list with 14643 entries.

#### Details

created using biomaRt package in May 2008

#### Examples

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

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
ccher-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**

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

**Description**

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

**Usage**

```r
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 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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