ccTutorial
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X ExpressionSet containing ChIP-chip data

Description
Preprocessed ChIP-chip expression 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-class, preprocess
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-class, mas5

Examples

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

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

**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))
```

**mm9genes**

*data frame of mm9 genes in Ensembl*

**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

```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);
  chromosomeNames(probeAnno)
## End(Not run)
```
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