Package ‘OMICsPCAdata’

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Type Package

Title Supporting data for package OMICsPCA

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Depends R (>= 3.5.0), MultiAssayExperiment

Suggests knitr, kableExtra, rmarkdown

biocViews RepositoryData, TechnologyData, ChIPSeqData, SequencingData, ExpressionData, ENCODE

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Description Supporting data for package OMICsPCA

License GPL-3

Encoding UTF-8

VignetteBuilder knitr

LazyData TRUE

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Contents

`clustered_data` *cluster object*

Description

a matrix containing cluster information

Usage

```
data("clustered_data")
```

Format

The format is: num [1:300, 1:5] 3.37 -5.26 2.07 2.32 1.94 ... - attr(*, "dimnames")=List of 2 ..$: chr [1:300] "ENST00000456433.1;ENST00000443722.1;ENST00000444457.1;ENST00000498530.1;ENST00000420236.2;E "ENST00000423207.2" "ENST00000429514.2;ENST00000263893.6;ENST00000492639.1;ENST00000495272.1;ENST00 "ENST00000487884.1" ... ..$: chr [1:5] "Dim.1" "Dim.2" "Dim.3" "Dim.4" ...

Examples

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

`groupinfo_ext` *An out put of create_group*

Description

An output of create_group()

Usage

```
data("groupinfo_ext")
```

Format

A data frame with 28770 observations on the following variable.

`group` a factor with levels `IntE` `NE` `RE` `WE`

Examples

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

`multi_assay` *Example data sets*

Description

Histone modification ChIP-seq and CAGE data

Usage

```
data("multi_assay")
```

Format

The datasets included in multi_assay are: 1) Histone modification ChIP-seq peaks of H2az, H3k9ac and H3k4me1. Each of these three datasets are in dataframe format, where the rows correspond to the TSSs and the columns correspond to various cell lines/tissues etc. Each value represents ChIP-seq peak intensity.

2) TSS expression data, measured by CAGE is also in data frame format and the row and column specification is same as the ChIP-seq data. Each value represents an normalized expression value (tpm).

Source

The Histone modification are collected from : https://www.encodeproject.org/matrix/?type=Experiment&assay_title=ChIP-seq&target.investigated_as=broad+histone+mark The DNaseI hypersensitivity (DHS) datasests are collected from : http://ftp.ebi.ac.uk/pub/databases/ensembl/encode/integration_data_jan2011/byDataType/openchrom/jan20

The Histone fand DHS files are downloaded as bigbed(.bb) format and converted to bed(.bed) format

The CAGE datasets are collected from : https://www.encodeproject.org/search/?type=Experiment&assay_slims=Transcriptio

Examples

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

`transcript_details` *details of GENCODE(v 17) TSSs*

Description

details of GENCODE(v 17) TSSs

Usage

```
data("transcript_details")
```

Format

A data frame with 194871 observations on the following 8 variables.

Examples

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

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