

Package ‘OMICsPCAdata’

November 30, 2023

Type Package
Title Supporting data for package OMICsPCA
Date 21/08/2018
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Version 1.21.0
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
git_url <https://git.bioconductor.org/packages/OMICsPCAdata>
git_branch devel
git_last_commit 5f51186
git_last_commit_date 2023-10-24
Repository Bioconductor 3.19
Date/Publication 2023-11-30

Table of contents:

clustered_data	2
groupinfo_ext	2
multi_assay	3
transcript_details	3
Index	5

clustered_data	<i>cluster object</i>
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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;ENST00000423207.2" "ENST00000429514.2;ENST00000263893.6;ENST00000492639.1;ENST00000495272.1;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	<i>An out put of create_group</i>
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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) datasets are collected from : http://ftp.ebi.ac.uk/pub/databases/ensembl/encode/integration_data_jan2011/byDataType/openchrom/jan2011

The Histone and 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_slms=Transcription

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) ...
```

Index

* datasets

clustered_data, [2](#)

groupinfo_ext, [2](#)

multi_assay, [3](#)

transcript_details, [3](#)

clustered_data, [2](#)

groupinfo_ext, [2](#)

multi_assay, [3](#)

transcript_details, [3](#)