Package: rWSBIM1322 (via r-universe)

August 31, 2024

Title Companion Package for WSBIM1322 Course

Version 0.3.2

Description Companion package for the WSBIM1322 course, distributing data and general documentation, and making course administration easier.

Depends R (>= 3.5.0),

Imports SummarizedExperiment, S4Vectors

Suggests rWSBIM1207, mzR, tidyverse, magrittr, Hiiragi2013, curatedTCGAData, ALL, Biostrings, Rtsne, factoextra, plotly, Gviz, caret, e1071, class, cluster, airway, pRolocdata

Remotes UCLouvain-CBIO/rWSBIM1207

License GPL-2

Encoding UTF-8

LazyData true

RoxygenNote 7.2.1

Repository https://uclouvain-cbio.r-universe.dev

RemoteUrl https://github.com/UCLouvain-CBIO/rWSBIM1322

RemoteRef HEAD

RemoteSha 782af41b081c3b900bf3575fe2bc6e8f3619b323

Contents

`cptac_se` *CPTAC data*

Description

The data stems from the 6th study of the Clinical Proteomic Technology Assessment for Cancer (CPTAC). The authors spiked the Sigma Universal Protein Standard mixture 1 (UPS1) containing 48 different human proteins in a protein background of 60 ng/microL Saccharomyces cerevisiae strain BY4741. Two different spike-in concentrations were used: 6A (0.25 fmol UPS1 proteins/microL) and 6B (0.74 fmol UPS1 proteins/microL). In this subset, we limited ourselves to the data of LTQ-Orbitrap W at site 56. The data were searched with MaxQuant version 1.5.2.8, and detailed search settings were described in Goeminne et al. (2016). Three replicates peptide quantitation data are available for each concentration.

Usage

```
cptac_se
```

Format

An object of class `SummarizedExperiment` with 4051 rows and 6 columns.

Details

The data are available as `SummarizedExperiment` objects.

See the proteomics tutorial from the Bioinformatics Summer School 2019 (https://lgatto.github.io/bioc-ms-prot/bss-lab.html) for scripts on how these data were processed.

Examples

```
library("SummarizedExperiment")
data(cptac_se)
cptac_se
data(cptac_se_prot)
cptac_se_prot
```

`g3` *Example for distances*

Description

This is a small toy example providing expression values for 5 genes and three samples from Olga Vitek. It is used to compare euclidean and correlation distances and the effect/importance of scaling.

Usage

```
g3
```

Format

An object of class `matrix` (inherits from `array`) with 3 rows and 5 columns.

Examples

```
data(g3)
g3
matplot(t(g3), type = "b", xlab = "Samples", ylab = "Expression")
```

`giris` *Expression data*

Description

This data is a copy of the `iris` data, reframed for biomedical course. It illustrates the expression of 4 genes, BRCA1, BRCA2, TP53 and A1CF, in 150 patients, that have been categorised in 3 catégories, A, B and C.

Usage

```
giris
```

Format

An object of class `data.frame` with 150 rows and 5 columns.

Examples

```
head(giris)
pairs(giris, col = giris$GRADE)

pca2 <- prcomp(giris2[, -5], scale = TRUE)
factoextra::fviz_pca_ind(pca2, col.ind = giris2$GRADE)
```

`hiiragi2013d` *Microarray expression data from Ohnishi et al. 2014.*

Description

The is a subset of the full Hiiragi 2013 dataset from the `Hiiragi2013` package. The data describes cell-to-cell expression variability followed by signal reinforcement progressively segregates early mouse lineages.

Usage

```
data("hiiragi2013df1")
data("hiiragi2013df2")
```

Source

The data originally come from the `Hiiragi2013` Bioconductor package. See `inst/script/hiiragi2013.R` to see how they have been converted.

References

Cell-to-cell expression variability followed by signal reinforcement progressively segregates early mouse lineages by Y. Ohnishi, W. Huber, A. Tsumura, M. Kang, P. Xenopoulos, K. Kurimoto, A. K. Oles, M. J. Arauzo-Bravo, M. Saitou, A.-K. Hadjantonakis and T. Hiiragi; Nature Cell Biology (2014) 16(1): 27-37. doi: 10.1038/ncb2881.

Examples

```
data(hiiragi2013df1)
data(hiiragi2013df2)
```

`kem2_se` *SummarizedExperiment data*

Description

This is a small RNA-Seq data set, build from the data returned by the `rWSBIM1207::kem2.tsv()` function.

Usage

```
kem2_se
```

Format

An object of class `SummarizedExperiment` with 4774 rows and 16 columns.

Examples

```
library("SummarizedExperiment")
data(kem2_se)
assay(kem2_se)
colData(kem2_se)
rowData(kem2_se)
```

`make_data` *Generate data*

Description

Generate data

Usage

```
make_data(noma)
```

Arguments

`noma`	‘character(1)‘ that can be coerced into a numeric

Value

A SummarizedExperimet

Examples

```
make_data("123")
```

`metab1` *Metabolomics data (from MSMB)*

Description

This data comes from the Modern *Statistics for Modern Biology* book and was originally called `mat1` from the `mat1xcms.RData` file. It contains quantitation data for 399 metabolites and 6 knockout and 6 wild-type samples.

Usage

```
metab1
```

Format

An object of class `matrix` (inherits from `array`) with 399 rows and 12 columns.

Examples

```
data(metab1)

dim(metab1)
metab1[1:10, 1:3]
```

---

recapSE1 *Recap SummarizedExperiment data*

Description

Several `SummarizedExperiment` datasets for the recap exercices in the conclusion chapter of the course.

Usage

```
recapSE1
```

Format

An object of class `SummarizedExperiment` with 1550 rows and 20 columns.

Examples

```
data(recapSE1)
recapSE1

data(recapSE2)
recapSE2
```

---

rWSBIM1322version *Package version*

Description

Package version

Usage

```
rWSBIM1322version()
```

Examples

```
## check the package version that is currently installed
rWSBIM1322version()
```

`tdata1` *Example data for t-tests illustration*

Description

See `scripts/randata.R` for how these data were generated.

Usage

```
tdata1
```

Format

An object of class `matrix` (inherits from `array`) with 100 rows and 6 columns.

Examples

```
data(tdata1)
head(tdata1)

data(tdata2)
tdata2

data(tdata3)
tdata3

data(tdata4)
tdata4
```

`up_selected` *Protein Uniprot identifiers*

Description

A character vector with Uniprot identifiers.

Usage

```
data("up_selected")
```

Examples

```
data(up_selected)
head(up_selected)
```

`xy` *Example data for PCA illustration*

Description

See `man/xy.R` for how these data were generated. `xy` is scaled, `xy0` is the orginal data.

Usage

```
xy
```

Format

An object of class `data.frame` with 20 rows and 2 columns.

Examples

```
data(xy)

xy0

xy
pca <- prcomp(xy)
summary(pca)
plot(pca)
biplot(pca)
```

Index