Package: rWSBIM2122 (via r-universe)

September 16, 2024

Title Companion Package for WSBIM2122 Course

Version 0.4.1

Description Companion package for the WSBIM2122 course, distributing data and general documentation, and making course administration easier.

Depends R (>= 3.5.0)

Suggests SummarizedExperiment, QFeatures, Spectra, clusterProfiler, biomaRt, org.Hs.eg.db, msigdbr, PSMatch, msdata, limma, DESeq2, tidyverse

Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.1

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

RemoteUrl https://github.com/UCLouvain-CBIO/rWSBIM2122

RemoteRef HEAD

RemoteSha 0bf852ac8f166a31081512e2c8ea5d319fd6509a

Contents

`gexp` *Single Gene Expression Data*

Description

A simple gene expression data in two groups. (Based on the `sleep` data).

Usage

```
gexp
```

Format

An object of class `data.frame` with 20 rows and 3 columns.

Examples

```
data(gexp)
gexp
```

`lmdata` *Gene expression data*

Description

Factorial design (2 factors with 2 levels each) with gene expression for 5 genes and 12 samples.

Usage

```
lmdata
```

Format

An object of class `matrix` (inherits from `array`) with 5 rows and 12 columns.

Examples

```
data(lmdata, verbose = TRUE)
lmdata
lmannot
```

`prepare_shell` *Prepare Shell data*

Description

A function used for its side effect. It creates the directory and files for the shell lesson.

Usage

```
prepare_shell(shell_dir = "wsbim2122_data", rm_dir = FALSE)
```

Arguments

`shell_dir`	`character(1)` with the name of the shell data directory. Default is `"wsbim2122_data"`.
`rm_dir`	`logical(1)` that defines whether `shell_dir` is going to be recursively removed. Default is `FALSE`.

Value

Invisibly returns `TRUE`.

Author(s)

Laurent Gatto

`rWSBIM2122version` *Package version*

Description

Package version

Usage

```
rWSBIM2122version()
```

Examples

```
## check the package version that is currently installed
rWSBIM2122version()
```

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