Package 'DEFormats'

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Type Package

Title Differential gene expression data formats converter

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URL https://github.com/aoles/DEFormats

BugReports https://github.com/aoles/DEFormats/issues

Description Convert between different data formats used by differential gene expression analysis tools.

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Imports checkmate, data.table, DESeq2, edgeR (>= 3.13.4), GenomicRanges, methods, S4Vectors, stats, SummarizedExperiment

Suggests BiocStyle (>= 1.8.0), knitr, rmarkdown, testthat

VignetteBuilder knitr

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`as.DESeqDataSet` *Convert to DESeqDataSet*

Description

Coerces an object to DESeqDataSet.

Usage

```
as.DESeqDataSet(x, ...)

## S3 method for class 'DGEList'
as.DESeqDataSet(x, ...)
```

Arguments

x	an R object
...	additional arguments to be passed to methods

Value

A `DESeqDataSet` object

Methods (by class)

- `as.DESeqDataSet(DGEList)`: Coerce `DGEList-class` objects to `DESeqDataSet`.

Author(s)

Andrzej Oleś <<andrzej.oles@gmail.com>>, 2016-2023

See Also

`as.DGEList`

Examples

```
require("edgeR")

counts = simulateRnaSeqData()
group = rep(c("case", "control"), each = 3)

dge = DGEList(counts = counts, group = group)
dge

as.DESeqDataSet(dge)
```

`as.DGEList` *Convert to DGEList*

Description

Coerces an object to DGEList.

Usage

```
as.DGEList(x, ...)

## S3 method for class 'DESeqDataSet'
as.DGEList(x, ...)
```

Arguments

x	an R object
...	additional arguments to be passed to methods

Value

A `DGEList` object.

Methods (by class)

- `as.DGEList(DESeqDataSet)`: Coerce `DESeqDataSet` objects to `DGEList-class`.

Author(s)

Andrzej Oleś <<andrzej.oles@gmail.com>>, 2016-2023

See Also

`as.DESeqDataSet`

Examples

```
require("DESeq2")

se = simulateRnaSeqData(output = "RangedSummarizedExperiment")
se

dds = DESeqDataSet(se, design = ~ condition)
dds

as.DGEList(dds)
```

DEFormats *Convert Between Differential Gene Expression Data Formats*

Description

DEFormats provides data converters between various formats used by different gene expression analysis packages.

Details

Currently the package supports data conversion between **DESeq2** and **edgeR**, i.e., between DESeqDataSet and DGEList objects, respectively.

Objects can be coerced using the following methods

- as.DESeqDataSet
- as.DGEList

Author(s)

Andrzej Oleś <<andrzej.oles@gmail.com>>, 2016-2023

DGEList *DGEList Constructor Generic*

Description

Creates a DGEList object.

Usage

```
DGEList(counts, ...)

## S4 method for signature 'RangedSummarizedExperiment'
DGEList(
  counts = new("RangedSummarizedExperiment"),
  lib.size = colData(counts)$lib.size,
  norm.factors = colData(counts)$norm.factors,
  samples = colData(counts),
  group = NULL,
  genes = as.data.frame(rowRanges(counts)),
  remove.zeros = FALSE
)
```

Arguments

counts	read counts, either a numeric matrix or a RangedSummarizedExperiment object.
...	other arguments are not currently used.
lib.size	numeric vector of library sizes (sequencing depths) for the samples. Defaults to colSums(counts).
norm.factors	numeric vector of normalization factors that modify the library sizes. Defaults to a vector of ones.
samples	data.frame containing sample information, with a row for each sample. This data.frame will be appended to the samples component of the DGEList object.
group	vector or factor giving the experimental group or treatment condition for each sample. Defaults to a single group.
genes	data.frame containing gene annotation.
remove.zeros	logical, whether to remove rows that have 0 total count.

Value

A DGEList object.

Author(s)

Andrzej Oleś <<andrzej.oles@gmail.com>>, 2016-2023

Examples

```
se = simulateRnaSeqData(output = "RangedSummarizedExperiment")

## Initialize a DGEList from a RangedSummarizedExperiment object
DGEList(se)
```

`simulateNormFactors` *Simulate Normalization Factors*

Description

Simulate gene-specific normalization factors for each sample of an RNA-seq experiment.

Usage

```
simulateNormFactors(n = 1000L, m = 6L, seed = 0L, ...)
```

Arguments

`n`	number of genes
`m`	number of samples
`seed`	a single integer value specifying the random number generator seed
`...`	arguments passed to `matrix`

Value

A matrix with `n` rows and `m` columns containing the normalization factors.

Author(s)

Andrzej Oleś <<andrzej.oles@gmail.com>>, 2016-2023

See Also

simulateRnaSeqData

Examples

```
require("DESeq2")

## normalization factors
se = simulateRnaSeqData(output = "RangedSummarizedExperiment")

dds = DESeqDataSet(se, design = ~ condition)

normalizationFactors(dds) = simulateNormFactors()
```

`simulateRnaSeqData` *Example counts table of RNA-seq data*

Description

Simulated expression data of an RNA-seq experiment.

Usage

```
simulateRnaSeqData(
  output = c("matrix", "RangedSummarizedExperiment"),
  n = 1000,
  m = 6,
  seed = 0L,
  ...
)
```

Arguments

`output`	output type
`n`	number of genes
`m`	number of samples
`seed`	a single integer value specifying the random number generator seed
`...`	arguments passed to `makeExampleDESeqDataSet`

Details

The count table is generated using the `makeExampleDESeqDataSet` method from the **DESeq2** package.

Value

Depending on the `output` setting a matrix or an `RangedSummarizedExperiment` object.

Author(s)

Andrzej Oleś <<andrzej.oles@gmail.com>>, 2016-2023

See Also

simulateNormFactors

Examples

```
## count data matrix
mx = simulateRnaSeqData()
head(mx)

## return an RangedSummarizedExperiment object
se = simulateRnaSeqData(output = "RangedSummarizedExperiment")
se
```

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