

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

biocViews ImmunoOncology, DifferentialExpression, GeneExpression,
RNASeq, Sequencing, Transcription

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as.DESeqDataSet	<i>Convert to DESeqDataSet</i>
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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

<code>x</code>	an R object
<code>...</code>	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 <code>colSums(counts)</code> .
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 <code>samples</code> component of the <code>DGEList</code> 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	<i>Simulate Normalization Factors</i>
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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	<i>Example counts table of RNA-seq data</i>
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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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