

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 *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)

- DGEList: Coerce [DGEList-class](#) objects to [DESeqDataSet](#).

Author(s)

Andrzej Oleś <<andrzej.oles@embl.de>>, 2016-2017

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	<i>Convert to DGEList</i>
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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)

- DESeqDataSet: Coerce [DESeqDataSet](#) objects to [DGEList-class](#).

Author(s)

Andrzej Oleś <<andrzej.oles@embl.de>>, 2016-2017

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@embl.de>>, 2016-2017

DGEList

*DGEList Constructor Generic***Description**

Creates a **DGEList** object.

Usage

```
DGEList(counts = matrix(0, 0, 0), lib.size = colSums(counts),
        norm.factors = rep(1, ncol(counts)), samples = NULL, group = NULL,
        genes = NULL, remove.zeros = FALSE)
```

```
## 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

<code>counts</code>	read counts, either a numeric matrix or a RangedSummarizedExperiment object.
<code>lib.size</code>	numeric vector giving the total count (sequence depth) for each library.
<code>norm.factors</code>	numeric vector of normalization factors that modify the library sizes.
<code>samples</code>	data frame containing information for each sample.
<code>group</code>	vector or factor giving the experimental group/condition for each sample/library.
<code>genes</code>	data frame containing annotation information for each gene.
<code>remove.zeros</code>	logical, whether to remove rows that have 0 total count.

Value

A [DGEList](#) object.

Author(s)

Andrzej Oleś <<andrzej.oles@embl.de>>, 2016-2017

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@embl.de>>, 2016-2017

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@embl.de>>, 2016-2017

See Also

[simulateNormFactors](#)

Examples

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

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

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