

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 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)

- 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

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