

Package ‘DEFormats’

August 22, 2025

Type Package

Title Differential gene expression data formats converter

Version 1.37.0

Encoding UTF-8

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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

RoxygenNote 7.2.3

git_url <https://git.bioconductor.org/packages/DEFormats>

git_branch devel

git_last_commit 9c9d687

git_last_commit_date 2025-04-15

Repository Bioconductor 3.22

Date/Publication 2025-08-22

Contents

as.DESeqDataSet	2
as.DGEList	3
DEFormats	4
DGEList	4
simulateNormFactors	5
simulateRnaSeqData	6
Index	8

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	<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)

- 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
```

Index

`as.DESeqDataSet`, [2](#), [3](#), [4](#)

`as.DGEList`, [2](#), [3](#), [4](#)

`DEFormats`, [4](#)

`DESeqDataSet`, [2–4](#)

`DGEList`, [3](#), [4](#), [4](#), [5](#)

`DGEList`, `RangedSummarizedExperiment`-method
(`DGEList`), [4](#)

`makeExampleDESeqDataSet`, [6](#)

`matrix`, [5](#)

`RangedSummarizedExperiment`, [5](#), [6](#)

`simulateNormFactors`, [5](#)

`simulateRnaSeqData`, [6](#)