

# Package ‘DEFormats’

October 16, 2019

**Type** Package

**Title** Differential gene expression data formats converter

**Version** 1.12.0

**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.

**License** GPL-3

**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** 6.0.1

**git\_url** <https://git.bioconductor.org/packages/DEFormats>

**git\_branch** RELEASE\_3\_9

**git\_last\_commit** 02c6ec6

**git\_last\_commit\_date** 2019-05-02

**Date/Publication** 2019-10-15

## R topics documented:

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

<b>Index</b>	<b>7</b>
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as.DESeqDataSet      *Convert to DESeqDataSet*

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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)
```

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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 <b>RangedSummarizedExperiment</b> 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 <a href="#">matrix</a>

**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()
```

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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 <a href="#">makeExampleDESeqDataSet</a>

### 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
```

# Index

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

DEFormats, [4](#)  
DEFormats-package (DEFormats), [4](#)  
DESeqDataSet, [2-4](#)  
DGEList, [3](#), [4](#), [4](#), [5](#)  
DGEList,RangedSummarizedExperiment-method  
(DGEList), [4](#)

makeExampleDESeqDataSet, [6](#)  
matrix, [5](#)

RangedSummarizedExperiment, [4](#), [6](#)

simulateNormFactors, [5](#)  
simulateRnaSeqData, [6](#)