

# Package ‘DEFormats’

May 15, 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.

**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** 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** 2025-05-15

## Contents

as.DESeqDataSet . . . . .	2
as.DGEList . . . . .	3
DEFormats . . . . .	4
DGEList . . . . .	4
simulateNormFactors . . . . .	5
simulateRnaSeqData . . . . .	6
<b>Index</b>	<b>8</b>

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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)
```

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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)

- `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)
```

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DEFormats

*Convert Between Differential Gene Expression Data Formats*

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### 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

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DGEList

*DGEList Constructor Generic*

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### 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 <a href="#">RangedSummarizedExperiment</a> 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	<code>data.frame</code> containing sample information, with a row for each sample. This <code>data.frame</code> 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	<code>data.frame</code> 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)
```

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simulateNormFactors     *Simulate Normalization Factors*

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

**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()
```

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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@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](#)