

# Package ‘DEFormats’

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**Type** Package

**Title** Differential gene expression data formats converter

**Version** 1.22.0

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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

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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)
```

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as.DGEList

*Convert to DGEList*

---

**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*

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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@embl.de>>, 2016-2017

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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 <a href="#">RangedSummarizedExperiment</a> 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)

```

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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 <code>matrix</code>

**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*

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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 <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
```

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