

# Package ‘DEFormats’

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**Type** Package

**Title** Differential gene expression data formats converter

**Version** 1.2.0

**Encoding** UTF-8

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**URL** <https://github.com/aoles/DEFormats>

**BugReports** <https://github.com/aoles/DEFormats/issues>

**Description** Covert between different data formats used by differential gene expression analysis tools.

**License** GPL-3

**Imports** checkmate, DESeq2, edgeR (>= 3.13.4), GenomicRanges, methods, stats, SummarizedExperiment

**Suggests** BiocStyle (>= 1.8.0), knitr, rmarkdown, testthat

**VignetteBuilder** knitr

**biocViews** DifferentialExpression, GeneExpression, RNASeq, Sequencing, Transcription

**RoxygenNote** 5.0.1

**NeedsCompilation** no

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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

### 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

### 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

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 = colData(counts)$group, 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

**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 <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

**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 <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

### See Also

[simulateNormFactors](#)

### Examples

```
## count data matrix  
mx = simulateRnaSeqData()  
head(mx)  
  
## return an RangedSummarizedExperiment object  
se = simulateRnaSeqData(output = "RangedSummarizedExperiment")  
se
```

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