

# Package ‘DEFormats’

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**Type** Package

**Title** Differential gene expression data formats converter

**Version** 1.35.0

**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

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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

*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)**

- `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

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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 colSums(counts).
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 samples component of the DGEList 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)
```

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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
```



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