

# Package ‘DEFormats’

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**Type** Package

**Title** Differential gene expression data formats converter

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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

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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)
```

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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 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*

---

**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 | <i>Example counts table of RNA-seq data</i> |
|--------------------|---------------------------------------------|

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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@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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