# 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

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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)

- `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)
```

---

`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*

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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 RangedSummarizedExperiment 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)
```

`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 `matrix` |

## 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()
```

`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 `makeExampleDESeqDataSet` |

## 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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