Package 'iSEEde'

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Title iSEE extension for panels related to differential expression analysis

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Description This package contains diverse functionality to extend the usage of the iSEE package, including additional classes for the panels or modes facilitating the analysis of differential expression results.
This package does not perform differential expression. Instead, it provides methods to embed precomputed differential expression results in a SummarizedExperiment object, in a manner that is compatible with interactive visualisation in iSEE applications.

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URL https://github.com/iSEE/iSEEde

BugReports https://support.bioconductor.org/t/iSEEde

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`contrastResultsNames` *Extract contrast results embedded in a SummarizedExperiment object*

Description

`contrastResults` returns either all contrasts results stored in `object` or a single contrast result by name.

`contrastResultsNames` returns the names of contrast results embedded in `object`.

Usage

```
contrastResultsNames(object)

contrastResults(object, name)
```

Arguments

`object`	A SummarizedExperiment object.
`name`	(Optional) Name of a single contrast result name to extract. Use `contrastResultsNames(object)` to list available names.

Value

For `contrastResultsNames`: the names of embedded contrast results available.

For `contrastResults`: a `DataFrame` of differential expression statistics.

If `name` is missing, `contrastResults` returns a nested `DataFrame` in which each column contains the results of a single contrast. If `name` is given, `contrastResults` returns a `DataFrame` that contains the results of a single contrast.

Examples

```
library("iSEEde")
library("airway")
library("DESeq2")
library("iSEE")

##
# Example data ----
##

data("airway")
airway$dex <- relevel(airway$dex, "untrt")

dds <- DESeqDataSet(airway, ~ 0 + dex + cell)

dds <- DESeq(dds)
res_deseq2 <- results(dds, contrast = list("dextrt", "dexuntrt"))
airway <- embedContrastResults(res_deseq2, airway, name = "dex: trt vs untrt")

##
# List result names ---
##

contrastResultsNames(airway)

##
# Extract results ---
##

contrastResults(airway)
contrastResults(airway, "dex: trt vs untrt")
```

`de-generics` *Generics for Differential Expression Results*

Description

An overview of the generics for accessing common pieces of information in differential expression results.

Definitions

- `pValue(x)` returns a named numeric vector of raw p-values.
- `log2FoldChange(x)` returns a named numeric vector of log2-fold-change values.
- `averageLog2(x)` returns a named numeric vector of average log2-expression values.

Author(s)

Kevin Rue-Albrecht

Examples

```
showMethods(pValue)
showMethods(log2FoldChange)
showMethods(averageLog2)
```

DETable-class *The DETable class*

Description

The DETable class is a RowTable subclass that is dedicated to creating a volcano plot. It retrieves the table of results for the selected differential expression contrast and creates an interactive table where each row represents a feature.

Slot overview

The following slots control the test procedure:

- `ContrastName`, a character scalar indicating the name of the contrast to display.
- `RoundDigits`, a logical scalar indicating whether to round numeric values (see `SignifDigits`).
- `SignifDigits`, an integer scalar indicating the number of significant digits to use for rounding numbers (see `RoundDigits`).

In addition, this class inherits all slots from its parent RowTable and Table classes.

Examples

```
x <- DETable()
x
```

`iSEEde-pkg` *iSEE extension for panels related to differential expression analysis*

Description

`iSEEde` is a package that provides panels for **iSEE**, facilitating the interactive visualisation of differential expression results.

Author(s)

Kevin Rue-Albrecht <kevin.rue-albrecht@imm.ox.ac.uk>

See Also

Useful links:

- https://github.com/iSEE/iSEEde
- Report bugs at https://support.bioconductor.org/t/iSEEde

Examples

```
library("iSEEde")
```

`iSEEDESeq2Results-class`
The iSEEDESeq2Results class

Description

The `iSEEDESeq2Results` class is used to provide a common interface to differential expression results produced by the **DESeq2** package. It provides methods to access common differential expression statistics (e.g., log2 fold-change, p-value, log2 average abundance).

Details

This class inherits all its slots directly from its parent class DataFrame.

Constructor

`iSEEDESeq2Results(data, row.names = rownames(data))` creates an instance of a `iSEEDESeq2Results` class, with:

`data` A `data.frame` produced by `DESeq2::results()` or `DESeq2::lfcShrink()`.

`row.names` The character vector of rownames for the SummarizedExperiment object in which the object is to be embedded. Must be a superset of `rownames(data)`.

Supported methods

- `embedContrastResults(x, se, name, ...)` embeds `x` in `se` under the identifier `name`. See `embedContrastResults()` for more details.
- `pValue(x)` returns the vector of raw p-values.
- `log2FoldChange(x)` returns the vector of log2-fold-change values.
- `averageLog2(x)` returns the vector of average log2-expression values.

Author(s)

Kevin Rue-Albrecht

Examples

```
library(DESeq2)

##
# From DESeq2::DESeq() ----
##

cnts <- matrix(rnbinom(n = 1000, mu = 100, size = 1 / 0.5), ncol = 10)
rownames(cnts) <- paste("Gene", 1:100)
cond <- factor(rep(1:2, each = 5))

# object construction
dds <- DESeqDataSetFromMatrix(cnts, DataFrame(cond), ~cond)

# standard analysis
dds <- DESeq(dds)
res <- results(dds)
head(res)

##
# iSEEDESeq2Results ----
##

# Embed the DESeq2 results in the SummarizedExperiment object
dds <- embedContrastResults(res, dds, name = "DESeq2")

##
# Access ----
##

contrastResultsNames(dds)
contrastResults(dds)
contrastResults(dds, "DESeq2")

head(pValue(contrastResults(dds, "DESeq2")))
head(log2FoldChange(contrastResults(dds, "DESeq2")))
head(averageLog2(contrastResults(dds, "DESeq2")))
```

iSEEedgeRResults-class *The iSEEedgeRResults class*

Description

The `iSEEedgeRResults` class is used to provide a common interface to differential expression results produced by the **edgeR** package. It provides methods to access common differential expression statistics (e.g., log fold-change, p-value, log2 average abundance).

Details

This class inherits all its slots directly from its parent class DataFrame.

Constructor

`iSEEedgeRResults(data, row.names = rownames(data))` creates an instance of a `iSEEedgeRResults` class, with:

`data` A `data.frame` produced by `edgeR::topTags()`.

`row.names` The character vector of rownames for the SummarizedExperiment object in which the object is to be embedded. Must be a superset of `rownames(data)`.

Supported methods

- `embedContrastResults(x, se, name, ...)` embeds `x` in `se` under the identifier `name`. See `embedContrastResults()` for more details.
- `pValue(x)` returns the vector of raw p-values.
- `log2FoldChange(x)` returns the vector of log2-fold-change values.
- `averageLog2(x)` returns the vector of average log2-expression values.

Author(s)

Kevin Rue-Albrecht

Examples

```
library(edgeR)
library(SummarizedExperiment)

##
# From edgeR::glmLRT() ----
##

nlibs <- 3
ngenes <- 100
dispersion.true <- 0.1
```

```
# Make first gene respond to covariate x
x <- 0:2
design <- model.matrix(~x)
beta.true <- cbind(Beta1=2,Beta2=c(2,rep(0,ngenes-1)))
mu.true <- 2^(beta.true %*% t(design))

# Generate count data
y <- rnbinom(ngenes*nlibs,mu=mu.true,size=1/dispersion.true)
y <- matrix(y,ngenes,nlibs)
colnames(y) <- c("x0","x1","x2")
rownames(y) <- paste("gene",1:ngenes,sep=".")
d <- DGEList(y)

# Normalize
d <- calcNormFactors(d)

# Fit the NB GLMs
fit <- glmFit(d, design, dispersion=dispersion.true)

# Likelihood ratio tests for trend
results <- glmLRT(fit, coef=2)
tt <- topTags(results)

##
# iSEEedgeRResults ----
##

# Simulate the original SummarizedExperiment object
se <- SummarizedExperiment(assays = list(counts = d$counts))

# Embed the edgeR results in the SummarizedExperiment object
se <- embedContrastResults(tt, se, name = "edgeR")

##
# Access ----
##

contrastResultsNames(se)
contrastResults(se)
contrastResults(se, "edgeR")

head(pValue(contrastResults(se, "edgeR")))
head(log2FoldChange(contrastResults(se, "edgeR")))
head(averageLog2(contrastResults(se, "edgeR")))
```

---

iSEELimmaResults-class

The iSEELimmaResults class

Description

The `iSEELimmaResults` class is used to provide a common interface to differential expression results produced by the **limma** package. It provides methods to access common differential expression statistics (e.g., log fold-change, p-value, log2 average abundance).

Details

This class inherits all its slots directly from its parent class DataFrame.

Constructor

`iSEELimmaResults(data, row.names = rownames(data))` creates an instance of a `iSEELimmaResults` class, with:

`data` A `data.frame` produced by `limma::topTable()`.

`row.names` The character vector of rownames for the SummarizedExperiment object in which the object is to be embedded. Must be a superset of `rownames(data)`.

Supported methods

- `embedContrastResults(x, se, name, class = "limma", ...)` embeds `x` in `se` under the identifier `name`. See `embedContrastResults()` for more details.
- `pValue(x)` returns the vector of raw p-values.
- `log2FoldChange(x)` returns the vector of log2-fold-change values.
- `averageLog2(x)` returns the vector of average log2-expression values.

Author(s)

Kevin Rue-Albrecht

Examples

```
library(limma)
library(SummarizedExperiment)

##
# From limma::lmFit() ----
##

sd <- 0.3 * sqrt(4 / rchisq(100, df = 4))
y <- matrix(rnorm(100 * 6, sd = sd), 100, 6)
rownames(y) <- paste("Gene", 1:100)
y[1:2, 4:6] <- y[1:2, 4:6] + 2
design <- cbind(Grp1 = 1, Grp2vs1 = c(0, 0, 0, 1, 1, 1))

fit <- lmFit(y, design)
fit <- eBayes(fit)
tt <- topTable(fit, coef = 2)
head(tt)
```

```
##
# iSEELimmaResults ----
##

# Simulate the original SummarizedExperiment object
se <- SummarizedExperiment(assays = list(counts = y))

# Embed the Limma-Voom results in the SummarizedExperiment object
se <- embedContrastResults(tt, se, name = "Limma-Voom", class = "limma")

##
# Access ----
##

contrastResultsNames(se)
contrastResults(se)
contrastResults(se, "Limma-Voom")

head(pValue(contrastResults(se, "Limma-Voom")))
head(log2FoldChange(contrastResults(se, "Limma-Voom")))
head(averageLog2(contrastResults(se, "Limma-Voom")))
```

`LogFCLogFCPlot-class` *The LogFCLogFCPlot class*

Description

The LogFCLogFCPlot class is a RowDataPlot subclass that is dedicated to comparing the log-fold-change value of two contrasts. It retrieves the log-fold change of the two selected contrasts and creates a row-based plot where each point represents a feature.

Slot overview

The following slots control the test procedure:

- `ContrastNameX`, a character scalar indicating the name of the contrast to display on the x-axis.
- `ContrastNameY`, a character scalar indicating the name of the contrast to display on the y-axis.

In addition, this class inherits all slots from its parent RowDotPlot, DotPlot, and Panel classes.

Examples

```
x <- LogFCLogFCPlot()
x
```

MAPlot-class *The MAPlot class*

Description

The MAPlot is a RowDataPlot subclass that is dedicated to creating an MA plot. It retrieves the log-fold change (M) and mean average (A) values and creates a row-based plot where each point represents a feature.

Slot overview

The following slots control the test procedure:

- `ContrastName`, a character scalar indicating the name of the contrast to display.

In addition, this class inherits all slots from its parent RowDotPlot, DotPlot, and Panel classes.

Examples

```
x <- MAPlot()
x
```

utils-SummarizedExperiment *Generics for Embbedding Results into a SummarizedExperiment Object*

Description

An overview of the generics for embedding results into a SummarizedExperiment object, in a format compatible with **iSEEde**.

Usage

```
embedContrastResults(x, se, name, ...)

embedContrastResultsMethods

## S4 method for signature 'ANY'
embedContrastResults(x, se, name, ...)

## S4 method for signature 'data.frame'
embedContrastResults(x, se, name, class, ...)
```

Arguments

x	Object to be embedded.
se	A SummarizedExperiment object.
name	Identifier for the embedded object.
...	Arguments passed to and from other methods.
class	Class to use for embedding x. Only used when class(x) does not uniquely identify the package that generated the object.

Format

embedContrastResultsMethods: Named character vector mapping keywords to class names designed to store differential expression results.

Value

An updated SummarizedExperiment object that contains the embedded object.

Definitions

- embedContrastResults(x, se, name, ...) embeds the results x in the SummarizedExperiment se.

Author(s)

Kevin Rue-Albrecht

Examples

```
embedContrastResultsMethods

showMethods(embedContrastResults)
```

VolcanoPlot-class *The VolcanoPlot class*

Description

The VolcanoPlot is a RowDataPlot subclass that is dedicated to creating a volcano plot. It retrieves the log-fold change and p-value from and creates a row-based plot where each point represents a feature.

Slot overview

The following slots control the test procedure:

- ContrastName, a character scalar indicating the name of the contrast to display.

In addition, this class inherits all slots from its parent RowDotPlot, DotPlot, and Panel classes.

Examples

```
x <- VolcanoPlot()
x
```

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