Package ‘iSEEpathways’

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Title  iSEE extension for panels related to pathway 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 pathway analysis results. This package does not perform pathway analysis. Instead, it provides methods to embed precomputed pathway analysis results in a SummarizedExperiment object, in a manner that is compatible with interactive visualisation in iSEE applications.

License  Artistic-2.0
URL  https://github.com/iSEE/iSEEpathways

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

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**FgseaEnrichmentPlot-class**

**Description**

The `FgseaEnrichmentPlot` is a `Panel` subclass where each row represents a set of features (i.e., rows). Selections in this panel can be transmitted to other row-oriented panels.

**Value**

`FgseaEnrichmentPlot()` returns an object of class `FgseaEnrichmentPlot`. In addition, this class inherits all slots from its parent `Panel` class.

**Slot overview**

The following slots control the test procedure:

- **ResultName**, a character scalar indicating the name of the pathway analysis result to display.
- **PathwayId**, a character scalar indicating the identifier of the pathway to display.
- **BrushData**, a list containing a Shiny brush along the x-axis (see `?brushedPoints`). Defaults to an empty list, i.e., no brush or lasso.
Examples

```r
x <- FgseaEnrichmentPlot(ResultName="fgsea", PathwayId="GO:0000002")
x
```

---

**iSEEfgseaResults-class**

*The iSEEfgseaResults class*

**Description**

The `iSEEfgseaResults` class is used to provide a common interface to pathway analysis results produced by the `fgsea` package. It provides methods to access the set of features in each pathway.

**Value**

`iSEEfgseaResults()` returns an object of class `iSEEfgseaResults`.

**Slot overview**

This class inherits all its slots directly from its parent class `iSEEpathwaysResults`.

**Constructor**

```r
iSEEfgseaResults(data, pathwayType, pathwaysList = NULL, featuresStats = NULL)
```

- **data** A `data.frame` produced by `fgsea::fgsea()`.
- **pathwayType** A character scalar specifying the type of pathway (e.g., "GO"). See `embedPathwaysResults`.
- **pathwaysList** A named list of pathways and associated feature identifiers.
- **featuresStats** Feature-level statistics used in the pathway analysis.

**Supported methods**

In the following code snippets, `x` is an instance of a `iSEEfgseaResults` class. Refer to the documentation for each method for more details on the remaining arguments.

- `embedPathwaysResults(x, se, name, pathwayType, ...)` embeds `x` in `se` under the identifier name. See `embedPathwaysResults()` for more details.
- `pathwaysList(x)` returns the named list of pathway identifiers and associated

**Author(s)**

Kevin Rue-Albrecht
Examples

library("fgsea")

##
## # Simulate example data
##

simulated_data <- simulateExampleData(n_pathways = 5, n_features = 100, pathway_sizes = 15:100)

pathways_list <- simulated_data$pathwaysList
features_stats <- simulated_data$featuresStat
se <- simulated_data$summarizedexperiment

##
## # Run pathway analysis ----
##

set.seed(42)
fgseaRes <- fgsea(pathways = pathways_list, 
                  stats = features_stats, 
                  minSize = 15, 
                  maxSize = 500)
head(fgseaRes[order(pval), ])

##
## # iSEEfgseaResults ----
##

# Embed the FGSEA results in the SummarizedExperiment object
se <- embedPathwaysResults(fgseaRes, se, name = "fgsea", class = "fgsea", 
                            pathwayType = "simulated", pathwaysList = pathways_list, featuresStats = features_stats)
se

##
## # Access ----
##

pathwaysResultsNames(se)
pPathwaysResults(se)
pPathwaysResults(se, "fgsea")

pathwayType(pPathwaysResults(se, "fgsea"))
head(lengths(pPathwaysList(pPathwaysResults(se, "fgsea"))))
head(featuresStats(pPathwaysResults(se, "fgsea")))
Description

iSEEpathways is a package that provides panels for iSEE, facilitating the interactive visualisation of pathway analysis results.

Author(s)

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

See Also

Useful links:

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

Examples

library("iSEEde")

devtools::load_all()

class_iSEEpathwaysResults()

class("iSEEpathwaysResults")

devtools::load_all()

class("iSEEpathwaysResults")
Generics for Pathway Analysis Results

Description
An overview of the generics for accessing common pieces of information in pathway analysis results.

Value
- `pathwayType(x)` returns a character scalar indicating the type of pathways analysed.
- `pathwaysList(x)` returns the named list of pathways used in the analysis, or `NULL`.
- `featuresStats(x)` returns the named numeric vector of feature-level statistics used in the analysis, or `NULL`.

Author(s)
Kevin Rue-Albrecht

Examples
- `showMethods(pathwayType)`
- `showMethods(pathwaysList)`
- `showMethods(featuresStats)`

Extract contrast results embedded in a `SummarizedExperiment` object

Description
`pathwaysResults` returns either all pathway analysis results stored in `object` or a single pathway analysis result by name.

`pathwaysResultsNames` returns the names of pathway analysis results embedded in `object`.

Usage
- `pathwaysResultsNames(object)`
- `pathwaysResults(object, name)`

Arguments
- `object` A `SummarizedExperiment` object.
- `name` (Optional) Name of a single pathway analysis result name to extract. Use `pathwaysResultsNames(object)` to list available names.
pathwaysResultsNames

Value

For pathwaysResultsNames: the names of embedded contrast results available.
For pathwaysResults: a list of differential expression statistics.
If name is missing, pathwaysResults returns a list in which each item contains the results of a single pathway analysis. If name is given, pathwaysResults returns a DataFrame that contains the results of a single pathway analysis.

Examples

library("fgsea")

##
# Simulate example data
##
simulated_data <- simulateExampleData(n_pathways = 5, n_features = 100, pathway_sizes = 15:100)

pathways_list <- simulated_data$pathwaysList
features_stats <- simulated_data$featuresStat
se <- simulated_data$summarizedexperiment

##
# Run pathway analysis ----
##
set.seed(42)
fgseaRes <- fgsea(pathways = pathways_list,
     stats = features_stats,
     minSize = 15,
     maxSize = 500)
head(fgseaRes[order(pval), ])

##
# iSEEfgseaResults ----
##
se <- embedPathwaysResults(fgseaRes, se, name = "fgsea", class = "fgsea", pathwayType = "GO",
     pathwaysList = pathways_list, featuresStats = features_stats)

##
# List result names ---
##
pathwaysResultsNames(se)

##
# Extract results ---
##
pathwaysResults(se)
pathwaysResults(se, "fgsea")
PathwaysTable-class  The PathwaysTable class

Description

The PathwaysTable is a Panel where each row represents a set of features (i.e., rows). Selections in this panel can be transmitted to other row-oriented panels.

Value

PathwaysTable() returns an object of class PathwaysTable.

Slot overview

The following slots control the test procedure:

• ResultName, a character scalar indicating the name of the pathway analysis result to display.

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

Examples

x <- PathwaysTable(ResultName="fgsea")
x

simulateExampleData  Simulate Example Data

Description

Simulates various pieces of data for the purpose of demonstration in vignettes and help pages.

Usage

simulateExampleData(
  n_pathways = 5000,  
  n_features = 15000,  
  n_samples = 8,  
  pathway_sizes = 15:500
)

Arguments

  n_pathways    integer scalar, number of pathways to simulate.
  n_features    integer scalar, number of features to simulate.
  n_samples     integer scalar, number of samples to simulate.
  pathway_sizes integer vector, possible sizes of pathway to sample from.
Details

At least for the time being, this function generates dummy data purely for the purpose of demonstrating the format of expected inputs.

As such, the independent pieces of simulated data are just that – independent – in the meaning that simulated counts, statistics, and pathways are not related numerically, and do not make any biological sense.

The only coherent piece of information is the set of feature identifiers, carefully coordinated between the rownames of the count matrix, the names of the feature statistics, and the set of features in the list of pathways, so that panels in the app can transmit and interpret that shared piece of information.

Value

A list of three elements:

- **pathwaysList** A named list of dummy pathways. Names represent pathway identifiers; values represent character vectors of feature identifiers.
- **featuresStat** A named numeric vector of dummy feature-wise statistics. Names represent feature identifiers; values represent 'scores' (e.g., log2 fold-change)
- **summarizedexperiment** A SummarizedExperiment object that contains a count matrix with rownames and colnames.

Examples

```r
set.seed(1)
simulated_data <- simulateExampleData()
head(lengths(simulated_data$pathwaysList))
head(simulated_data$featuresStat)
```

---

**utils-SummarizedExperiment**

*Generics for Embedding Pathway Analysis Results into a SummarizedExperiment Object*

---

Description

An overview of the generics for embedding pathway analysis results into a SummarizedExperiment object, in a format compatible with iSEEpathways.

Usage

```r
embedPathwaysResults(x, se, name, pathwayType, ...)
```

```r
## S4 method for signature 'data.frame'
embedPathwaysResults(x, se, name, class, pathwayType, ...)
```
Arguments

- `x` Object to be embedded.
- `se` A SummarizedExperiment object.
- `name` Identifier for the embedded object.
- `pathwayType` Character scalar indicating the type of pathway. See Details.
- `...` Arguments passed to individual constructors of pathway analysis result classes.
- `class` Class to use for embedding `x`. Only used when `class(x)` does not uniquely identify the package that generated the object `x`.

Format

`embedPathwaysResultsMethods`: Named character vector mapping keywords to class names designed to store pathway analysis results.

Details

The argument `pathwayType` is used to identify the function mapping a certain type of pathway identifier to the corresponding feature identifiers. Pathway mapping functions must be registered as a named list using `registerAppOptions(se, Pathways.map.functions = list(...))`, where the name matching `pathwayType` identifies the function to use to map pathway identifiers to feature identifiers in a given pathway analysis result, e.g.

```r
library(org.Hs.eg.db)
map_GO <- function(pathway_id) {
  mapIds(org.Hs.eg.db, pathway_id, "ENSEMBL", keytype = "GOALL", multiVals = "CharacterList"))[[pathway_id]]
}
se <- registerAppOptions(se, Pathways.map.functions = list(GO = map_GO))
```

See vignette("integration", package = "iSEEpathways") for examples.

Value

`embedPathwaysResults` returns an updated SummarizedExperiment object that contains the embedded object.

Definitions

- `embedPathwaysResults(x, se, name, pathwayType, ...)` embeds the results `x` in the SummarizedExperiment `se` under the key `name`; `pathwayType` is a character scalar required to identify a function mapping a pathway identifier to associated feature identifiers; additional named arguments in `...` are passed to the constructor of the pathway results class.

Author(s)

Kevin Rue-Albrecht
Examples

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