Package ‘Rcolombos’

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Type Package

Title Interface to Colombos Compendia using the Exposed REST API

Version 2.0.2

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Description Provides programmatic access to Colombos, a web based interface for exploring and analyzing comprehensive organism-specific cross-platform expression compendia of bacterial organisms.

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Depends httr

Repository CRAN

URL `http://colombos.net/`,`http://legacyv2.colombos.net/`

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R topics documented:

`advanced_search` *This method mimics the advanced_search functionality of Colombos. It takes a series of parameters, representing the different settings available on Colombos advanced search and returns a list containing the locustags (gene_names), contrasts and M-values for the current selection.*

Description

This method mimics the advanced_search functionality of Colombos. It takes a series of parameters, representing the different settings available on Colombos advanced search and returns a list containing the locustags (gene_names), contrasts and M-values for the current selection.

Usage

```
advanced_search(organism = NULL, g_ids = NULL, geneNames = FALSE, c_ids,
  by = "genes", g_search_type, ann_type, c_search_type)
```

Arguments

`organism`	A character containing the organism id: use `listOrganisms` to display the available organisms.
`g_ids`	A vector of strings representing contrast_id, go terms, experiment id or condition id according the search type.
`geneNames`	boolean if == FALSE (default) return the locustag otherwise the gene_name for the selected genes.
`c_ids`	A vector of strings representing contrast_id, go terms, experiment id or condition id according the search type.
`by`	A string eithes genes, contrasts, both allowing the selection by genes entities, contrast entities or both.
`g_search_type`	A string either genes, go or annotation.
`ann_type`	A string containing the selected gene_annotation_type: use `listEntities` to display the available entities.
`c_search_type`	A string either contrast_names. experiment, go, condition use `listOrganisms` to display the available organisms.

Value

A data.frame containing locustag (gene_names), contrasts and M-values for the current organism and genes.

References

http://colombos.net

Examples

```
## Not run:
 library("Rcolombos")

 # modules by gene entities
 g.gn <- advanced_search(organism="bsubt",
                     g_ids=c("cgeB","yfnG"),
                     by="genes", g_search_type="genes")
 g.go <- advanced_search(organism="bsubt",
                     g_ids="response to antibiotic, transcription",
                     by="genes", g_search_type="go")
 g.anno <- advanced_search(organism="bsubt",
                     g_ids="biotin-carboxyl carrier protein assembly",
                     by="genes", g_search_type="annotation", ann_type="Pathway")

 # modules by contrast entities
 c.cn <- advanced_search(organism="bsubt",
                 c_ids=c("GSM27217.ch2-vs-GSM27217.ch1","GSM27218.ch1-vs-GSM27218.ch2"),
                     by="contrasts", c_search_type="contrast_names")
 c.go <- advanced_search(organism="bsubt",
                     c_ids="response to antibiotic, transcription",
                     by="contrasts", c_search_type="go")
 c.exp <- advanced_search(organism="bsubt",
                     c_ids="GSE22296", by="contrasts", c_search_type="experiment")
 c.cond <- advanced_search(organism="bsubt",
 c_ids=c("DAPTOMYCIN","H2O2","HPUra","IPTG","MMC","MNCL2","MOENOMYCIN","RAMOPLANIN"),
 by="contrasts", c_search_type="condition")

 # modules by both gene and contrast entities
 b.go.cn <- advanced_search(organism="bsubt",
                     g_ids="response to antibiotic, transcription", geneNames=F,
                 c_ids=c("GSM27217.ch2-vs-GSM27217.ch1","GSM27218.ch1-vs-GSM27218.ch2"),
                     g_search_type="go", c_search_type="contrast_names", by="both")
 b.gn.ge <- advanced_search(organism="bsubt", g_ids=c("BSU00020","BSU00100"),
                     geneNames=F, c_ids="GSE22296", g_search_type="genes",
                     c_search_type="experiment", by="both")
 b.go.ge <- advanced_search(organism="bsubt", g_ids="response to antibiotic, transcription",
                     geneNames=F, c_ids="GSE22296", g_search_type="go",
                     c_search_type="experiment", by="both")
 b.gn.cn <- advanced_search(organism="bsubt",
                    g_ids=c("dnaA","dnaN","yaaA","recF","yaaB","gyrB"), geneNames=FALSE,
                  c_ids=c("GSM27217.ch2-vs-GSM27217.ch1","GSM27218.ch1-vs-GSM27218.ch2",
                     "GSM27219.ch2-vs-GSM27219.ch1","GSM27278.ch2-vs-GSM27278.ch1",
                     "GSM27279.ch1-vs-GSM27279.ch2"),
                     g_search_type="genes", c_search_type="contrast_names", by="both")
 heatmap(as.matrix(b.gn.cn), col=terrain.colors(15))

## End(Not run)
```

`advanced_search_by_both` *Accessory function allowing the advanced_search by both g_ids and c_ids*

Description

Accessory function allowing the advanced_search by both g_ids and c_ids

Usage

```
advanced_search_by_both(organism, g_ids, geneNames, c_ids, g_search_type,
  ann_type, c_search_type)
```

Arguments

`organism`	A character containing the organism id: use `listOrganisms` to display the available organisms.
`g_ids`	A vector of strings representing contrast_id, go terms, experiment id or condition id according the search type.
`geneNames`	boolean if == FALSE (default) return the locustag otherwise the gene_name for the selected genes.
`c_ids`	A vector of strings representing contrast_id, go terms, experiment id or condition id according the search type.
`g_search_type`	A string either genes, go or annotation.
`ann_type`	A string containing the selected gene_annotation_type: use `listEntities` to display the available entities.
`c_search_type`	A string either contrast_names. experiment, go, condition.

Value

A data.frame containing locustag (gene_names), contrasts and M-values for the current organism and genes.

References

http://colombos.net

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advanced_search_by_contrasts

Accessory function allowing the advanced_search by contrast_ids, go, experiment, condition

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Description

Accessory function allowing the advanced_search by contrast_ids, go, experiment, condition

Usage

```
advanced_search_by_contrasts(organism = NULL, ids = NULL,
  geneNames = FALSE, c_search_type = NULL)
```

Arguments

`organism`	A character containing the organism id: use `listOrganisms` to display the available organisms.
`ids`	A vector of strings representing contrast_id, go terms, experiment id or condition id according the search type.
`geneNames`	boolean if == FALSE (default) return the locustag otherwise the gene_name for the selected genes.
`c_search_type`	A string either contrast_names. experiment, go, condition.

Value

A data.frame containing locustag (gene_names), contrasts and M-values for the current organism and genes.

References

http://colombos.net

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advanced_search_by_genes

Accessory function allowing the advanced_search by gene_ids, go, annotation

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Description

Accessory function allowing the advanced_search by gene_ids, go, annotation

Usage

```
advanced_search_by_genes(organism = "bsubt", ids = NULL,
  geneNames = FALSE, g_search_type = "genes", ann_type)
```

Arguments

`organism`	A character containing the organism id: use `listOrganisms` to display the available organisms.
`ids`	A vector of strings representing gene_id, go terms or annotation entities according the search type.
`geneNames`	boolean if == FALSE (default) return the locustag otherwise the gene_name for the selected genes.
`g_search_type`	A string either genes, go or annotation.
`ann_type`	A string containing the selected gene_annotation_type: use `listEntities` to display the available entities.

Value

A data.frame containing locustag (gene_names), contrasts and M-values for the current organism and genes.

References

http://colombos.net

`getCompendium` *This method allows to download/import the full compendium for the selected organism*

Description

This method allows to download/import the full compendium for the selected organism

Usage

```
getCompendium(organism = "hpylo", path = NULL)
```

Arguments

`organism`	A character containing the organism id: use `listOrganisms` to display the available organisms.
`path`	A string indicating the path where the file will be either downloaded or read, if already retrieved

Value

A list containing two or three data.frames.

In case `switchVersion` is equal to 2:

`exprdata`	the full compendium for the selected organism
`condannot`	The condition annotation for the selected organism

In case `switchVersion` is equal to 3:

`exprdata`	the full compendium for the selected organism
`refannot`	The condition annotation for the reference contrasts
`testannot`	The condition annotation for the test contrasts

References

http://colombos.net

Examples

```
## Not run:
library('Rcolombos')
hpylo <- getCompendium("hpylo")

## End(Not run)
```

`get_contrast_annotations` *This method allows to retrieve all the annotations for the Reference and Test conditions for a selected organism (nickname) and for a user specified contrast name. Please be aware that only one contrast is allowed in input. It returns a list containing both ReferenceAnnnotation and TestAnnotation. and return the available entities*

Description

This method allows to retrieve all the annotations for the Reference and Test conditions for a selected organism (nickname) and for a user specified contrast name. Please be aware that only one contrast is allowed in input. It returns a list containing both ReferenceAnnnotation and TestAnnotation. and return the available entities

Usage

```
get_contrast_annotations(organism = "bsubt",
  contrast_name = "GSM27217.ch2-vs-GSM27217.ch1")
```

Arguments

`organism`	A character containing the organism id: use `listOrganisms` to display the available organisms.
`contrast_name`	annotation A character containing the selected contrast_name type: use `listContrasts` to display the available contrast names.

Value

A list of two data.frame, ReferenceAnnnotation and TestAnnotation, containing 2 columns: both the properties and the values for the selected contrast

References

http://colombos.net

Examples

```
## Not run:
 library("Rcolombos")
 out <- get_contrast_annotations(organism="bsubt",
 contrast_name="GSM27217.ch2-vs-GSM27217.ch1")

## End(Not run)
```

`listAnnotationTypes` *This method takes as parameter a string (the nickname of an organism) and returns a character vector corresponding to the currently available annotation type for the selected organism.*

Description

This method takes as parameter a string (the nickname of an organism) and returns a character vector corresponding to the currently available annotation type for the selected organism.

Usage

```
listAnnotationTypes(organism = "ecoli")
```

Arguments

`organism`	A character containing the organism id: use `listOrganisms` to display the available organisms.

Value

A data.frame containing the name and description of the annotation for the selected organism.

References

http://colombos.net

Examples

```
## Not run:
library('Rcolombos')
listAnnotationTypes()

## End(Not run)
```

`listContrasts` *This method takes as parameter a single string, representing an organism, and returns a character vector corresponding to the currently available organisms.*

Description

This method takes as parameter a single string, representing an organism, and returns a character vector corresponding to the currently available organisms.

Usage

```
listContrasts(organism = "ecoli")
```

Arguments

`organism`	A character containing the organism id: use `listOrganisms` to display the available organisms.

Value

A data.frame containing the contrasts and GSM of all the contrasts for the selected organism.

References

http://colombos.net

Examples

```
## Not run:
library('Rcolombos')
listContrasts()

## End(Not run)
```

`listEntities` *This method takes a string containing the nickname for the selected organism and a string containing the annotation type and return the available entities*

Description

This method takes a string containing the nickname for the selected organism and a string containing the annotation type and return the available entities

Usage

```
listEntities(organism = "ecoli", annotation = "Pathway")
```

Arguments

`organism`	A character containing the organism id: use `listOrganisms` to display the available organisms.
`annotation`	A character containing the selected annotation type: use `listAnnotationTypes` to display the available types.

Value

A vector containing the available entities for the selected annotation type.

References

http://colombos.net

Examples

```
## Not run:
 library("Rcolombos")
 pathway_entities <- listEntities(organism="bsubt", annotation="Pathway")
 Tr_entities <- listEntities("bsubt","Transcriptional regulation")

## End(Not run)
```

`listGenes` *This method takes as parameter a single string, representing an organism, and returns a character vector corresponding to the currently available organisms.*

Description

This method takes as parameter a single string, representing an organism, and returns a character vector corresponding to the currently available organisms.

Usage

```
listGenes(organism = "ecoli")
```

Arguments

`organism`	A character containing the organism id: use `listOrganisms` to display the available organisms.

Value

A data.frame containing the locustag and description of all the genes for the selected organism.

References

http://colombos.net

Examples

```
## Not run:
library('Rcolombos')
listGenes()

## End(Not run)
```

`listOrganisms` *Returns a character vector corresponding to the currently available organisms.*

Description

Returns a character vector corresponding to the currently available organisms.

Usage

```
listOrganisms()
```

Value

A list containing the currently available organisms.

References

http://colombos.net

Examples

```
library('Rcolombos')
listOrganisms()
```

`parseCompendium` *This method allows importing the full compendium for the selected organism from a local file*

Description

This method allows importing the full compendium for the selected organism from a local file

Usage

```
parseCompendium(destfile)
```

Arguments

`destfile`	A character containing the full path of the downloaded file

Value

A list containing two or three data.frames.

In case `switchVersion` is equal to 2:

`exprdata`	the full compendium for the selected organism
`condannot`	The condition annotation for the selected organism

In case `switchVersion` is equal to 3:

`exprdata`	the full compendium for the selected organism
`refannot`	The condition annotation for the reference contrasts
`testannot`	The condition annotation for the test contrasts

References

http://colombos.net

Examples

```
## Not run:
library('Rcolombos')
mtube <- parseCompendium("mtube_compendium_data.zip")

## End(Not run)
```

`quick_search` *This method mimics the quick_search functionality of Colombos. It takes a string containg the nickname for the selected organism and a vector of string representing the genes of interest for the specified organism and returns a list containing the locustags (gene_names), contrasts and M-values for the current selection.*

Description

This method mimics the quick_search functionality of Colombos. It takes a string containg the nickname for the selected organism and a vector of string representing the genes of interest for the specified organism and returns a list containing the locustags (gene_names), contrasts and M-values for the current selection.

Usage

```
quick_search(organism = "ecoli", genes, geneNames = FALSE)
```

Arguments

`organism`	A character containing the organism id: use `listOrganisms` to display the available organisms.
`genes`	A vector of strings representing the genes of interest.
`geneNames`	boolean if == FALSE (default) returns the locustag otherwise the gene_name for the selected genes.

Value

A data.frame containing locustag (gene_names), contrasts and M-values for the current organism and genes.

References

http://colombos.net

Examples

```
## Not run:
 library("Rcolombos")
 my_module <- quick_search(organism="ecoli",
                     genes=c("b0400","b2805","b0567"),
                     geneNames=FALSE)
 heatmap(as.matrix(my_module), col=terrain.colors(15))

## End(Not run)
```

`Rcolombos` *Interface to Colombos Compendia using the Exposed REST API*

Description

Provides programmatic access to Colombos, a web based interface for exploring and analyzing comprehensive organism-specific cross-platform expression compendia of bacterial organisms.

`switchVersion` *Select the COLOMBOS REST API version to be used for retrieving data*

Description

Select the COLOMBOS REST API version to be used for retrieving data

Usage

```
switchVersion(version = 3)
```

Arguments

`version`	positive number 2 or 3 - 3 (current REST API version) as default

References

http://colombos.net

Examples

```
## Not run:
library('Rcolombos')
switchVersion (version = 2) # switch from COLOMBOS REST API 3 to 2

## End(Not run)
```

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