

Package ‘Rcolombos’

March 4, 2015

Type Package

Title Interface to Colombos Compendia using the Exposed REST API

Version 1.5.2

Date 2013-06-26

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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/>

Collate 'Rcolombos.R' 'utilities.R' 'zzz.R'

NeedsCompilation no

Date/Publication 2015-03-04 09:36:00

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advanced_search	<i>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.</i>
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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 either 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", "H202", "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>

advanced_search_by_contrasts

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

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>

advanced_search_by_genes

Accessory function allowing the advanced_search by gene_ids, go, annotation

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	<i>This method allows to download/import the full compendium for the selected organism</i>
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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 three data.frame:

exprdata	the full compendium for the selected organism
condannot	The condition annotation for the selected organism
condontol	the condition ontology for the selected organism

References

<http://colombos.net>

Examples

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

listAnnotationTypes	<i>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.</i>
---------------------	---

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

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	<i>This method takes a string containing the nickname for the selected organism and a string containing the annotation type and return the available entities</i>
--------------	---

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

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	<i>Returns a character vector corresponding to the currently available organisms.</i>
---------------	---

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

```
## Not run:  
library('Rcolombos')  
listOrganisms()  
  
## End(Not run)
```

parseCompendium	<i>This method allows importing the full compendium for the selected organism from a local file</i>
-----------------	---

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 three data.frame:

exprdata	the full compendium for the selected organism
condannot	The condition annotation for the selected organism
condontol	the condition ontology for the selected organism

References

<http://colombos.net>

Examples

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

quick_search	<i>This method mimics the quick_search functionality of Colombos. It takes a string containing 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.</i>
--------------	--

Description

This method mimics the `quick_search` functionality of `Colombos`. It takes a string containing 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

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

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