Package ‘Rcolombos’
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Title Interface to Colombos Compendia using the Exposed REST API
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Author Paolo Sonego <paolo.sonego@fmach.it>
Maintainer Paolo Sonego <paolo.sonego@fmach.it>
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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advanced_search

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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 eithers 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","yfG"),
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=c("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=c("GSE22296", g_search_type="genes", c_search_type="experiment", by="both")
b.go.ge <- advanced_search(organism="bsubt", g_ids=c("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.

genNames 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)
getCompendium

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
**get_contrast_annotations**

**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**

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

---

**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 Reference Annotation and Test Annotation, and return the available entities.

**Usage**

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

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, ReferenceAnnotation 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.
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')
listAnnotationTypes()

## 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('Rcologos')
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 destfile
```

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>destfile</td>
<td>A character containing the full path of the downloaded file</td>
</tr>
</tbody>
</table>

Value
A list containing two or three data.frames.
In case `switchVersion` is equal to 2:

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>exprdata</td>
<td>the full compendium for the selected organism</td>
</tr>
<tr>
<td>condannot</td>
<td>The condition annotation for the selected organism</td>
</tr>
</tbody>
</table>

In case `switchVersion` is equal to 3:

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>exprdata</td>
<td>the full compendium for the selected organism</td>
</tr>
<tr>
<td>refannot</td>
<td>The condition annotation for the reference contrasts</td>
</tr>
<tr>
<td>testannot</td>
<td>The condition annotation for the test contrasts</td>
</tr>
</tbody>
</table>

References
http://colombos.net
quick_search

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 containing the nickname for the selected organism and a vector of strings 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 containing the nickname for the selected organism and a vector of strings 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

```r
## Not run:
library("Rcolombos")
my_module <- quick_search(organism="coli",
genesis=c("b0400","b2805","b0567"),
genename=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

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

#### Arguments

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

#### References

http://colombos.net

#### Examples

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

## End(Not run)
```
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