

Package ‘SynergizeR’

February 19, 2015

Type Package

Title Interface to The Synergizer service for translating between sets of biological identifiers.

Version 0.2

Date 2011-10-11

Author Paolo Sonogo <paolo.sonogo@gmail.com>

Maintainer Paolo Sonogo <paolo.sonogo@gmail.com>

Description This package provides programmatic access to The Synergizer service for translating between sets of biological identifiers.

Depends R (>= 2.11.0), RJSONIO, RCurl

License GPL-2

LazyLoad yes

Collate 'metamethods.r' 'synergizer.r' 'zzz.r'

Repository CRAN

Repository/R-Forge/Project synergizer

Repository/R-Forge/Revision 12

Date/Publication 2011-11-16 12:46:33

NeedsCompilation no

R topics documented:

available_authorities	2
available_domains	2
available_ranges	3
available_species	4
server_version	5
synergizer	5

Index	7
--------------	----------

`available_authorities` *Returns a character vector corresponding to the currently available authorities.*

Description

Returns a character vector corresponding to the currently available authorities.

Value

A list containing the currently available authorities.

References

<http://llama.mshri.on.ca/synergizer/translate/>

Examples

```
## Not run:
library('SynergizerR')
available_authorities()
## End(Not run)
```

`available_domains` *Takes as parameters two strings, representing an authority and a species, and returns a character vector corresponding to the currently available domain namespaces for the chosen authority and species.*

Description

Takes as parameters two strings, representing an authority and a species, and returns a character vector corresponding to the currently available domain namespaces for the chosen authority and species.

Usage

```
available_domains(authority = "ensembl", species = "Homo sapiens")
```

Arguments

<code>authority</code>	A character containing any authoritative sources of identifier-mapping information
<code>species</code>	A character containing the Species. Note that the range of species supported depends on the choice of authority. Examples: <i>Homo sapiens</i> , <i>Mus musculus</i> .

Value

A vector containing the currently available domain namespaces for the chosen authority and species.

References

<http://llama.mshri.on.ca/synergizer/translate/>

Examples

```
## Not run:
library('SynergizerR')
available_domains('ensembl', 'homo sapiens')
## End(Not run)
```

available_ranges	<i>Takes as parameters three strings, representing an authority, a species, and a domain namespace, and returns a character vector corresponding to the currently available range namespaces for the chosen authority, species, and domain namespace.</i>
------------------	---

Description

Takes as parameters three strings, representing an authority, a species, and a domain namespace, and returns a character vector corresponding to the currently available range namespaces for the chosen authority, species, and domain namespace.

Usage

```
available_ranges(authority = "ensembl", species = "Homo sapiens", domain = "hgnc_symbol")
```

Arguments

authority	A character containing any authoritative sources of identifier-mapping information.
species	A character containing the Species. Note that the range of species supported depends on the choice of authority. Examples: Homo sapiens, Mus musculus.
domain	This is the "namespace" (naming scheme) of the database identifiers the user wishes to translate. Examples: embl, ipi

Value

A vector containing the currently available range namespaces for the chosen authority, species, and domain namespace.

References

<http://llama.mshri.on.ca/synergizer/translate/>

Examples

```
## Not run:  
library('SynergizerR')  
available_ranges('ensembl', 'homo sapiens', 'hgnc_symbol')  
## End(Not run)
```

available_species	<i>This method takes as parameter a single string, representing an authority, and returns a character vector corresponding to the currently available species for the chosen authority.</i>
-------------------	---

Description

This method takes as parameter a single string, representing an authority, and returns a character vector corresponding to the currently available species for the chosen authority.

Usage

```
available_species(authority = "ensembl")
```

Arguments

authority	A character containing any authoritative sources of identifier-mapping information.
-----------	---

Value

A vector containing the currently available species for the chosen authority.

References

<http://llama.mshri.on.ca/synergizer/translate/>

Examples

```
## Not run:  
library('SynergizerR')  
available_species('ensembl')  
## End(Not run)
```

server_version	<i>Returns current version of the Synergizer server as a string.</i>
----------------	--

Description

Returns current version of the Synergizer server as a string.

Value

A one-element character vector containing current version of the Synergizer server

References

<http://llama.mshri.on.ca/synergizer/translate/>

Examples

```
## Not run:
library('SynergizerR')
server_version()
## End(Not run)
```

synergizer	<i>Translate a set of biological identifiers into an selected alternative.</i>
------------	--

Description

This function will translate between sets of biological identifiers.

Usage

```
synergizer(authority = "ensembl", species = "Homo sapiens", domain = "hgnc_symbol", range = "entrezg
```

Arguments

authority	A character containing any authoritative sources of identifier-mapping information.
species	A character containing the Species. Note that the range of species supported depends on the choice of authority. Examples: Homo sapiens, Mus musculus.
domain	This is the "namespace" (naming scheme) of the database identifiers the user wishes to translate. Examples: embl, ipi
range	This is the "namespace" (naming scheme) to which the user wishes to translate the input identifiers. Examples: embl, ipi
ids	a vector containing the ids to be translated
file	NULL or a string containing the name of the file where the ids will be saved

Value

A vector containing the translated ids.

References

<http://llama.mshri.on.ca/synergizer/translate/>

Examples

```
## Not run:  
library('SynergizerR')  
symbols.ids <- synergizer( authority = "ensembl", species = "Homo sapiens", domain="affy_hg_u95av2", range="hgnc."  
entrez.ids <- synergizer( authority = "ensembl", species = "Homo sapiens", domain="hgnc_symbol", range="entrezgen."  
## End(Not run)
```

Index

`available_authorities`, [2](#)

`available_domains`, [2](#)

`available_ranges`, [3](#)

`available_species`, [4](#)

`server_version`, [5](#)

`synergizer`, [5](#)