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 Sonego <paolo.sonego@gmail.com>

Maintainer Paolo Sonego <paolo.sonego@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

```r
## 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

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

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.
available_ranges

Value

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

References

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

Examples

```r
## not run:
library('SynergizerR')
available_domains('ensembl','homo sapiens')
## end not run
```

available_ranges

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.

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

```r
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/
available_species

### Examples

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

---

**available_species**  
*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.*

---

**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**

```r
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**

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

Returns current version of the Synergizer server as a string.

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

Translate a set of biological identifiers into an selected alternative.

Description

This function will translate between sets of biological identifiers.

Usage

synergizer(authority = "ensembl", species = "Homo sapiens", domain = "hgnc_symbol", range = "entrezgene")

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>authority</td>
<td>A character containing any authoritative sources of identifier-mapping information.</td>
</tr>
<tr>
<td>species</td>
<td>A character containing the Species. Note that the range of species supported depends on the choice of authority. Examples: Homo sapiens, Mus musculus.</td>
</tr>
<tr>
<td>domain</td>
<td>This is the &quot;namespace&quot; (naming scheme) of the database identifiers the user wishes to translate. Examples: embl,ipi</td>
</tr>
<tr>
<td>range</td>
<td>This is the &quot;namespace&quot; (naming scheme) to which the user wishes to translate the input identifiers. Examples: embl,ipi</td>
</tr>
<tr>
<td>ids</td>
<td>a vector containing the ids to be translated</td>
</tr>
<tr>
<td>file</td>
<td>NULL or a string containing the name of the file where the ids will be saved</td>
</tr>
</tbody>
</table>
Value

A vector containing the translated ids.

References

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

Examples

```r
## Not run:
library('SynergizerR')
symbols.ids <- synergizer( authority = "ensembl", species = "Homo sapiens", domain="affy_hg_u95av2", range="hgnc_symbol", ids=c("19S9_at","1U0S_at","14U4_at") )
entrez.ids <- synergizer( authority = "ensembl", species = "Homo sapiens", domain="hgnc_symbol", range="entrezgene", ids=c("snph","pja1","prkdc","radR1l1","rorc","kcnk16") )
## End(Not run)
```
Index

availableAuthorities, 2
availableDomains, 2
availableRanges, 3
availableSpecies, 4
serverVersion, 5
synergizer, 5