

# Package ‘SynergizeR’

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**Type** Package

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

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**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'

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

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### 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)
```

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`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.*

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### 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

`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*.

**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)
```

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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>
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**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)
```

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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>
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## 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.
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## 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)
```

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

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

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