Package 'ritis'

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Title Integrated Taxonomic Information System Client

Description An interface to the Integrated Taxonomic Information System ('ITIS')
(<https://www.itis.gov>). Includes functions to work with the 'ITIS' REST
API methods (<https://www.itis.gov/ws_description.html>), as well as the
'Solr' web service (<https://www.itis.gov/solr_documentation.html>).

Version 1.0.0

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URL <https://github.com/ropensci/ritis> (devel)

<https://docs.ropensci.org/ritis/> (docs)

BugReports <https://github.com/ropensci/ritis/issues>

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tibble

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R **topics documented:**

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ritis-package   *ritis*

Description

Interface to Integrated Taxonomic Information (ITIS)

ritis package API

All functions that start with `itis_` work with the ITIS Solr API described at https://www.itis.gov/solr_documentation.html, which uses the package **solrium**, and these functions have you use the **solrium** function interfaces, so you can pass on parameters to the **solrium** functions - so the **solrium** docs are important here.

All other functions work with the ITIS REST API described at https://www.itis.gov/ws_description.html. For these methods, they can grab data in either JSON or XML format. JSON is the default. We parse the JSON to R native format, either data.frame, character string, or list. You can get raw JSON as a character string back, or raw XML as a character string, and then parse yourself with **jsonlite** or **xml2**

You'll also be interested in the taxize book https://taxize.dev/

Terminology

- "mononomial": a taxonomic name with one part, e.g, *Poa*
- "binomial": a taxonomic name with two parts, e.g, *Poa annua*
- "trinomial": a taxonomic name with three parts, e.g, *Poa annua annua*

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---

accepted_names   *Get accepted names from tsn*

Description

Get accepted names from tsn

Usage

```
accepted_names(tsn, wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to [crul::HttpClient](#)

Value

Zero row data.frame if the name is accepted, otherwise a data.frame with information on the currently accepted name

Examples

```
## Not run:
# TSN accepted - good name, empty data.frame returned
accepted_names(tsn = 208527)

# TSN not accepted - input TSN is old name, non-empty data.frame returned
accepted_names(tsn = 504239)

# raw json
accepted_names(tsn = 208527, raw = TRUE)

## End(Not run)
```

---

any_match_count   *Get any match count.*

Description

Get any match count.

Usage

```
any_match_count(x, wt = "json", raw = FALSE, ...)
```

Arguments

x	text or taxonomic serial number (TSN) (character or numeric)
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to [crul::HttpClient](#)

Value

An integer containing the number of matches the search will return.

Examples

```
## Not run:
any_match_count(x = 202385)
any_match_count(x = "dolphin")
any_match_count(x = "dolphin", wt = "xml")

## End(Not run)
```

---

comment_detail   *Get comment detail from TSN*

Description

Get comment detail from TSN

Usage

```
comment_detail(tsn, wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to crul::HttpClient

Value

A data.frame with results.

Examples

```
## Not run:
comment_detail(tsn=180543)
comment_detail(tsn=180543, wt = "xml")

## End(Not run)
```

---

common_names   *Get common names from tsn*

Description

Get common names from tsn

Usage

```
common_names(tsn, wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to [crul::HttpClient](#)

Value

a data.frame

Examples

```
## Not run:
common_names(tsn=183833)
common_names(tsn=183833, wt = "xml")

## End(Not run)
```

---

core_metadata   *Get core metadata from tsn*

Description

Get core metadata from tsn

Usage

```
core_metadata(tsn, wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to [crul::HttpClient](#)

Examples

```
## Not run:
# coverage and currrency data
core_metadata(tsn=28727)
core_metadata(tsn=28727, wt = "xml")
# no coverage or currrency data
core_metadata(183671)
core_metadata(183671, wt = "xml")

## End(Not run)
```

---

coverage	*Get coverge from tsn*

Description

Get coverge from tsn

Usage

```
coverage(tsn, wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to [crul::HttpClient](#)

Examples

```
## Not run:
# coverage data
coverage(tsn=28727)
# no coverage data
coverage(526852)
coverage(526852, wt = "xml")

## End(Not run)
```

---

credibility   *Get credibility rating from tsn*

Description

Get credibility rating from tsn

Usage

```
credibility_rating(tsn, wt = "json", raw = FALSE, ...)

credibility_ratings(wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to crul::HttpClient

Details

methods:

- credibility_rating: Get credibility rating for a tsn
- credibility_ratings: Get possible credibility ratings

Value

a data.frame

Examples

```
## Not run:
credibility_rating(tsn = 526852)
credibility_rating(526852, wt = "xml")
credibility_rating(526852, raw = TRUE)

credibility_ratings()
credibility_ratings(wt = "xml")
credibility_ratings(raw = TRUE)

## End(Not run)
```

---

currency   *Get currency from tsn*

Description

Get currency from tsn

Usage

```
currency(tsn, wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to [crul::HttpClient](#)

Value

a data.frame

Examples

```
## Not run:
# currency data
currency(tsn=28727)
currency(tsn=28727, wt = "xml")
# no currency dat
currency(526852)
currency(526852, raw = TRUE)

## End(Not run)
```

---

date_data   *Get date data from tsn*

Description

Get date data from tsn

Usage

```
date_data(tsn, wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to crul::HttpClient

Examples

```
## Not run:
date_data(tsn = 180543)
date_data(180543, wt = "xml")
date_data(180543, wt = "json", raw = TRUE)

## End(Not run)
```

---

description	*Get description of the ITIS service*

Description

Get description of the ITIS service

Usage

```
description(wt = "json", raw = FALSE, ...)
```

Arguments

wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to crul::HttpClient

Value

a string, the ITIS web service description

Examples

```
## Not run:
description()
description(wt = "xml")

## End(Not run)
```

---

experts   *Get expert information for the TSN.*

Description

Get expert information for the TSN.

Usage

```
experts(tsn, wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to [crul::HttpClient](#)

Examples

```
## Not run:
experts(tsn = 180544)
experts(180544, wt = "xml")
experts(180544, raw = TRUE)

## End(Not run)
```

---

full_record   *Get full record from TSN or lsid*

Description

Get full record from TSN or lsid

Usage

```
full_record(tsn = NULL, lsid = NULL, wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
lsid	lsid for a taxonomic group (character)
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to [crul::HttpClient](#)

Examples

```
## Not run:
# from tsn
full_record(tsn = 50423)
full_record(tsn = 202385)
full_record(tsn = 183833)

full_record(tsn = 183833, wt = "xml")
full_record(tsn = 183833, raw = TRUE)

# from lsid
full_record(lsid = "urn:lsid:itis.gov:itis_tsn:180543")
full_record(lsid = "urn:lsid:itis.gov:itis_tsn:180543")

## End(Not run)
```

---

geographic_divisions   *Get geographic divisions from tsn*

Description

Get geographic divisions from tsn

Usage

```
geographic_divisions(tsn, wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to [crul::HttpClient](#)

Examples

```
## Not run:
geographic_divisions(tsn = 180543)

geographic_divisions(tsn = 180543, wt = "xml")

geographic_divisions(tsn = 180543, wt = "json", raw = TRUE)

## End(Not run)
```

---

geographic_values *Get all possible geographic values*

Description

Get all possible geographic values

Usage

```
geographic_values(wt = "json", raw = FALSE, ...)
```

Arguments

wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to [crul::HttpClient](#)

Value

character vector of geographic names

Examples

```
## Not run:
geographic_values()
geographic_values(wt = "xml")
geographic_values(wt = "json", raw = TRUE)

## End(Not run)
```

---

global_species_completeness
Get global species completeness from tsn

Description

Get global species completeness from tsn

Usage

```
global_species_completeness(tsn, wt = "json", raw = FALSE, ...)
```

Arguments

`tsn`	TSN for a taxonomic group (numeric). Required.
`wt`	(character) One of "json" or "xml". Required.
`raw`	(logical) Return raw JSON or XML as character string. Required. Default: `FALSE`
`...`	curl options passed on to [crul::HttpClient](#)

Examples

```
## Not run:
global_species_completeness(tsn = 180541)
global_species_completeness(180541, wt = "xml")
global_species_completeness(180541, wt = "json", raw = TRUE)

## End(Not run)
```

---

hierarchy	*Get hierarchy down from tsn*

Description

Get hierarchy down from tsn

Usage

```
hierarchy_down(tsn, wt = "json", raw = FALSE, ...)

hierarchy_up(tsn, wt = "json", raw = FALSE, ...)

hierarchy_full(tsn, wt = "json", raw = FALSE, ...)
```

Arguments

`tsn`	TSN for a taxonomic group (numeric). Required.
`wt`	(character) One of "json" or "xml". Required.
`raw`	(logical) Return raw JSON or XML as character string. Required. Default: `FALSE`
`...`	curl options passed on to [crul::HttpClient](#)

Details

Hierarchy methods:

- hierarchy_down: Get hierarchy down from tsn
- hierarchy_up: Get hierarchy up from tsn
- hierarchy_full: Get full hierarchy from tsn

Examples

```
## Not run:
## Full down (class Mammalia)
hierarchy_down(tsn=179913)

## Full up (genus Agoseris)
hierarchy_up(tsn=36485)

## Full hierarchy
### genus Liatris
hierarchy_full(tsn=37906)
### get raw data back
hierarchy_full(tsn=37906, raw = TRUE)
### genus Baetis, get xml back
hierarchy_full(100800, wt = "xml")

## End(Not run)
```

---

itis_facet   *ITIS Solr facet*

Description

ITIS Solr facet

Usage

```
itis_facet(..., proxy = NULL, callopts = list())
```

Arguments

...	Arguments passed on to the `params` parameter of the [solrium::solr_facet()](#) function. See [solr_fields](#) for possible parameters, and examples below
proxy	List of arguments for a proxy connection, including one or more of: url, port, username, password, and auth. See [crul::proxy()](#) for help, which is used to construct the proxy connection.
callopts	Curl options passed on to [crul::HttpClient](#)

Examples

```
## Not run:
itis_facet(q = "rank:Species", rows = 0, facet.field = "kingdom")$facet_fields

x <- itis_facet(q = "hierarchySoFar:*$Aves$* AND rank:Species AND usage:valid",
    facet.pivot = "nameWInd,vernacular", facet.limit = -1, facet.mincount = 1,
    rows = 0)
head(x$facet_pivot$`nameWInd,vernacular`)

## End(Not run)
```

---

itis_group   *ITIS Solr group search*

Description

ITIS Solr group search

Usage

```
itis_group(..., proxy = NULL, callopts = list())
```

Arguments

...	Arguments passed on to the `params` parameter of the `solrium::solr_group()` function. See solr_fields for possible parameters, and examples below
proxy	List of arguments for a proxy connection, including one or more of: url, port, username, password, and auth. See `crul::proxy()` for help, which is used to construct the proxy connection.
callopts	Curl options passed on to crul::HttpClient

Examples

```
## Not run:
x <- itis_group(q = "nameWOInd:/[A-Za-z0-9]*[%20]{0,0}*/",
   group.field = 'rank', group.limit = 3)
head(x)

## End(Not run)
```

---

itis_highlight   *ITIS Solr highlight*

Description

ITIS Solr highlight

Usage

```
itis_highlight(..., proxy = NULL, callopts = list())
```

Arguments

...	Arguments passed on to the `params` parameter of the `solrium::solr_highlight()` function. See solr_fields for possible parameters, and examples below
proxy	List of arguments for a proxy connection, including one or more of: url, port, username, password, and auth. See `crul::proxy()` for help, which is used to construct the proxy connection.
callopts	Curl options passed on to crul::HttpClient

Examples

```
## Not run:
itis_highlight(q = "rank:Species", hl.fl = 'rank', rows=10)

## End(Not run)
```

---

itis_search   *ITIS Solr search*

Description

ITIS Solr search

Usage

```
itis_search(..., proxy = NULL, callopts = list())
```

Arguments

...	Arguments passed on to the params parameter of the [solrium::solr_search()](#) function. See [solr_fields](#) for possible parameters, and examples below
proxy	List of arguments for a proxy connection, including one or more of: url, port, username, password, and auth. See [crul::proxy()](#) for help, which is used to construct the proxy connection.
callopts	Curl options passed on to [crul::HttpClient](#)

Details

The syntax for this function can be a bit hard to grasp. See https://itis.gov/solr_examples.html for help on generating the syntax ITIS wants for specific searches.

References

https://www.itis.gov/solr_documentation.html

Examples

```
## Not run:
itis_search(q = "tsn:182662")

# get all orders within class Aves (birds)
z <- itis_search(q = "rank:Class AND nameWOInd:Aves")
hierarchy_down(z$tsn)

# get taxa "downstream" from a target taxon
## taxize and taxizedb packages have downstream() fxns, but
## you can do a similar thing here by iteratively drilling down
## the taxonomic hierarchy
```

```
## here, we get families within Aves
library(data.table)
aves <- itis_search(q = "rank:Class AND nameWOInd:Aves")
aves_orders <- hierarchy_down(aves$tsn)
aves_families <- lapply(aves_orders$tsn, hierarchy_down)
rbindlist(aves_families)

# the tila operator
itis_search(q = "nameWOInd:Liquidamber\\ styraciflua~0.4")

# matches only monomials
itis_search(q = "nameWOInd:/[A-Za-z0-9]*[ ]{0,0}*/")

# matches only binomials
itis_search(q = "nameWOInd:/[A-Za-z0-9]*[ ]{1,1}[A-Za-z0-9]*/")

# matches only trinomials
itis_search(q = "nameWOInd:/[A-Za-z0-9]*[ ]{1,1}[A-Za-z0-9]*[ ]{1,1}[A-Za-z0-9]*/")

# matches binomials or trinomials
itis_search(q = "nameWOInd:/[A-Za-z0-9]*[ ]{1,1}[A-Za-z0-9]*[ ]{0,1}[A-Za-z0-9]*/")

itis_search(q = "nameWOInd:Poa\\ annua")

# pagination
itis_search(q = "nameWOInd:/[A-Za-z0-9]*[ ]{0,0}*/", rows = 2)
itis_search(q = "nameWOInd:/[A-Za-z0-9]*[ ]{0,0}*/", rows = 200)

# select fields to return
itis_search(q = "nameWOInd:/[A-Za-z0-9]*[ ]{0,0}*/",
   fl = c('nameWInd', 'tsn'))

## End(Not run)
```

---

jurisdiction	*Get jurisdictional origin from tsn*

Description

Get jurisdictional origin from tsn

Usage

```
jurisdictional_origin(tsn, wt = "json", raw = FALSE, ...)

jurisdiction_origin_values(wt = "json", raw = FALSE, ...)

jurisdiction_values(wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: `FALSE`
...	curl options passed on to [crul::HttpClient](#)

Details

Jurisdiction methods:

- jurisdictional_origin: Get jurisdictional origin from tsn
- jurisdiction_origin_values: Get jurisdiction origin values
- jurisdiction_values: Get all possible jurisdiction values

Value

- jurisdictional_origin: data.frame
- jurisdiction_origin_values: data.frame
- jurisdiction_values: character vector

Examples

```
## Not run:
jurisdictional_origin(tsn=180543)
jurisdictional_origin(tsn=180543, wt = "xml")

jurisdiction_origin_values()

jurisdiction_values()

## End(Not run)
```

---

kingdoms   *Get kingdom names from tsn*

Description

Get kingdom names from tsn

Usage

```
kingdom_name(tsn, wt = "json", raw = FALSE, ...)

kingdom_names(wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to crul::HttpClient

Details

- kingdom_name: Get kingdom name for a TSN

- kingdom_names: Get all possible kingdom names

Examples

```
## Not run:
kingdom_name(202385)
kingdom_name(202385, wt = "xml")
kingdom_names()

## End(Not run)
```

---

last_change_date   *Provides the date the ITIS database was last updated*

Description

Provides the date the ITIS database was last updated

Usage

```
last_change_date(wt = "json", raw = FALSE, ...)
```

Arguments

wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to crul::HttpClient

Value

character value with a date

Examples

```
## Not run:
last_change_date()
last_change_date(wt = "xml")

## End(Not run)
```

---

lsid2tsn	*Gets the TSN corresponding to the LSID, or an empty result if there is no match.*

Description

Gets the TSN corresponding to the LSID, or an empty result if there is no match.

Usage

```
lsid2tsn(lsid, wt = "json", raw = FALSE, ...)
```

Arguments

lsid	(character) lsid for a taxonomic group. Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to crul::HttpClient

Examples

```
## Not run:
lsid2tsn(lsid="urn:lsid:itis.gov:itis_tsn:28726")
lsid2tsn(lsid="urn:lsid:itis.gov:itis_tsn:28726", wt = "xml")
lsid2tsn("urn:lsid:itis.gov:itis_tsn:0")
lsid2tsn("urn:lsid:itis.gov:itis_tsn:0", wt = "xml")

## End(Not run)
```

---

other_sources   *Returns a list of the other sources used for the TSN.*

Description

Returns a list of the other sources used for the TSN.

Usage

```
other_sources(tsn, wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to [crul::HttpClient](#)

Examples

```
## Not run:
# results
other_sources(tsn=182662)
# no results
other_sources(tsn=2085272)
# get xml
other_sources(tsn=182662, wt = "xml")

## End(Not run)
```

---

parent_tsn   *Returns the parent TSN for the entered TSN.*

Description

Returns the parent TSN for the entered TSN.

Usage

```
parent_tsn(tsn, wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to crul::HttpClient

Value

a data.frame

Examples

```
## Not run:
parent_tsn(tsn = 202385)
parent_tsn(tsn = 202385, raw = TRUE)
parent_tsn(tsn = 202385, wt = "xml")

## End(Not run)
```

---

publications	*Returns a list of the pulications used for the TSN.*

Description

Returns a list of the pulications used for the TSN.

Usage

```
publications(tsn, wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to crul::HttpClient

Value

a data.frame

Examples

```
## Not run:
publications(tsn = 70340)
publications(tsn = 70340, wt = "xml")

publications(tsn = 70340, verbose = TRUE)

## End(Not run)
```

---

rank_name   *Returns the kingdom and rank information for the TSN.*

Description

Returns the kingdom and rank information for the TSN.

Usage

```
rank_name(tsn, wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to crul::HttpClient

Value

a data.frame, with rank name and other info

Examples

```
## Not run:
rank_name(tsn = 202385)

## End(Not run)
```

---

rank_names   *Provides a list of all the unique rank names contained in the database and their kingdom and rank ID values.*

Description

Provides a list of all the unique rank names contained in the database and their kingdom and rank ID values.

Usage

```
rank_names(wt = "json", raw = FALSE, ...)
```

Arguments

wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to crul::HttpClient

Value

a data.frame, with columns:

- kingdomname
- rankid
- rankname

Examples

```
## Not run:
rank_names()

## End(Not run)
```

---

record   *Gets a record from an LSID*

Description

Gets a record from an LSID

Usage

```
record(lsid, wt = "json", raw = FALSE, ...)
```

Arguments

lsid	lsid for a taxonomic group (character). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: `FALSE`
...	curl options passed on to [crul::HttpClient](#)

Details

Gets the partial ITIS record for the TSN in the LSID, found by comparing the TSN in the search key to the TSN field. Returns an empty result set if there is no match or the TSN is invalid.

Value

a data.frame

Examples

```
## Not run:
record(lsid = "urn:lsid:itis.gov:itis_tsn:180543")

## End(Not run)
```

---

review_year   *Returns the review year for the TSN.*

Description

Returns the review year for the TSN.

Usage

```
review_year(tsn, wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: `FALSE`
...	curl options passed on to [crul::HttpClient](#)

Value

a data.frame

Examples

```
## Not run:
review_year(tsn = 180541)

## End(Not run)
```

---

scientific_name	*Returns the scientific name for the TSN. Also returns the component parts (names and indicators) of the scientific name.*

Description

Returns the scientific name for the TSN. Also returns the component parts (names and indicators) of the scientific name.

Usage

```
scientific_name(tsn, wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to [crul::HttpClient](#)

Value

a data.frame

Examples

```
## Not run:
scientific_name(tsn = 531894)

## End(Not run)
```

---

search_anymatch *Search for any match*

Description

Search for any match

Usage

```
search_anymatch(x, wt = "json", raw = FALSE, ...)
```

Arguments

x	text or taxonomic serial number (TSN) (character or numeric)
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to [crul::HttpClient](#)

Value

a data.frame

See Also

[search_any_match_paged](#)

Examples

```
## Not run:
search_anymatch(x = 202385)
search_anymatch(x = "dolphin")
# no results
search_anymatch(x = "Pisces")

## End(Not run)
```

search_any_match_paged

Search for any matched page

Description

Search for any matched page

Usage

```
search_any_match_paged(
  x,
  pagesize = NULL,
  pagenum = NULL,
  ascend = NULL,
  wt = "json",
  raw = FALSE,
  ...
)
```

Arguments

x	text or taxonomic serial number (TSN) (character or numeric)
pagesize	An integer containing the page size (numeric)
pagenum	An integer containing the page number (numeric)
ascend	A boolean containing true for ascending sort order or false for descending (logical)
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to crul::HttpClient

Value

a data.frame

a data.frame

See Also

search_anymatch

Examples

```
## Not run:
search_any_match_paged(x=202385, pagesize=100, pagenum=1, ascend=FALSE)
search_any_match_paged(x="Zy", pagesize=100, pagenum=1, ascend=FALSE)

## End(Not run)
```

---

search_common *Search for tsn by common name*

Description

Search for tsn by common name

Usage

```
search_common(x, from = "all", wt = "json", raw = FALSE, ...)
```

Arguments

x	text or taxonomic serial number (TSN) (character or numeric)
from	(character) One of "all", "begin", or "end". See Details.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: `FALSE`
...	curl options passed on to [crul::HttpClient](#)

Details

The `from` parameter:

- all - Search against the `searchByCommonName` API route, which searches entire name string
- begin - Search against the `searchByCommonNameBeginsWith` API route, which searches for a match at the beginning of a name string
- end - Search against the `searchByCommonNameEndsWith` API route, which searches for a match at the end of a name string

Value

a data.frame

See Also

[search_scientific()](#)

Examples

```
## Not run:
search_common("american bullfrog")
search_common("ferret-badger")
search_common("polar bear")

# comparison: all, begin, end
search_common("inch")
search_common("inch", from = "begin")
search_common("inch", from = "end")

# end
search_common("snake", from = "end")

## End(Not run)
```

---

search_scientific   *Search by scientific name*

Description

Search by scientific name

Usage

```
search_scientific(x, wt = "json", raw = FALSE, ...)
```

Arguments

x	text or taxonomic serial number (TSN) (character or numeric)
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to crul::HttpClient

Value

a data.frame

See Also

search_common

Examples

```
## Not run:
search_scientific("Tardigrada")
search_scientific("Quercus douglasii")

## End(Not run)
```

---

solr   *ITIS Solr Methods*

Description

ITIS provides access to their data via their Solr service described at `https://www.itis.gov/solr_documentation.html`. This is a powerful interace to ITIS data as you have access to a very flexible query interface.

Details

See solr_fields and `https://www.itis.gov/solr_documentation.html` for guidance on available fields.

Functions

- `itis_search()` - Search
- `itis_group()` - Group
- `itis_highlight()` - Highlight
- `itis_facet()` - Facet

---

solr_fields   *List of fields that can be used in solr functions*

Description

Each element in the list has a list of length tree, with:

Format

A list of length 36

Details

- field: the field name, this is the name you can use in your queries
- definition: the definition of the field
- example: an example value

Source

`https://www.itis.gov/solr_documentation.html`

---

synonym_names   *Returns a list of the synonyms (if any) for the TSN.*

Description

Returns a list of the synonyms (if any) for the TSN.

Usage

```
synonym_names(tsn, wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to [crul::HttpClient](#)

Value

a data.frame

Examples

```
## Not run:
synonym_names(tsn=183671) # tsn not accepted
synonym_names(tsn=526852) # tsn accepted

## End(Not run)
```

---

taxon_authorship   *Returns the author information for the TSN.*

Description

Returns the author information for the TSN.

Usage

```
taxon_authorship(tsn, wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to [crul::HttpClient](#)

Value

a data.frame

Examples

```
## Not run:
taxon_authorship(tsn = 183671)

## End(Not run)
```

---

terms	*Get ITIS terms, i.e., tsn's, authors, common names, and scientific names*

Description

Get ITIS terms, i.e., tsn's, authors, common names, and scientific names

Usage

```
terms(query, what = "both", wt = "json", raw = FALSE, ...)
```

Arguments

query	One or more common or scientific names, or partial names
what	One of both (search common and scientific names), common (search just common names), or scientific (search just scientific names)
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to [crul::HttpClient](#)

Examples

```
## Not run:
# Get terms searching both common and scientific names
terms(query='bear')

# Get terms searching just common names
terms(query='tarweed', "common")

# Get terms searching just scientific names
terms(query='Poa annua', "scientific")

# many at once
terms(query=c('Poa annua', 'Pinus contorta'), "scientific")

## End(Not run)
```

---

tsn2lsid	*Gets the unique LSID for the TSN, or an empty result if there is no match.*

Description

Gets the unique LSID for the TSN, or an empty result if there is no match.

Usage

```
tsn2lsid(tsn, wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to crul::HttpClient

Value

a character string, an LSID, or NULL if nothing found

Examples

```
## Not run:
tsn2lsid(tsn = 155166)
tsn2lsid(tsn = 333333333)
tsn2lsid(155166, raw = TRUE)
tsn2lsid(155166, wt = "xml")

## End(Not run)
```

`tsn_by_vernacular_language`

Get tsn by vernacular language

Description

Get tsn by vernacular language

Usage

```
tsn_by_vernacular_language(language, wt = "json", raw = FALSE, ...)
```

Arguments

language	A string containing the language. This is a language string, not the international language code (character)
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to [crul::HttpClient](#)

Value

a data.frame

Examples

```
## Not run:
tsn_by_vernacular_language(language = "french")

## End(Not run)
```

`unacceptability_reason`

Returns the unacceptability reason, if any, for the TSN.

Description

Returns the unacceptability reason, if any, for the TSN.

Usage

```
unacceptability_reason(tsn, wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to [crul::HttpClient](#)

Examples

```
## Not run:
unacceptability_reason(tsn = 183671)

## End(Not run)
```

---

usage   *Returns the usage information for the TSN.*

Description

Returns the usage information for the TSN.

Usage

```
usage(tsn, wt = "json", raw = FALSE, ...)
```

Arguments

tsn	TSN for a taxonomic group (numeric). Required.
wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to [crul::HttpClient](#)

Examples

```
## Not run:
usage(tsn = 526852)
usage(tsn = 526852, raw = TRUE)
usage(tsn = 526852, wt = "xml")

## End(Not run)
```

---

vernacular_languages *Provides a list of the unique languages used in the vernacular table.*

Description

Provides a list of the unique languages used in the vernacular table.

Usage

```
vernacular_languages(wt = "json", raw = FALSE, ...)
```

Arguments

wt	(character) One of "json" or "xml". Required.
raw	(logical) Return raw JSON or XML as character string. Required. Default: FALSE
...	curl options passed on to crul::HttpClient

Value

a character vector of verncular names

Examples

```
## Not run:
vernacular_languages()

## End(Not run)
```

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