Package ‘TNRS’

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Title  Taxonomic Name Resolution Service
Version  0.3.0
Description  Provides access to the Taxonomic Name Resolution Service <https://github.com/ojalaquellueva/tnrsapi> through R. The user supplies plant taxonomic names and the package returns resolved taxonomic names along with information on decisions. Optionally, the package can also be used to parse taxonomic names.

License  MIT + file LICENSE
Encoding  UTF-8
LazyData  true
Imports  jsonlite, httr
Suggests  knitr, rmarkdown, testthat, vcr (>= 0.6.0), devtools
VignetteBuilder  knitr
RoxygenNote  7.1.2
Depends  R (>= 2.10)
NeedsCompilation  no
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R topics documented:

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TNRS  Resolve plant taxonomic names

Description

Resolve plant taxonomic names.

Usage

TNRS(
  taxonomic_names,
  sources = c("tropicos", "wcvp"),
  classification = "tropicos",
  mode = "resolve",
  matches = "best",
  accuracy = NULL,
  ...
)

Arguments

taxonomic_names  Data.frame containing two columns: 1) Row number, 2) Taxonomic names to be resolved (or parsed). Alternatively, a character vector of names can be supplied.
sources  Character vector. Taxonomic sources to use. Default is c("tropicos","wcvp"). Options include "tropicos", "usda", "wfo", and "wcvp".
classification  Character. Family classification to use. Currently options include "tropicos" (the default), which is equivalent to APGIII, and "wfo".
mode  Character. Options are "resolve" and "parse". Default option is "resolve"
matches  Character. Should all matches be returned ("all") or only the best match ("best", the default)?
accuracy  numeric. If specified, only matches with a score greater than or equal to the supplied accuracy level will be returned. If left NULL, the default threshold will be used.
...  Additional parameters passed to internal functions

Value

Dataframe containing TNRS results.

Note

usda = United States Department of Agriculture, wfo = World Flora Online, wcvp = World Checklist of Vascular Plants.
Examples

```r
## Not run:
# Take a subset of the testfile to speed up runtime
tnrs_testfile <- tnrs_testfile[1:20,]

results <- TNRS(taxonomic_names = tnrs_testfile)

# Inspect the results
head(results, 10)

## End(Not run)
```

TNRS_base

Resolve a small batch of plant taxonomic names

Description

Resolve a small batch of plant taxonomic names

Usage

```r
TNRS_base(
  taxonomic_names,
  sources = c("tropicos", "wcvp"),
  classification = "tropicos",
  mode = "resolve",
  matches = "best",
  accuracy = NULL,
  ...
)
```

Arguments

taxonomic_names  Data.frame containing two columns: 1) Row number, 2) Taxonomic names to be resolved (or parsed). Alternatively, a character vector of names can be supplied.
sources  Character. Taxonomic sources to use. Default is c("tropicos","wcvp"). Options include "tropicos", "usda", "wfo", and "wcvp".
classification  Character. Family classification to use. Currently options include "tropicos" (the default), which is equivalent to APGIII, and "wfo".
mode  Character. Options are "resolve" and "parse". Default option is "resolve"
matches  Character. Should all matches be returned ("all") or only the best match ("best", the default)?
accuracy  numeric. If specified, only matches with a score greater than or equal to the supplied accuracy level will be returned.
...  Additonal parameters passed to internal functions
Value

Dataframe containing TNRS results.

Note

This function is primarily used as an internal function of TNRS and can only handle relatively small batches of names.

usda = United States Department of Agriculture, wfo = World Flora Online, wcvp = World Checklist of Vascular Plants.

---

**TNRS_citations**

*Get citation information*

Description

Returns information needed to cite the TNRS

Usage

TNRS_citations(...)

Arguments

... Additional parameters passed to internal functions

Value

Dataframe containing bibtex-formatted citation information

Note

This function provides citation information in bibtex format that can be used with reference manager software (e.g. Paperpile, Zotero). Please do remember to cite both the sources and the TNRS, as the TNRS couldn’t exist without these sources!

Examples

```r
{
  citation_info <- TNRS_citations()
}
```
Description

Returns metadata on TNRS including version and citation information

Usage

TNRS_metadata(bibtex_file = NULL)

Arguments

bibtex_file Optional output file for writing bibtex citations.

Value

List containing: (1) bibtex-formatted citation information, (2) information about TNRS data sources, and (3) TNRS version information.

Note

This function provides citation information in bibtex format that can be used with reference manager software (e.g. Paperpile, Zotero). Please remember to cite both the sources and the TNRS, as the TNRS couldn’t exist without these sources!

This function is a wrapper that returns the output of the functions TNRS_citations, TNRS_sources, and TNRS_version.

Examples

```
 metadata <- TNRS_metadata()
```

Description

Return metadata about the current TNRS sources

Usage

TNRS_sources(…)

Arguments

... Additional parameters passed to internal functions

Value

Dataframe containing information about the sources used in the current TNRS version.

Examples

```r
{  
sources <- TNRS_sources()
}
```

---

**tnrs_testfile**

*100 scientific names.*

---

Description

A dataset containing scientific names for 100 taxa. Names vary in accuracy and correctness.

Usage

`tnrs_testfile`

Format

A data frame with 100 rows and 2 variables:

- **ID** Unique integer identifying each row
- **taxon** Scientific name, possibly containing errors ...

Source

https://github.com/ojalaquellueva/TNRSapi
TNRS_version

Get metadata on current TNRS version

Description
Return metadata about the current TNRS version

Usage
TNRS_version(...)

Arguments
... Additional parameters passed to internal functions

Value
Dataframe containing current TNRS version number, build date, and code version.

Examples
{
    TNRS_version_metadata <- TNRS_version()
}

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