Package ‘TNRS’

March 30, 2021

Title Taxonomic Name Resolution Service
Version 0.1.0
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, RCurl, rjson
Suggests knitr, rmarkdown, testthat, devtools
VignetteBuilder knitr
RoxygenNote 7.1.1
Depends R (>= 2.10)
NeedsCompilation no
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Repository CRAN
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.TNRS_base

Description

Resolve a small batch of plant taxonomic names

Usage

.TNRS_base(
  taxonomic_names,  
sources = "tpl,tropicos,usda",  
classification = "tropicos",  
mode = "resolve",  
matches = "best"
)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>taxonomic_names</td>
<td>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.</td>
</tr>
<tr>
<td>sources</td>
<td>Character. Taxonomic sources to use. Default is &quot;tpl,tropicos,usda&quot;. Options include tpl,tropicos,usda,ncbi</td>
</tr>
<tr>
<td>classification</td>
<td>Character. Family classification to use. Currently the only options is &quot;tropicos&quot;, which is equivalent to APGIII.</td>
</tr>
<tr>
<td>mode</td>
<td>Character. Options are &quot;resolve&quot; and &quot;parse&quot;. Default option is &quot;resolve&quot;</td>
</tr>
<tr>
<td>matches</td>
<td>Character. Should all matches be returned (&quot;all&quot;) or only the best match (&quot;best&quot;, the default)?</td>
</tr>
</tbody>
</table>

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.
TNRS

TNRS

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Resolve plant taxonomic names

**Description**

Resolve plant taxonomic names.

**Usage**

```r
TNRS(
  taxonomic_names,
  sources = "tpl,tropicos,usda",
  classification = "tropicos",
  mode = "resolve",
  matches = "best"
)
```

**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 "tpl,tropicos,usda". Options include tpl,tropicos,usda,ncbi
- `classification`: Character. Family classification to use. Currently the only options is "tropicos", which is equivalent to APGIII.
- `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)?

**Value**

Dataframe containing TNRS results.

**Examples**

```r

# 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)
```

**TNRS_citations**  
*Get citation information*

**Description**

Returns information needed to cite the TNRS

**Usage**

TNRS_citations()

**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()
}
```

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**TNRS_metadata**  
*Get TNRS metadata*

**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

```{r}
metadata <- TNRS_metadata()
```

---

**TNRS_sources**

*Get information on sources used by the TNRS*

**Description**

Return metadata about the current TNRS sources

**Usage**

```
TNRS_sources()
```

**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

```r
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](https://github.com/ojalaquellueva/TNRSapi)

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### TNRS_version

Get metadata on current TNRS version

#### Description

Return metadata about the current TNRS version

#### Usage

```r
TNRS_version()
```

#### Value

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

#### Examples

```r
{
    TNRS_version_metadata <- TNRS_version()
}
```
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