

# 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	<i>Resolve a single batch of (plant) taxonomic names</i>
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### 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

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.

### Note

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

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**TNRS***Resolve plant taxonomic names*

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**Description**

Resolve plant taxonomic names.

**Usage**

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

**Arguments**

<code>taxonomic_names</code>	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.
<code>sources</code>	Character. Taxonomic sources to use. Default is "tpl,tropicos,usda". Options include tpl,tropicos,usda,ncbi
<code>classification</code>	Character. Family classification to use. Currently the only options is "tropicos", which is equivalent to APGIII.
<code>mode</code>	Character. Options are "resolve" and "parse". Default option is "resolve"
<code>matches</code>	Character. Should all matches be returned ("all") or only the best match ("best", the default)?

**Value**

Dataframe containing TNRS results.

**Examples**

```
{  
  #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)  
}
```

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TNRS_citations	<i>Get citation information</i>
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**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**

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

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TNRS_metadata	<i>Get TNRS metadata</i>
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**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()  
}
```

---

TNRS\_sources

*Get information on sources used by the TNRS*

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**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**

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

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tnrs_testfile	<i>100 scientific names.</i>
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**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>

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TNRS_version	<i>Get metadata on current TNRS version</i>
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**Description**

Return metadata about the current TNRS version

**Usage**

```
TNRS_version()
```

**Value**

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

**Examples**

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

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