

# Package ‘TNRS’

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**Title** Taxonomic Name Resolution Service

**Version** 0.3.5

**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** 7.2.3

**Depends** R (>= 3.5.0)

**NeedsCompilation** no

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TNRS	<i>Resolve plant taxonomic names</i>
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**Description**

Resolve plant taxonomic names.

**Usage**

```
TNRS(
  taxonomic_names,
  sources = c("wcvp", "wfo"),
  classification = "wfo",
  mode = "resolve",
  matches = "best",
  accuracy = NULL,
  skip_internet_check = FALSE,
  ...
)
```

**Arguments**

taxonomic_names	Data.frame containing two columns: 1) Row number, 2) Taxonomic names to be resolved (or parsed). Note that these two columns must be in this order. Alternatively, a character vector of names can be supplied.
sources	Character. Taxonomic sources to use. Default is c("wcvp", "wfo"). Options include "wfo", "wcvp", and "cact". Use TNRS_sources() for more information.
classification	Character. Family classification to use. Currently options include "wfo" (the default).
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.
skip_internet_check	Should the check for internet connectivity be skipped? Default is FALSE.
...	Additional parameters passed to internal functions

**Value**

Dataframe containing TNRS results.

**Note**

wfo = World Flora Online, wcvp = World Checklist of Vascular Plants, cact = Cactaceae at Caryophyllales.org.

For queries of more than 5000 names, the function will automatically divide the query into batches of 5000 names and then run the batches one after the other. Thus, for very large queries this may take some time. When this is the case, a progress bar will be displayed.

**IMPORTANT:** Note that parallelization of queries is automatically handled by the API, and so there is no need to further parallelize in R (in fact, doing so may actually slow things down!).

**Examples**

```
## 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)
```

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TNRS\_base

*Resolve a small batch of plant taxonomic names*

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**Description**

Resolve a small batch of plant taxonomic names

**Usage**

```
TNRS_base(  
  taxonomic_names,  
  sources = c("wcvp", "wfo"),  
  classification = "wfo",  
  mode = "resolve",  
  matches = "best",  
  accuracy = NULL,  
  skip_internet_check = FALSE,  
  ...  
)
```

**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("wcvp", "wfo"). Options include "wfo", and "wcvp".
classification	Character. Family classification to use. Currently options include "wfo" (the default).
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.
skip_internet_check	Should the check for internet connectivity be skipped? Default is FALSE.
...	Additional 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.

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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(skip_internet_check = FALSE, ...)
```

**Arguments**

skip_internet_check	Should the check for internet connectivity be skipped? Default is FALSE.
...	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**

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

---

TNRS\_metadata

*Get TNRS metadata*

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**Description**

Returns metadata on TNRS including version and citation information

**Usage**

```
TNRS_metadata(bibtex_file = NULL, skip_internet_check = FALSE)
```

**Arguments**

`bibtex_file` Optional output file for writing bibtex citations.

`skip_internet_check`

Should the check for internet connectivity be skipped? Default is FALSE.

**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()
}
```

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TNRS_sources	<i>Get information on sources used by the TNRS</i>
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**Description**

Return metadata about the current TNRS sources

**Usage**

```
TNRS_sources(skip_internet_check = FALSE, ...)
```

**Arguments**

```
skip_internet_check      Should the check for internet connectivity be skipped? Default is FALSE.
...                       Additional parameters passed to internal functions
```

**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(skip_internet_check = FALSE, ...)
```

**Arguments**

`skip_internet_check`

Should the check for internet connectivity be skipped? Default is FALSE.

`...`

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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