

Package: rgnparser (via r-universe)

August 30, 2026

Title Parse Scientific Names

Description Parse scientific names using 'gnparser'
(<https://github.com/gnames/gnparser>), written in Go.
'gnparser' parses scientific names into their component parts;
it utilizes a Parsing Expression Grammar specifically for
scientific names.

Version 0.3.0

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URL <https://docs.ropensci.org/rgnparser/>,
<https://github.com/ropensci/rgnparser>

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

Roxygen list(markdown = TRUE)

Encoding UTF-8

Language en-US

SystemRequirements gnparser (<https://github.com/gnames/gnparser>)

Imports sys, tibble, jsonlite, readr, lifecycle

Suggests testthat

RoxygenNote 7.2.3

Config/pak/sysreqs libx11-dev

Repository <https://ropensci.r-universe.dev>

Date/Publication 2026-05-29 14:59:30 UTC

RemoteUrl <https://github.com/ropensci/rgnparser>

RemoteRef main

RemoteSha f3fa6f483d8f798284c37da9693ce905fa378986

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rgnparser-package	<i>rgnparser</i>
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Description

Parse scientific names using gnparser

gn_debug	<i>gn_debug</i>
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Description

DEFUNCT

Usage

gn_debug(...)

Arguments

... ignored

gn_parse	<i>gn_parse</i>
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Description

extract names using gnparsers

Usage

```
gn_parse(
  x,
  threads = 1,
  batch_size = NULL,
  ignore_tags = FALSE,
  cultivar = FALSE,
  capitalize = FALSE,
  diaereses = FALSE,
  details = FALSE
)
```

Arguments

x	(character) vector of scientific names. required
threads	(integer/numeric) number of threads to run for parallel processing. Setting to NULL will use all threads available. default: 1
batch_size	(integer/numeric) maximum number of names in a batch send for processing. default: NULL
ignore_tags	(logical) ignore HTML entities and tags when parsing. default: FALSE
cultivar	(logical) adds support for botanical cultivars like <i>Sarracenia flava</i> 'Maxima' and graft-chimaeras like + <i>Crataegomespilus</i> . default: FALSE
capitalize	(logical) capitalizes the first letter of name-strings. default: FALSE
diaereses	(logical) preserves diaereses within names, e.g. <i>Leptochloöpsis virgata</i> . The stemmed canonical name will be generated without diaereses. default: FALSE
details	(logical) Return more details for a parsed name

Value

a list

Examples

```
trys <- function(x) try(x, silent=TRUE)
if (interactive()) {
  x <- c("Quadrella steyermarkii (Standl.) Iltis & Cornejo",
        "Parus major Linnaeus, 1788", "Helianthus annuus var. texanus")
}
```

```

trys(gn_parse(x[1]))
trys(gn_parse(x[2]))
trys(gn_parse(x[3]))
trys(gn_parse(x))
# details
w <- trys(gn_parse(x, details = TRUE))
w[[1]]$details # details for one name
lapply(w, "[", "details") # details for all names
z <- trys(gn_parse(x, details = FALSE)) # compared to regular
z
}

```

gn_parse_tidy

gn_parse_tidy

Description

extract names using gnparser into a tidy tibble

Usage

```

gn_parse_tidy(
  x,
  threads = 1,
  batch_size = NULL,
  cultivar = FALSE,
  capitalize = FALSE,
  diaereses = FALSE,
  ignore_tags = FALSE
)

```

Arguments

x	(character) vector of scientific names. required
threads	(integer/numeric) number of threads to run for parallel processing. Setting to NULL will use all threads available. default: 1
batch_size	(integer/numeric) maximum number of names in a batch send for processing. default: NULL
cultivar	(logical) adds support for botanical cultivars like <i>Sarracenia flava</i> 'Maxima' and graft-chimaeras like + <i>Crataegomespilus</i> . default: FALSE
capitalize	(logical) capitalizes the first letter of name-strings. default: FALSE
diaereses	(logical) preserves diaereses within names, e.g. <i>Leptochloöpsis virgata</i> . The stemmed canonical name will be generated without diaereses. default: FALSE
ignore_tags	(logical) ignore HTML entities and tags when parsing. default: FALSE

Details

This function focuses on a data.frame result that's easy to munge downstream - note that this function does not do additional details as does [gn_parse\(\)](#).

Value

a data.frame

Examples

```
trys <- function(x) try(x, silent=TRUE)
if (interactive()) {
  x <- c("Quadrella steyermarkii (Standl.) Iltis & Cornejo",
        "Parus major Linnaeus, 1788", "Helianthus annuus var. texanus")
  trys(gn_parse_tidy(x))
}
```

gn_version

gn_version

Description

get gnparser version information

Usage

gn_version()

Value

named list, with version and build

Examples

```
trys <- function(x) try(x, silent=TRUE)
if (interactive()) {
  trys(gn_version())
}
```

install_gnparser

Install gnparser

Description**[Deprecated]****Reason for deprecating:**

The function used to download the appropriate gnparser executable for your platform and try to copy it to a system directory so **rgnparser** can run the gnparser command. This function was deprecated to stay in compliance with CRAN policies ("Packages should not write in the user's home filespace, nor anywhere else on the file system apart from the R session's temporary directory")

Solution:

Please install gnparser by hand. For Linux and Mac users, installing with your usual package manager such as homebrew is the easiest, see gnparser documentation for more details: <https://github.com/gnames/gnparser#installation>

Usage

```
install_gnparser(version, force)
```

Arguments

version	The gnparser version number, e.g., 1.0.0; the default latest means the latest version (fetched from GitLab releases). Alternatively, this argument can take a file path of the zip archive or tarball of gnparser that has already been downloaded from GitLab, in which case it will not be downloaded again. The minimum version is v1.0.0 because gnparser v1 introduced breaking changes - and we don't support older versions of gnparser here.
force	Whether to install gnparser even if it has already been installed. This may be useful when upgrading gnparser.

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