

# Package: rgnparser (via r-universe)

October 6, 2024

**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

**License** MIT + file LICENSE

**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

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

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

**RemoteRef** main

**RemoteSha** 2be26db42f0cce1e6f88f12ccc8abe379ddc0460

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

Parse scientific names using gnparsers

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gn_debug	<i>gn_debug</i>
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**Description**

DEFUNCT

**Usage**

```
gn_debug(...)
```

**Arguments**

...	ignored
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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
}

```

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gn\_parse\_tidy

*gn\_parse\_tidy*


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**Description**

extract names using gnparsr 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*

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**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())
}
```

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`install_gnparser`*Install gnparser*

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**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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