Package: fungaltraits (via r-universe)

May 28, 2026

Title A dynamically-updating versioned trait database for fungi

Version 0.0.3

Date 2018-04-11

Description A functional trait database for fungi.

Depends R (>= 3.1.0)

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LazyData true

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Imports tidyr, datastorr (>= 0.0.3)

Suggests testthat

RoxygenNote 5.0.1

Config/pak/sysreqs libicu-dev libssl-dev

Repository https://traitecoevo.r-universe.dev

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RemoteUrl https://github.com/traitecoevo/fungaltraits

RemoteRef HEAD

RemoteSha 2a3671647afc82f101bb00b3ff3d99da0630388a

Contents

`fungal_traits` *Fungal trait database*

Description

This function provides access to the fungal traits database

Usage

```
fungal_traits(version = NULL, path = NULL)

fungal_traits_versions(local = TRUE, path = NULL)

fungal_traits_version_current(local = TRUE, path = NULL)

fungal_traits_del(version, path = NULL)
```

Arguments

`version`	Version number. The default will load the most recent version on your computer or the most recent version known to the package if you have never downloaded the data before. With `plant_lookup_del`, specifying `version=NULL` will delete *all* data sets.
`path`	Path to store the data at. If not given, `datastorr` will use `rappdirs` to find the best place to put persistent application data on your system. You can delete the persistent data at any time by running `mydata_del(NULL)` (or `mydata_del(NULL, path)` if you use a different path).
`local`	Logical indicating if local or github versions should be polled. With any luck, `local=FALSE` is a superset of `local=TRUE`. For `mydata_version_current`, if `TRUE`, but there are no local versions, then we do check for the most recent github version.

Details

The data within this lookup table comes from many original sources. For speedy access to the data within R use this function. For access to the full meta-data, download the zip file associated with the Github release.

Examples

```
#
# see the format of the resource
#
head(fungal_traits())
#
#
```

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