

Package ‘mauricer’

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Type Package

Title Install 'BEAST2' Packages

Version 2.0.5

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Description 'BEAST2' (<<http://www.beast2.org>>) is a widely used Bayesian phylogenetic tool, that uses DNA/RNA/protein data and many model priors to create a posterior of jointly estimated phylogenies and parameters.
'BEAST2' is commonly accompanied by 'BEAUti 2' (<<http://www.beast2.org>>), which, among others, allows one to install 'BEAST2' package.
This package allows to install 'BEAST2' packages from 'R'.

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

Depends beastier

Imports stringr

Suggests beautiful, curl, knitr, rmarkdown, testit, testthat (>= 2.1.0)

VignetteBuilder knitr

URL <https://github.com/ropensci/mauricer>

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

SystemRequirements BEAST2 (<http://www.beast2.org/>)

NeedsCompilation no

Repository CRAN

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get_beast2_pkg_names *List all BEAST2 packages available and installed*

Description

Will [stop](#) if there is no internet connection

Usage

```
get_beast2_pkg_names()
```

Value

a data frame

Author(s)

Richèl J.C. Bilderbeek

Examples

```
library(testthat)

if (is_beast2_installed() && curl::has_internet()) {
  df <- get_beast2_pkg_names()
  expect_true("name" %in% names(df))
  expect_true("installed_version" %in% names(df))
  expect_true("latest_version" %in% names(df))
  expect_true("dependencies" %in% names(df))
  expect_true("description" %in% names(df))
}
```

| | |
|--------------|---|
| get_mrc_path | <i>Get the full path of a file in the inst/extdata folder</i> |
|--------------|---|

Description

Get the full path of a file in the inst/extdata folder

Usage

```
get_mrc_path(filename)
```

Arguments

filename the file's name, without the path

Value

the full path of the filename, if and only if the file is present. Will stop otherwise.

Author(s)

Richèl J.C. Bilderbeek

See Also

for more files, use [get_mrc_paths](#)

Examples

```
library(testthat)

expect_true(file.exists(get_mrc_path("anthus_aco_sub.fas")))
expect_true(file.exists(get_mrc_path("anthus_nd2_sub.fas")))
```

| | |
|---------------|---|
| get_mrc_paths | <i>Get the full paths of files in the 'inst/extdata' folder</i> |
|---------------|---|

Description

Get the full paths of files in the 'inst/extdata' folder

Usage

```
get_mrc_paths(filenamees)
```

Arguments

filenames the files' names, without the path

Value

the filenames' full paths, if and only if all files are present. Will stop otherwise.

Author(s)

Richèl J.C. Bilderbeek

See Also

for one file, use [get_mrc_path](#)

Examples

```
filenames <- get_mrc_paths(c("anthus_aco_sub.fas", "anthus_nd2_sub.fas"))  
  
library(testthat)  
expect_true(all(file.exists(filenames)))
```

install_beast2_pkg *Install a BEAST2 package*

Description

Install a BEAST2 package

Usage

```
install_beast2_pkg(name)
```

Arguments

name the package's name

Value

nothing. It does install the BEAST2 package

Author(s)

Richèl J.C. Bilderbeek

Examples

```
library(testthat)

# Only install a package on Travis,
# if BEAST2 is installed and the package is not
if (is_on_travis() &&
    is_beast2_installed()
    && !is_beast2_ns_pkg_installed())
) {
  install_beast2_pkg("NS")
  expect_true(is_beast2_ns_pkg_installed())
}
```

is_beast2_ns_pkg_installed

Determine if the BEAST2 NS package is installed

Description

Determine if the BEAST2 NS package is installed

Usage

```
is_beast2_ns_pkg_installed()
```

Value

TRUE if the BEAST2 NS package is installed, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
library(testthat)

if (is_beast2_installed()) {
  print(
    paste(
      "Is the BEAST2 NS package installed:",
      is_beast2_ns_pkg_installed()
    )
  )
}
```

`is_beast2_pkg_installed`*Checks if a BEAST2 package is already installed.*

Description

To be able to check this, an internet connection is needed. Without an internet connection, NULL is returned.

Usage

```
is_beast2_pkg_installed(name)
```

Arguments

| | |
|------|---------------------|
| name | BEAST2 package name |
|------|---------------------|

Value

- TRUE if the BEAST2 package is installed
- FALSE if the BEAST2 package is not installed
- NULL if there is no internet connection

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [is_beast2_ns_pkg_installed](#) to see if the NS package is installed without an internet connection

Examples

```
library(testthat)

if (is_beast2_installed() && curl::has_internet()) {
  print(
    paste(
      "Is the Beasy BEAST2 package installed:",
      is_beast2_pkg_installed("Beasy")
    )
  )
}
```

mauricer *mauricer: Install BEAST2 packages.*

Description

'BEAST2' (<<http://www.beast2.org>>) is a widely used Bayesian phylogenetic tool, that uses DNA/RNA/protein data and many model priors to create a posterior of jointly estimated phylogenies and parameters.

Details

'BEAST2' is commonly accompanied by 'BEAUi 2' (<<http://www.beast2.org>>), which, among others, allows one to install 'BEAST2' package. This package allows to install 'BEAST2' packages from 'R'.

See Also

[mauricer](#) is part of the *babette* package suite:

- [babette](#): work with BEAST2
- [beautier](#): create BEAST2 input files
- [beastier](#): run BEAST2
- [mauricer](#): install BEAST2 packages
- [tracerer](#): parse and analyse BEAST2 output

`uninstall_beast2_pkg` *Uninstall a BEAST2 package*

Description

Uninstall a BEAST2 package

Usage

```
uninstall_beast2_pkg(name)
```

Arguments

name the package's name

Value

nothing. It does install the BEAST2 package

Author(s)

Richèl J.C. Bilderbeek

Examples

```
library(testthat)

# Only install a package on Travis, if BEAST2 is installed
# and the package is not
if (is_on_travis() &&
    is_beast2_installed() &&
    curl::has_internet() &&
    !is_beast2_pkg_installed("Beasy"))
) {
  install_beast2_pkg("Beasy")
  expect_true(is_beast2_pkg_installed("Beasy"))

  uninstall_beast2_pkg("Beasy")
  expect_false(is_beast2_pkg_installed("Beasy"))
}
```


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