

# Package ‘mauricer’

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**Type** Package

**Title** Install 'BEAST2' Packages

**Version** 2.1

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**Description** 'BEAST2' (<<https://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' (<<https://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** 7.1.1

**Depends** beastier

**Imports** curl, stringr

**Suggests** beautier, knitr, rmarkdown, testit, testthat (>= 2.1.0)

**VignetteBuilder** knitr

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

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

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

**NeedsCompilation** no

**Repository** CRAN

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default_params_doc	<i>This function does nothing. It is intended to inherit is parameters' documentation.</i>
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Description

This function does nothing. It is intended to inherit is parameters' documentation.

Usage

default\_params\_doc(has\_internet, name)

Arguments

- has\_internet      boolean to indicate if the user has access to the internet. By default, this value equals the result of curl::has\_internet
- name              the package's name

Note

This is an internal function, so it should be marked with @noRd. This is not done, as this will disallow all functions to find the documentation parameters

Author(s)

Richèl J.C. Bilderbeek

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get\_beast2\_pkg\_names    *Get all BEAST2 package names*

---

## Description

List all BEAST2 packages that are available and installed. Will [stop](#) if there is no internet connection

## Usage

```
get_beast2_pkg_names(has_internet = curl::has_internet())
```

## Arguments

**has\_internet**    boolean to indicate if the user has access to the internet. By default, this value equals the result of `curl::has_internet`

## Value

a data frame with columns

1. name package name, for example, codebdmm
2. installed\_version the installed version, for example, 2.6.2. installed\_version will be NA if the package is not installed
3. latest\_version version number of the latest version, for example, 2.6.3
4. dependencies packages the package depends on, for example BEASTLabs, GEO\_SPHERE. dependencies will be empty if there are no dependencies
5. description description of the package, for example Nested sampling for model selection and posterior inference

## Author(s)

Richèl J.C. Bilderbeek

## Examples

```
if (is_beast2_installed() && curl::has_internet()) {  
  get_beast2_pkg_names()  
}
```

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get_mrc_path	<i>Get the full path of a mauricer file</i>
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**Description**

Get the full path of a file in the inst/extdata folder. If there is no mauricer file, [get\\_mrc\\_path](#) will [stop](#).

**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**

```
get_mrc_path("anthus_aco_sub.fas")
```

---

get_mrc_paths	<i>Get the full path of one or more mauricer files</i>
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---

**Description**

Get the full paths of files in the inst/extdata folder. If there is a mauricer file absent, [get\\_mrc\\_paths](#) will [stop](#).

**Usage**

```
get_mrc_paths(fileNames)
```

**Arguments**

fileNames	the files' names, without the path
-----------	------------------------------------

**Value**

the filenames' full paths

**Author(s)**

Richèl J.C. Bilderbeek

**See Also**

for one file, use [get\\_mrc\\_path](#)

**Examples**

```
get_mrc_paths(c("anthus_aco_sub.fas", "anthus_nd2_sub.fas"))
```

---

install_beast2_pkg	<i>Install a BEAST2 package</i>
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---

**Description**

Install a BEAST2 package. If the package is already installed, (see [is\\_beast2\\_pkg\\_installed](#)), this function [stops](#).

**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**

```
## Not run:  
install_beast2_pkg("NS")  
  
## End(Not run)
```

is\_beast2\_ns\_pkg\_installed

*Is the BEAST2 NS package installed?*

---

### Description

Determine if the BEAST2 NS package is installed.

### Usage

```
is_beast2_ns_pkg_installed()
```

### Details

Unlike [is\\_beast2\\_pkg\\_installed](#), this function does not need an internet connection. Instead, the function calls BEAST2 to read a BEAST2 XML file that uses NS.

### Value

TRUE if the BEAST2 NS package is installed, FALSE otherwise

### Author(s)

Richèl J.C. Bilderbeek

### Examples

```
## Not run:  
  is_beast2_ns_pkg_installed()  
  
## End(Not run)
```

---

is\_beast2\_pkg\_installed

*Is a BEAST2 package installed?*

---

### Description

Checks if a BEAST2 package is installed.

### Usage

```
is_beast2_pkg_installed(name, has_internet = curl::has_internet())
```

**Arguments**

name	the package's name
has_internet	boolean to indicate if the user has access to the internet. By default, this value equals the result of <code>curl::has_internet</code>

**Details**

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

**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**

```
## Not run:
  is_beast2_pkg_installed("Beasy")

## End(Not run)
```

---

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

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uninstall\_beast2\_pkg    *Uninstall a BEAST2 package*

---

**Description**

Uninstall a BEAST2 package

**Usage**

```
uninstall_beast2_pkg(name, has_internet = curl::has_internet())
```

**Arguments**

name	the package's name
has_internet	boolean to indicate if the user has access to the internet. By default, this value equals the result of <code>curl::has_internet</code>

**Value**

nothing. It does install the BEAST2 package

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
## Not run:  
  uninstall_beast2_pkg("Beasy")  
  
## End(Not run)
```



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