

# Package ‘beastier’

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**Type** Package

**Title** Call 'BEAST2'

**Version** 2.2.1

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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 a command-line tool.  
This package provides a way to call 'BEAST2' from an 'R' function call.

**License** GPL-3

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<https://github.com/ropensci/beastier/>

**BugReports** <https://github.com/ropensci/beastier>

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---

are\_beast2\_input\_lines

*Would these lines of text, when written to a file, result in a valid BEAST2 input file?*

---

### Description

Would these lines of text, when written to a file, result in a valid BEAST2 input file?

### Usage

```
are_beast2_input_lines(
  lines,
  verbose = FALSE,
  method = ifelse(is_on_ci(), "deep", "fast"),
  beast2_path = get_default_beast2_path()
)
```

### Arguments

lines	lines of text
verbose	if TRUE, additional information is displayed, that is potentially useful in debugging
method	the method to check. Can be 'deep' or 'fast'. The 'deep' method uses BEAST2 to validate the complete file. The 'fast' method uses some superficial tests (for example: if all IDs are unique)
beast2_path	name of either a BEAST2 binary file (usually simply beast) or a BEAST2 jar file (usually has a .jar extension). Use <a href="#">get_default_beast2_bin_path</a> to get the default BEAST binary file's path Use <a href="#">get_default_beast2_jar_path</a> to get the default BEAST jar file's path

### Value

TRUE if the text is valid, FALSE if not

### Author(s)

Richèl J.C. Bilderbeek

### See Also

Use [is\\_beast2\\_input\\_file](#) to check a file

### Examples

```
if (is_beast2_installed() && is_on_ci()) {
  get_beastier_path("anthus_2_4.xml")
}
```

---

`are_beast2_input_lines_deep`

*Would these lines of text, when written to a file, result in a valid BEAST2 input file?*

---

## Description

Would these lines of text, when written to a file, result in a valid BEAST2 input file?

## Usage

```
are_beast2_input_lines_deep(  
  lines,  
  verbose = FALSE,  
  beast2_path = get_default_beast2_path()  
)
```

## Arguments

<code>lines</code>	lines of text
<code>verbose</code>	if TRUE, additional information is displayed, that is potentially useful in debugging
<code>beast2_path</code>	name of either a BEAST2 binary file (usually simply <code>beast</code> ) or a BEAST2 jar file (usually has a <code>.jar</code> extension). Use <a href="#">get_default_beast2_bin_path</a> to get the default BEAST binary file's path Use <a href="#">get_default_beast2_jar_path</a> to get the default BEAST jar file's path

## Value

TRUE if the text is valid, FALSE if not

## Author(s)

Richèl J.C. Bilderbeek

## See Also

Use [is\\_beast2\\_input\\_file](#) to check a file

## Examples

```
if (is_beast2_installed() && is_on_ci()) {  
  beast2_filename <- get_beastier_path("anthus_2_4.xml")  
  text <- readLines(beast2_filename)  
  testit::assert(are_beast2_input_lines_deep(text))  
}
```

---

```
are_beast2_input_lines_fast
```

*Would these lines of text, when written to a file, result in a valid BEAST2 input file?*

---

### Description

Would these lines of text, when written to a file, result in a valid BEAST2 input file?

### Usage

```
are_beast2_input_lines_fast(lines)
```

### Arguments

lines	lines of text
-------	---------------

### Value

TRUE if the text is valid, FALSE if not

### Author(s)

Richèl J.C. Bilderbeek

### See Also

Use [is\\_beast2\\_input\\_file](#) to check a file

### Examples

```
beast2_filename <- get_beastier_path("anthus_2_4.xml")
text <- readLines(beast2_filename)

# TRUE
are_beast2_input_lines_fast(text)
```

---

are\_identical\_alignments

*Determines if the two alignments are equal*

---

### **Description**

Determines if the two alignments are equal

### **Usage**

are\_identical\_alignments(p, q)

### **Arguments**

p	the first alignment
q	the second alignment

### **Value**

TRUE or FALSE

### **Author(s)**

Richèl J.C. Bilderbeek

---

beast2\_internal\_filenames\_to\_table

*Convert a beast2\_internal\_filenames to a table*

---

### **Description**

Convert a beast2\_internal\_filenames to a table

### **Usage**

beast2\_internal\_filenames\_to\_table(beast2\_internal\_filenames)

### **Arguments**

beast2\_internal\_filenames  
a list of internally used BEAST2 filenames, as created by [create\\_beast2\\_internal\\_filenames](#)

---

`beast2_options_to_table`*Convert a beast2\_options to a table*

---

**Description**

Convert a `beast2_options` to a table

**Usage**

```
beast2_options_to_table(beast2_options)
```

**Arguments**

`beast2_options` a set of BEAST2 options, that are the R equivalent of the BEAST2 command-line options, as can be created by [create\\_beast2\\_options](#)

---

`beastier`*beastier: A package to call BEAST2.*

---

**Description**

`beastier` allows to call BEAST2, a popular Bayesian phylogenetics tool, using an R interface. 'beastier' closely follows the interface of BEAST2, including its default settings.

**See Also**

These are packages associated with `beastier`:

- The package `beautier` can create BEAST2 input files from R
- The package `tracrer` can parse BEAST2 output files from R
- The package `babette` combines the functionality of `beautier`, `beastier` and `tracrer` into a single workflow

**Examples**

```
beast2_options <- create_beast2_options(  
  input_filename = get_beastier_path("2_4.xml")  
)  
  
if (is_beast2_installed() && is_on_ci()) {  
  run_beast2_from_options(beast2_options)  
}
```



---

beastier_report	Create a <i>beastier</i> report, to be used when reporting bugs
-----------------	---

---

**Description**

Create a [beastier](#) report, to be used when reporting bugs

**Usage**

```
beastier_report()
```

---

check_beast2	Check if BEAST2 is installed properly.
--------------	--

---

**Description**

Calls stop if BEAST2 is improperly installed

**Usage**

```
check_beast2(beast2_path = get_default_beast2_path())
```

**Arguments**

beast2_path	name of either a BEAST2 binary file (usually simply <code>beast</code> ) or a BEAST2 jar file (usually has a <code>.jar</code> extension). Use <a href="#">get_default_beast2_bin_path</a> to get the default BEAST binary file's path Use <a href="#">get_default_beast2_jar_path</a> to get the default BEAST jar file's path
-------------	---

**Value**

nothing

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
if (is_beast2_installed()) {  
  check_beast2()  
}
```

check\_beast2\_internal\_filenames

*Check if the `beast2_internal_filenames` is a valid BEAST2 internal filenames object.*

---

### Description

Calls stop if the BEAST2 internal filenames object is invalid

### Usage

```
check_beast2_internal_filenames(beast2_internal_filenames)
```

### Arguments

`beast2_internal_filenames`  
a list of internally used BEAST2 filenames, as created by [create\\_beast2\\_internal\\_filenames](#)

### Value

nothing

### Author(s)

Richèl J.C. Bilderbeek

### See Also

Use [create\\_beast2\\_internal\\_filenames](#) to create a valid BEAST2 internal filenames object

### Examples

```
if (beastier::is_beast2_installed()) {  
  check_beast2_internal_filenames(  
    create_beast2_internal_filenames(  
      create_beast2_options(  
        input_filename = get_beastier_path("2_4.xml")  
      )  
    )  
  )  
}
```

---

check\_beast2\_internal\_filenames\_data\_types

*Check if the `beast2_internal_filenames`, which is a list, has all elements of the right data types*

---

**Description**

Calls stop if not.

**Usage**

```
check_beast2_internal_filenames_data_types(beast2_internal_filenames)
```

**Arguments**

`beast2_internal_filenames`

a list of internally used BEAST2 filenames, as created by [create\\_beast2\\_internal\\_filenames](#)

**Value**

nothing

**Author(s)**

Richèl J.C. Bilderbeek

**See Also**

Use [check\\_beast2\\_internal\\_filenames](#) to check the entire `beast2_internal_filenames` object

---

check\_beast2\_internal\_filenames\_filenames\_differ

*Check if the filenames in `beast2_internal_filenames` differ*

---

**Description**

Calls stop if not.

**Usage**

```
check_beast2_internal_filenames_filenames_differ(beast2_internal_filenames)
```

**Arguments**

`beast2_internal_filenames`

a list of internally used BEAST2 filenames, as created by [create\\_beast2\\_internal\\_filenames](#)

**Value**

nothing

**Author(s)**

Richèl J.C. Bilderbeek

**See Also**

Use [check\\_beast2\\_internal\\_filenames](#) to check the entire `beast2_internal_filenames` object

---

`check_beast2_internal_filenames_names`

*Check if the `beast2_internal_filenames`, which is a list, has all the elements needed.*

---

**Description**

Calls `stop` if not.

**Usage**

```
check_beast2_internal_filenames_names(beast2_internal_filenames)
```

**Arguments**

`beast2_internal_filenames`  
a list of internally used BEAST2 filenames, as created by [create\\_beast2\\_internal\\_filenames](#)

**Value**

nothing

**Author(s)**

Richèl J.C. Bilderbeek

**See Also**

Use [check\\_beast2\\_internal\\_filenames](#) to check the entire `beast2_internal_filenames` object

---

check\_beast2\_options *Check if the beast2\_options is a valid BEAST2 options object.*

---

**Description**

Calls stop if the BEAST2 option object is invalid

**Usage**

```
check_beast2_options(beast2_options)
```

**Arguments**

beast2\_options a set of BEAST2 options, that are the R equivalent of the BEAST2 command-line options, as can be created by [create\\_beast2\\_options](#)

**Value**

nothing

**Author(s)**

Richèl J.C. Bilderbeek

**See Also**

Use [create\\_beast2\\_options](#) to create a valid BEAST2 options object

**Examples**

```
check_beast2_options(create_beast2_options())
```

---

check\_beast2\_optionses *Check if the beast2\_options is a valid BEAST2 options object.*

---

**Description**

Calls stop if the BEAST2 option object is invalid

**Usage**

```
check_beast2_optionses(beast2_optionses)
```

**Arguments**

beast2\_optionses

list of one or more `beast2_options` structures, as can be created by [create\\_beast2\\_options](#).  
Use of reduplicated plural to achieve difference with `beast2_options`

**Value**

nothing

**Author(s)**

Richèl J.C. Bilderbeek

**See Also**

Use [create\\_beast2\\_options](#) to create a valid BEAST2 options object

**Examples**

```
check_beast2_optionses(list(create_beast2_options()))
```

---

```
check_beast2_options_data_types
```

*Check if the `beast2_options`, which is a list, has all elements of the right data types*

---

**Description**

Calls stop if not.

**Usage**

```
check_beast2_options_data_types(beast2_options)
```

**Arguments**

`beast2_options` a set of BEAST2 options, that are the R equivalent of the BEAST2 command-line options, as can be created by [create\\_beast2\\_options](#)

**Value**

nothing

**Author(s)**

Richèl J.C. Bilderbeek

**See Also**

Use [check\\_beast2\\_options](#) to check the entire `beast2_options` object

---

`check_beast2_options_do_not_overwrite_existing_files`

*Check if the `beast2_options` will not overwrite existing files, when the `'overwrite'` options is set to FALSE*

---

**Description**

Will `stop` if a file is threatened to be overwritten

**Usage**

```
check_beast2_options_do_not_overwrite_existing_files(  
  beast2_options,  
  beast2_internal_filenames  
)
```

**Arguments**

`beast2_options` a set of BEAST2 options, that are the R equivalent of the BEAST2 command-line options, as can be created by [create\\_beast2\\_options](#)

`beast2_internal_filenames`  
a list of internally used BEAST2 filenames, as created by [create\\_beast2\\_internal\\_filenames](#)

**Author(s)**

Richèl J.C. Bilderbeek

---

`check_beast2_options_filenames_differ`

*Check if the filenames in `beast2_options` differ*

---

**Description**

Calls `stop` if not.

**Usage**

```
check_beast2_options_filenames_differ(beast2_options)
```

**Arguments**

`beast2_options` a set of BEAST2 options, that are the R equivalent of the BEAST2 command-line options, as can be created by [create\\_beast2\\_options](#)

**Value**

nothing

**Author(s)**

Richèl J.C. Bilderbeek

**See Also**

Use [check\\_beast2\\_options](#) to check the entire `beast2_options` object

---

`check_beast2_options_names`

*Check if the `beast2_options`, which is a list, has all the elements needed.*

---

**Description**

Calls `stop` if not.

**Usage**

```
check_beast2_options_names(beast2_options)
```

**Arguments**

`beast2_options` a set of BEAST2 options, that are the R equivalent of the BEAST2 command-line options, as can be created by [create\\_beast2\\_options](#)

**Value**

nothing

**Author(s)**

Richèl J.C. Bilderbeek

**See Also**

Use [check\\_beast2\\_options](#) to check the entire `beast2_options` object



---

check_beast2_path	<i>Checks the BEAST2 .jar path. Will stop if there is a problem with the BEAST2 .jar path.</i>
-------------------	--

---

### Description

Checks the BEAST2 .jar path. Will stop if there is a problem with the BEAST2 .jar path.

### Usage

```
check_beast2_path(beast2_path)
```

### Arguments

beast2_path	name of either a BEAST2 binary file (usually simply <code>beast</code> ) or a BEAST2 jar file (usually has a <code>.jar</code> extension). Use <a href="#">get_default_beast2_bin_path</a> to get the default BEAST binary file's path Use <a href="#">get_default_beast2_jar_path</a> to get the default BEAST jar file's path
-------------	---

### Value

nothing. Will call `stop` if the BEAST2 .jar path has a problem

### Author(s)

Richèl J.C. Bilderbeek

### Examples

```
if (is_beast2_installed()) {  
  beast2_path <- get_default_beast2_jar_path()  
  check_beast2_path(beast2_path)  
}
```

---

check_can_create_file	<i>Check that a file can be created at a certain path.</i>
-----------------------	--

---

### Description

Will `stop` if not. Will `stop` if the file already exists. Does so by creating an empty file at the path, and then deleting it.

### Usage

```
check_can_create_file(filename, overwrite = TRUE)
```

**Arguments**

filename        file that may or may not be created  
overwrite       if TRUE, if filename already exists, it will be deleted by this function

**Author(s)**

Richèl J.C. Bilderbeek

---

check\_input\_filename    *Checks the input filename. Will stop if there is a problem with the input filename.*

---

**Description**

Checks the input filename. Will stop if there is a problem with the input filename.

**Usage**

```
check_input_filename(input_filename)
```

**Arguments**

input\_filename    the name of a BEAST2 input XML file. This file usually has an .xml extension. Use [create\\_temp\\_input\\_filename](#) to create a temporary filename with that extension.

**Value**

nothing. Will call [stop](#) if the input file is invalid

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
check_input_filename(  
  get_beastier_path("beast2_example_output.log")  
)
```

---

check_n_threads	<i>Check if the input is a valid number of threads.</i>
-----------------	---

---

**Description**

Will [stop](#) if not.

**Usage**

```
check_n_threads(n_threads)
```

**Arguments**

n_threads	the number of computational threads to use. Use <a href="#">NA</a> to use the BEAST2 default of 1.
-----------	--

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
# Can have 1 or more threads
check_n_threads(1)
check_n_threads(2)
# Can have NA threads
check_n_threads(NA)
```

---

check_os	<i>Checks if the operating system is supported</i>
----------	--

---

**Description**

Checks if the operating system is supported

**Usage**

```
check_os(os)
```

**Arguments**

os	name of the operating system, must be <code>unix</code> (Linux, Mac) or <code>win</code> (Windows)
----	--

**Value**

nothing. Will stop if the OS is unsupported

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
check_os("mac")
check_os("unix")
check_os("win")
```

---

check_rng_seed	<i>Check if the input is a valid RNG seed.</i>
----------------	--

---

**Description**

Will [stop](#) if not.

**Usage**

```
check_rng_seed(rng_seed)
```

**Arguments**

rng_seed	the random number generator seed of the BEAST2 run. Must be a non-zero positive integer value or <a href="#">NA</a> . If rng_seed is <a href="#">NA</a> , BEAST2 will pick a random seed
----------	--

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
# Numbers from 1 and higher are valid RNG seeds
check_rng_seed(1)
check_rng_seed(2)
# Also NA is a valid RNG seed
check_rng_seed(NA)
```

---

```
create_beast2_internal_filenames
```

*Create a list with the internally used BEAST2 filenames*

---

**Description**

Create a list with the internally used BEAST2 filenames

**Usage**

```
create_beast2_internal_filenames(beast2_options)
```

**Arguments**

`beast2_options` a set of BEAST2 options, that are the R equivalent of the BEAST2 command-line options, as can be created by [create\\_beast2\\_options](#)

**Value**

a list with the internally used BEAST2 filenames

**Examples**

```
beast2_options <- create_beast2_options(  
  input_filename = get_beastier_path("2_4.xml")  
)  
if (is_beast2_installed()) {  
  create_beast2_internal_filenames(beast2_options)  
}
```

---

```
create_beast2_options
```

*Function to create a set of BEAST2 options.*

---

**Description**

These BEAST2 options are the R equivalent of the command-line options.

**Usage**

```
create_beast2_options(  
  input_filename = create_temp_input_filename(),  
  output_state_filename = create_temp_state_filename(),  
  rng_seed = NA,  
  n_threads = NA,  
  use_beagle = FALSE,  
  overwrite = TRUE,
```

```

beast2_path = get_default_beast2_path(),
verbose = FALSE,
output_log_filename = "deprecated",
output_trees_filenames = "deprecated",
beast2_working_dir = "deprecated"
)

```

## Arguments

**input\_filename** the name of a BEAST2 input XML file. This file usually has an `.xml` extension. Use [create\\_temp\\_input\\_filename](#) to create a temporary filename with that extension.

**output\_state\_filename** name of the `.xml` state file to create. Use [create\\_temp\\_state\\_filename](#) to create a temporary filename with that extension.

**rng\_seed** the random number generator seed of the BEAST2 run. Must be a non-zero positive integer value or `NA`. If `rng_seed` is `NA`, BEAST2 will pick a random seed

**n\_threads** the number of computational threads to use. Use `NA` to use the BEAST2 default of 1.

**use\_beagle** use BEAGLE if present

**overwrite** if `TRUE`: overwrite the `.log` and `.trees` files if one of these exists. If `FALSE`, BEAST2 will not be started if

- the `.log` file exists
- the `.trees` files exist
- the `.log` file created by BEAST2 exists
- the `.trees` files created by BEAST2 exist

**beast2\_path** name of either a BEAST2 binary file (usually simply `beast`) or a BEAST2 jar file (usually has a `.jar` extension). Use [get\\_default\\_beast2\\_bin\\_path](#) to get the default BEAST binary file's path Use [get\\_default\\_beast2\\_jar\\_path](#) to get the default BEAST jar file's path

**verbose** if `TRUE`, additional information is displayed, that is potentially useful in debugging

**output\_log\_filename** name of the `.log` file to create

**output\_trees\_filenames** one or more names for `.trees` file to create. There will be one `.trees` file created per alignment in the input file. The number of alignments must equal the number of `.trees` filenames, else an error is thrown. Alignments are sorted alphabetically by their IDs

**beast2\_working\_dir** a folder where BEAST2 can work in isolation. For each BEAST2 run, a new subfolder is created in that folder. Within this folder, BEAST2 is allowed to create all of its output files, without the risk of overwriting existing ones, allowing BEAST2 to run in multiple parallel processes.

**Value**

a BEAST2 options structure

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
beast2_options <- create_beast2_options()
check_beast2_options(beast2_options)
```

---

create\_beast2\_run\_cmd *Creates the terminal command to run BEAST2*

---

**Description**

Creates the terminal command to run BEAST2

**Usage**

```
create_beast2_run_cmd(
  input_filename,
  output_state_filename,
  rng_seed = NA,
  n_threads = NA,
  use_beagle = FALSE,
  overwrite = FALSE,
  beast2_path = get_default_beast2_path()
)
```

**Arguments**

input_filename	the name of a BEAST2 input XML file. This file usually has an .xml extension. Use <a href="#">create_temp_input_filename</a> to create a temporary filename with that extension.
output_state_filename	name of the BEAST2 output file that stores the state (usually has a .xml.state extension)
rng_seed	the random number generator seed of the BEAST2 run. Must be a non-zero positive integer value or <b>NA</b> . If rng_seed is <b>NA</b> , BEAST2 will pick a random seed
n_threads	the number of computational threads to use. Use <b>NA</b> to use the BEAST2 default of 1.
use_beagle	use BEAGLE if present

overwrite	if TRUE: overwrite the .log and .trees files if one of these exists. If FALSE, BEAST2 will not be started if <ul style="list-style-type: none"> <li>• the .log file exists</li> <li>• the .trees files exist</li> <li>• the .log file created by BEAST2 exists</li> <li>• the .trees files created by BEAST2 exist</li> </ul>
beast2_path	name of either a BEAST2 binary file (usually simply beast) or a BEAST2 jar file (usually has a .jar extension). Use <a href="#">get_default_beast2_bin_path</a> to get the default BEAST binary file's path Use <a href="#">get_default_beast2_jar_path</a> to get the default BEAST jar file's path

**Value**

a character vector with the command and arguments to call BEAST2

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
if (is_beast2_installed()) {
  cmds <- create_beast2_run_cmd(
    input_filename = "input.xml",
    output_state_filename = "output.xml.state",
    beast2_path = get_default_beast2_jar_path()
  )
  testit::assert(cmds[2] == "-cp")
}
```

---

```
create_beast2_validate_cmd
```

*Creates the terminal command to validate a BEAST2 input file*

---

**Description**

Creates the terminal command to validate a BEAST2 input file

**Usage**

```
create_beast2_validate_cmd(
  input_filename,
  beast2_path = get_default_beast2_path()
)
```



## Arguments

- `input_filename` the name of a BEAST2 input XML file. This file usually has an `.xml` extension. Use [create\\_temp\\_input\\_filename](#) to create a temporary filename with that extension.
- `beast2_path` name of either a BEAST2 binary file (usually simply `beast`) or a BEAST2 jar file (usually has a `.jar` extension). Use [get\\_default\\_beast2\\_bin\\_path](#) to get the default BEAST binary file's path Use [get\\_default\\_beast2\\_jar\\_path](#) to get the default BEAST jar file's path

## Value

a character vector, of which the first element is the command (`java`, in this case), and the others are arguments (`-jar`, in this case, followed by more arguments).

## Author(s)

Richèl J.C. Bilderbeek

## Examples

```
if (is_beast2_installed() && is_on_ci()) {  
  cmds <- create_beast2_validate_cmd(  
    input_filename = "input.xml"  
  )  
  testit::assert(cmds[2] == "-cp")  
}
```

---

`create_beast2_validate_cmd_bin`

*Creates the terminal command to validate a BEAST2 input file using a call to the launcher.jar file*

---

## Description

Creates the terminal command to validate a BEAST2 input file using a call to the launcher.jar file

## Usage

```
create_beast2_validate_cmd_bin(  
  input_filename,  
  beast2_bin_path = get_default_beast2_bin_path()  
)
```

**Arguments**

- `input_filename` the name of a BEAST2 input XML file. This file usually has an `.xml` extension. Use `create_temp_input_filename` to create a temporary filename with that extension.
- `beast2_bin_path` name of the BEAST2 binary file (usually simply `beast`). Use `get_default_beast2_bin_path` to get the default BEAST binary file's path

**Value**

a character vector, of which the first element is the command (`java`, in this case), and the others are arguments (`-jar`, in this case, followed by more arguments).

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
if (is_beast2_installed() && is_on_ci()) {
  cmds <- create_beast2_validate_cmd_bin(
    input_filename = "input.xml"
  )
  testit::assert(length(cmds) == 3)
  testit::assert(cmds[2] == "-validate")
}
```

---

`create_beast2_validate_cmd_jar`

*Creates the terminal command to validate a BEAST2 input file using a call to the launcher.jar file*

---

**Description**

Creates the terminal command to validate a BEAST2 input file using a call to the `launcher.jar` file

**Usage**

```
create_beast2_validate_cmd_jar(
  input_filename,
  beast2_jar_path = get_default_beast2_jar_path()
)
```

**Arguments**

- `input_filename` the name of a BEAST2 input XML file. This file usually has an `.xml` extension. Use [create\\_temp\\_input\\_filename](#) to create a temporary filename with that extension.
- `beast2_jar_path` name of the BEAST2 jar file (usually has a `.jar` extension). Use [get\\_default\\_beast2\\_jar\\_path](#) to get the default BEAST jar file's path

**Value**

a character vector, of which the first element is the command (`java`, in this case), and the others are arguments (`-jar`, in this case, followed by more arguments).

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
if (is_beast2_installed() && is_on_ci()) {
  cmds <- create_beast2_validate_cmd_jar(
    input_filename = "input.xml"
  )
  testit::assert(length(cmds) == 6)
  testit::assert(cmds[2] == "-cp")
}
```

---

```
create_beast2_version_cmd
```

*Creates the terminal command to version a BEAST2 input file*

---

**Description**

Creates the terminal command to version a BEAST2 input file

**Usage**

```
create_beast2_version_cmd(beast2_path = beastier::get_default_beast2_path())
```

**Arguments**

- `beast2_path` name of either a BEAST2 binary file (usually simply `beast`) or a BEAST2 jar file (usually has a `.jar` extension). Use [get\\_default\\_beast2\\_bin\\_path](#) to get the default BEAST binary file's path Use [get\\_default\\_beast2\\_jar\\_path](#) to get the default BEAST jar file's path

**Value**

a character vector, of which the first element is the command (java, in this case), and the others are arguments (-jar, in this case, followed by more arguments).

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
if (is_beast2_installed() && is_on_ci()) {
  cmds <- create_beast2_version_cmd()
  testit::assert(cmds[2] == "-cp")
}
```

---

create\_beast2\_version\_cmd\_bin

*Creates the terminal command to version a BEAST2 input file using a call to the launcher . jar file*

---

**Description**

Creates the terminal command to version a BEAST2 input file using a call to the launcher . jar file

**Usage**

```
create_beast2_version_cmd_bin(beast2_bin_path = get_default_beast2_bin_path())
```

**Arguments**

beast2\_bin\_path

name of the BEAST2 binary file (usually simply beast). Use [get\\_default\\_beast2\\_bin\\_path](#) to get the default BEAST binary file's path

**Value**

a character vector, of which the first element is the command (java, in this case), and the others are arguments (-jar, in this case, followed by more arguments).

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
if (is_beast2_installed() && is_on_ci()) {
  cmds <- create_beast2_version_cmd_bin()
  testit::assert(length(cmds) == 2)
  testit::assert(cmds[2] == "-version")
}
```

---

```
create_beast2_version_cmd_jar
```

*Creates the terminal command to version a BEAST2 input file using a call to the launcher . jar file*

---

### Description

Creates the terminal command to version a BEAST2 input file using a call to the launcher . jar file

### Usage

```
create_beast2_version_cmd_jar(beast2_jar_path = get_default_beast2_jar_path())
```

### Arguments

beast2\_jar\_path

name of the BEAST2 jar file (usually has a . jar extension). Use [get\\_default\\_beast2\\_jar\\_path](#) to get the default BEAST jar file's path

### Value

a character vector, of which the first element is the command (java, in this case), and the others are arguments (-jar, in this case, followed by more arguments).

### Author(s)

Richèl J.C. Bilderbeek

### Examples

```
if (is_beast2_installed()) {
  cmds <- create_beast2_version_cmd_jar()
  testit::assert(length(cmds) == 5)
  testit::assert(cmds[2] == "-cp")
}
```

---

```
create_mcbette_beast2_options
```

*Create a beast2\_options structure for mcbette*

---

### Description

Create a `beast2_options` structure to be used for `mcbette` (a package that allows one to do model comparison). The generated filenames indicating `mcbette` usage, as well as the correct BEAST2 binary type

**Usage**

```

create_mcbette_beast2_options(
  input_filename = beastier::create_temp_input_filename(),
  output_state_filename = beastier::create_temp_state_filename(),
  rng_seed = NA,
  n_threads = NA,
  use_beagle = FALSE,
  overwrite = TRUE,
  beast2_bin_path = beastier::get_default_beast2_bin_path(),
  verbose = FALSE
)

```

**Arguments**

input_filename	the name of a BEAST2 input XML file. This file usually has an .xml extension. Use <a href="#">create_temp_input_filename</a> to create a temporary filename with that extension.
output_state_filename	name of the .xml state file to create. Use <a href="#">create_temp_state_filename</a> to create a temporary filename with that extension.
rng_seed	the random number generator seed of the BEAST2 run. Must be a non-zero positive integer value or <code>NA</code> . If <code>rng_seed</code> is <code>NA</code> , BEAST2 will pick a random seed
n_threads	the number of computational threads to use. Use <code>NA</code> to use the BEAST2 default of 1.
use_beagle	use BEAGLE if present
overwrite	if TRUE: overwrite the .log and .trees files if one of these exists. If FALSE, BEAST2 will not be started if <ul style="list-style-type: none"> <li>• the .log file exists</li> <li>• the .trees files exist</li> <li>• the .log file created by BEAST2 exists</li> <li>• the .trees files created by BEAST2 exist</li> </ul>
beast2_bin_path	name of the BEAST2 binary file (usually simply <code>beast</code> ). Use <a href="#">get_default_beast2_bin_path</a> to get the default BEAST binary file's path
verbose	if TRUE, additional information is displayed, that is potentially useful in debugging

**Author(s)**

Richèl J.C. Bilderbeek

**See Also**

to create a regular (that is, not intended for model comparison) BEAST2 options structure, use [create\\_beast2\\_options](#)

**Examples**

```
create_mcbette_beast2_options()
```

---

```
create_temp_input_filename
```

*Create a temporary filename for the BEAST2 XML filename*

---

**Description**

Create a temporary filename for the BEAST2 XML filename

**Usage**

```
create_temp_input_filename()
```

---

```
create_temp_state_filename
```

*Create a temporary file for the BEAST2 XML output file that stores its state.*

---

**Description**

Create a temporary file for the BEAST2 XML output file that stores its state.

**Usage**

```
create_temp_state_filename()
```

---

```
default_params_doc
```

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

---

**Description**

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

**Usage**

```
default_params_doc(  
    beast2_bin_path,  
    beast2_folder,  
    beast2_internal_filenames,  
    beast2_jar_path,  
    beast2_options,  
    beast2_optionses,  
    beast2_path,  
    beast2_version,  
    beast2_working_dir,  
    clock_model,  
    clock_models,  
    crown_age,  
    crown_ages,  
    fasta_filename,  
    fasta_filenames,  
    fixed_crown_age,  
    fixed_crown_ages,  
    initial_phylogenies,  
    input_filename,  
    mcmc,  
    misc_options,  
    n_taxa,  
    n_threads,  
    os,  
    output_filename,  
    output_log_filename,  
    output_state_filename,  
    output_trees_filenames,  
    overwrite,  
    rename_fun,  
    rng_seed,  
    sequence_length,  
    site_model,  
    site_models,  
    tree_prior,  
    tree_priors,  
    use_beagle,  
    verbose  
)
```

**Arguments**

`beast2_bin_path` name of the BEAST2 binary file (usually simply `beast`). Use [get\\_default\\_beast2\\_bin\\_path](#) to get the default BEAST binary file's path

`beast2_folder` the folder where the BEAST2 is installed. Note that this is not the folder



where the BEAST2 executable is installed: the BEAST2 executable is in a subfolder. Use [get\\_default\\_beast2\\_folder](#) to get the default BEAST2 folder. Use [get\\_default\\_beast2\\_bin\\_path](#) to get the full path to the default BEAST2 executable.

beast2_internal_filenames	a list of internally used BEAST2 filenames, as created by <a href="#">create_beast2_internal_filenames</a>
beast2_jar_path	name of the BEAST2 jar file (usually has a .jar extension). Use <a href="#">get_default_beast2_jar_path</a> to get the default BEAST jar file's path
beast2_options	a set of BEAST2 options, that are the R equivalent of the BEAST2 command-line options, as can be created by <a href="#">create_beast2_options</a>
beast2_optionses	list of one or more <code>beast2_options</code> structures, as can be created by <a href="#">create_beast2_options</a> . Use of reduplicated plural to achieve difference with <code>beast2_options</code>
beast2_path	name of either a BEAST2 binary file (usually simply <code>beast</code> ) or a BEAST2 jar file (usually has a .jar extension). Use <a href="#">get_default_beast2_bin_path</a> to get the default BEAST binary file's path Use <a href="#">get_default_beast2_jar_path</a> to get the default BEAST jar file's path
beast2_version	the version of BEAST2. By default, this is the version as returned by <a href="#">get_default_beast2_version</a>
beast2_working_dir	a folder where BEAST2 can work in isolation. For each BEAST2 run, a new subfolder is created in that folder. Within this folder, BEAST2 is allowed to create all of its output files, without the risk of overwriting existing ones, allowing BEAST2 to run in multiple parallel processes.
clock_model	a <code>beautier</code> clock model
clock_models	a list of one or more <code>beautier</code> clock models
crown_age	the crown age of the phylogeny
crown_ages	the crown ages of the phylogenies. Set to NA if the crown age needs to be estimated
fasta_filename	a FASTA filename.
fasta_filenames	One or more FASTA filenames.
fixed_crown_age	determines if the phylogeny's crown age is fixed. If FALSE, crown age is estimated by BEAST2. If TRUE, the crown age is fixed to the crown age of the initial phylogeny.
fixed_crown_ages	one or more booleans to determine if the phylogenies' crown ages are fixed. If FALSE, crown age is estimated by BEAST2. If TRUE, the crown age is fixed to the crown age of the initial phylogeny.
initial_phylogenies	one or more MCMC chain's initial phylogenies. Each one set to NA will result in BEAST2 using a random phylogeny. Else the phylogeny is assumed to be of class <code>ape::phylo</code> .

input_filename	the name of a BEAST2 input XML file. This file usually has an .xml extension. Use <a href="#">create_temp_input_filename</a> to create a temporary filename with that extension.
mcmc	one beautier MCMC
misc_options	one beautier misc_options object
n_taxa	The number of taxa
n_threads	the number of computational threads to use. Use <a href="#">NA</a> to use the BEAST2 default of 1.
os	name of the operating system, must be unix (Linux, Mac) or win (Windows)
output_filename	Name of the XML parameter file created by this function. BEAST2 uses this file as input.
output_log_filename	name of the .log file to create
output_state_filename	name of the .xml.state file to create. Use <a href="#">create_temp_state_filename</a> to create a temporary filename with that extension.
output_trees_filenames	one or more names for .trees file to create. There will be one .trees file created per alignment in the input file. The number of alignments must equal the number of .trees filenames, else an error is thrown. Alignments are sorted alphabetically by their IDs
overwrite	if TRUE: overwrite the .log and .trees files if one of these exists. If FALSE, BEAST2 will not be started if <ul style="list-style-type: none"> <li>• the .log file exists</li> <li>• the .trees files exist</li> <li>• the .log file created by BEAST2 exists</li> <li>• the .trees files created by BEAST2 exist</li> </ul>
rename_fun	a function to rename a filename, as can be checked by <a href="#">check_rename_fun</a> . This function should have one argument, which will be a filename or <a href="#">NA</a> . The function should <a href="#">return</a> one filename (when passed one filename) or one <a href="#">NA</a> (when passed one <a href="#">NA</a> ). Example rename functions are: <ul style="list-style-type: none"> <li>• <a href="#">get_remove_dir_fun</a> get a function that removes the directory paths from the filenames, in effect turning these into local files</li> <li>• <a href="#">get_replace_dir_fun</a> get a function that replaces the directory paths from the filenames</li> <li>• <a href="#">get_remove_hex_fun</a> get a function that removes the hex string from filenames. For example, <code>tracelog_82c1a522040.log</code> becomes <code>tracelog.log</code></li> </ul>
rng_seed	the random number generator seed of the BEAST2 run. Must be a non-zero positive integer value or <a href="#">NA</a> . If <code>rng_seed</code> is <a href="#">NA</a> , BEAST2 will pick a random seed
sequence_length	a DNA sequence length, in base pairs
site_model	a beautier site model

site_models	one or more beautier site models
tree_prior	a beautier tree prior
tree_priors	one or more beautier tree priors
use_beagle	use BEAGLE if present
verbose	if TRUE, additional information is displayed, that is potentially useful in debugging

**Value**

Nothing. This is an internal function that does nothing

**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

---

do_minimal_run	<i>Do a minimal BEAST2 run</i>
----------------	--------------------------------

---

**Description**

To achieve this, [run\\_beast2\\_from\\_options](#) is called.

**Usage**

```
do_minimal_run()
```

**Value**

The text sent to STDOUT and STDERR. It will create the files with name output\_state\_filename

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
if (is_beast2_installed() && is_on_ci()) {
  do_minimal_run()
}
```

get\_alignment\_ids\_from\_xml\_filename

*Get the alignment ID from a file with one alignment*

---

### Description

Get the alignment ID from a file with one alignment

### Usage

```
get_alignment_ids_from_xml_filename(xml_filename)
```

### Arguments

xml\_filename    name of a BEAST2 XML input filename

### Value

one or more alignment IDs

### Author(s)

Richèl J.C. Bilderbeek

### Examples

```
# test_output_0
get_alignment_ids_from_xml_filename(get_beastier_path("2_4.xml"))
# c("anthus_aco", "anthus_nd2")
get_alignment_ids_from_xml_filename(get_beastier_path("anthus_15_15.xml"))
```

---

get\_beast2\_example\_filename

*Get the full path of a BEAST2 example file*

---

### Description

Will [stop](#) if the filename is not a BEAST2 example file

### Usage

```
get_beast2_example_filename(
  filename,
  beast2_folder = get_default_beast2_folder()
)
```

### Arguments

filename	name of the BEAST2 example file. This should exclude the full path; this function exists to add that full path
beast2_folder	the folder where the BEAST2 is installed. Note that this is not the folder where the BEAST2 executable is installed: the BEAST2 executable is in a subfolder. Use <a href="#">get_default_beast2_folder</a> to get the default BEAST2 folder. Use <a href="#">get_default_beast2_bin_path</a> to get the full path to the default BEAST2 executable.

### Examples

```
if (is_beast2_installed()) {  
  get_beast2_example_filename("testJukesCantor.xml")  
}
```

---

get\_beast2\_example\_filenames

*Get a list with the full paths of all BEAST2 example filenames*

---

### Description

Get a list with the full paths of all BEAST2 example filenames

### Usage

```
get_beast2_example_filenames(beast2_folder = get_default_beast2_folder())
```

### Arguments

beast2_folder	the folder where the BEAST2 is installed. Note that this is not the folder where the BEAST2 executable is installed: the BEAST2 executable is in a subfolder. Use <a href="#">get_default_beast2_folder</a> to get the default BEAST2 folder. Use <a href="#">get_default_beast2_bin_path</a> to get the full path to the default BEAST2 executable.
---------------	--

### Value

a list with the full paths of all BEAST2 example filenames

---

```
get_beast2_main_class_name
```

*Get the BEAST2 main class name.*

---

### Description

One way to fix the error no main manifest attribute is to specify the main class name.

### Usage

```
get_beast2_main_class_name()
```

---

```
get_beast2_options_filenames
```

*Extract the filenames from a beast2\_options*

---

### Description

Extract the filenames from a beast2\_options

### Usage

```
get_beast2_options_filenames(beast2_options)
```

### Arguments

`beast2_options` a set of BEAST2 options, that are the R equivalent of the BEAST2 command-line options, as can be created by [create\\_beast2\\_options](#)

### Author(s)

Richèl J.C. Bilderbeek

### Examples

```
beast2_options <- beastier::create_beast2_options()
get_beast2_options_filenames(beast2_options)
```

---

get\_beast2\_version      *Get the BEAST2 version*

---

**Description**

Get the BEAST2 version

**Usage**

```
get_beast2_version(beast2_path = get_default_beast2_path())
```

**Arguments**

beast2\_path      name of either a BEAST2 binary file (usually simply `beast`) or a BEAST2 jar file (usually has a `.jar` extension). Use [get\\_default\\_beast2\\_bin\\_path](#) to get the default BEAST binary file's path Use [get\\_default\\_beast2\\_jar\\_path](#) to get the default BEAST jar file's path

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
if (is_beast2_installed() && is_on_ci()) {  
  get_beast2_version()  
}
```

---

get\_beastier\_path      *Get the full path of a file in the inst/extdata folder*

---

**Description**

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

**Usage**

```
get_beastier_path(filename)
```

**Arguments**

filename      the file's name, without the path

**Value**

the full path to the filename. Will stop if the file is absent in the `inst/extdata` folder

**Author(s)**

Richèl J.C. Bilderbeek

**See Also**

for more files, use [get\\_beastier\\_paths](#)

**Examples**

```
get_beastier_path("beast2_example_output.log")
get_beastier_path("beast2_example_output.trees")
get_beastier_path("beast2_example_output.xml")
get_beastier_path("beast2_example_output.xml.state")
```

---

get\_beastier\_paths      *Get the full paths of files in the inst/extdata folder*

---

**Description**

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

**Usage**

```
get_beastier_paths(filenamees)
```

**Arguments**

filenamees      the files' names, without the path

**Value**

the filenamees' full paths. Will stop if a file is absent in the inst/extdata folder

**Author(s)**

Richèl J.C. Bilderbeek

**See Also**

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



## Examples

```
get_beastier_paths(  
  c(  
    "beast2_example_output.log",  
    "beast2_example_output.trees",  
    "beast2_example_output.xml",  
    "beast2_example_output.xml.state"  
  )  
)
```

---

```
get_default_beast2_bin_path
```

*Get the default BEAST2 binary file (beast, that is) path*

---

## Description

Get the default BEAST2 binary file (beast, that is) path

## Usage

```
get_default_beast2_bin_path(  
  beast2_folder = get_default_beast2_folder(),  
  os = rappdirs::app_dir()$os  
)
```

## Arguments

**beast2\_folder** the folder where the BEAST2 is installed. Note that this is not the folder where the BEAST2 executable is installed: the BEAST2 executable is in a subfolder. Use [get\\_default\\_beast2\\_folder](#) to get the default BEAST2 folder. Use [get\\_default\\_beast2\\_bin\\_path](#) to get the full path to the default BEAST2 executable.

**os** name of the operating system, must be unix (Linux, Mac) or win (Windows)

## Value

the default BEAST2 binary file's path

## Author(s)

Richèl J.C. Bilderbeek

## See Also

Use [get\\_default\\_beast2\\_folder](#) to get the default folder in which BEAST2 is installed. Use [install\\_beast2](#) with default arguments to install BEAST2 to this location.

**Examples**

```
if (is_beast2_installed() && rappdirs::app_dir()$os == "unix") {
  testit::assert(
    grepl(
      "beast/bin/beast",
      get_default_beast2_bin_path()
    )
  )
}
```

---

get\_default\_beast2\_download\_url

*Get the default BEAST2 download URL, which depends on the operating system*

---

**Description**

Get the default BEAST2 download URL, which depends on the operating system

**Usage**

```
get_default_beast2_download_url(
  beast2_version = beastier::get_default_beast2_version(),
  os = rappdirs::app_dir()$os
)
```

**Arguments**

**beast2\_version** the version of BEAST2. By default, this is the version as returned by [get\\_default\\_beast2\\_version](#)

**os** name of the operating system, must be unix (Linux, Mac) or win (Windows)

**Value**

the URL where BEAST2 can be downloaded from

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
get_default_beast2_download_url()
```

---

```
get_default_beast2_download_url_linux
```

*Get the BEAST2 download URL for Linux*

---

**Description**

Get the BEAST2 download URL for Linux

**Usage**

```
get_default_beast2_download_url_linux(  
    beast2_version = beastier::get_default_beast2_version()  
)
```

**Arguments**

`beast2_version` the version of BEAST2. By default, this is the version as returned by [get\\_default\\_beast2\\_version](#)

**Value**

the URL where BEAST2 can be downloaded from

**Author(s)**

Richèl J.C. Bilderbeek

---

```
get_default_beast2_download_url_win
```

*Get the BEAST2 download URL for Windows*

---

**Description**

Get the BEAST2 download URL for Windows

**Usage**

```
get_default_beast2_download_url_win(  
    beast2_version = beastier::get_default_beast2_version()  
)
```

**Arguments**

`beast2_version` the version of BEAST2. By default, this is the version as returned by [get\\_default\\_beast2\\_version](#)

**Value**

the URL where BEAST2 can be downloaded from

**Author(s)**

Richèl J.C. Bilderbeek

---

get\_default\_beast2\_folder

*Get the path to the folder where this package installs BEAST2 by default*

---

**Description**

Get the path to the folder where this package installs BEAST2 by default

**Usage**

```
get_default_beast2_folder()
```

**Value**

the path to the folder where this package installs BEAST2 by default

**Author(s)**

Richèl J.C. Bilderbeek

**See Also**

Use [get\\_default\\_beast2\\_jar\\_path](#) to get the path to the BEAST2 jar file, when installed by this package Use [install\\_beast2](#) with default arguments to install BEAST2 to this folder.

**Examples**

```
print(get_default_beast2_folder())
```

---

get\_default\_beast2\_jar\_path

*Get the default BEAST2 jar file's path*

---

**Description**

Get the default BEAST2 jar file's path

**Usage**

```
get_default_beast2_jar_path(  
  beast2_folder = beastier::get_default_beast2_folder(),  
  os = rappdirs::app_dir()$os  
)
```

**Arguments**

- `beast2_folder` the folder where the BEAST2 is installed. Note that this is not the folder where the BEAST2 executable is installed: the BEAST2 executable is in a sub-folder. Use [get\\_default\\_beast2\\_folder](#) to get the default BEAST2 folder. Use [get\\_default\\_beast2\\_bin\\_path](#) to get the full path to the default BEAST2 executable.
- `os` name of the operating system, must be `unix` (Linux, Mac) or `win` (Windows)

**Value**

the default BEAST2 jar file's path

**Author(s)**

Richèl J.C. Bilderbeek

**See Also**

Use [get\\_default\\_beast2\\_folder](#) to get the default folder in which BEAST2 is installed. Use [install\\_beast2](#) with default arguments to install BEAST2 to this location.

**Examples**

```
get_default_beast2_jar_path()
```

---

```
get_default_beast2_path
```

*Get the default BEAST2 path*

---

**Description**

Get the default BEAST2 path

**Usage**

```
get_default_beast2_path()
```

**Value**

the default BEAST2 path

**Author(s)**

Richèl J.C. Bilderbeek

**See Also**

Use [get\\_default\\_beast2\\_bin\\_path](#) to get the default path to the BEAST2 binary file. Use [get\\_default\\_beast2\\_jar\\_path](#) to get the default path to the BEAST2 jar file. Use [get\\_default\\_beast2\\_folder](#) to get the default folder in which BEAST2 is installed. Use [install\\_beast2](#) with default arguments to install BEAST2 to this location.

**Examples**

```
if (is_beast2_installed()) {  
  get_default_beast2_path()  
}
```

---

`get_default_beast2_version`

*Get the default BEAST2 version that is used by beastier*

---

**Description**

Get the default BEAST2 version that is used by beastier

**Usage**

```
get_default_beast2_version()
```

**Value**

the BEAST2 version

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
get_default_beast2_version()
```

---

*get\_default\_java\_path* *Obtains the default path to the Java executable*

---

**Description**

Obtains the default path to the Java executable

**Usage**

```
get_default_java_path(os = rappdirs::app_dir())$os
```

**Arguments**

os                    name of the operating system, must be unix (Linux, Mac) or win (Windows)

**Value**

the default path to the Java executable

**Author(s)**

Richèl J.C. Bilderbeek

---

*get\_duplicate\_param\_ids*  
*Find duplicate RealParameter IDs*

---

**Description**

Find duplicate RealParameter IDs

**Usage**

```
get_duplicate_param_ids(text)
```

**Arguments**

text                    the XML as text

**Value**

a vector of duplicate IDs, will be empty if all IDs are unique

**Author(s)**

Richèl J.C. Bilderbeek

**See Also**

to see if all IDs are unique, use [has\\_unique\\_ids](#)

**Examples**

```
line_1 <- "<parameter id=\"RealParameter.1\" ...</parameter>"
line_2 <- "<parameter id=\"RealParameter.2\" ...</parameter>"
testit::assert(
  length(get_duplicate_param_ids(c(line_1, line_2))) == 0)
testit::assert(
  get_duplicate_param_ids(
    c(line_1, line_1)) == c("RealParameter.1")
)
testit::assert(
  get_duplicate_param_ids(
    c(line_2, line_2)) == c("RealParameter.2")
)
```

---

get\_java\_version

*Get the Java version*

---

**Description**

Get the Java version

**Usage**

```
get_java_version()
```

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
if (is_beast2_installed() && is_on_ci()) {
  get_java_version()
}
```



---

get\_trees\_filenames    *Get the .trees filenames that BEAST2 will produce*

---

**Description**

Get the .trees filenames that BEAST2 will produce

**Usage**

```
get_trees_filenames(input_filename)
```

**Arguments**

input\_filename    the name of a BEAST2 input XML file. This file usually has an .xml extension. Use [create\\_temp\\_input\\_filename](#) to create a temporary filename with that extension.

**Value**

character vector with the names of the .trees files that BEAST2 will produce

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
get_trees_filenames(get_beastier_path("2_4.xml"))  
get_trees_filenames(get_beastier_path("anthus_2_4.xml"))
```

---

gives\_beast2\_warning    *Determines if BEAST2 issues a warning when using the BEAST2 XML input file*

---

**Description**

Determines if BEAST2 issues a warning when using the BEAST2 XML input file

**Usage**

```
gives_beast2_warning(  
  filename,  
  verbose = FALSE,  
  beast2_path = get_default_beast2_path()  
)
```

**Arguments**

filename	name of the BEAST2 XML input file
verbose	if TRUE, additional information is displayed, that is potentially useful in debugging
beast2_path	name of either a BEAST2 binary file (usually simply <code>beast</code> ) or a BEAST2 jar file (usually has a <code>.jar</code> extension). Use <a href="#">get_default_beast2_bin_path</a> to get the default BEAST binary file's path Use <a href="#">get_default_beast2_jar_path</a> to get the default BEAST jar file's path

**Value**

TRUE if the file produces a BEAST2 warning, FALSE if not

**Author(s)**

Richèl J.C. Bilderbeek

**See Also**

Use [is\\_beast2\\_input\\_file](#) to check if a file is a valid BEAST2 input file. Use [are\\_beast2\\_input\\_lines](#) to check if the text (for example, as loaded from a file) to be valid BEAST2 input.

**Examples**

```
if (is_beast2_installed() &&
    is_on_ci() &&
    rappdirs::app_dir()$os == "unix") {

  # This file is OK for BEAST2, no warning, returns FALSE
  gives_beast2_warning(filename = get_beastier_path("2_4.xml"))

  # BEAST2 will give a warning on this file, returns TRUE
  gives_beast2_warning(
    filename = get_beastier_path("beast2_warning.xml")
  )
}
```

---

has\_unique\_ids

*Determine if the XML text has unique parameter IDs*

---

**Description**

Determine if the XML text has unique parameter IDs

**Usage**

```
has_unique_ids(text)
```

**Arguments**

text            the XML as text

**Value**

TRUE if all parameter IDs are unique, FALSE otherwise

**Author(s)**

Richèl J.C. Bilderbeek

**See Also**

to obtain the duplicate parameter IDs, use [get\\_duplicate\\_param\\_ids](#)

**Examples**

```
line_1 <- "<parameter id=\"RealParameter.1\" ...</parameter>"
line_2 <- "<parameter id=\"RealParameter.2\" ...</parameter>"
# Unique IDs
has_unique_ids(c(line_1, line_2))
# No unique ID
has_unique_ids(c(line_1, line_1))
```

---

install_beast2	<i>Install BEAST2 Installs BEAST2 of the default version (see <a href="#">get_default_beast2_version</a>), but another version can also be specified</i>
----------------	--

---

**Description**

Install BEAST2 Installs BEAST2 of the default version (see [get\\_default\\_beast2\\_version](#)), but another version can also be specified

**Usage**

```
install_beast2(
  folder_name = rappdirs::user_data_dir(),
  beast2_version = beastier::get_default_beast2_version(),
  verbose = FALSE,
  os = rappdirs::app_dir()$os
)
```

**Arguments**

folder_name	name of the folder where the BEAST2 files will be put. The name of the BEAST2 binary file will be at [folder_name]/beast/bin/beast The name of the BEAST2 jar file will be at [folder_name]/beast/lib/launcher.jar
beast2_version	the version of BEAST2. By default, this is the version as returned by <a href="#">get_default_beast2_version</a>
verbose	if TRUE, additional information is displayed, that is potentially useful in debugging
os	name of the operating system, must be unix (Linux, Mac) or win (Windows)

**Value**

Nothing. Will install BEAST2

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
## Not run:
  install_beast2()

## End(Not run)
```

---

is\_alignment

*Determines if the input is an alignment of type [DNABin](#)*

---

**Description**

Determines if the input is an alignment of type [DNABin](#)

**Usage**

```
is_alignment(input)
```

**Arguments**

input	The input to be tested
-------	------------------------

**Value**

TRUE or FALSE

**Author(s)**

Richèl J.C. Bilderbeek

---

is\_beast2\_input\_file *Is a file a valid BEAST2 input file?*

---

### Description

Is a file a valid BEAST2 input file?

### Usage

```
is_beast2_input_file(  
    filename,  
    show_warnings = FALSE,  
    verbose = FALSE,  
    beast2_path = get_default_beast2_path()  
)
```

### Arguments

filename	name of the BEAST2 XML input file
show_warnings	if TRUE, warnings will shown
verbose	if TRUE, additional information is displayed, that is potentially useful in debugging
beast2_path	name of either a BEAST2 binary file (usually simply <code>beast</code> ) or a BEAST2 jar file (usually has a <code>.jar</code> extension). Use <a href="#">get_default_beast2_bin_path</a> to get the default BEAST binary file's path Use <a href="#">get_default_beast2_jar_path</a> to get the default BEAST jar file's path

### Value

TRUE if the file is valid, FALSE if not

### Note

this function only works on standard BEAST2 input files: if a BEAST2 input file is modified to use a certain BEAST2 package, this function will label it as an invalid file

### Author(s)

Richèl J.C. Bilderbeek

### See Also

Use [are\\_beast2\\_input\\_lines](#) to check the lines

**Examples**

```

if (is_beast2_installed() && is_on_ci()) {

  filename <- get_beastier_path("anthus_2_4.xml")
  # TRUE, this is a BEAST2 input file
  is_beast2_input_file(filename)

  filename <- get_beastier_path("beast2_example_output.log")
  # FALSE, this is not a BEAST2 input file,
  # it is a BEAST2 output log file instead
  is_beast2_input_file(filename)
}

```

---

is\_beast2\_installed    *Checks if BEAST2 is installed*

---

**Description**

Checks if BEAST2 is installed

**Usage**

```

is_beast2_installed(
  folder_name = get_default_beast2_folder(),
  os = rappdirs::app_dir()$os
)

```

**Arguments**

folder_name	name of the folder where the BEAST2 files are put. The name of the BEAST2 binary file will be at [folder_name]/beast/bin/beast The name of the BEAST2 jar file will be at [folder_name]/beast/lib/launcher.jar
os	name of the operating system, must be unix (Linux, Mac) or win (Windows)

**Value**

TRUE if BEAST2 is installed

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```

if (is_beast2_installed()) {
  print("BEAST2 is installed")
}

```

---

is_bin_path	<i>Is the path a path to the BEAST2 binary file? Does not check if the file at that path is present</i>
-------------	---

---

**Description**

Is the path a path to the BEAST2 binary file? Does not check if the file at that path is present

**Usage**

```
is_bin_path(path)
```

**Arguments**

path            a string to a path

**Value**

TRUE if the path is a path to a BEAST2 binary file

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
if (is_beast2_installed()) {  
  # TRUE  
  is_bin_path("beast")  
  is_bin_path("BEAST.exe")  
  is_bin_path(get_default_beast2_bin_path())  
  # FALSE  
  is_bin_path("launcher.jar")  
  is_bin_path(get_default_beast2_jar_path())  
}
```

---

is_jar_path	<i>Is the path a path to the BEAST2 jar file? Does not check if the file at that path is present</i>
-------------	--

---

**Description**

Is the path a path to the BEAST2 jar file? Does not check if the file at that path is present

**Usage**

```
is_jar_path(path)
```

**Arguments**

path                    a string to a path

**Value**

TRUE if the path is a path to a BEAST2 jar file

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
# Returns TRUE
is_jar_path("beast.jar")
is_jar_path("launcher.jar")
is_jar_path(get_default_beast2_jar_path())
# Returns FALSE
is_jar_path("beast")
is_jar_path(get_default_beast2_bin_path())
```

---

is\_on\_appveyor

*Determines if the environment is AppVeyor*

---

**Description**

Determines if the environment is AppVeyor

**Usage**

```
is_on_appveyor()
```

**Value**

TRUE if run on AppVeyor, FALSE otherwise

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
if (is_on_appveyor()) {
  print("Running on AppVeyor")
}
```



---

is_on_ci	<i>Determines if the environment is a continuous integration service</i>
----------	--

---

**Description**

Determines if the environment is a continuous integration service

**Usage**

```
is_on_ci()
```

**Value**

TRUE if run on AppVeyor or Travis CI, FALSE otherwise

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
if (is_on_ci()) {  
  print("Running on a continuous integration service")  
}
```

---

is_on_travis	<i>Determines if the environment is Travis CI</i>
--------------	---

---

**Description**

Determines if the environment is Travis CI

**Usage**

```
is_on_travis()
```

**Value**

TRUE if run on Travis CI, FALSE otherwise

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
if (is_on_travis()) {  
  print("Running on Travis CI")  
}
```

print\_beast2\_internal\_filenames

*Print a beast2\_internal\_filenames as a table*

---

### **Description**

Print a beast2\_internal\_filenames as a table

### **Usage**

```
print_beast2_internal_filenames(beast2_internal_filenames)
```

### **Arguments**

beast2\_internal\_filenames

a list of internally used BEAST2 filenames, as created by [create\\_beast2\\_internal\\_filenames](#)

---

print\_beast2\_options *Pretty-print a beast2\_options*

---

### **Description**

Pretty-print a beast2\_options

### **Usage**

```
print_beast2_options(beast2_options)
```

### **Arguments**

beast2\_options a set of BEAST2 options, that are the R equivalent of the BEAST2 command-line options, as can be created by [create\\_beast2\\_options](#)

---

`remove_file_if_present`*Remove a file if it is present*

---

**Description**

Remove a file if it is present

**Usage**

```
remove_file_if_present(filename)
```

**Arguments**

filename          name of a file

---

`rename_beast2_options_filenames`*Rename the filenames in the BEAST2 options*

---

**Description**

Rename the filenames in the BEAST2 options

**Usage**

```
rename_beast2_options_filenames(beast2_options, rename_fun)
```

**Arguments**

beast2\_options    a set of BEAST2 options, that are the R equivalent of the BEAST2 command-line options, as can be created by [create\\_beast2\\_options](#)

rename\_fun        a function to rename a filename, as can be checked by [check\\_rename\\_fun](#). This function should have one argument, which will be a filename or `NA`. The function should [return](#) one filename (when passed one filename) or one `NA` (when passed one `NA`). Example rename functions are:

- [get\\_remove\\_dir\\_fun](#) get a function that removes the directory paths from the filenames, in effect turning these into local files
- [get\\_replace\\_dir\\_fun](#) get a function that replaces the directory paths from the filenames
- [get\\_remove\\_hex\\_fun](#) get a function that removes the hex string from filenames. For example, `tracelog_82c1a522040.log` becomes `tracelog.log`

---

run_beast2	<i>Run BEAST2</i>
------------	-------------------

---

### Description

Run BEAST2

### Usage

```
run_beast2(
  input_filename,
  output_log_filename = "output_log_filename_is_deprecated",
  output_trees_filenames = "output_trees_filenames_is_deprecated",
  output_state_filename = create_temp_state_filename(),
  rng_seed = NA,
  n_threads = NA,
  use_beagle = FALSE,
  overwrite = TRUE,
  beast2_working_dir = "beast2_working_dir_is_deprecated",
  beast2_path = get_default_beast2_path(),
  verbose = FALSE
)
```

### Arguments

input_filename	the name of a BEAST2 input XML file. This file usually has an .xml extension. Use <a href="#">create_temp_input_filename</a> to create a temporary filename with that extension.
output_log_filename	name of the .log file to create
output_trees_filenames	one or more names for .trees file to create. There will be one .trees file created per alignment in the input file. The number of alignments must equal the number of .trees filenames, else an error is thrown. Alignments are sorted alphabetically by their IDs
output_state_filename	name of the .xml.state file to create. Use <a href="#">create_temp_state_filename</a> to create a temporary filename with that extension.
rng_seed	the random number generator seed of the BEAST2 run. Must be a non-zero positive integer value or <b>NA</b> . If rng_seed is <b>NA</b> , BEAST2 will pick a random seed
n_threads	the number of computational threads to use. Use <b>NA</b> to use the BEAST2 default of 1.
use_beagle	use BEAGLE if present
overwrite	if TRUE: overwrite the .log and .trees files if one of these exists. If FALSE, BEAST2 will not be started if

- the .log file exists
- the .trees files exist
- the .log file created by BEAST2 exists
- the .trees files created by BEAST2 exist

beast2\_working\_dir

a folder where BEAST2 can work in isolation. For each BEAST2 run, a new subfolder is created in that folder. Within this folder, BEAST2 is allowed to create all of its output files, without the risk of overwriting existing ones, allowing BEAST2 to run in multiple parallel processes.

beast2\_path

name of either a BEAST2 binary file (usually simply `beast`) or a BEAST2 jar file (usually has a `.jar` extension). Use [get\\_default\\_beast2\\_bin\\_path](#) to get the default BEAST binary file's path Use [get\\_default\\_beast2\\_jar\\_path](#) to get the default BEAST jar file's path

verbose

if TRUE, additional information is displayed, that is potentially useful in debugging

### Value

The text sent to STDOUT and STDERR. It will create the file with name `output_state_filenames`

### Author(s)

Richèl J.C. Bilderbeek

### Examples

```
if (is_beast2_installed() && is_on_ci()) {
  run_beast2(
    input_filename = get_beastier_path("2_4.xml")
  )
}
```

---

run\_beast2\_from\_options

*Run BEAST2*

---

### Description

Run BEAST2

### Usage

```
run_beast2_from_options(beast2_options = create_beast2_options())
```

**Arguments**

beast2\_options a set of BEAST2 options, that are the R equivalent of the BEAST2 command-line options, as can be created by [create\\_beast2\\_options](#)

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
if (is_beast2_installed() && is_on_ci()) {  
  beast2_options <- create_beast2_options(  
    input_filename = get_beastier_path("2_4.xml")  
  )  
  run_beast2_from_options(beast2_options)  
}
```

---

save_lines	<i>Save text (a container of strings) to a file</i>
------------	---

---

**Description**

Save text (a container of strings) to a file

**Usage**

```
save_lines(filename, lines)
```

**Arguments**

filename filename of the file to have the text written to  
lines lines of text to be written to file

**Value**

Nothing. Will save the lines to file

**Author(s)**

Richèl J.C. Bilderbeek

**Examples**

```
text <- c("hello", "world")  
filename <- tempfile(fileext = ".txt")  
save_lines(filename = filename, lines = text)
```

---

save\_nexus\_as\_fasta     *Save a NEXUS file as a FASTA file*

---

### Description

Save a NEXUS file as a FASTA file

### Usage

```
save_nexus_as_fasta(nexus_filename, fasta_filename)
```

### Arguments

nexus\_filename    name of an existing NEXUS file  
 fasta\_filename    name of the FASTA file to be created

---

uninstall\_beast2     *Uninstall BEAST2*

---

### Description

Uninstall BEAST2

### Usage

```
uninstall_beast2(  
  folder_name = rappdirs::user_data_dir(),  
  os = rappdirs::app_dir()$os,  
  verbose = FALSE  
)
```

### Arguments

folder\_name        name of the folder where the BEAST2 files are installed. The name of the BEAST2 binary file will be at [folder\_name]/beast/bin/beast The name of the BEAST2 jar file will be at [folder\_name]/beast/lib/launcher.jar  
 os                 name of the operating system, must be unix (Linux, Mac) or win (Windows)  
 verbose            if TRUE, additional information is displayed, that is potentially useful in debugging

### Author(s)

Richèl J.C. Bilderbeek

**Examples**

```
## Not run:
  uninstall_beast2()

## End(Not run)
```

---

update_beastier	<i>Update all beastier dependencies, by installing their latest versions</i>
-----------------	--

---

**Description**

Update all beastier dependencies, by installing their latest versions

**Usage**

```
update_beastier()
```

**Author(s)**

Richèl J.C. Bilderbeek

---

upgrade_beast2	<i>Upgrade BEAST2.</i>
----------------	------------------------

---

**Description**

Will [stop](#) if BEAST2 is not installed

**Usage**

```
upgrade_beast2(
  folder_name = rappdirs::user_data_dir(),
  os = rappdirs::app_dir()$os
)
```

**Arguments**

folder_name	name of the folder where the BEAST2 files will be put. The name of the BEAST2 binary file will be at [folder_name]/beast/bin/beast The name of the BEAST2 jar file will be at [folder_name]/beast/lib/launcher.jar
os	name of the operating system, must be unix (Linux, Mac) or win (Windows)

**Author(s)**

Richèl J.C. Bilderbeek



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