

Package ‘mcbette’

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Title Model Comparison Using 'babette'

Version 1.15

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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. 'mcbette' allows to do a Bayesian model comparison over some site and clock models, using 'babette' (<<https://github.com/ropensci/babette/>>).

License GPL-3

RoxygenNote 7.2.1

VignetteBuilder knitr

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

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

Imports babette (>= 2.3), beautier (>= 2.6.2), beastier (>= 2.4.6), curl, devtools, mauricer (>= 2.5), Rmpfr, testit, txtplot

Suggests ape, ggplot2, hunspell, knitr, lintr, markdown, nLTT, phangorn, rappdirs, rmarkdown, spelling, stringr, testthat (>= 2.1.0), tracerer

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NeedsCompilation no

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calc_weights	<i>Calculate the weights for each marginal likelihood</i>
--------------	-----------------------------------------------------------

Description

Calculate the weights for each marginal likelihood

Usage

```
calc_weights(marg_lik)
```

Arguments

marg_lik (non-log) marginal likelihood estimates

Value

the weight of each marginal likelihood estimate, which will sum up to 1.0

Author(s)

Richèl J.C. Bilderbeek

Examples

```
# Evidences (aka marginal likelihoods) can be very small
evidences <- c(0.0001, 0.0002, 0.0003, 0.0004)

# Sum will be 1.0
calc_weights(evidences)

beastier::check_empty_beastier_folders()
```

can_run_mcbette	<i>Can 'mcbette' run?</i>
-----------------	---------------------------

Description

Can 'mcbette' run? Will return **TRUE** if:

- (1) Running on Linux or MacOS
- (2) BEAST2 is installed
- (3) The BEAST2 NS package is installed

Usage

```
can_run_mcbette(beast2_folder = beastier::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 [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. Use [get_default_beast2_jar_path](#) to get the full path to the default BEAST2 jar file.

Author(s)

Richèl J.C. Bilderbeek

Examples

```
can_run_mcbette()

beastier::check_empty_beastier_folders()
```

check_beast2_ns_pkg *Checks if the BEAST2 'NS' package is installed.*

Description

Checks if the BEAST2 'NS' package is installed. Will [stop](#) if not

Usage

```
check_beast2_ns_pkg(beast2_bin_path = beastier::get_default_beast2_bin_path())
```

Arguments

beast2_bin_path
path to the the BEAST2 binary file

check_marg_lik *Check if the marg_lik are of the same type as returned by [est_marg_lik](#).*

Description

[stop](#) if not.

Usage

```
check_marg_lik(marg_lik)
```

Arguments

marg_lik a table of (estimated) marginal likelihoods, as, for example, created by [est_marg_lik](#). This [data.frame](#) has the following columns:

- site_model_name: name of the site model, must be an element of [get_site_model_names](#)
- clock_model_name: name of the clock model, must be an element of [get_clock_model_names](#)
- tree_prior_name: name of the tree prior, must be an element of [get_tree_prior_names](#)
- marg_log_lik: estimated marginal (natural) log likelihood
- marg_log_lik_sd: estimated error of marg_log_lik
- weight: relative model weight, a value from 1.0 (all evidence is in favor of this model combination) to 0.0 (no evidence in favor of this model combination)
- ess: effective sample size of the marginal likelihood estimation

Use [get_test_marg_lik](#) to get a test marg_lik. Use [is_marg_lik](#) to determine if a marg_lik is valid. Use [check_marg_lik](#) to check that a marg_lik is valid.

check_mcbette_state *Check if the mcbette_state is valid.*

Description

Check if the mcbette_state is valid. Will [stop](#) otherwise.

Usage

```
check_mcbette_state(mcbette_state)
```

Arguments

mcbette_state the [mcbette](#) state, which is a [list](#) with the following elements:

- `beast2_installed` [TRUE](#) if BEAST2 is installed, [FALSE](#) otherwise
- `ns_installed` [NA](#) if BEAST2 is not installed. [TRUE](#) if the BEAST2 NS package is installed [FALSE](#) if the BEAST2 NS package is not installed

Author(s)

Richèl J.C. Bilderbeek

default_params_doc *Documentation of general function arguments. This function does nothing. It is intended to inherit function argument documentation.*

Description

Documentation of general function arguments. This function does nothing. It is intended to inherit function argument documentation.

Usage

```
default_params_doc(  
  beast2_bin_path,  
  beast2_folder,  
  beast2_working_dir,  
  beast2_options,  
  beast2_optionses,  
  clock_model,  
  clock_models,  
  epsilon,  
  fasta_filename,  
  inference_model,  
  inference_models,
```

```

marg_liks,
mcbette_state,
mcmc,
os,
rng_seed,
site_model,
site_models,
tree_prior,
tree_priors,
verbose
)

```

Arguments

beast2_bin_path	path to the the BEAST2 binary file
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. Use get_default_beast2_jar_path to get the full path to the default BEAST2 jar file.
beast2_working_dir	folder in which BEAST2 will run and produce intermediate files. By default, this is a temporary folder
beast2_options	a <code>beast2_options</code> structure, as can be created by create_mcbette_beast2_options .
beast2_optionses	list of one or more <code>beast2_options</code> structures, as can be created by create_mcbette_beast2_options . Use of reduplicated plural to achieve difference with <code>beast2_options</code>
clock_model	a clock model, as can be created by create_clock_model
clock_models	a list of one or more clock models, as can be created by create_clock_models
epsilon	measure of relative accuracy. Smaller values result in longer, more precise estimations
fasta_filename	name of the FASTA file
inference_model	an inference model, as can be created by create_inference_model
inference_models	a list of one or more inference models, as can be created by create_inference_model
marg_liks	a table of (estimated) marginal likelihoods, as, for example, created by est_marg_liks . This <code>data.frame</code> has the following columns: <ul style="list-style-type: none"> • <code>site_model_name</code>: name of the site model, must be an element of get_site_model_names • <code>clock_model_name</code>: name of the clock model, must be an element of get_clock_model_names • <code>tree_prior_name</code>: name of the tree prior, must be an element of get_tree_prior_names • <code>marg_log_lik</code>: estimated marginal (natural) log likelihood

- `marg_log_lik_sd`: estimated error of `marg_log_lik`
- `weight`: relative model weight, a value from 1.0 (all evidence is in favor of this model combination) to 0.0 (no evidence in favor of this model combination)
- `ess`: effective sample size of the marginal likelihood estimation

Use `get_test_marg_lik` to get a test `marg_lik`s. Use `is_marg_lik` to determine if a `marg_lik`s is valid. Use `check_marg_lik` to check that a `marg_lik`s is valid.

<code>mcbette_state</code>	the <code>mcbette</code> state, which is a <code>list</code> with the following elements: <ul style="list-style-type: none"> • <code>beast2_installed</code> <code>TRUE</code> if BEAST2 is installed, <code>FALSE</code> otherwise • <code>ns_installed</code> <code>NA</code> if BEAST2 is not installed. <code>TRUE</code> if the BEAST2 NS package is installed <code>FALSE</code> if the BEAST2 NS package is not installed
<code>mcmc</code>	an MCMC for the Nested Sampling run, as can be created by <code>create_mcmc_nested_sampling</code>
<code>os</code>	name of the operating system, must be <code>unix</code> (Linux, Mac) or <code>win</code> (Windows)
<code>rng_seed</code>	a random number generator seed used for the BEAST2 inference
<code>site_model</code>	a site model, as can be created by <code>create_site_model</code>
<code>site_models</code>	a list of one or more site models, as can be created by <code>create_site_models</code>
<code>tree_prior</code>	a tree prior, as can be created by <code>create_tree_prior</code>
<code>tree_priors</code>	a list of one or more tree priors, as can be created by <code>create_tree_priors</code>
<code>verbose</code>	if <code>TRUE</code> show debug output

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

<code>est_marg_lik</code>	<i>Estimate the marginal likelihood for an inference model.</i>
---------------------------	-----------------------------------------------------------------

Description

Estimate the marginal likelihood for an inference model.

Usage

```
est_marg_lik(
  fasta_filename,
  inference_model = beautier::create_ns_inference_model(),
  beast2_options = beastier::create_mcbette_beast2_options(),
  os = rappdirs::app_dir()$os
)
```

Arguments

fasta_filename name of the FASTA file
inference_model
 an inference model, as can be created by [create_inference_model](#)
beast2_options a `beast2_options` structure, as can be created by [create_mcbette_beast2_options](#).
os name of the operating system, must be `unix` (Linux, Mac) or `win` (Windows)

Value

a [list](#) showing the estimated marginal likelihoods (and its estimated error), its items are::

- `marg_log_lik`: estimated marginal (natural) log likelihood
- `marg_log_lik_sd`: estimated error of `marg_log_lik`
- `esses` the Effective Sample Size

Author(s)

Richèl J.C. Bilderbeek

See Also

- [can_run_mcbette](#): see if 'mcbette' can run
- [est_marg_lik](#): estimate multiple marginal likelihoods

Examples

```

if (can_run_mcbette()) {
  # An example FASTA file
  fasta_filename <- system.file("extdata", "simple.fas", package = "mcbette")

  # A testing inference model with inaccurate (thus fast) marginal
  # likelihood estimation
  inference_model <- beautier::create_ns_inference_model()

  # Shorten the run, by doing a short (dirty, unreliable) MCMC
  inference_model$mcmc <- beautier::create_test_ns_mcmc()

  # Setup the options for BEAST2 to be able to call BEAST2 packages
  beast2_options <- beautier::create_mcbette_beast2_options()

  # Estimate the marginal likelihood
  est_marg_lik(
    fasta_filename = fasta_filename,
    inference_model = inference_model,
    beast2_options = beast2_options
  )

  beautier::check_empty_beautier_folders()
}

```

est_marg_lik *Estimate the marginal likelihoods for one or more inference models*

Description

Estimate the marginal likelihoods (aka evidence) for one or more inference models, based on a single alignment. Also, the marginal likelihoods are compared, resulting in a relative weight for each model, where a relative weight of a model close to 1.0 means that that model is way likelier than the others.

Usage

```
est_marg_lik(
  fasta_filename,
  inference_models = list(beautier::create_inference_model(mcmc =
    beautier::create_ns_mcmc())),
  beast2_optionses = rep(list(beastier::create_mcbette_beast2_options()), times =
    length(inference_models)),
  verbose = FALSE,
  os = rappdirs::app_dir()$os
)
```

Arguments

`fasta_filename` name of the FASTA file

`inference_models`
a list of one or more inference models, as can be created by [create_inference_model](#)

`beast2_optionses`
list of one or more `beast2_options` structures, as can be created by [create_mcbette_beast2_options](#).
Use of reduplicated plural to achieve difference with `beast2_options`

`verbose` if TRUE show debug output

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

Details

In the process, multiple (temporary) files are created (where `[x]` denotes the index in a list)

- `beast2_optionses[x]$input_filename` path to the the BEAST2 XML input file
- `beast2_optionses[x]$output_state_filename` path to the BEAST2 XML state file
- `inference_models[x]$mcmc$tracelog$filename` path to the BEAST2 trace file with parameter estimates
- `inference_models[x]$mcmc$treelog$filename` path to the BEAST2 trees file with the posterior trees
- `inference_models[x]$mcmc$screenlog$filename` path to the BEAST2 screen output file

These file can be deleted manually by [bbt_delete_temp_files](#), else these will be deleted automatically by the operating system.

Value

a [data.frame](#) showing the estimated marginal likelihoods (and its estimated error) per combination of models. Columns are:

- `site_model_name`: name of the site model
- `clock_model_name`: name of the clock model
- `tree_prior_name`: name of the tree prior
- `marg_log_lik`: estimated marginal (natural) log likelihood
- `marg_log_lik_sd`: estimated error of `marg_log_lik`
- `weight`: relative model weight, a value from 1.0 (all evidence is in favor of this model combination) to 0.0 (no evidence in favor of this model combination)
- `ess`: effective sample size of the marginal likelihood estimation

Author(s)

Richèl J.C. Bilderbeek

See Also

- [can_run_mcbette](#): see if 'mcbette' can run
- [est_marg_lik](#): estimate multiple marginal likelihood of a single inference mode

Examples

```
if (can_run_mcbette()) {

  # Use an example FASTA file
  fasta_filename <- system.file("extdata", "simple.fas", package = "mcbette")

  # Create two inference models
  inference_model_1 <- beautier::create_ns_inference_model(
    site_model = beautier::create_jc69_site_model()
  )
  inference_model_2 <- beautier::create_ns_inference_model(
    site_model = beautier::create_hky_site_model()
  )

  # Shorten the run, by doing a short (dirty, unreliable) MCMC
  inference_model_1$mcmc <- beautier::create_test_ns_mcmc()
  inference_model_2$mcmc <- beautier::create_test_ns_mcmc()

  # Combine the inference models
  inference_models <- list(inference_model_1, inference_model_2)

  # Create the BEAST2 options, that will write the output
  # to different (temporary) filenames
  beast2_options_1 <- beastier::create_mcbette_beast2_options()
  beast2_options_2 <- beastier::create_mcbette_beast2_options()
}
```

```

# Combine the two BEAST2 options sets,
# use reduplicated plural
beast2_optionses <- list(beast2_options_1, beast2_options_2)

# Compare the models
marg_lik <- est_marg_lik(
  fasta_filename,
  inference_models = inference_models,
  beast2_optionses = beast2_optionses
)

# Interpret the results
interpret_marg_lik_estimates(marg_lik)

beastier::check_empty_beastier_folders()
}

```

get_mcbette_state *Get the current state of [mcbette](#)*

Description

Get the current state of [mcbette](#)

Usage

```
get_mcbette_state(beast2_folder = beastier::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 [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. Use [get_default_beast2_jar_path](#) to get the full path to the default BEAST2 jar file.

Value

a [list](#) with the following elements:

- `beast2_installed` [TRUE](#) if BEAST2 is installed, [FALSE](#) otherwise
- `ns_installed` [TRUE](#) if the BEAST2 NS package is installed [FALSE](#) if the BEAST2 or the BEAST2 NS package is not installed

Examples

```

get_mcbette_state()

beastier::check_empty_beastier_folders()

```

get_test_marg_lik *Get testing marg_lik*

Description

Get testing marg_lik

Usage

```
get_test_marg_lik()
```

Examples

```
get_test_marg_lik()
beastier::check_empty_beastier_folders()
```

interpret_bayes_factor
Interpret a Bayes factor

Description

Interpret a Bayes factor, using the interpretation from [1].

Usage

```
interpret_bayes_factor(bayes_factor)
```

Arguments

bayes_factor Bayes factor to be interpreted

Details

- [1] H. Jeffreys (1961). The Theory of Probability (3rd ed.). Oxford. p. 432

Value

a string with the interpretation in English

Author(s)

Richèl J.C. Bilderbeek

Examples

```
interpret_bayes_factor(0.5)

beastier::check_empty_beastier_folders()
```

```
interpret_marg_lik_estimates
```

Interpret the marginal likelihood estimates

Description

Interpret the marginal likelihood estimates as created by [est_marg_lik](#)s.

Usage

```
interpret_marg_lik_estimates(marg_lik)
```

Arguments

`marg_lik` a table of (estimated) marginal likelihoods, as, for example, created by [est_marg_lik](#)s. This [data.frame](#) has the following columns:

- `site_model_name`: name of the site model, must be an element of [get_site_model_names](#)
- `clock_model_name`: name of the clock model, must be an element of [get_clock_model_names](#)
- `tree_prior_name`: name of the tree prior, must be an element of [get_tree_prior_names](#)
- `marg_log_lik`: estimated marginal (natural) log likelihood
- `marg_log_lik_sd`: estimated error of `marg_log_lik`
- `weight`: relative model weight, a value from 1.0 (all evidence is in favor of this model combination) to 0.0 (no evidence in favor of this model combination)
- `ess`: effective sample size of the marginal likelihood estimation

Use [get_test_marg_lik](#) to get a test `marg_lik`s. Use [is_marg_lik](#) to determine if a `marg_lik` is valid. Use [check_marg_lik](#) to check that a `marg_lik` is valid.

Author(s)

Richèl J.C. Bilderbeek

is_marg_lik	<i>Determine if the marg_lik is valid</i>
-------------	-------------------------------------------

Description

Determine if the marg_lik is valid

Usage

```
is_marg_lik(marg_lik, verbose = FALSE)
```

Arguments

marg_lik	<p>a table of (estimated) marginal likelihoods, as, for example, created by est_marg_lik. This data.frame has the following columns:</p> <ul style="list-style-type: none"> • site_model_name: name of the site model, must be an element of get_site_model_names • clock_model_name: name of the clock model, must be an element of get_clock_model_names • tree_prior_name: name of the tree prior, must be an element of get_tree_prior_names • marg_log_lik: estimated marginal (natural) log likelihood • marg_log_lik_sd: estimated error of marg_log_lik • weight: relative model weight, a value from 1.0 (all evidence is in favor of this model combination) to 0.0 (no evidence in favor of this model combination) • ess: effective sample size of the marginal likelihood estimation <p>Use get_test_marg_lik to get a test marg_lik. Use is_marg_lik to determine if a marg_lik is valid. Use check_marg_lik to check that a marg_lik is valid.</p>
verbose	if TRUE show debug output

Value

TRUE if the argument is a valid marg_lik, FALSE otherwise

mcbette	<i>mcbette: Model Comparison Using Babette</i>
---------	------------------------------------------------

Description

'mcbette' does a model comparing using [babette](#), where the models are Bayesian phylogenetic models, as created by [create_inference_model](#).

Details

The main function is [est_marg_lik](#)s, which estimate the marginal likelihoods (aka evidence) for one or more inference models, based on a single alignment. Also, the marginal likelihoods are compared, resulting in a relative weight for each model, where a relative weight of a model close to 1.0 means that that model is way likelier than the others.

In the process, multiple (temporary) files are created (where [x] denotes the index in a list)

- `beast2_optionses[x]$input_filename` path to the the BEAST2 XML input file
- `beast2_optionses[x]$output_state_filename` path to the BEAST2 XML state file
- `inference_models[x]$mcmc$tracelog$filename` path to the BEAST2 trace file with parameter estimates
- `inference_models[x]$mcmc$treelog$filename` path to the BEAST2 trees file with the posterior trees
- `inference_models[x]$mcmc$screenlog$filename` path to the BEAST2 screen output file

These file can be deleted manually by [bbt_delete_temp_files](#), else these will be deleted automatically by the operating system.

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [can_run_mcbette](#) to see if 'mcbette' can run.

Examples

```
if (can_run_mcbette()) {

  # An example FASTA file
  fasta_filename <- system.file("extdata", "simple.fas", package = "mcbette")

  inference_model_1 <- beautier::create_ns_inference_model(
    site_model = beautier::create_jc69_site_model()
  )
  inference_model_2 <- beautier::create_ns_inference_model(
    site_model = beautier::create_gtr_site_model()
  )

  # Shorten the run, by doing a short (dirty, unreliable) MCMC
  inference_model_1$mcmc <- beautier::create_test_ns_mcmc()
  inference_model_2$mcmc <- beautier::create_test_ns_mcmc()

  inference_models <- c(list(inference_model_1), list(inference_model_2))

  # Estimate the marginal log-likelihoods of the two models
  marg_lik <- est_marg_lik(
    fasta_filename = fasta_filename,
```

```
    inference_models = inference_models
  )

  # Interpret the results
  interpret_marg_lik_estimates(marg_lik)

  beastier::check_empty_beastier_folders()
  beastier::remove_beastier_folders()
}
```

mcbette_report

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

Description

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

Usage

```
mcbette_report(beast2_folder = beastier::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 [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. Use [get_default_beast2_jar_path](#) to get the full path to the default BEAST2 jar file.

Value

nothing. It is intended that the output (not the return value) is copy-pasted from screen.

Author(s)

Richèl J.C. Bilderbeek

Examples

```
mcbette_report()
```

mcbette_self_test	<i>Performs a minimal mcbette run</i>
-------------------	-------------------------------------------------------

Description

Performs a minimal [mcbette](#) run

Usage

```
mcbette_self_test(beast2_folder = beastier::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 [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. Use [get_default_beast2_jar_path](#) to get the full path to the default BEAST2 jar file.

plot_marg_lik	<i>Plot the marg_lik</i>
---------------	--------------------------

Description

Plot the `marg_lik`

Usage

```
plot_marg_lik(marg_lik)
```

Arguments

`marg_lik` a table of (estimated) marginal likelihoods, as, for example, created by [est_marg_lik](#). This [data.frame](#) has the following columns:

- `site_model_name`: name of the site model, must be an element of [get_site_model_names](#)
- `clock_model_name`: name of the clock model, must be an element of [get_clock_model_names](#)
- `tree_prior_name`: name of the tree prior, must be an element of [get_tree_prior_names](#)
- `marg_log_lik`: estimated marginal (natural) log likelihood
- `marg_log_lik_sd`: estimated error of `marg_log_lik`
- `weight`: relative model weight, a value from 1.0 (all evidence is in favor of this model combination) to 0.0 (no evidence in favor of this model combination)

- `ess`: effective sample size of the marginal likelihood estimation
- Use [get_test_marg_lik](#)s to get a test `marg_lik`s. Use [is_marg_lik](#)s to determine if a `marg_lik`s is valid. Use [check_marg_lik](#)s to check that a `marg_lik`s is valid.

Value

a [ggplot](#)

set_mcbette_state *Set the [mcbette](#) state.*

Description

Set the [mcbette](#) state to having BEAST2 installed with or without installing the BEAST2 NS package.

Usage

```
set_mcbette_state(
  mcbette_state,
  beast2_folder = beastier::get_default_beast2_folder(),
  verbose = FALSE
)
```

Arguments

`mcbette_state` the [mcbette](#) state, which is a [list](#) with the following elements:

- `beast2_installed` **TRUE** if BEAST2 is installed, **FALSE** otherwise
- `ns_installed` **NA** if BEAST2 is not installed. **TRUE** if the BEAST2 NS package is installed **FALSE** if the BEAST2 NS package is not installed

`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. Use [get_default_beast2_jar_path](#) to get the full path to the default BEAST2 jar file.

`verbose` if **TRUE** show debug output

Note

In newer versions of BEAST2, BEAST2 comes pre-installed with the BEAST2 NS package. For such a version, one cannot install BEAST2 without NS. A warning will be issues if one intends to only install BEAST2 (i.e. without the BEAST2 NS package) and gets the BEAST2 NS package installed as a side effect as well.

Also, installing or uninstalling a BEAST2 package from a BEAST2 installation will affect all installations.

See Also

- Use [get_mcbette_state](#) to get the current [mcbette](#) state
- Use [check_mcbette_state](#) to check the current [mcbette](#) state

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