

Package: tracerer (via r-universe)

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Type Package

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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. 'Tracer' (<<https://github.com/beast-dev/tracer/>>) is a GUI tool to parse and analyze the files generated by 'BEAST2'. This package provides a way to parse and analyze 'BEAST2' input files without active user input, but using R function calls instead.

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Imports jsonlite, Rcpp

Suggests ape, ggplot2, knitr, phangorn, rappdirs, rmarkdown, spelling, testthat (>= 3.0.0)

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RoxygenNote 7.3.3

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

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

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calc_act

Calculate the auto-correlation time, alternative implementation

Description

Calculate the auto-correlation time, alternative implementation

Usage

```
calc_act(trace, sample_interval)
```

Arguments

```
trace          the values
sample_interval the interval in timesteps between samples
```

Value

the auto_correlation time

Author(s)

The original Java version of the algorithm was from Remco Bouckaert, ported to R and adapted by Richèl J.C. Bilderbeek

See Also

Java code can be found here: <https://github.com/CompEvol/beast2/blob/9f040ed0357c4b946ea276a481a4c654ad4fsrc/beast/core/util/ESS.java#L161> # nolint URLs can be long

Examples

```
trace <- sin(seq(from = 0.0, to = 2.0 * pi, length.out = 100))
# 38.18202
calc_act(trace = trace, sample_interval = 1)
```

calc_act_cpp	<i>Calculate the auto correlation time from https://github.com/beast-dev/beast-mcmc/blob/800817772033c13061f026226e41128d21fd14f3/src/dr/inference/trace/TraceCorrelation.java#L159 # nolint</i>
--------------	--

Description

Calculate the auto correlation time from <https://github.com/beast-dev/beast-mcmc/blob/800817772033c13061f026226e41128d21fd14f3/src/dr/inference/trace/TraceCorrelation.java#L159> # nolint

Usage

```
calc_act_cpp(sample, sample_interval)
```

Arguments

sample sample
sample_interval
 sample interval

Value

the auto correlation time

Author(s)

Richèl J.C. Bilderbeek

calc_act_r	<i>Calculate the auto-correlation time using only R. Consider using calc_act instead, as it is orders of magnitude faster</i>
------------	---

Description

Calculate the auto-correlation time using only R. Consider using [calc_act](#) instead, as it is orders of magnitude faster

Usage

```
calc_act_r(trace, sample_interval)
```

Arguments

trace the values
sample_interval
 the interval in timesteps between samples

Value

the auto correlation time

Author(s)

The original Java version of the algorithm was from Remco Bouckaert, ported to R and adapted by Richèl J.C. Bilderbeek

See Also

Java code can be found here: <https://github.com/CompEvol/beast2/blob/9f040ed0357c4b946ea276a481a4c654ad4fsrc/beast/core/util/ESS.java#L161> # nolint URLs can be long

Examples

```
trace <- sin(seq(from = 0.0, to = 2.0 * pi, length.out = 100))
calc_act_r(trace = trace, sample_interval = 1) # 38.18202
```

calc_ess	<i>Calculates the Effective Sample Size</i>
----------	---

Description

Calculates the Effective Sample Size

Usage

```
calc_ess(trace, sample_interval)
```

Arguments

trace	the values without burn-in
sample_interval	the interval in timesteps between samples

Value

the effective sample size

Author(s)

The original Java version of the algorithm was from Remco Bouckaert, ported to R and adapted by Richèl J.C. Bilderbeek

See Also

Java code can be found here: <https://github.com/CompEvol/beast2/blob/9f040ed0357c4b946ea276a481a4c654ad4fsrc/beast/core/util/ESS.java#L161> # nolint URLs can be long

Examples

```
filename <- get_tracerer_path("beast2_example_output.log")
estimates <- parse_beast_tracelog_file(filename)
calc_ess(estimates$posterior, sample_interval = 1000)
```

calc_esses	<i>Calculates the Effective Sample Sizes from a parsed BEAST2 log file</i>
------------	--

Description

Calculates the Effective Sample Sizes from a parsed BEAST2 log file

Usage

```
calc_esses(traces, sample_interval)
```

Arguments

traces	a dataframe with traces with removed burn-in
sample_interval	the interval in timesteps between samples

Value

the effective sample sizes

Author(s)

Richèl J.C. Bilderbeek

Examples

```
# Parse an example log file
estimates <- parse_beast_tracelog_file(
  get_tracerer_path("beast2_example_output.log")
)

# Calculate the effective sample sizes of all parameter estimates
calc_esses(estimates, sample_interval = 1000)
```

calc_geom_mean	<i>Calculate the geometric mean</i>
----------------	-------------------------------------

Description

Calculate the geometric mean

Usage

```
calc_geom_mean(values)
```

Arguments

values a numeric vector of values

Value

returns the geometric mean if all values are at least zero, else returns NA

Author(s)

Richèl J.C. Bilderbeek

calc_hpd_interval	<i>Calculate the Highest Probability Density of an MCMC trace that has its burn-in removed</i>
-------------------	--

Description

Calculate the Highest Probability Density of an MCMC trace that has its burn-in removed

Usage

```
calc_hpd_interval(trace, proportion = 0.95)
```

Arguments

trace a numeric vector of parameter estimates obtained from an MCMC run. Must have its burn-in removed

proportion the proportion of numbers within the interval. For example, use 0.95 for a 95 percentage interval

Value

a numeric vector, with at index 1 the lower boundary of the interval, and at index 2 the upper boundary of the interval

Author(s)

The original Java version of the algorithm was from J. Heled, ported to R and adapted by Richèl J.C. Bilderbeek

See Also

The function [remove_burn_in](#) removes a burn-in. The Java code that inspired this function can be found here: <https://github.com/beast-dev/beast-mcmc/blob/98705c59db65e4f406a420bbade949aeecfe05d0/src/dr/stats/DiscreteStatistics.java#L317> # nolint URLs can be long

Examples

```

estimates <- parse_beast_tracelog_file(
  get_tracerer_path("beast2_example_output.log")
)
tree_height_trace <- remove_burn_in(
  estimates$TreeHeight,
  burn_in_fraction = 0.1
)

# Values will be 0.453 and 1.816
calc_hpd_interval(tree_height_trace, proportion = 0.95)

```

calc_mode	<i>Calculate the mode of values If the distribution is bi or multimodal or uniform, NA is returned</i>
-----------	--

Description

Calculate the mode of values If the distribution is bi or multimodal or uniform, NA is returned

Usage

```
calc_mode(values)
```

Arguments

values numeric vector to calculate the mode of

Value

the mode of the trace

Author(s)

Richèl J.C. Bilderbeek

Examples

```

# In a unimodal distribution, find the value that occurs most
calc_mode(c(1, 2, 2))
calc_mode(c(1, 1, 2))

# For a uniform distribution, NA is returned
tracerer::calc_mode(c(1, 2))

```

`calc_std_error_of_mean_cpp`*Calculates the standard error of the mean*

Description

Calculates the standard error of the mean

Usage

```
calc_std_error_of_mean_cpp(sample)
```

Arguments

sample numeric vector of values

Value

the standard error of the mean

Author(s)

Richèl J.C. Bilderbeek

`calc_stderr_mean`*Calculate the standard error of the mean*

Description

Calculate the standard error of the mean

Usage

```
calc_stderr_mean(trace)
```

Arguments

trace the values

Value

the standard error of the mean

Author(s)

The original Java version of the algorithm was from Remco Bouckaert, ported to R and adapted by Richèl J.C. Bilderbeek

See Also

Java code can be found here: <https://github.com/beast-dev/beast-mcmc/blob/800817772033c13061f026226e41128src/dr/inference/trace/TraceCorrelation.java#L159> # nolint URLs can be long

Examples

```
trace <- sin(seq(from = 0.0, to = 2.0 * pi, length.out = 100))
calc_stderr_mean(trace) # 0.4347425
```

calc_summary_stats	<i>Calculates the Effective Sample Sizes of one estimated variable's trace</i>
--------------------	--

Description

Calculates the Effective Sample Sizes of one estimated variable's trace

Usage

```
calc_summary_stats(traces, sample_interval)
```

Arguments

traces	one or more traces, supplies as either, (1) a numeric vector or, (2) a data frame of numeric values.
sample_interval	the interval (the number of state transitions between samples) of the MCMC run that produced the trace. Using a different sample_interval than the actually used sampling interval will result in bogus return values.

Value

the summary statistics of the traces. If one numeric vector is supplied, a list is returned with the elements listed below. If the traces are supplied as a data frame, a data frame is returned with the elements listed below as column names.

The elements are:

- mean: mean
- stderr_mean: standard error of the mean
- stdev: standard deviation
- variance: variance
- mode: mode
- geom_mean: geometric mean
- hpd_interval_low: lower bound of 95% highest posterior density
- hpd_interval_high: upper bound of 95% highest posterior density
- act: auto correlation time
- ess: effective sample size

Note

This function assumes the burn-in is removed. Use [remove_burn_in](#) (on a vector) or [remove_burn_ins](#) (on a data frame) to remove the burn-in.

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [calc_summary_stats_trace](#) to calculate the summary statistics of one trace (stored as a numeric vector). Use [calc_summary_stats_traces](#) to calculate the summary statistics of more traces (stored as a data frame).

Examples

```
estimates_all <- parse_beast_tracelog_file(
  get_tracerer_path("beast2_example_output.log")
)
estimates <- remove_burn_ins(estimates_all, burn_in_fraction = 0.1)

# From a single variable's trace
calc_summary_stats(
  estimates$posterior,
  sample_interval = 1000
)

# From all variables' traces
calc_summary_stats(
  estimates,
  sample_interval = 1000
)
```

calc_summary_stats_trace

Calculates the Effective Sample Sizes of one estimated variable's trace

Description

Calculates the Effective Sample Sizes of one estimated variable's trace

Usage

```
calc_summary_stats_trace(trace, sample_interval)
```

Arguments

trace a numeric vector of values. Assumes the burn-in is removed.
sample_interval the interval in timesteps between samples

Value

the effective sample sizes

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [remove_burn_in](#) to remove the burn-in of a trace

Examples

```
estimates_all <- parse_beast_tracelog_file(
  get_tracerer_path("beast2_example_output.log")
)
estimates <- remove_burn_ins(estimates_all, burn_in_fraction = 0.1)

calc_summary_stats_trace(
  estimates$posterior,
  sample_interval = 1000
)
```

calc_summary_stats_traces

Calculates the Effective Sample Sizes of the traces of multiple estimated variables

Description

Calculates the Effective Sample Sizes of the traces of multiple estimated variables

Usage

```
calc_summary_stats_traces(traces, sample_interval)
```

Arguments

traces a data frame with traces of estimated parameters. Assumes the burn-ins are removed.

sample_interval the interval in timesteps between samples

Value

the effective sample sizes

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [remove_burn_ins](#) to remove the burn-ins of all traces

Examples

```
estimates_all <- parse_beast_tracelog_file(
  get_tracerer_path("beast2_example_output.log")
)
estimates <- remove_burn_ins(estimates_all, burn_in_fraction = 0.1)

calc_summary_stats_traces(
  estimates,
  sample_interval = 1000
)
```

check_trace

Check if the trace is a valid. Will [stop](#) if not

Description

Check if the trace is a valid. Will [stop](#) if not

Usage

```
check_trace(trace)
```

Arguments

trace the values

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_trace(seq(1, 2))
```

count_trees_in_file	<i>Count the number of trees in a .trees file</i>
---------------------	---

Description

Count the number of trees in a .trees file

Usage

```
count_trees_in_file(trees_filename)
```

Arguments

trees_filename name of a BEAST2 posterior .trees file, as can be read using [parse_beast_trees](#)

Value

the number of trees

Author(s)

Richèl J.C. Bilderbeek

See Also

if the .trees file is invalid, use [is_trees_file](#) with verbose = TRUE for the reason

cs_std_dev	<i>Calculate the corrected sample standard deviation</i>
------------	--

Description

Calculate the corrected sample standard deviation

Usage

```
cs_std_dev(values)
```

Arguments

values numeric values

Value

the corrected sample standard deviation

Author(s)

Richèl J.C. Bilderbeek

default_params_doc	<i>Documentation of general function arguments</i>
--------------------	--

Description

This function does nothing. It is intended to inherit function argument documentation.

Usage

```
default_params_doc(
  log_filename,
  sample_interval,
  state_filename,
  trace,
  tracelog_filename,
  trees_filename,
  trees_filenames,
  verbose
)
```

Arguments

log_filename	deprecated name of the BEAST2 tracelog .log output file. Use tracelog_filename instead
sample_interval	the interval in timesteps between samples
state_filename	name of the BEAST2 state .xml.state output file
trace	the values
tracelog_filename	name of the BEAST2 tracelog .log output file, as can be read using parse_beast_tracelog_file
trees_filename	name of a BEAST2 posterior .trees file, as can be read using parse_beast_trees
trees_filenames	the names of one or more a BEAST2 posterior .trees file. Each .trees file can be read using parse_beast_trees
verbose	set to TRUE for more 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

```
extract_operators_lines
```

Extract the JSON lines out of a .xml.state with the unparsed BEAST2 MCMC operator acceptances file with the operators

Description

Extract the JSON lines out of a .xml.state with the unparsed BEAST2 MCMC operator acceptances file with the operators

Usage

```
extract_operators_lines(filename)
```

Arguments

filename name of the BEAST2 .xml.state output file

Value

the JSON lines of a .xml.state file with the unparsed BEAST2 MCMC operator acceptances

Author(s)

Richèl J.C. Bilderbeek

```
get_tracerer_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_tracerer_path(filename)
```

Arguments

filename the file's name, without the path

Value

the full path to the filename

Author(s)

Richèl J.C. Bilderbeek

See Also

for more files, use [get_tracerer_paths](#)

Examples

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

<code>get_tracerer_paths</code>	<i>Get the full paths of files in the inst/extdata folder</i>
---------------------------------	---

Description

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

Usage

```
get_tracerer_paths(filenamees)
```

Arguments

filenamees the files' names, without the path

Value

the filenamees' full paths

Author(s)

Richèl J.C. Bilderbeek

See Also

for one file, use [get_tracerer_path](#)

Examples

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

```
get_tracerer_tempfilename
```

Get a temporary filename

Description

Get a temporary filename, similar to [tempfile](#), except that it always writes to a temporary folder named [tracerer](#).

Usage

```
get_tracerer_tempfilename(pattern = "file", fileext = "")
```

Arguments

pattern	a non-empty character vector giving the initial part of the name.
fileext	a non-empty character vector giving the file extension

Value

name for a temporary file

Note

this function is added to make sure no temporary cache files are left undeleted

is_posterior	<i>Determines if the input is a BEAST2 posterior</i>
--------------	--

Description

Determines if the input is a BEAST2 posterior

Usage

```
is_posterior(x)
```

Arguments

x the input

Value

TRUE if the input contains all information of a BEAST2 posterior. Returns FALSE otherwise.

Author(s)

Richèl J.C. Bilderbeek

Examples

```
trees_filename <- get_tracerer_path("beast2_example_output.trees")
tracelog_filename <- get_tracerer_path("beast2_example_output.log")
posterior <- parse_beast_posterior(
  trees_filename = trees_filename,
  tracelog_filename = tracelog_filename
)
is_posterior(posterior)
```

is_trees_file	<i>Measure if a file a valid BEAST2 .trees file</i>
---------------	---

Description

Measure if a file a valid BEAST2 .trees file

Usage

```
is_trees_file(trees_filename, verbose = FALSE)
```

Arguments

trees_filename name of a BEAST2 posterior .trees file, as can be read using [parse_beast_trees](#)
 verbose set to TRUE for more output

Value

TRUE if trees_filename is a valid .trees file

Author(s)

Richèl J.C. Bilderbeek

See Also

Most of the work is done by [read.nexus](#)

Examples

```
# TRUE
is_trees_file(get_tracerer_path("beast2_example_output.trees"))
is_trees_file(get_tracerer_path("unplottable_anthus_aco.trees"))
is_trees_file(get_tracerer_path("anthus_2_4_a.trees"))
is_trees_file(get_tracerer_path("anthus_2_4_b.trees"))
# FALSE
is_trees_file(get_tracerer_path("mcbette_issue_8.trees"))
```

is_trees_posterior	<i>Determines if the input is a BEAST2 posterior, as parsed by parse_beast_trees</i>
--------------------	--

Description

Determines if the input is a BEAST2 posterior, as parsed by parse_beast_trees

Usage

```
is_trees_posterior(x)
```

Arguments

x the input

Value

TRUE or FALSE

Author(s)

Richèl J.C. Bilderbeek

parse_beast_log	<i>Deprecated function to parse a BEAST2 .log output file. Use parse_beast_tracelog_file instead</i>
-----------------	--

Description

Deprecated function to parse a BEAST2 .log output file. Use [parse_beast_tracelog_file](#) instead

Usage

```
parse_beast_log(tracelog_filename, filename = "deprecated")
```

Arguments

tracelog_filename	name of the BEAST2 tracelog .log output file, as can be read using parse_beast_tracelog_file
filename	deprecated name of the BEAST2 .log output file

Value

data frame with the parameter estimates

Author(s)

Richèl J.C. Bilderbeek

Examples

```
# Deprecated
parse_beast_log(
  tracelog_filename = get_tracerer_path("beast2_example_output.log")
)
# Use the function 'parse_beast_tracelog_file' instead
parse_beast_tracelog_file(
  tracelog_filename = get_tracerer_path("beast2_example_output.log")
)
```

parse_beast_output_files	<i>Parse all BEAST2 output files</i>
--------------------------	--------------------------------------

Description

Parse all BEAST2 output files

Usage

```
parse_beast_output_files(log_filename, trees_filenames, state_filename)
```

Arguments

`log_filename` deprecated name of the BEAST2 tracelog .log output file. Use `tracelog_filename` instead

`trees_filenames` the names of one or more a BEAST2 posterior .trees file. Each .trees file can be read using [parse_beast_trees](#)

`state_filename` name of the BEAST2 state .xml.state output file

Value

a list with the following elements:

- `estimates`: parameter estimates
- `[alignment_id]_trees`: the phylogenies in the BEAST2 posterior. `[alignment_id]` is the ID of the alignment.
- `operators`: the BEAST2 MCMC operator acceptances

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [remove_burn_ins](#) to remove the burn-in from `out$estimates`

Examples

```
trees_filenames <- get_tracerer_path("beast2_example_output.trees")
log_filename <- get_tracerer_path("beast2_example_output.log")
state_filename <- get_tracerer_path("beast2_example_output.xml.state")
parse_beast_output_files(
  log_filename = log_filename,
  trees_filenames = trees_filenames,
  state_filename = state_filename
)
```

parse_beast_posterior *Parses BEAST2 output files to a posterior*

Description

Parses BEAST2 output files to a posterior

Usage

```
parse_beast_posterior(  
  trees_filenames,  
  tracelog_filename,  
  log_filename = "deprecated"  
)
```

Arguments

trees_filenames	the names of one or more a BEAST2 posterior .trees file. Each .trees file can be read using parse_beast_trees
tracelog_filename	name of the BEAST2 tracelog .log output file, as can be read using parse_beast_tracelog_file
log_filename	deprecated name of the BEAST2 tracelog .log output file. Use tracelog_filename instead

Value

a list with the following elements:

- estimates: parameter estimates
- [alignment_id]_trees: the phylogenies in the BEAST2 posterior. [alignment_id] is the ID of the alignment.

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [remove_burn_ins](#) to remove the burn-ins from the posterior's estimates (posterior\$estimates)

Examples

```

trees_filenames <- get_tracerer_path("beast2_example_output.trees")
tracelog_filename <- get_tracerer_path("beast2_example_output.log")
posterior <- parse_beast_posterior(
  trees_filenames = trees_filenames,
  tracelog_filename = tracelog_filename
)

```

```

parse_beast_state_operators

```

Parses a BEAST2 state .xml.state output file to get only the operators acceptances

Description

Parses a BEAST2 state .xml.state output file to get only the operators acceptances

Usage

```

parse_beast_state_operators(
  state_filename = get_tracerer_path("beast2_example_output.xml.state"),
  filename = "deprecated"
)

```

Arguments

state_filename	name of the BEAST2 state .xml.state output file
filename	deprecated name of the BEAST2 .xml.state output file, use state_filename instead

Value

data frame with all the operators' success rates

Author(s)

Richèl J.C. Bilderbeek

Examples

```

parse_beast_state_operators(
  state_filename = get_tracerer_path("beast2_example_output.xml.state")
)

```

`parse_beast_tracelog_file`*Parses a BEAST2 tracelog .log output file*

Description

Parses a BEAST2 tracelog .log output file

Usage

```
parse_beast_tracelog_file(tracelog_filename)
```

Arguments

tracelog_filename

name of the BEAST2 tracelog .log output file, as can be read using [parse_beast_tracelog_file](#)

Value

data frame with the parameter estimates

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [remove_burn_ins](#) to remove the burn-in from the returned parameter estimates. Use [save_beast_estimates](#) to save the estimates to a .log file.

Examples

```
parse_beast_tracelog_file(  
  tracelog_filename = get_tracerer_path("beast2_example_output.log")  
)
```

`parse_beast_trees`*Parses a BEAST2 .trees output file*

Description

Parses a BEAST2 .trees output file

Usage

```
parse_beast_trees(filename)
```

Arguments

filename name of the BEAST2 .trees output file

Value

the phylogenies in the posterior

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [save_beast_trees](#) to save the phylogenies to a .trees file. Use [is_trees_file](#) with verbose = TRUE to find out why a file is invalid

Examples

```
trees_filename <- get_tracerer_path("beast2_example_output.trees")
parse_beast_trees(trees_filename)
```

remove_burn_in	<i>Removed the burn-in from a trace</i>
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Description

Removed the burn-in from a trace

Usage

```
remove_burn_in(trace, burn_in_fraction)
```

Arguments

trace the values
burn_in_fraction the fraction that needs to be removed, must be [0,1>

Value

the values with the burn-in removed

Author(s)

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Examples

```
# Create a trace from one to and including ten
v <- seq(1, 10)

# Remove the first ten percent of its values,
# in this case removes the first value, which is one
w <- remove_burn_in(trace = v, burn_in_fraction = 0.1)
```

remove_burn_ins	<i>Removed the burn-ins from a data frame</i>
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Description

Removed the burn-ins from a data frame

Usage

```
remove_burn_ins(traces, burn_in_fraction = 0.1)
```

Arguments

traces	a data frame with traces
burn_in_fraction	the fraction that needs to be removed, must be $[0, 1>$. Its default value of 10 as of Tracer

Value

the data frame with the burn-in removed

Author(s)

Richèl J.C. Bilderbeek

save_beast_estimates	<i>Save the BEAST2 estimates as a BEAST2 .log file There will be some differences: a BEAST2 .log file also saves the model as comments and formats the numbers in a way non-standard to R</i>
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Description

Save the BEAST2 estimates as a BEAST2 .log file There will be some differences: a BEAST2 .log file also saves the model as comments and formats the numbers in a way non-standard to R

Usage

```
save_beast_estimates(estimates, filename)
```

Arguments

estimates	a data frame of BEAST2 parameter estimates
filename	name of the .log file to save to

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [parse_beast_log](#) to read a BEAST2 .log file

save_beast_trees	<i>Save the BEAST2 trees as a BEAST2 .log file There will be some differences: a BEAST2 .log file also saves the model as comments and formats the numbers in a way non-standard to R</i>
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Description

Save the BEAST2 trees as a BEAST2 .log file There will be some differences: a BEAST2 .log file also saves the model as comments and formats the numbers in a way non-standard to R

Usage

```
save_beast_trees(trees, filename)
```

Arguments

trees	BEAST2 posterior trees, of type <code>ape::multiPhylo</code>
filename	name of the .trees file to save to

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [parse_beast_log](#) to read a BEAST2 .log file

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