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.

License GPL-3

Imports jsonlite, Rcpp

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

VignetteBuilder knitr

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

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

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Contents

calc_act . . . 2
calc_act_cpp . . . 3
calc_act_r . . . 4
calc_ess . . . 5
calc_esses . . . 6
calc_geom_mean . . . 6
calc_hpd_interval . . . 7
calc_mode . . . 8
calc_std_error_of_mean_cpp . . . 9
calc_stderr_mean . . . 9
calc_summary_stats . . . 10
calc_summary_stats_trace . . . 11
calc_summary_stats_traces . . . 12
check_trace . . . 13
count_trees_in_file . . . 14
cs_std_dev . . . 14
default_params_doc . . . 15
extract_operators_lines . . . 16
get_tracerer_path . . . 16
get_tracerer_paths . . . 17
get_tracerer_tempfilename . . . 18
is_posterior . . . 19
is_trees_file . . . 19
is_trees_posterior . . . 20
parse_beast_log . . . 21
parse_beast_output_files . . . 21
parse_beast_posterior . . . 23
parse_beast_state_operators . . . 24
parse_beast_tracelog_file . . . 25
parse_beast_trees . . . 25
remove_burn_in . . . 26
remove_burn_ins . . . 27
save_beast_estimates . . . 27
save_beast_trees . . . 28

Index **29**

`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/9f040ed0357c4b946ea276a481a4c654ad4f
src/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 *Calculate the auto correlation time from https://github.com/beast-dev/beast-mcmc/blob/800817772033c13061f026226e41128d21fd14f3/src/dr/inference/trace/TraceCorrelation.java#L159 # nolint*

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` *Calculate the auto-correlation time using only R. Consider using calc_act instead, as it is orders of magnitude faster*

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/9f040ed0357c4b946ea276a481a4c654ad4f
src/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 *Calculates the Effective Sample Size*

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/9f040ed0357c4b946ea276a481a4c654ad4f
src/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 *Calculates the Effective Sample Sizes from a parsed BEAST2 log file*

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 *Calculate the geometric mean*

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

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

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/800817772033c13061f026226e41128
src/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` *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(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 *Count the number of trees in a* .trees *file*

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 *Calculate the corrected sample standard deviation*

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 *Documentation of general function arguments*

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")
```

`get_tracerer_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_tracerer_paths(filenames)
```

Arguments

`filenames`	the files' names, without the path

Value

the filenames' full paths

Author(s)

Richèl J.C. Bilderbeek

See Also

for one file, use `get_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 *Determines if the input is a BEAST2 posterior*

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 *Measure if a file a valid BEAST2* .trees *file*

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

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` *Deprecated function to parse a BEAST2* `.log` *output file. Use parse_beast_tracelog_file instead*

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` *Parse all BEAST2 output files*

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 *Removed the burn-in from a trace*

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)

Richèl J.C. Bilderbeek

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` *Removed the burn-ins from a data frame*

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` *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*

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` *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*

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 `ape::multiPhylo`
`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

Index

calc_act, 2, *4*
calc_act_cpp, 3
calc_act_r, 4
calc_ess, 5
calc_esses, 6
calc_geom_mean, 6
calc_hpd_interval, 7
calc_mode, 8
calc_std_error_of_mean_cpp, 9
calc_stderr_mean, 9
calc_summary_stats, 10
calc_summary_stats_trace, 11, *11*
calc_summary_stats_traces, *11*, 12
check_trace, 13
count_trees_in_file, 14
cs_std_dev, 14

default_params_doc, 15

extract_operators_lines, 16

get_tracerer_path, 16, *17*
get_tracerer_paths, 17, *17*
get_tracerer_tempfilename, 18

is_posterior, 19
is_trees_file, *14*, 19, *26*
is_trees_posterior, 20

parse_beast_log, 21, *28*
parse_beast_output_files, 21
parse_beast_posterior, 23
parse_beast_state_operators, 24
parse_beast_tracelog_file, *15*, *21*, *23*, 25, *25*
parse_beast_trees, *14, 15*, *19*, *22, 23*, 25

read.nexus, *20*
remove_burn_in, *7*, *11, 12*, 26
remove_burn_ins, *11*, *13*, *22, 23*, *25*, 27

save_beast_estimates, *25*, 27
save_beast_trees, *26*, 28
stop, *13*

tempfile, *18*
tracerer, *18*