

Package ‘Cer2016’

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Type Package

Title Phylogeny Summary Statistics Demonstrated

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Author Richel Bilderbeek <richel@richelbilderbeek.nl>

Maintainer Richel Bilderbeek <richel@richelbilderbeek.nl>

Description This package contains multiple phylogeny summary statistics: SummaryStatisticA, SummaryStatisticB, SummaryStatisticC and SummaryStatisticD. These statistics are demonstrated on phylogenies created by the protracted and the (non-protracted) birth-death model.

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LazyData TRUE

Requires adephylo, ape, nLTT, PBD, phangorn, phytools, rBEAST, ribir, testit, tools, TreeSim

Suggests ape, ggplot2, gridExtra, knitr, lintr, rmarkdown, testit, testthat

RoxygenNote 5.0.1

URL <https://github.com/richelbilderbeek/Cer2016>

BugReports <https://github.com/richelbilderbeek/Cer2016/issues>

VignetteBuilder knitr

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add_alignments	<i>Add an alignment to a file</i>
----------------	-----------------------------------

Description

Add an alignment to a file

Usage

```
add_alignments(filename)
```

Arguments

filename	Parameter filename
----------	--------------------

Value

Nothing, modifies the parameter file

Author(s)

Richel Bilderbeek

add_outgroup_to_phylogeny	<i>Adds an outgroup to a phylogeny</i>
---------------------------	--

Description

Adds an outgroup to a phylogeny

Usage

```
add_outgroup_to_phylogeny(phylogeny, stem_length, outgroup_name = "Outgroup")
```

Arguments

phylogeny	a phylogeny
stem_length	How long will the length of the outgroup be before the crown?
outgroup_name	How is the outgroup named?

Value

A phylogeny, of type phylo

Author(s)

Richel Bilderbeek

add_pbd_output	<i>Adds a pbd_sim result to a file</i>
----------------	--

Description

Adds a pbd_sim result to a file

Usage

```
add_pbd_output(filename)
```

Arguments

filename	Parameter filename
----------	--------------------

Value

Nothing, modifies the parameter file

Author(s)

Richel Bilderbeek

add_posteriors	<i>Add BEAST2 posteriors to a file</i>
----------------	--

Description

Add BEAST2 posteriors to a file

Usage

```
add_posteriors(filename, skip_if_output_present = FALSE)
```

Arguments

filename	Parameter filename
skip_if_output_present	skip if output files are present, else remove these and start a new BEAST2 run

Value

Nothing, modifies the parameter file

Author(s)

Richel Bilderbeek

`add_species_trees_with_outgroup`*Add a species tree with outgroup to a file*

Description

Add a species tree with outgroup to a file

Usage

```
add_species_trees_with_outgroup(filename)
```

Arguments

filename	Parameter filename
----------	--------------------

Value

Nothing, modifies the parameter file

Author(s)

Richel Bilderbeek

`branch_sorter`*Sorts branches for the NRBS analysis*

Description

Sorts branches for the NRBS analysis

Usage

```
branch_sorter(phylogeny)
```

Arguments

phylogeny	A phylogeny of class 'phylo'
-----------	------------------------------

Value

something

Author(s)

Femke Thon

branch_sorter_from_file
sorts branches for the NRBS analysis

Description

sorts branches for the NRBS analysis

Usage

branch_sorter_from_file(filename)

Arguments

tree1, tree2, the trees that are to be sorted.

Value

a sorted tree1 and tree2

Author(s)

Femke Thon

check_progress *Function that shows how much parameter files are present, and how far the pipeline has gotten*

Description

Function that shows how much parameter files are present, and how far the pipeline has gotten

Usage

check_progress(folder = ".")

Arguments

folder The folder containing the parameter files

Value

A data table showing the progress

Author(s)

Richel Bilderbeek

collect_files_gammas	<i>Collects the gamma statistics of all phylogenies belonging to a multiple parameter file in the melted/uncast/long form</i>
----------------------	---

Description

Collects the gamma statistics of all phylogenies belonging to a multiple parameter file in the melted/uncast/long form

Usage

```
collect_files_gammas(filenamees, verbose = FALSE)
```

Arguments

filenamees	names of the parameter file
verbose	give verbose output, should be TRUE or FALSE

Value

A list with two dataframes of gamma statistics

collect_file_gammas	<i>Collects the gamm statistics of all phylogenies belonging to a parameter file in the melted/uncast/long form</i>
---------------------	---

Description

Collects the gamm statistics of all phylogenies belonging to a parameter file in the melted/uncast/long form

Usage

```
collect_file_gammas(filename, verbose = FALSE)
```

Arguments

filename	name of the parameter file
verbose	give verbose output, should be TRUE or FALSE

Value

A dataframe of gamma statistics of each phylogeny in time

Examples

```
filename <- find_path("toy_example_3.RDa")
df <- collect_file_gammas(filename)
testit::assert(names(df) == c("species_tree_gammas", "posterior_gammas"))
testit::assert(names(df$species_tree_gammas)
  == c("species_tree", "gamma_stat")
)
testit::assert(nrow(df$species_tree_gammas) == 2)
testit::assert(nrow(df$posterior_gammas) == 80)
```

```
collect_gamma_statistics
```

Collects the gamma statistics of all phylogenies in the melted/uncast/long form

Description

Collects the gamma statistics of all phylogenies in the melted/uncast/long form

Usage

```
collect_gamma_statistics(phylogenies)
```

Arguments

phylogenies the phylogenies, supplied as either a list or a multiPhylo object, where the phylogenies are of type 'phylo'

Value

A dataframe of gamma statistics of each phylogeny in time

```
collect_parameters      Creates tidy data of all parameter files
```

Description

Creates tidy data of all parameter files

Usage

```
collect_parameters(filenamees, verbose = FALSE)
```

Arguments

filenamees names of the parameter files
 verbose give verbose output, should be TRUE or FALSE

Author(s)

Richel Bilderbeek

Examples

```
filenames <- c(
  find_path("article_0_0_0_0.RDa"),
  find_path("article_0_1_4_0_2.RDa"),
  find_path("toy_example_1.RDa")
)
df <- collect_parameters(filenames)
testit::assert(nrow(df) == 3)
```

collect_posterior_filenames

Collect posterior filenames

Description

Collect posterior filenames

Usage

```
collect_posterior_filenames(parameter_filename)
```

Arguments

parameter_filename
Name of a parameter file

Value

generates species tree files from the posterior

Author(s)

Richel Bilderbeek and Jolien Gay

Examples

```
parameter_filename <- find_path("toy_example_1.RDa")
posterior_filenames <- collect_posterior_filenames(parameter_filename)
trees_filename <- find_path("toy_example_1_1_1_1.trees")
testit::assert(length(posterior_filenames) == 1)
testit::assert(posterior_filenames[1] == trees_filename)
```

`collect_posterior_gammas`*Collect the gamma statistics of the BEAST2 posteriors*

Description

Collect the gamma statistics of the BEAST2 posteriors

Usage

```
collect_posterior_gammas(filename)
```

Arguments

filename name of the file containing the parameters and results

Value

a data frame

Author(s)

Richel Bilderbeek

Examples

```
filename <- find_path("toy_example_3.RDa")
df <- collect_posterior_gammas(filename)
testit::assert(names(df) ==
  c("species_tree", "alignment", "beast_run", "gamma_stat")
)
testit::assert(nrow(df) == 80)
```

`collect_posterior_nltts`*Collect the nLTT values of the BEAST2 posteriors*

Description

Collect the nLTT values of the BEAST2 posteriors

Usage

```
collect_posterior_nltts(filename, dt = 0.001)
```

Arguments

filename	name of the file containing the parameters and results
dt	the resolution of the nLTT plot, must be in range <0,1>, default is 0.001

Value

a data frame

Author(s)

Richel Bilderbeek

collect_species_tree_gammas

Collect the gamma statistics of the species trees with outgroup

Description

Collect the gamma statistics of the species trees with outgroup

Usage

```
collect_species_tree_gammas(filename, verbose = FALSE)
```

Arguments

filename	name of the file containing the parameters and results
verbose	give verbose output, should be TRUE or FALSE

Value

a data frame

Author(s)

Richel Bilderbeek

Examples

```
filename <- find_path("toy_example_1.RDa")
df <- collect_species_tree_gammas(filename)
testit::assert(names(df) == c("species_tree", "gamma_stat"))
testit::assert(nrow(df) == 1)
testit::assert(abs(df$gamma_stat - -0.8205514) < 0.0001)
```

`collect_species_tree_nltts`*Collect the nLTT values of the species trees with outgroup*

Description

Collect the nLTT values of the species trees with outgroup

Usage

```
collect_species_tree_nltts(filename, dt = 0.001)
```

Arguments

filename	name of the file containing the parameters and results
dt	the resolution of the nLTT plot, must be in range <0,1>, default is 0.001

Value

a data frame

Author(s)

Richel Bilderbeek

Examples

```
dt <- 0.1
filename <- find_path("toy_example_3.RDa")
df <- collect_species_tree_nltts(filename, dt = dt)
testit::assert(names(df) == c("species_tree", "t", "nltt"))
testit::assert(nrow(df) == 2 * (1 + (1/dt)))
```

`convert_alignment_to_beast_input_file`*Convert an alignment and parameters to a BEAST XML input file*

Description

Convert an alignment and parameters to a BEAST XML input file

Usage

```
convert_alignment_to_beast_input_file(alignment_dnabin, mcmc_chainlength,
  rng_seed = 42, beast_filename, temp_fasta_filename)
```

Arguments

alignment_dnabin the DNA alignment of type DNABin
 mcmc_chainlength the BEAST2 MCMC chain length
 rng_seed random number generator seed
 beast_filename the filename of the XML BEAST2 input file created
 temp_fasta_filename the name of a temporary file created

Value

Nothing, creates a file called 'beast_filename'

Author(s)

Richel Bilderbeek

convert_alignment_to_beast_posterior
Convert an alignment to a BEAST2 XML input file

Description

Convert an alignment to a BEAST2 XML input file

Usage

```
convert_alignment_to_beast_posterior(alignment_dnabin, mcmc_chainlength,
  base_filename, rng_seed = 42, beast_bin_path = "",
  beast_jar_path = find_beast_jar_path(), skip_if_output_present = FALSE)
```

Arguments

alignment_dnabin The alignmentnet
 mcmc_chainlength The length of the MCMC chain BEAST2 will generate
 base_filename The base of the filename (the part without the extension)
 rng_seed The random number generator seed used by BEAST2
 beast_bin_path Where the binary 'beast' can be found
 beast_jar_path Where the jar 'beast.jar' can be found
 skip_if_output_present skip if output files are present, else remove these and start a new BEAST2 run

Value

A BEAST2 posterior

Author(s)

Richel Bilderbeek

convert_alignment_to_fasta

Convert an alignment (of type DNABin) to a FASTA file

Description

Convert an alignment (of type DNABin) to a FASTA file

Usage

```
convert_alignment_to_fasta(alignment_dnabin, filename)
```

Arguments

alignment_dnabin

DNA alignment of type DNABin

filename

FASTA filename the alignment will be saved to

Value

Nothing, it will create a FASTA file

Author(s)

Richel Bilderbeek

convert_phylogeny_to_alignment

Converts a phylogeny to a random DNA alignment

Description

Converts a phylogeny to a random DNA alignment

Usage

```
convert_phylogeny_to_alignment(phylogeny, sequence_length, mutation_rate = 1)
```

Arguments

phylogeny a phylogeny
sequence_length the number of nucleotides to alignment will have per taxon
mutation_rate the rate per nucleotide to change, per million years

Value

an alignment

Author(s)

Richel Bilderbeek

extract_erg	<i>Extract the ERG ('Extinction Rate of a Good species') parameter value from a file</i>
-------------	--

Description

Extract the ERG ('Extinction Rate of a Good species') parameter value from a file

Usage

```
extract_erg(file)
```

Arguments

file A loaded parameter file

Value

the value of the ERG parameter

Author(s)

Richel Bilderbeek

Examples

```
file <- read_file(find_path("toy_example_1.RDa"))  
erg <- extract_erg(file)  
testit::assert(erg >= 0.0)
```

extract_eri	<i>Extract the ERI ('Extinction Rate of an Incipient species') parameter value from a file</i>
-------------	--

Description

Extract the ERI ('Extinction Rate of an Incipient species') parameter value from a file

Usage

```
extract_eri(file)
```

Arguments

file	A loaded parameter file
------	-------------------------

Value

the value of the ERI parameter

Author(s)

Richel Bilderbeek

Examples

```
file <- read_file(find_path("toy_example_1.RDa"))
eri <- extract_eri(file)
testit::assert(eri >= 0.0)
```

extract_scr	<i>Extract the SCR ('Speciation Completion Rate') parameter value from a file</i>
-------------	---

Description

Extract the SCR ('Speciation Completion Rate') parameter value from a file

Usage

```
extract_scr(file)
```

Arguments

file	A loaded parameter file
------	-------------------------

Value

the value of the SCR parameter

Author(s)

Richel Bilderbeek

Examples

```
file <- read_file(find_path("toy_example_1.RDa"))
scr <- extract_scr(file)
testit::assert(scr >= 0.0)
```

extract_sirg	<i>Extract the SIRG ('Speciation Initial Rate of a Good species') parameter value from a file</i>
--------------	---

Description

Extract the SIRG ('Speciation Initial Rate of a Good species') parameter value from a file

Usage

```
extract_sirg(file)
```

Arguments

file	A loaded parameter file
------	-------------------------

Value

the value of the SIRG parameter

Author(s)

Richel Bilderbeek

Examples

```
file <- read_file(find_path("toy_example_1.RDa"))
sirg <- extract_sirg(file)
testit::assert(sirg >= 0.0)
```

extract_siri	<i>Extract the SIRI ('Speciation Initial Rate of an Incipient species') parameter value from a file</i>
--------------	---

Description

Extract the SIRI ('Speciation Initial Rate of an Incipient species') parameter value from a file

Usage

```
extract_siri(file)
```

Arguments

file	A loaded parameter file
------	-------------------------

Value

the value of the SIRI parameter

Author(s)

Richel Bilderbeek

Examples

```
file <- read_file(find_path("toy_example_1.RDa"))
siri <- extract_siri(file)
testit::assert(siri >= 0.0)
```

find_beast_bin_path	<i>Find the path of the BEAST2 binary file</i>
---------------------	--

Description

Find the path of the BEAST2 binary file

Usage

```
find_beast_bin_path()
```

Value

the path of the BEAST2 binary file

find_beast_jar_path	<i>Find the path of the BEAST2 jar file</i>
---------------------	---

Description

Find the path of the BEAST2 jar file

Usage

```
find_beast_jar_path()
```

Value

the path of the BEAST2 jar file

find_beast_posterior_test_filename	<i>Find the path of known-to-be-valid BEAST2 posterior file</i>
------------------------------------	---

Description

Find the path of known-to-be-valid BEAST2 posterior file

Usage

```
find_beast_posterior_test_filename()
```

Value

the path of a known-to-be-valid BEAST2 posterior file

find_path	<i>Finds the full path of a file</i>
-----------	--------------------------------------

Description

Finds the full path of a file

Usage

```
find_path(filename)
```

Arguments

filename	the name of a file
----------	--------------------

Value

the full path of the filename if an existing file could be found, stops otherwise

Author(s)

Richel Bilderbeek

Examples

```
path <- find_path("toy_example_1.RDa")
testit::assert(file.exists(path))
```

```
get_phylogeny_crown_age
```

Obtain the crown age of a phylony

Description

Obtain the crown age of a phylony

Usage

```
get_phylogeny_crown_age(phylogeny)
```

Arguments

phylogeny The phylogeny to obtain the crown age of

Value

the age of the phylogeny

Author(s)

Richel Bilderbeek

is_alignment	<i>Determines if the input is an alignment of type DNABin</i>
--------------	---

Description

Determines if the input is an alignment of type DNABin

Usage

```
is_alignment(input)
```

Arguments

input	The input to be testes
-------	------------------------

Value

TRUE or FALSE

Author(s)

Richel Bilderbeek

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

Description

Determines if the input is a BEAST2 posterior

Usage

```
is_beast_posterior(x)
```

Arguments

x	the input
---	-----------

Value

TRUE or FALSE

Author(s)

Richel Bilderbeek

is_pbd_sim_output	<i>Does not use pbd_sim()\$stree, but generates these like PBD does</i>
-------------------	---

Description

Does not use pbd_sim()\$stree, but generates these like PBD does

Usage

```
is_pbd_sim_output(pbd_sim_output, verbose = FALSE)
```

Arguments

pbd_sim_output	the argument tested to output of PBD::pbd_sim
verbose	will the function show why the input is determined not to be output of PBD::pbd_sim

Value

TRUE or FALSE

Author(s)

Richel Bilderbeek

is_phylogeny	<i>Checks if the input is a phylogeny</i>
--------------	---

Description

Checks if the input is a phylogeny

Usage

```
is_phylogeny(x)
```

Arguments

x	input to be checked
---	---------------------

Value

TRUE or FALSE

Author(s)

Richel Bilderbeek

is_valid_file	<i>Checks if a file is a valid parameter file</i>
---------------	---

Description

Checks if a file is a valid parameter file

Usage

```
is_valid_file(filename, verbose = FALSE)
```

Arguments

filename	the name of the file to be checked
verbose	give verbose output, should be TRUE or FALSE

Value

TRUE or FALSE

Author(s)

Richel Bilderbeek

Examples

```
testit::assert(is_valid_file(find_path("toy_example_1.RDa")))
testit::assert(!is_valid_file(find_path("toy_example_1_1_1_1.trees")))
```

is_whole_number	<i>Checks if x is a single, whole-number variable</i>
-----------------	---

Description

Checks if x is a single, whole-number variable

Usage

```
is_whole_number(x, tolerance = .Machine$double.eps^0.5)
```

Arguments

x	the number to check
tolerance	the maximum error a number may deviate from a whole number, before it is labeled as a floating point value

Value

TRUE or FALSE

Author(s)

Richel Bilderbeek

load_parameters_from_file

Load parameters from file

Description

Load parameters from file

Usage

```
load_parameters_from_file(filename)
```

Arguments

filename name of the parameter file

Value

a data frame with all parameters

Author(s)

Richel Bilderbeek

normalized_rooted_branch_score

calculates the normalized rooted branch score

Description

calculates the normalized rooted branch score

Usage

```
normalized_rooted_branch_score(filenamees)
```

Arguments

filenamees the filenames

Value

the normalized rooted branch score

Author(s)

Femke Thon

plot_alignments	<i>Plot alignments</i>
-----------------	------------------------

Description

Plot alignments

Usage

plot_alignments(filename)

Arguments

filename name of the parameter file

Author(s)

Richel Bilderbeek

plot_extant_incipient_tree	<i>Plot the extant incipient species tree</i>
----------------------------	---

Description

Plot the extant incipient species tree
Plot the extant incipient species tree

Usage

plot_extant_incipient_tree(filename)

plot_extant_incipient_tree(filename)

Arguments

filename name of the parameter file

Value

Nothing. It does produce a plot

Author(s)

Richel Bilderbeek

plot_posterior_nltts *Plot multiple BEAST2 posteriors*

Description

Plot multiple BEAST2 posteriors

Usage

```
plot_posterior_nltts(filename, dt = 0.001)
```

Arguments

filename	name of the file containing the parameters and results
dt	the resolution of the nLTT plot, must be in range <0,1>, default is 0.001

Value

Nothing, produces a plot

Author(s)

Richel Bilderbeek

plot_posterior_samples
 Plot a random posterior phylogeny

Description

Plot a random posterior phylogeny

Usage

```
plot_posterior_samples(filename)
```

Arguments

filename	a filename
----------	------------

Value

Nothing, but it does generate some plots

Author(s)

Richel Bilderbeek

plot_posterior_sample_nltts
Plot the nLTTs of the posterior

Description

Plot the nLTTs of the posterior

Usage

```
plot_posterior_sample_nltts(filename, dt = 0.001)
```

Arguments

filename	a filename
dt	the resolution of the nLTT plot, must be in range <0,1>, default is 0.001

Value

Nothing, but it does generate some plots

Author(s)

Richel Bilderbeek

plot_species_tree_with_outgroup
Plot

Description

Plot

Usage

```
plot_species_tree_with_outgroup(filename)
```

Arguments

filename a file name

Value

Nothing, but it does generate plots

Author(s)

Richel Bilderbeek

plot_species_tree_with_outgroup_nltt

Plot species_tree_with_outgroup_nltt

Description

Plot species_tree_with_outgroup_nltt

Usage

```
plot_species_tree_with_outgroup_nltt(filename, dt = 0.001)
```

Arguments

filename parameter filename

dt the resolution of the nLTT plot, must be in range <0,1>, default is 0.001

Author(s)

Richel Bilderbeek

read_file

Read a parameter (.RDa) file

Description

Read a parameter (.RDa) file

Usage

```
read_file(filename)
```

Arguments

filename name of the parameter (.RDa) file

Value

the file as R data

Author(s)

Richel Bilderbeek

Examples

```
file <- read_file(find_path("toy_example_1.RDa"))
print(names(file))
```

```
sample_species_trees_from_pbd_sim_output
```

Samples species trees from PBD::pbd_sim its output It does not use pbd_sim()\$stree, but generates these like PBD does.

Description

Samples species trees from PBD::pbd_sim its output It does not use pbd_sim()\$stree, but generates these like PBD does.

Usage

```
sample_species_trees_from_pbd_sim_output(n, pbd_sim_output)
```

Arguments

n The number of species trees to sample
pbd_sim_output The output generated by PBD::pbd_sim

Value

A list of length n, containing the n sampled species trees

Author(s)

Richel Bilderbeek, inspired by Rampal Etienne's PBD::pbd_sim function

`save_parameters_to_file`*Creates a valid parameter file*

Description

Creates a valid parameter file

Usage

```
save_parameters_to_file(rng_seed, sirg, siri, scr, erg, eri, age,  
    n_species_trees_samples, mutation_rate, n_alignments, sequence_length,  
    mcmc_chainlength, n_beast_runs, filename)
```

Arguments

<code>rng_seed</code>	the random number generator seed
<code>sirg</code>	the species initiation rate of the good species
<code>siri</code>	the speciation-initiation rate of the incipient species
<code>scr</code>	the rate at which incipient species become good
<code>erg</code>	the rate at which good species get extinct
<code>eri</code>	the rate at which incipient species get extinct
<code>age</code>	crown age of the phylogeny
<code>n_species_trees_samples</code>	the number of species trees that will be sampled from an incipient species tree
<code>mutation_rate</code>	the probability per nucleotide to mutate at a DNA replication
<code>n_alignments</code>	the number of alignments simulated per species tree
<code>sequence_length</code>	the simulated DNA sequence length in nucleotides
<code>mcmc_chainlength</code>	the length of the MCMC chain that BEAST2 will run
<code>n_beast_runs</code>	the number of BEAST2 runs per DNA alignments
<code>filename</code>	the name of the parameter file that will be created by this function

Value

Nothing, it will create a file with filename ‘filename’

Author(s)

Richel Bilderbeek

show_parameter_files *Creates a nice knitr::table to show one or more parameter files*

Description

Creates a nice knitr::table to show one or more parameter files

Usage

```
show_parameter_files(filenamees, verbose = FALSE)
```

Arguments

filenamees	names of the parameter files
verbose	give verbose output, should be TRUE or FALSE

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