

Package ‘beautier’

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Title 'BEAUti' from R

Version 2.6.12

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.

'BEAUti 2' (which is part of 'BEAST2') is a GUI tool that allows users to specify the many possible setups and generates the XML file 'BEAST2' needs to run. This package provides a way to create 'BEAST2' input files without active user input, but using R function calls instead.

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RoxygenNote 7.2.3

VignetteBuilder knitr

URL <https://docs.ropensci.org/beautier/>,
<https://github.com/ropensci/beautier>

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

Imports ape, rappdirs, purrr, rlang (>= 1.1.0), seqinr, stringr

Suggests knitr, markdown, readr, rmarkdown, testthat (>= 2.1.0)

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Contents

alpha_parameter_to_xml	12
are_clock_models	13
are_equal_mcmcs	14
are_equal_screenlogs	15
are_equal_tracelogs	16
are_equal_treelogs	17
are_equal_xml_files	18
are_equal_xml_lines	19
are_equivalent_xml_files	20
are_equivalent_xml_lines	21
are_equivalent_xml_lines_all	21
are_equivalent_xml_lines_loggers	22
are_equivalent_xml_lines_operators	23
are_equivalent_xml_lines_section	23
are_fasta_filenames	24
are_ids	25
are_init_clock_models	26
are_init_mrca_priors	26
are_init_site_models	27
are_init_tree_priors	27
are_mrca_align_ids_in_fasta	28
are_mrca_priors	28
are_mrca_taxon_names_in_fasta	29
are_rln_clock_models	30
are_site_models	30
are_tree_priors	31
bd_tree_prior_to_xml_prior_distr	32
beta_parameter_to_xml	33
b_pop_sizes_parameter_to_xml	34
b_pop_sizes_param_to_xml	35
cbs_tree_prior_to_xml_prior_distr	35

ccp_tree_prior_to_xml_prior_distr	36
ccp_tree_prior_to_xml_state	37
cep_tree_prior_to_xml_prior_distr	38
check_alignment_id	39
check_beauti_options	40
check_clock_model	40
check_clock_models	41
check_empty_beautier_folder	42
check_filename	43
check_file_and_model_agree	44
check_file_exists	44
check_gamma_site_model	45
check_gamma_site_model_names	46
check_gtr_site_model	46
check_gtr_site_model_names	47
check_inference_model	48
check_inference_models	49
check_is_monophyletic	50
check_log_mode	50
check_log_sort	51
check_mcmc	51
check_mcmc_list_element_names	52
check_mcmc_values	53
check_mrca_prior	53
check_mrca_prior_name	54
check_mrca_prior_names	55
check_mrca_prior_taxa_names	55
check_ns_mcmc	56
check_param	56
check_param_names	57
check_param_types	58
check_phylogeny	58
check_rename_fun	59
check_rln_clock_model	60
check_screenlog	60
check_screenlog_names	61
check_screenlog_values	62
check_site_model	62
check_site_models	63
check_site_model_names	64
check_site_model_types	65
check_store_every	65
check_strict_clock_model	66
check_tn93_site_model	66
check_tn93_site_model_names	67
check_tracelog	68
check_tracelog_names	68
check_tracelog_values	69

check_treelog	69
check_treelog_names	70
check_treelog_values	71
check_tree_prior	71
check_tree_priors	72
clock_model_to_xml_operators	73
clock_model_to_xml_prior_distr	74
clock_model_to_xml_state	75
clock_model_to_xml_tracelog	75
clock_model_to_xml_treelogger	76
clock_rate_param_to_xml	77
compare_lines	78
count_trailing_spaces	79
create_alpha_param	80
create_bd_tree_prior	81
create_beast2_beast_xml	82
create_beast2_input	83
create_beast2_input_beast	84
create_beast2_input_data	85
create_beast2_input_data_sequences	86
create_beast2_input_distr	87
create_beast2_input_distr_lh	88
create_beast2_input_distr_prior	89
create_beast2_input_file	90
create_beast2_input_file_from_model	92
create_beast2_input_from_model	93
create_beast2_input_init	94
create_beast2_input_map	95
create_beast2_input_operators	96
create_beast2_input_run	96
create_beast2_input_state	98
create_beautier_tempfolder	99
create_beauti_options	99
create_beauti_options_v2_4	101
create_beauti_options_v2_6	101
create_beta_distr	103
create_beta_param	104
create_branch_rate_model_xml	105
create_b_pop_sizes_param	106
create_cbs_tree_prior	107
create_ccp_tree_prior	108
create_ccp_tree_prior	109
create_clock_model	111
create_clock_models	112
create_clock_models_from_names	113
create_clock_model_from_name	114
create_clock_rate_param	115
create_clock_rate_state_node_parameter_xml	116

create_data_xml	117
create_distr	118
create_exp_distr	119
create_freq_param	120
create_gamma_distr	121
create_gamma_site_model	122
create_gtr_site_model	124
create_gtr_subst_model_xml	126
create_hky_site_model	126
create_hky_subst_model_xml	127
create_inference_model	128
create_inv_gamma_distr	129
create_jc69_site_model	131
create_jc69_subst_model_xml	132
create_kappa_1_param	132
create_kappa_2_param	133
create_kappa_param	133
create_lambda_param	134
create_laplace_distr	135
create_loggers_xml	136
create_log_normal_distr	137
create_mcmc	139
create_mean_param	140
create_mrca_prior	141
create_mu_param	143
create_m_param	144
create_normal_distr	145
create_ns_inference_model	147
create_ns_mcmc	148
create_one_div_x_distr	149
create_param	151
create_poisson_distr	152
create_rate_ac_param	153
create_rate_ag_param	154
create_rate_at_param	155
create_rate_categories_state_node_xml	156
create_rate_cg_param	157
create_rate_ct_param	158
create_rate_gt_param	159
create_rln_clock_branch_rate_model_xml	160
create_rln_clock_model	161
create_scale_param	162
create_screenlog	164
create_screenlog_xml	165
create_sigma_param	165
create_site_model	166
create_site_models	168
create_site_models_from_names	169

create_site_model_from_name	170
create_site_model_parameters_xml	171
create_site_model_xml	172
create_strict_clock_branch_rate_model_xml	173
create_strict_clock_model	174
create_strict_clock_rate_scaler_operator_xml	175
create_subst_model_xml	176
create_s_param	177
create_temp_screenlog_filename	178
create_temp_tracelog_filename	179
create_temp_treelog_filename	180
create_test_inference_model	180
create_test_mcmc	182
create_test_ns_inference_model	183
create_test_ns_mcmc	184
create_test_screenlog	186
create_test_tracelog	187
create_test_treelog	188
create_tn93_site_model	189
create_tn93_subst_model_xml	190
create_tracelog	191
create_tracelog_xml	192
create_trait_set_string	192
create_treelog	193
create_treelog_xml	194
create_tree_likelihood_distr_xml	195
create_tree_prior	196
create_tree_priors	197
create_ucl_d_mean_state_node_param_xml	198
create_ucl_d_stdev_state_node_param_xml	199
create_uniform_distr	200
create_xml_declaration	201
create_yule_tree_prior	202
default_parameters_doc	203
default_params_doc	204
distr_to_xml	210
distr_to_xml_beta	211
distr_to_xml_exp	211
distr_to_xml_inv_gamma	212
distr_to_xml_laplace	212
distr_to_xml_log_normal	213
distr_to_xml_normal	213
distr_to_xml_one_div_x	214
distr_to_xml_poisson	214
distr_to_xml_uniform	215
extract_xml_loggers_from_lines	215
extract_xml_operators_from_lines	216
extract_xml_section_from_lines	216

fasta_file_to_sequences	217
find_clock_model	217
find_first_regex_line	218
find_first_xml_opening_tag_line	218
find_last_regex_line	219
find_last_xml_closing_tag_line	220
freq_equilibrium_to_xml	220
freq_param_to_xml	221
gamma_distr_to_xml	222
gamma_site_models_to_xml_prior_distr	223
gamma_site_model_to_xml_prior_distr	223
gamma_site_model_to_xml_state	224
get_alignment_id	225
get_alignment_ids	226
get_alignment_ids_from_fasta_filenames	227
get_beautier_folder	228
get_beautier_path	228
get_beautier_paths	229
get_beautier_tempfilename	230
get_clock_models_ids	230
get_clock_model_name	231
get_clock_model_names	232
get_crown_age	232
get_default_beast_namespace	233
get_default_beast_namespace_v2_4	234
get_default_beast_namespace_v2_6	234
get_distr_names	235
get_distr_n_params	235
get_fasta_filename	236
get_file_base_sans_ext	237
get_freq_equilibrium_names	238
get_gamma_site_model_n_distrs	238
get_gamma_site_model_n_params	239
get_has_non_strict_clock_model	240
get_inference_model_filenames	241
get_log_modes	242
get_log_sorts	242
get_mcmc_filenames	243
get_n_taxa	244
get_operator_id_pre	244
get_param_names	245
get_remove_dir_fun	246
get_remove_hex_fun	246
get_replace_dir_fun	247
get_site_models_n_distrs	248
get_site_models_n_params	249
get_site_model_names	250
get_site_model_n_distrs	250

get_site_model_n_params	251
get_taxa_names	252
get_tree_priors_n_distrs	253
get_tree_priors_n_params	253
get_tree_prior_names	254
get_tree_prior_n_distrs	255
get_tree_prior_n_params	256
get_xml_closing_tag	257
get_xml_opening_tag	258
gtr_site_model_to_xml_prior_distr	258
gtr_site_model_to_xml_state	259
has_mrca_prior	260
has_mrca_prior_with_distr	261
has_rln_clock_model	262
has_strict_clock_model	263
has_tip_dating	264
has_xml_closing_tag	265
has_xml_opening_tag	265
has_xml_short_closing_tag	266
hky_site_model_to_xml_prior_distr	267
hky_site_model_to_xml_state	267
indent	268
init_bd_tree_prior	269
init_beta_distr	269
init_ccp_tree_prior	270
init_cep_tree_prior	270
init_clock_models	271
init_distr	272
init_exp_distr	272
init_gamma_distr	273
init_gamma_site_model	273
init_gtr_site_model	274
init_hky_site_model	275
init_inference_model	276
init_inv_gamma_distr	276
init_jc69_site_model	277
init_laplace_distr	278
init_log_normal_distr	278
init_mrca_prior	279
init_mrca_priors	280
init_normal_distr	280
init_one_div_x_distr	281
init_param	281
init_poisson_distr	282
init_rln_clock_model	283
init_site_models	284
init_strict_clock_model	284
init_tn93_site_model	285

init_tree_priors	286
init_uniform_distr	287
init_yule_tree_prior	287
interspace	288
is_alpha_param	288
is_bd_tree_prior	289
is_beauti_options	290
is_beta_distr	291
is_beta_param	292
is_b_pop_sizes_param	293
is_cbs_tree_prior	294
is_ccp_tree_prior	295
is_cep_tree_prior	296
is_clock_model	297
is_clock_model_name	298
is_clock_rate_param	299
is_default_mcmc	300
is_distr	301
is_distr_name	302
is_exp_distr	303
is_freq_equilibrium_name	304
is_freq_param	305
is_gamma_distr	306
is_gamma_site_model	307
is_gtr_site_model	308
is_hky_site_model	309
is_id	310
is_inference_model	311
is_init_bd_tree_prior	311
is_init_beta_distr	312
is_init_cbs_tree_prior	312
is_init_ccp_tree_prior	313
is_init_cep_tree_prior	313
is_init_clock_model	314
is_init_distr	314
is_init_exp_distr	315
is_init_gamma_distr	315
is_init_gamma_site_model	316
is_init_gtr_site_model	316
is_init_hky_site_model	317
is_init_inv_gamma_distr	318
is_init_jc69_site_model	319
is_init_laplace_distr	320
is_init_log_normal_distr	320
is_init_mrca_prior	321
is_init_normal_distr	321
is_init_one_div_x_distr	322
is_init_param	322

is_init_poisson_distr	323
is_init_rln_clock_model	323
is_init_site_model	324
is_init_strict_clock_model	324
is_init_tn93_site_model	325
is_init_tree_prior	325
is_init_uniform_distr	326
is_init_yule_tree_prior	327
is_inv_gamma_distr	327
is_in_patterns	328
is_jc69_site_model	329
is_kappa_1_param	330
is_kappa_2_param	331
is_kappa_param	332
is_lambda_param	333
is_laplace_distr	334
is_log_normal_distr	335
is_mcmc	336
is_mcmc_nested_sampling	337
is_mean_param	338
is_mrca_align_ids_in_fastas	339
is_mrca_align_id_in_fasta	340
is_mrca_prior	341
is_mrca_prior_with_distr	342
is_mu_param	342
is_m_param	343
is_normal_distr	344
is_one_bool	345
is_one_div_x_distr	346
is_one_double	347
is_one_empty_string	348
is_one_int	349
is_one_na	350
is_one_string	350
is_one_string_that_is_a_number	351
is_on_appveyor	352
is_on_ci	353
is_on_github_actions	353
is_on_travis	354
is_param	355
is_param_name	356
is_phylo	357
is_poisson_distr	358
is_rate_ac_param	359
is_rate_ag_param	360
is_rate_at_param	361
is_rate_cg_param	362
is_rate_ct_param	363

is_rate_gt_param	365
is_rln_clock_model	366
is_scale_param	367
is_sigma_param	368
is_site_model	369
is_site_model_name	370
is_strict_clock_model	371
is_s_param	372
is_tn93_site_model	373
is_tree_prior	374
is_tree_prior_name	375
is_uniform_distr	375
is_xml	376
is_yule_tree_prior	377
jc69_site_model_to_xml_state	378
kappa_param_to_xml	378
mcmc_to_xml_run	379
mcmc_to_xml_run_default	380
mcmc_to_xml_run_nested_sampling	381
mrca_priors_to_xml_prior_distr	382
mrca_prior_to_xml_prior_distr	382
mrca_prior_to_xml_state	383
mrca_prior_to_xml_taxonset	384
mrca_prior_to_xml_trace_log	385
m_param_to_xml	386
no_taxa_to_xml_tree	386
parameter_to_xml	387
parameter_to_xml_kappa_1	388
parameter_to_xml_kappa_2	389
parameter_to_xml_lambda	389
parameter_to_xml_mean	390
parameter_to_xml_mu	390
parameter_to_xml_rate_ac	391
parameter_to_xml_rate_ag	392
parameter_to_xml_rate_at	392
parameter_to_xml_rate_cg	393
parameter_to_xml_rate_ct	394
parameter_to_xml_rate_gt	394
parameter_to_xml_scale	395
parameter_to_xml_sigma	396
remove_beautier_folder	396
remove_empty_lines	397
remove_multiline	398
rename_inference_model_filenames	398
rename_mcmc_filenames	399
rln_clock_model_to_xml_mean_rate_prior	401
rln_clock_model_to_xml_operators	401
rln_clock_model_to_xml_prior_distr	402

rln_clock_model_to_xml_state	403
rln_clock_model_to_xml_tracelog	404
rnd_phylo_to_xml_init	405
site_models_to_xml_operators	406
site_models_to_xml_prior_distr	406
site_models_to_xml_tracelog	407
site_model_to_xml_operators	408
site_model_to_xml_prior_distr	408
site_model_to_xml_state	410
site_model_to_xml_tracelog	410
strict_clock_model_to_xml_operators	411
strict_clock_model_to_xml_prior_distr	412
strict_clock_model_to_xml_state	413
strict_clock_model_to_xml_tracelog	413
s_parameter_to_xml	414
taxa_to_xml_tree	415
tipdate_taxa_to_xml_trait	416
tipdate_taxa_to_xml_tree	417
tn93_site_model_to_xml_prior_distr	417
tn93_site_model_to_xml_state	418
tree_model_to_tracelog_xml	419
tree_priors_to_xml_prior_distr	420
tree_priors_to_xml_tracelog	421
tree_prior_to_xml_operators	422
tree_prior_to_xml_prior_distr	422
tree_prior_to_xml_state	423
tree_prior_to_xml_tracelog	424
unindent	425
yule_tree_prior_to_xml_operators	425
yule_tree_prior_to_xml_prior_distr	426
Index	427

alpha_parameter_to_xml

Internal function

Description

Converts an alpha parameter to XML

Usage

alpha_parameter_to_xml(alpha_parameter, beauti_options)

Arguments

alpha_parameter
 an alpha parameter, as created by [create_alpha_param](#)
 beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

the parameter as XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
remove_beautier_folder()
check_empty_beautier_folder()

# The alpha parameter must be initialized, i.e. have an ID
alpha_parameter_to_xml(
  alpha_parameter = create_alpha_param(id = "1"),
  beauti_options = create_beauti_options()
)

check_empty_beautier_folder()
```

are_clock_models	<i>Determine if x consists out of clock_models objects</i>
------------------	--

Description

Determine if x consists out of clock_models objects

Usage

```
are_clock_models(x)
```

Arguments

x the object to check if it consists out of clock_models objects

Value

TRUE if x, or all elements of x, are clock_model objects

Author(s)

Richèl J.C. Bilderbeek

Examples

```

check_empty_beautier_folder()

rln_clock_model <- create_rln_clock_model()
strict_clock_model <- create_strict_clock_model()
both_clock_models <- list(rln_clock_model, strict_clock_model)
# TRUE
are_clock_models(rln_clock_model)
are_clock_models(strict_clock_model)
are_clock_models(both_clock_models)

# FALSE
are_clock_models(NA)
are_clock_models(NULL)
are_clock_models("nonsense")
are_clock_models(create_jc69_site_model())

check_empty_beautier_folder()

```

are_equal_mcmc

*Determine if two MCMCs are equal.***Description**

Will [stop](#) if the arguments are not MCMCs.

Usage

```
are_equal_mcmc(mcmc_1, mcmc_2)
```

Arguments

mcmc_1	an MCMC, as created by create_mcmc
mcmc_2	an MCMC, as created by create_mcmc

Value

TRUE if the two MCMCs are equal

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_mcmc](#) to create an MCMC

Examples

```
if (is_on_ci()) {  
  
  check_empty_beautier_folder()  
  
  mcmc_1 <- create_mcmc(chain_length = 1000)  
  mcmc_2 <- create_mcmc(chain_length = 314)  
  # TRUE  
  are_equal_mcmc(mcmc_1, mcmc_1)  
  # FALSE  
  are_equal_mcmc(mcmc_1, mcmc_2)  
  
  check_empty_beautier_folder()  
}
```

are_equal_screenlogs *Determine if two screenlogs are equal.*

Description

Will [stop](#) if the arguments are not screenlogs.

Usage

```
are_equal_screenlogs(screenlog_1, screenlog_2)
```

Arguments

screenlog_1 an screenlog, as created by [create_screenlog](#)
screenlog_2 an screenlog, as created by [create_screenlog](#)

Value

TRUE if the two screenlogs are equal

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_screenlog](#) to create an screenlog

Examples

```

check_empty_beautier_folder()

screenlog_1 <- create_screenlog(log_every = 1000)
screenlog_2 <- create_screenlog(log_every = 314)
# TRUE
are_equal_screenlogs(screenlog_1, screenlog_1)
# FALSE
are_equal_screenlogs(screenlog_1, screenlog_2)

check_empty_beautier_folder()

```

are_equal_tracelogs *Determine if two tracelogs are equal.*

Description

Will [stop](#) if the arguments are not tracelogs.

Usage

```
are_equal_tracelogs(tracelog_1, tracelog_2)
```

Arguments

tracelog_1	an tracelog, as created by create_tracelog
tracelog_2	an tracelog, as created by create_tracelog

Value

TRUE if the two tracelogs are equal

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_tracelog](#) to create an tracelog

Examples

```

check_empty_beautier_folder()

tracelog_1 <- create_tracelog(log_every = 1000)
tracelog_2 <- create_tracelog(log_every = 314)
# TRUE
are_equal_tracelogs(tracelog_1, tracelog_1)
# FALSE

```



```
are_equal_tracelogs(tracelog_1, tracelog_2)

check_empty_beautier_folder()
```

are_equal_treelogs	<i>Determine if two treelogs are equal.</i>
--------------------	---

Description

Will [stop](#) if the arguments are not treelogs.

Usage

```
are_equal_treelogs(treelog_1, treelog_2)
```

Arguments

treelog_1	an treelog, as created by create_treelog
treelog_2	an treelog, as created by create_treelog

Value

TRUE if the two treelogs are equal

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_treelog](#) to create an treelog

Examples

```
check_empty_beautier_folder()

treelog_1 <- create_treelog(log_every = 1000)
treelog_2 <- create_treelog(log_every = 314)
# TRUE
are_equal_treelogs(treelog_1, treelog_1)
# FALSE
are_equal_treelogs(treelog_1, treelog_2)

check_empty_beautier_folder()
```

are_equal_xml_files *Determine if XML files result in equal trees*

Description

Determine if XML files result in equal trees

Usage

```
are_equal_xml_files(filename_1, filename_2, section)
```

Arguments

filename_1	name of a first XML file
filename_2	name of a second XML file
section	name of an XML section. Assumes that there is one line that starts with <section (excluding whitespace) and one line that is </section> (also excluding whitespace)

Value

TRUE if the two sections of the XML files are equal, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

to check for equivalence, use [are_equivalent_xml_files](#)

Examples

```
check_empty_beautier_folder()

are_equal_xml_files(
  filename_1 = get_beautier_path("2_4.xml"),
  filename_2 = get_beautier_path("2_6_0.xml"),
  section = "taxonset"
)

check_empty_beautier_folder()
```

are_equal_xml_lines	<i>Determine if XML lines result in equal trees</i>
---------------------	---

Description

Determine if XML lines result in equal trees

Usage

```
are_equal_xml_lines(lines_1, lines_2, section)
```

Arguments

lines_1	lines of a first XML file
lines_2	lines of a second XML file
section	name of an XML section. Assumes that there is one line that starts with <section (excluding whitespace) and one line that is </section> (also excluding whitespace)

Value

TRUE if the two sections of the XML files are equal, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

are_equal_xml_lines(
  lines_1 = readLines(get_beautier_path("2_4.xml")),
  lines_2 = readLines(get_beautier_path("2_6_0.xml")),
  section = "taxonset"
)

check_empty_beautier_folder()
```

`are_equivalent_xml_files`*Internal function*

Description

Internal function used for debugging to determine if XML files result in equivalent trees

Usage

```
are_equivalent_xml_files(filename_1, filename_2, section = NA)
```

Arguments

<code>filename_1</code>	name of a first XML file
<code>filename_2</code>	name of a second XML file
<code>section</code>	the name of the XML section, use NA to check the whole file

Value

TRUE if the two XML files result in equivalent trees, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

to check for equality, use `are_equal_xml_files`

Examples

```
check_empty_beautier_folder()

are_equivalent_xml_files(
  filename_1 = get_beautier_path("2_4.xml"),
  filename_2 = get_beautier_path("2_6_0.xml")
)

check_empty_beautier_folder()
```

`are_equivalent_xml_lines`*Determine if XML lines result in equivalent trees*

Description

Determine if XML lines result in equivalent trees

Usage

```
are_equivalent_xml_lines(lines_1, lines_2, section = NA, verbose = FALSE)
```

Arguments

<code>lines_1</code>	lines of a first XML file
<code>lines_2</code>	lines of a second XML file
<code>section</code>	the name of the XML section
<code>verbose</code>	if TRUE, additional information is displayed, that is potentially useful in debugging

Value

TRUE if the two XML lines result in equivalent trees, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

`are_equivalent_xml_lines_all`*Determine if XML lines result in equivalent trees*

Description

Determine if XML lines result in equivalent trees

Usage

```
are_equivalent_xml_lines_all(lines_1, lines_2, verbose = FALSE)
```

Arguments

<code>lines_1</code>	lines of a first XML file
<code>lines_2</code>	lines of a second XML file
<code>verbose</code>	if TRUE, additional information is displayed, that is potentially useful in debugging

Value

TRUE if the two XML lines result in equivalent trees, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

are_equivalent_xml_lines_loggers

Determine if XML operator lines result in equivalent trees

Description

Determine if XML operator lines result in equivalent trees

Usage

```
are_equivalent_xml_lines_loggers(lines_1, lines_2, verbose = FALSE)
```

Arguments

lines_1	lines of a first XML file
lines_2	lines of a second XML file
verbose	if TRUE, additional information is displayed, that is potentially useful in debugging

Value

TRUE if the two XML lines result in equivalent trees, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

`are_equivalent_xml_lines_operators`*Determine if XML operator lines result in equivalent trees*

Description

Determine if XML operator lines result in equivalent trees

Usage

```
are_equivalent_xml_lines_operators(lines_1, lines_2, verbose = FALSE)
```

Arguments

<code>lines_1</code>	lines of a first XML file
<code>lines_2</code>	lines of a second XML file
<code>verbose</code>	if TRUE, additional information is displayed, that is potentially useful in debugging

Value

TRUE if the two XML lines result in equivalent trees, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

`are_equivalent_xml_lines_section`*Determine if XML lines result in equivalent trees*

Description

Determine if XML lines result in equivalent trees

Usage

```
are_equivalent_xml_lines_section(lines_1, lines_2, section, verbose = FALSE)
```

Arguments

<code>lines_1</code>	lines of a first XML file
<code>lines_2</code>	lines of a second XML file
<code>section</code>	the name of the XML section
<code>verbose</code>	if TRUE, additional information is displayed, that is potentially useful in debugging

Value

TRUE if the two XML lines result in equivalent trees, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

are_fasta_filenames *Checks if all filenames have a FASTA filename extension*

Description

Checks if all filenames have a FASTA filename extension

Usage

```
are_fasta_filenames(filenames)
```

Arguments

filenames filenames

Value

TRUE if all filenames have a FASTA filename extension

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# TRUE
are_fasta_filenames("1.fas")
are_fasta_filenames("1.fasta")
are_fasta_filenames("1.FAS")
are_fasta_filenames("1.FASTA")
are_fasta_filenames(c("1.fas", "2.fas"))

# FALSE
are_fasta_filenames("")
are_fasta_filenames(NA)
are_fasta_filenames(NULL)
are_fasta_filenames(Inf)
are_fasta_filenames("1.fasX")
are_fasta_filenames(c("1.fas", "2.exe"))
are_fasta_filenames(c("1.bat", "2.exe"))
```



```
check_empty_beautier_folder()
```

are_ids	<i>Determine if x consists out of IDs</i>
---------	---

Description

Determine if x consists out of IDs

Usage

```
are_ids(x)
```

Arguments

x the object to check if it consists out of IDs

Value

TRUE if x, or all elements of x, are IDs

Author(s)

Richèl J.C. Bilderbeek

See Also

to check one ID, use [is_id](#)

Examples

```
check_empty_beautier_folder()

# TRUE
are_ids("anthus_aco")
are_ids(c("anthus_aco", "anthus_nd2"))
are_ids(list("anthus_aco", "anthus_nd2"))
are_ids(c(1, 2))
are_ids(1)

# FALSE
are_ids(NULL)
are_ids(NA)
are_ids(c())
are_ids(ape::rcoal(3))
are_ids(c(ape::rcoal(3), ape::rcoal(4)))

check_empty_beautier_folder()
```

are_init_clock_models *Determine if x consists out of initialized clock_models objects*

Description

Determine if x consists out of initialized clock_models objects

Usage

```
are_init_clock_models(x)
```

Arguments

x the object to check if it consists out of initialized clock_models objects

Value

TRUE if x, or all elements of x, are initialized clock_model objects

Author(s)

Richèl J.C. Bilderbeek

are_init_mrca_priors *Determine if x consists out of initialized MRCA priors*

Description

Determine if x consists out of initialized MRCA priors

Usage

```
are_init_mrca_priors(x)
```

Arguments

x the object to check if it consists out of initialized MRCA priors

Value

TRUE if x, or all elements of x, are initialized MRCA priors

Author(s)

Richèl J.C. Bilderbeek

are_init_site_models *Determine if x consists out of initialized site_models objects*

Description

Determine if x consists out of initialized site_models objects

Usage

```
are_init_site_models(x)
```

Arguments

x the object to check if it consists out of initialized site_models objects

Value

TRUE if x, or all elements of x, are initialized site_model objects

Author(s)

Richèl J.C. Bilderbeek

are_init_tree_priors *Determine if x consists out of initialized tree_priors objects*

Description

Determine if x consists out of initialized tree_priors objects

Usage

```
are_init_tree_priors(x)
```

Arguments

x the object to check if it consists out of initialized tree_priors objects

Value

TRUE if x, or all elements of x, are initialized tree_prior objects

Author(s)

Richèl J.C. Bilderbeek

are_mrca_align_ids_in_fasta

Determine if the MRCA priors' alignment IDs are present in the FASTA files

Description

Determine if the MRCA priors' alignment IDs are present in the FASTA files

Usage

```
are_mrca_align_ids_in_fasta(mrca_prior, fasta_filename)
```

Arguments

mrca_prior a Most Recent Common Ancestor prior, as returned by [create_mrca_prior](#)

fasta_filename a FASTA filename. Use [get_fasta_filename](#) to obtain a testing FASTA filename. Note that BEAST2 also supports missing data, by using a dash (-) or question mark (?) as a sequence.

Value

TRUE if all the MRCA priors' alignment IDs are present in the FASTA files. Returns FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

are_mrca_priors

Determine if x consists out of MRCA priors

Description

Determine if x consists out of MRCA priors

Usage

```
are_mrca_priors(mrca_priors)
```

Arguments

mrca_priors a list of one or more Most Recent Common Ancestor priors, as returned by [create_mrca_prior](#)

Value

TRUE if x, or all elements of x, are MRCA priors. Returns FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

are_mrca_taxon_names_in_fasta

Determine if the MRCA priors' taxa names are present in the FASTA files

Description

Determine if the MRCA priors' taxa names are present in the FASTA files

Usage

```
are_mrca_taxon_names_in_fasta(mrca_prior, fasta_filename)
```

Arguments

mrca_prior a Most Recent Common Ancestor prior, as returned by [create_mrca_prior](#)

fasta_filename a FASTA filename. Use [get_fasta_filename](#) to obtain a testing FASTA filename. Note that BEAST2 also supports missing data, by using a dash (-) or question mark (?) as a sequence.

Value

TRUE if the MRCA priors' taxa names are present in the FASTA files. FALSE otherwise.

Author(s)

Richèl J.C. Bilderbeek

`are_rln_clock_models` *Are the clock models Relaxed Log-Normal clock models?*

Description

Are the clock models Relaxed Log-Normal clock models?

Usage

```
are_rln_clock_models(clock_models)
```

Arguments

`clock_models` a list of one or more clock models, as returned by [create_clock_model](#)

Value

vector of booleans with the same length as the number of clock models in `clock_models`. Each *nth* element is TRUE if the *nth* element in `clock_models` is a relaxed log-normal clock model, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

`are_site_models` *Determine if x consists out of site_models objects*

Description

Determine if x consists out of site_models objects

Usage

```
are_site_models(x)
```

Arguments

`x` the object to check if it consists out of site_models objects

Value

TRUE if x, or all elements of x, are site_model objects

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_site_model](#) to create a site model

Examples

```
check_empty_beautier_folder()

jc69_site_model <- create_jc69_site_model()
gtr_site_model <- create_gtr_site_model()
both_site_models <- list(jc69_site_model, gtr_site_model)

# TRUE
are_site_models(jc69_site_model)

# TRUE
are_site_models(gtr_site_model)

# TRUE
are_site_models(both_site_models)

check_empty_beautier_folder()
```

are_tree_priors	<i>Determine if x consists out of tree_priors objects</i>
-----------------	---

Description

Determine if x consists out of tree_priors objects

Usage

```
are_tree_priors(x)
```

Arguments

x the object to check if it consists out of tree_priors objects

Value

TRUE if x, or all elements of x, are tree_prior objects

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_yule_tree_prior](#) to create a Yule tree prior

Examples

```
check_empty_beautier_folder()

yule_tree_prior <- create_yule_tree_prior()
bd_tree_prior <- create_bd_tree_prior()
both_tree_priors <- list(yule_tree_prior, bd_tree_prior)
# TRUE
are_tree_priors(yule_tree_prior)
# TRUE
are_tree_priors(bd_tree_prior)
# TRUE
are_tree_priors(both_tree_priors)

check_empty_beautier_folder()
```

bd_tree_prior_to_xml_prior_distr

Creates the tree prior section in the prior section of the prior section of the distribution section of a BEAST2 XML parameter file for a Birth-Death tree prior

Description

Creates the tree prior section in the prior section of the prior section of the distribution section of a BEAST2 XML parameter file for a Birth-Death tree prior

Usage

```
bd_tree_prior_to_xml_prior_distr(bd_tree_prior, beauti_options)
```

Arguments

bd_tree_prior a Birth-Death tree prior, as created by [create_bd_tree_prior](#)
beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# <distribution id="posterior" spec="util.CompoundDistribution">
#   <distribution id="prior" spec="util.CompoundDistribution">
#     HERE, where the ID of the distribution is 'prior'
#   </distribution>
#   <distribution id="likelihood" ...>
#   </distribution>
# </distribution>

check_empty_beautier_folder()
```

beta_parameter_to_xml *Internal function*

Description

Converts a beta parameter to XML

Usage

```
beta_parameter_to_xml(beta_parameter, beauti_options = create_beauti_options())
```

Arguments

beta_parameter a beta parameter, as created by [create_beta_param](#)

beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

the parameter as XML text

Author(s)

Richèl J.C. Bilderbeek

`b_pop_sizes_parameter_to_xml`
Internal function

Description

Converts a Bayesian population sizes parameter to XML

Usage

```
b_pop_sizes_parameter_to_xml(  
  b_pop_sizes_parameter,  
  beauti_options = create_beauti_options()  
)
```

Arguments

`b_pop_sizes_parameter`
a Bayesian population size parameter, as created by [create_b_pop_sizes_param](#)
`beauti_options` one BEAUti options object, as returned by [create_beauti_options](#)

Value

the parameter as XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
b_pop_sizes_parameter_to_xml(  
  b_pop_sizes_parameter = create_b_pop_sizes_param(id = 42),  
  beauti_options = create_beauti_options()  
)  
b_pop_sizes_parameter_to_xml(  
  b_pop_sizes_parameter = create_b_pop_sizes_param(id = 42, upper = Inf),  
  beauti_options = create_beauti_options()  
)
```

`b_pop_sizes_param_to_xml`*Internal function*

Description

Converts a 'bPopSizes' parameter to XML

Usage

```
b_pop_sizes_param_to_xml(  
  b_pop_sizes_param,  
  beauti_options = create_beauti_options()  
)
```

Arguments

`b_pop_sizes_param`

a Bayesian population size parameter, as created by [create_b_pop_sizes_param](#)

`beauti_options` one BEAUti options object, as returned by [create_beauti_options](#)

Value

the parameter as XML text

Author(s)

Richèl J.C. Bilderbeek

`cbs_tree_prior_to_xml_prior_distr`

Creates the tree prior section in the prior section of the prior section of the distribution section of a BEAST2 XML parameter file for a Birth-Death tree prior

Description

Creates the tree prior section in the prior section of the prior section of the distribution section of a BEAST2 XML parameter file for a Birth-Death tree prior

Usage

```
cbs_tree_prior_to_xml_prior_distr(cbs_tree_prior, beauti_options)
```

Arguments

cbs_tree_prior a Coalescent Bayesian Skyline tree prior, as returned by [create_cbs_tree_prior](#)
 beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# <distribution id="posterior" spec="util.CompoundDistribution">
#   <distribution id="prior" spec="util.CompoundDistribution">
#     HERE, where the ID of the distribution is 'prior'
#   </distribution>
#   <distribution id="likelihood" ...>
#   </distribution>
# </distribution>

check_empty_beautier_folder()
```

```
ccp_tree_prior_to_xml_prior_distr
```

Creates the tree prior section in the prior section of the prior section of the distribution section of a BEAST2 XML parameter file for a Coalescent Constant Population tree prior

Description

Creates the tree prior section in the prior section of the prior section of the distribution section of a BEAST2 XML parameter file for a Coalescent Constant Population tree prior

Usage

```
ccp_tree_prior_to_xml_prior_distr(ccp_tree_prior, beauti_options)
```

Arguments

ccp_tree_prior a Coalescent Constant Population tree prior, as returned by [create_ccp_tree_prior](#)
 beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# <distribution id="posterior" spec="util.CompoundDistribution">
#   <distribution id="prior" spec="util.CompoundDistribution">
#     HERE, where the ID of the distribution is 'prior'
#   </distribution>
# <distribution id="likelihood" ...>
#   </distribution>
# </distribution>

check_empty_beautier_folder()
```

ccp_tree_prior_to_xml_state

Convert a CCP tree prior to the XML as part of the state section

Description

Convert a CCP tree prior to the XML as part of the state section

Usage

```
ccp_tree_prior_to_xml_state(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

XML as text

Examples

```

check_empty_beautier_folder()

# Need an ID and initial value
inference_model <- create_inference_model(
  tree_prior = create_ccp_tree_prior(
    id = "anthus_nd2_sub",
    pop_size_distr = create_normal_distr(
      id = 123,
      value = 3.14
    )
  )
)

ccp_tree_prior_to_xml_state(inference_model)

check_empty_beautier_folder()

```

```
cep_tree_prior_to_xml_prior_distr
```

Creates the tree prior section in the prior section of the prior section of the distribution section of a BEAST2 XML parameter file for a Coalescent Exponential Population tree prior

Description

Creates the tree prior section in the prior section of the prior section of the distribution section of a BEAST2 XML parameter file for a Coalescent Exponential Population tree prior

Usage

```
cep_tree_prior_to_xml_prior_distr(cep_tree_prior, beauti_options)
```

Arguments

`cep_tree_prior` a Coalescent Exponential Population tree prior, as returned by [create_cep_tree_prior](#)
`beauti_options` one BEAUti options object, as returned by [create_beauti_options](#)

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```

check_empty_beautier_folder()

# <distribution id="posterior" spec="util.CompoundDistribution">
#   <distribution id="prior" spec="util.CompoundDistribution">
#     HERE, where the ID of the distribution is 'prior'
#   </distribution>
#   <distribution id="likelihood" ...>
#     </distribution>
# </distribution>

check_empty_beautier_folder()

```

check_alignment_id	<i>Check if the alignment_id is valid.</i>
--------------------	--

Description

Will [stop](#) if not.

Usage

```
check_alignment_id(alignment_id)
```

Arguments

alignment_id ID of the alignment, as returned by [get_alignment_id](#). Keep at NA to have it initialized automatically

Value

nothing, will [stop](#) if needed

Examples

```

check_empty_beautier_folder()

# anthus_aco_sub
alignment_id <- get_alignment_id("/home/homer/anthus_aco_sub.fas")
check_alignment_id(alignment_id)

check_empty_beautier_folder()

```

`check_beauti_options` *Check if the beauti_options is a valid beauti_options object.*

Description

Calls stop if the beauti_options object is invalid

Usage

```
check_beauti_options(beauti_options)
```

Arguments

`beauti_options` one BEAUti options object, as returned by [create_beauti_options](#)

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_beauti_options](#) to create a valid BEAUti options setup

Examples

```
check_empty_beautier_folder()

check_beauti_options(create_beauti_options())

check_empty_beautier_folder()
```

`check_clock_model` *Check if the clock model is a valid clock model.*

Description

Calls stop if the clock model is invalid

Usage

```
check_clock_model(clock_model)
```


Arguments

clock_model a clock model, as returned by [create_clock_model](#)

Value

TRUE if clock_model is a valid clock model

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_clock_model](#) to create a valid clock model

Examples

```
check_empty_beautier_folder()

check_clock_model(create_strict_clock_model())
check_clock_model(create_rln_clock_model())

check_empty_beautier_folder()
```

check_clock_models *Check if the object is a list of one or more clock models.*

Description

Will [stop](#) if the object is not a list of one or more clock models.

Usage

```
check_clock_models(clock_models)
```

Arguments

clock_models the object to be checked if it is a list of one or more valid clock models

Value

nothing. Will [stop](#) if the object is not a list of one or more clock models.

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_clock_model](#) to create a valid clock model

Examples

```
check_empty_beautier_folder()

check_clock_models(create_strict_clock_model())
check_clock_models(list(create_strict_clock_model()))
check_clock_models(
  list(create_strict_clock_model(), create_rln_clock_model())
)

check_empty_beautier_folder()
```

check_empty_beautier_folder

Internal function

Description

Internal function to verify that, if there are ‘beautier’ temporary files created, these are also cleaned up, as by CRAN policy.

Usage

```
check_empty_beautier_folder(beautier_folder = get_beautier_folder())
```

Arguments

beautier_folder
the path to the [beautier](#) temporary files folder

Details

If the ‘beautier’ folder does not exist, this function does nothing. If there are folder and/or files in the ‘beautier’ folder, an error is given.

Value

No return value, called for side effects.

Author(s)

Richèl J.C. Bilderbeek

See Also

use [remove_beautier_folder](#) to remove the default ‘beautier’ folder

Examples

```
remove_beautier_folder()

check_empty_beautier_folder()

remove_beautier_folder()
```

check_filename	<i>Check if the 'filename' is valid</i>
----------------	---

Description

Calls stop if the filename is invalid

Usage

```
check_filename(filename, allow_empty_str = FALSE, allow_na = FALSE)
```

Arguments

filename	a filename, as can be checked by check_filename
allow_empty_str	allow a string to be empty
allow_na	allow NA

Value

The filename (invisibly)

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

check_filename("trace.log")
check_filename("my.trees")

check_empty_beautier_folder()
```

check_file_and_model_agree

Checks if the input FASTA file and the inference model agree.

Description

Will [stop](#) if not

Usage

```
check_file_and_model_agree(input_filename, inference_model)
```

Arguments

input_filename A FASTA filename. Use [get_fasta_filename](#) to obtain a testing FASTA filename.

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

nothing, will [stop](#) if needed

check_file_exists

Function to check if a file exists. Calls stop if the file is absent

Description

Function to check if a file exists. Calls stop if the file is absent

Usage

```
check_file_exists(filename, filename_description = NA)
```

Arguments

filename name of the file

filename_description

description of the filename

Value

nothing. Will stop if the file is absent, with a proper error message

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

check_file_exists(get_beautier_path("anthus_aco_sub.fas"))

check_empty_beautier_folder()
```

`check_gamma_site_model`

Checks if the parameter is a valid gamma site model

Description

Checks if the parameter is a valid gamma site model

Usage

```
check_gamma_site_model(gamma_site_model)
```

Arguments

`gamma_site_model`
a site model's gamma site model, as returned by [create_gamma_site_model](#)

Value

nothing. Will call stop if the argument is not a valid gamma site model

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

check_gamma_site_model(create_gamma_site_model())

check_empty_beautier_folder()
```

check_gamma_site_model_names

Checks if the gamma site model has the right list elements' names

Description

Checks if the gamma site model has the right list elements' names

Usage

```
check_gamma_site_model_names(gamma_site_model)
```

Arguments

gamma_site_model

a site model's gamma site model, as returned by [create_gamma_site_model](#)

Value

nothing. Will call stop if the argument is not a valid gamma site model

Author(s)

Richèl J.C. Bilderbeek

check_gtr_site_model *Check if the gtr_site_model is a valid GTR nucleotide substitution model.*

Description

Use [create_gtr_site_model](#) to create a valid GTR nucleotide substitution model.

Usage

```
check_gtr_site_model(gtr_site_model)
```

Arguments

gtr_site_model a GTR site model, as returned by [create_gtr_site_model](#)

Value

TRUE is the gtr_site_model is a valid GTR nucleotide substitution model, FALSE otherwise

Examples

```
check_empty_beautier_folder()

check_gtr_site_model(create_gtr_site_model())

check_empty_beautier_folder()
```

`check_gtr_site_model_names`

Check if the `gtr_site_model` has the list elements of a valid `gtr_site_model` object.

Description

Calls stop if an element is missing

Usage

```
check_gtr_site_model_names(gtr_site_model)
```

Arguments

`gtr_site_model` a GTR site model, as returned by [create_gtr_site_model](#)

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_gtr_site_model](#) to create a valid `gtr_site_model`

check_inference_model *Check if the supplied object is a valid Bayesian phylogenetic inference model.*

Description

Calls stop if the supplied object is not a valid Bayesian phylogenetic inference model.

Usage

```
check_inference_model(inference_model)
```

Arguments

inference_model
a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_inference_model](#) to create a valid Bayesian phylogenetic inference model

Examples

```
check_empty_beautier_folder()

check_inference_model(create_inference_model())

check_empty_beautier_folder()
```

`check_inference_models`*Check if the inference_model is a valid BEAUti inference model.*

Description

Calls stop if not.

Usage

```
check_inference_models(inference_models)
```

Arguments

`inference_models`

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

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_inference_model](#) to create a valid BEAST2 options object

Examples

```
check_empty_beautier_folder()
```

```
check_inference_models(list(create_inference_model()))
```

```
check_empty_beautier_folder()
```

check_is_monophyletic *Check if is_monophyletic has a valid value.*

Description

Will [stop](#) if not.

Usage

```
check_is_monophyletic(is_monophyletic)
```

Arguments

is_monophyletic
boolean to indicate monophyly is assumed in a Most Recent Common Ancestor prior, as returned by [create_mrca_prior](#)

Value

No return value, called for side effects

check_log_mode *Check if the supplied mode is a valid logging mode.*

Description

Check if the supplied mode is a valid logging mode.

Usage

```
check_log_mode(mode)
```

Arguments

mode mode how to log. Valid are tree, autodetect and compound

Value

No return value, called for side effects

check_log_sort	<i>Check if the supplied sort is a valid logging sorting option.</i>
----------------	--

Description

Check if the supplied sort is a valid logging sorting option.

Usage

```
check_log_sort(sort)
```

Arguments

sort	how to sort the entries in a log. Valid are smart, none and alphabetic
------	--

Value

No return value, called for side effects

check_mcmc	<i>Check if the MCMC is a valid MCMC object.</i>
------------	--

Description

Calls stop if the MCMC is invalid

Usage

```
check_mcmc(mcmc)
```

Arguments

mcmc	one MCMC. Use create_mcmc to create an MCMC. Use create_ns_mcmc to create an MCMC for a Nested Sampling run. Use check_mcmc to check if an MCMC is valid. Use rename_mcmc_filenames to rename the filenames in an MCMC.
------	---

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_mcmc](#) to create a valid MCMC

Examples

```
check_empty_beautier_folder()

check_mcmc(create_mcmc())

check_empty_beautier_folder()
```

check_mcmc_list_element_names

Check if the MCMC has the list elements of a valid MCMC object.

Description

Calls stop if an element is missing

Usage

```
check_mcmc_list_element_names(mcmc)
```

Arguments

mcmc	one MCMC. Use create_mcmc to create an MCMC. Use create_ns_mcmc to create an MCMC for a Nested Sampling run. Use check_mcmc to check if an MCMC is valid. Use rename_mcmc_filenames to rename the filenames in an MCMC.
------	---

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_mcmc](#) to create a valid MCMC

check_mcmc_values	<i>Check if the MCMC has the list elements with valid values for being a valid MCMC object.</i>
-------------------	---

Description

Calls stop if a value is invalid

Usage

```
check_mcmc_values(mcmc)
```

Arguments

mcmc	one MCMC. Use create_mcmc to create an MCMC. Use create_ns_mcmc to create an MCMC for a Nested Sampling run. Use check_mcmc to check if an MCMC is valid. Use rename_mcmc_filenames to rename the filenames in an MCMC.
------	---

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_mcmc](#) to create a valid MCMC

check_mrca_prior	<i>Check if the MRCA prior is a valid MRCA prior.</i>
------------------	---

Description

Calls stop if the MRCA prior is invalid.

Usage

```
check_mrca_prior(mrca_prior)
```

Arguments

mrca_prior	a Most Recent Common Ancestor prior, as returned by create_mrca_prior
------------	---

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_mrca_prior](#) to create a valid MRCA prior

Examples

```
check_empty_beautier_folder()

fasta_filename <- get_beautier_path("anthus_aco.fas")
mrca_prior <- create_mrca_prior(
  alignment_id = get_alignment_id(fasta_filename = fasta_filename),
  taxa_names = get_taxa_names(filename = fasta_filename)
)
mrca_prior <- create_mrca_prior(
  alignment_id = get_alignment_id(fasta_filename = fasta_filename),
  taxa_names = get_taxa_names(filename = fasta_filename)
)
check_mrca_prior(mrca_prior)

check_empty_beautier_folder()
```

check_mrca_prior_name *Check if mrca_prior_name is a valid MRCA prior name.*

Description

A valid MRCA prior name is either [NA](#) or one character string. Will [stop](#) if not.

Usage

```
check_mrca_prior_name(mrca_prior_name)
```

Arguments

mrca_prior_name

the unique name of the MRCA prior, for example a genus, family, order or even class name. Leave at [NA](#) to have it named automatically.

Value

No return value, called for side effects

`check_mrca_prior_names`*Check if the MRCA prior, which is a list, has all the named elements.*

Description

Calls stop if not.

Usage

```
check_mrca_prior_names(mrca_prior)
```

Arguments

`mrca_prior` a Most Recent Common Ancestor prior, as returned by [create_mrca_prior](#)

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [check_mrca_prior](#) to check the entire MRCA prior

`check_mrca_prior_taxa_names`*Check the MRCA prior's taxon names are valid.*

Description

Will [stop](#) if not.

Usage

```
check_mrca_prior_taxa_names(taxa_names)
```

Arguments

`taxa_names` names of the taxa, as returned by [get_taxa_names](#). Keep at NA to have it initialized automatically, using all taxa in the alignment

Value

No return value, called for side effects

check_ns_mcmc	<i>Check if this an MCMC that uses Nested Sampling to estimate a marginal likelihood.</i>
---------------	---

Description

Will [stop](#) if not, else will do nothing

Usage

```
check_ns_mcmc(mcmc)
```

Arguments

mcmc	one MCMC. Use create_mcmc to create an MCMC. Use create_ns_mcmc to create an MCMC for a Nested Sampling run. Use check_mcmc to check if an MCMC is valid. Use rename_mcmc_filenames to rename the filenames in an MCMC.
------	---

Value

No return value, called for side effects

Author(s)

Richèl J.C. Bilderbeek

See Also

use [create_ns_mcmc](#) to create an MCMC that uses Nested Sampling to estimate a marginal likelihood

check_param	<i>Check if the parameter is a valid parameter</i>
-------------	--

Description

Calls stop if the parameter is invalid

Usage

```
check_param(param)
```

Arguments

param	a parameter, as can be created by create_param .
-------	--

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_param](#) to create a valid parameter

Examples

```
check_empty_beautier_folder()

check_param(create_alpha_param())
check_param(create_beta_param())

check_empty_beautier_folder()
```

check_param_names	<i>Check if the param has the list elements of a valid param object.</i>
-------------------	--

Description

Calls stop if an element is missing

Usage

```
check_param_names(param)
```

Arguments

param a parameter, as can be created by [create_param](#).

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_param](#) to create a valid param

check_param_types	<i>Check if the param has the list elements of the right type for a valid param object.</i>
-------------------	---

Description

Calls stop if an element has the incorrect type

Usage

```
check_param_types(param)
```

Arguments

param a parameter, as can be created by [create_param](#).

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_param](#) to create a valid param

check_phylogeny	<i>Check if the phylogeny is a valid phylogeny object.</i>
-----------------	--

Description

Calls stop if the phylogeny is invalid

Usage

```
check_phylogeny(phylogeny)
```

Arguments

phylogeny a phylogeny of type phylo from the ape package

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use `ape::read.tree` to create a phylogeny

Examples

```
check_empty_beautier_folder()

# Must do nothing on phylogenies
phylogeny <- ape::read.tree(text = "(A:1, B:1):1;")
check_phylogeny(phylogeny)

check_empty_beautier_folder()
```

check_rename_fun

Check if the rename function is a valid filename rename function

Description

Will [stop](#) if not

Usage

```
check_rename_fun(rename_fun)
```

Arguments

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

- [get_remove_dir_fun](#) get a function that removes the directory paths from the filenames, in effect turning these into local files
- [get_replace_dir_fun](#) get a function that replaces the directory paths from the filenames
- [get_remove_hex_fun](#) get a function that removes the hex string from filenames. For example, `tracelog_82c1a522040.log` becomes `tracelog.log`

Value

No return value, called for side effects

Author(s)

Richèl J.C. Bilderbeek

`check_rln_clock_model` *Check if the clock model is a valid clock model.*

Description

Calls `stop` if the clock model is invalid

Usage

```
check_rln_clock_model(clock_model)
```

Arguments

`clock_model` a clock model, as returned by [create_clock_model](#)

Value

TRUE if `clock_model` is a valid clock model

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_clock_model](#) to create a valid clock model

Examples

```
check_empty_beautier_folder()

check_rln_clock_model(create_rln_clock_model())

check_empty_beautier_folder()
```

`check_screenlog` *Check if a screenlog is valid.*

Description

Will call [stop](#) if not.

Usage

```
check_screenlog(screenlog)
```

Arguments

screenlog a screenlog, as created by [create_screenlog](#)

Value

No return value, called for side effects

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

check_screenlog(create_test_screenlog())

check_empty_beautier_folder()
```

check_screenlog_names *Check if the screenlog has the list elements of a valid screenlog object.*

Description

Calls stop if an element is missing

Usage

```
check_screenlog_names(screenlog)
```

Arguments

screenlog a screenlog, as created by [create_screenlog](#)

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_screenlog](#) to create a valid screenlog

`check_screenlog_values`

Check if the screenlog has the list elements with valid values for being a valid screenlog object.

Description

Calls stop if a value is invalid

Usage

```
check_screenlog_values(screenlog)
```

Arguments

`screenlog` a screenlog, as created by [create_screenlog](#)

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_screenlog](#) to create a valid screenlog

`check_site_model`

Check if the site model is a valid site model

Description

Calls stop if the site models are invalid

Usage

```
check_site_model(site_model)
```

Arguments

`site_model` a site model, as returned by [create_site_model](#)

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_site_model](#) to create a valid site model

Examples

```
check_empty_beautier_folder()

check_site_model(create_jc69_site_model())
check_site_model(create_hky_site_model())
check_site_model(create_tn93_site_model())
check_site_model(create_gtr_site_model())

# Can use list of one site model
check_site_model(list(create_jc69_site_model()))

check_empty_beautier_folder()
```

check_site_models	<i>Check if the object is a list of one or more site models.</i>
-------------------	--

Description

Will [stop](#) if the object is not a list of one or more site models.

Usage

```
check_site_models(site_models)
```

Arguments

site_models the object to be checked if it is a list of one or more valid site models

Value

nothing. Will [stop](#) if the object is not a list of one or more site models.

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_site_model](#) to create a valid site model

Examples

```
check_empty_beautier_folder()

check_site_models(create_jc69_site_model())
check_site_models(list(create_jc69_site_model()))
check_site_models(
  list(create_jc69_site_model(), create_gtr_site_model())
)

check_empty_beautier_folder()
```

check_site_model_names

Check if the site_model has the list elements of a valid site_model object.

Description

Calls stop if an element is missing

Usage

```
check_site_model_names(site_model)
```

Arguments

site_model a site model, as returned by [create_site_model](#)

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_site_model](#) to create a valid site_model

`check_site_model_types`

Check if the `site_model` has the list elements of the right type for a valid `site_model` object.

Description

Calls `stop` if an element has the incorrect type

Usage

```
check_site_model_types(site_model)
```

Arguments

`site_model` a site model, as returned by [create_site_model](#)

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_site_model](#) to create a valid `site_model`

`check_store_every`

Check if `store_every` holds a valid value

Description

Will [stop](#) if not

Usage

```
check_store_every(store_every)
```

Arguments

`store_every` number of states the MCMC will process before the posterior's state will be saved to file. Use -1 or NA to use the default frequency.

Value

No return value, called for side effects

`check_strict_clock_model`*Check if the clock model is a valid clock model.*

Description

Calls stop if the clock model is invalid

Usage

```
check_strict_clock_model(clock_model)
```

Arguments

`clock_model` a clock model, as returned by [create_clock_model](#)

Value

TRUE if `clock_model` is a valid clock model

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_clock_model](#) to create a valid clock model

Examples

```
check_empty_beautier_folder()

check_strict_clock_model(create_strict_clock_model())

check_empty_beautier_folder()
```

`check_tn93_site_model` *Check if the tn93_site_model is a valid TN93 nucleotide substitution model.*

Description

Use [create_tn93_site_model](#) to create a valid TN93 nucleotide substitution model.

Usage

```
check_tn93_site_model(tn93_site_model)
```

Arguments

tn93_site_model
a TN93 site model, as returned by [create_tn93_site_model](#)

Value

No return value, called for side effects

Examples

```
check_empty_beautier_folder()

check_tn93_site_model(create_tn93_site_model())

check_empty_beautier_folder()
```

```
check_tn93_site_model_names
```

Check if the tn93_site_model has the list elements of a valid tn93_site_model object.

Description

Calls stop if an element is missing

Usage

```
check_tn93_site_model_names(tn93_site_model)
```

Arguments

tn93_site_model
a TN93 site model, as returned by [create_tn93_site_model](#)

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_tn93_site_model](#) to create a valid tn93_site_model

check_tracelog	<i>Check if a tracelog is valid.</i>
----------------	--------------------------------------

Description

Will call [stop](#) if not.

Usage

check_tracelog(tracelog)

Arguments

tracelog a tracelog, as created by [create_tracelog](#)

Value

No return value, called for side effects

check_tracelog_names	<i>Check if the tracelog has the list elements of a valid tracelog object.</i>
----------------------	--

Description

Calls stop if an element is missing

Usage

check_tracelog_names(tracelog)

Arguments

tracelog a tracelog, as created by [create_tracelog](#)

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_tracelog](#) to create a valid tracelog

check_tracelog_values	<i>Check if the tracelog has the list elements with valid values for being a valid tracelog object.</i>
-----------------------	---

Description

Calls stop if a value is invalid

Usage

```
check_tracelog_values(tracelog)
```

Arguments

tracelog	a tracelog, as created by create_tracelog
----------	---

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_tracelog](#) to create a valid tracelog

check_treelog	<i>Check if a treelog is valid.</i>
---------------	-------------------------------------

Description

Will call [stop](#) if not.

Usage

```
check_treelog(treelog)
```

Arguments

treelog	a treelog, as created by create_treelog
---------	---

Value

No return value, called for side effects

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()
```

```
check_treelog(create_test_treelog())
```

```
check_empty_beautier_folder()
```

check_treelog_names	<i>Check if the treelog has the list elements of a valid treelog object.</i>
---------------------	--

Description

Calls stop if an element is missing

Usage

```
check_treelog_names(treelog)
```

Arguments

treelog a treelog, as created by [create_treelog](#)

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_treelog](#) to create a valid treelog

check_treelog_values	<i>Check if the treelog has the list elements with valid values for being a valid treelog object.</i>
----------------------	---

Description

Calls stop if a value is invalid

Usage

```
check_treelog_values(treelog)
```

Arguments

treelog a treelog, as created by [create_treelog](#)

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_treelog](#) to create a valid treelog

check_tree_prior	<i>Check if the tree prior is a valid tree prior</i>
------------------	--

Description

Calls stop if the tree priors are invalid

Usage

```
check_tree_prior(tree_prior)
```

Arguments

tree_prior a tree priors, as returned by [create_tree_prior](#)

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_tree_prior](#) to create a valid tree prior

Examples

```
check_empty_beautier_folder()

check_tree_prior(create_yule_tree_prior())
check_tree_prior(create_bd_tree_prior())
check_tree_prior(create_cbs_tree_prior())
check_tree_prior(create_ccp_tree_prior())
check_tree_prior(create_cep_tree_prior())

# Can use list of one tree prior
check_tree_prior(list(create_yule_tree_prior()))

check_empty_beautier_folder()
```

check_tree_priors	<i>Check if the object is a list of one or more tree priors.</i>
-------------------	--

Description

Will [stop](#) if the object is not a list of one or more tree priors.

Usage

```
check_tree_priors(tree_priors)
```

Arguments

tree_priors the object to be checked if it is a list of one or more valid tree priors

Value

nothing. Will [stop](#) if the object is not a list of one or more tree priors.

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_tree_prior](#) to create a valid tree prior

Examples

```
check_empty_beautier_folder()

check_tree_priors(create_yule_tree_prior())
check_tree_priors(list(create_yule_tree_prior()))
check_tree_priors(list(create_yule_tree_prior(), create_bd_tree_prior()))

check_empty_beautier_folder()
```

clock_model_to_xml_operators
Internal function

Description

Converts a clock model to the operators section of the XML as text

Usage

```
clock_model_to_xml_operators(inference_model)
```

Arguments

`inference_model`
a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

a character vector of XML strings

Author(s)

Richèl J.C. Bilderbeek

clock_model_to_xml_prior_distr
Internal function

Description

Internal function to converts a clock model to the prior section of the XML as text

Usage

```
clock_model_to_xml_prior_distr(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

a character vector of XML strings

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()
# <distribution id="posterior" spec="util.CompoundDistribution">
#   <distribution id="prior" spec="util.CompoundDistribution">
#     HERE, where the ID of the distribution is 'prior'
#   </distribution>
#   <distribution id="likelihood" ...>
#   </distribution>
# </distribution>
clock_model_to_xml_prior_distr(
  inference_model = create_inference_model()
)
check_empty_beautier_folder()
```

`clock_model_to_xml_state`*Internal function*

Description

Converts a clock model to the state section of the XML as text

Usage

```
clock_model_to_xml_state(inference_model)
```

Arguments

`inference_model`

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

lines of XML text, without indentation nor state tags

Author(s)

Richèl J.C. Bilderbeek

`clock_model_to_xml_tracelog`*Internal function*

Description

Creates the clock model's XML for the tracelog section

Usage

```
clock_model_to_xml_tracelog(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

a character vector of XML strings

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# <logger id="tracelog" ...>
#'   # Here
# </logger>

check_empty_beautier_folder()
```

clock_model_to_xml_treelogger

Convert a clock model to the XML of the TreeLogger

Description

Convert a clock model to the XML of the TreeLogger

Usage

```
clock_model_to_xml_treelogger(clock_model)
```

Arguments

clock_model a clock model, as returned by [create_clock_model](#)

Value

a character vector of XML strings

Note

This is an internal function, so it should be marked with @export. This is not done, as this will disallow all functions to find the documentation parameters

Author(s)

Richèl J.C. Bilderbeek

clock_rate_param_to_xml

Internal function

Description

Converts a clockRate parameter to XML

Usage

```
clock_rate_param_to_xml(  
  clock_rate_param,  
  beauti_options = create_beauti_options()  
)
```

Arguments

clock_rate_param
a clockRate parameter, a numeric value, as created by [create_clock_rate_param](#)

beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

the parameter as XML text

Author(s)

Richèl J.C. Bilderbeek

compare_lines	<i>Internal function</i>
---------------	--------------------------

Description

Internal debug function to compare the actually created lines to expected lines using any diff tool

Usage

```
compare_lines(
  lines,
  expected,
  section = NA,
  created_lines_filename = get_beautier_tempfilename(pattern = "created", fileext =
    ".xml"),
  expected_lines_filename = get_beautier_tempfilename(pattern = "expected", fileext =
    ".xml")
)
```

Arguments

lines	the created lines
expected	the expected/goal/target lines
section	the XML section. Leave at NA to compare all lines
created_lines_filename	name of the file where the (section of the) created lines are stored
expected_lines_filename	name of the file where the (section of the) expected lines are stored

Value

nothing. Instead, two files are created, with the names `created_lines_filename` and `expected_lines_filename` that contain the section under investigation, so that a diff tool can compare these

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# Creates temporary files in beautier folder
compare_lines(
  lines = readLines(get_beautier_path("bd_2_4.xml")),
  expected = readLines(get_beautier_path("bd_2_4.xml"))
)
```

```
remove_beautier_folder()
check_empty_beautier_folder()
```

count_trailing_spaces *Count the number of spaces before the first character*

Description

Count the number of spaces before the first character

Usage

```
count_trailing_spaces(line)
```

Arguments

line	line of text
------	--------------

Value

the number of spaces before the first character

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# 0
count_trailing_spaces("x")
# 1
count_trailing_spaces(" y")
# 2
count_trailing_spaces(" <")
# 0
count_trailing_spaces("")
# 1
count_trailing_spaces(" ")
# 2
count_trailing_spaces("  ")

check_empty_beautier_folder()
```

create_alpha_param	Create a parameter called alpha
--------------------	---------------------------------

Description

Create a parameter called alpha

Usage

```
create_alpha_param(id = NA, value = 0)
```

Arguments

id	the parameter's ID
value	value of the parameter

Value

a parameter called alpha

Note

this parameter is used in a beta distribution (as returned by [create_beta_distr](#)) and gamma distribution (as returned by [create_gamma_distr](#)) and inverse-gamma distribution (as returned by [create_inv_gamma_distr](#)). It cannot be estimated (as a hyper parameter) yet.

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_param](#) contains a list of all parameters that can be created

Examples

```
if (is_on_ci()) {  
  
  # Create the parameter  
  alpha_param <- create_alpha_param()  
  
  # Use the parameter in a distribution  
  beta_distr <- create_beta_distr(  
    alpha = alpha_param  
  )  
  
  # Use the distribution to create a BEAST2 input file  
  beast2_input_file <- get_beautier_tempfilename()  
  create_beast2_input_file(  
    beast2_input_file,  
    beta_distr,  
    alpha_param  
  )  
}
```



```
    input_filename = get_fasta_filename(),
    beast2_input_file,
    tree_prior = create_yule_tree_prior(
        birth_rate_distr = beta_distr
    )
)
file.remove(beast2_input_file)

remove_beautier_folder()
}
```

create_bd_tree_prior *Create a Birth-Death tree prior*

Description

Create a Birth-Death tree prior

Usage

```
create_bd_tree_prior(
  id = NA,
  birth_rate_distr = create_uniform_distr(),
  death_rate_distr = create_uniform_distr()
)
```

Arguments

id	the ID of the alignment
birth_rate_distr	the birth rate distribution, as created by a create_distr function
death_rate_distr	the death rate distribution, as created by a create_distr function

Value

a Birth-Death tree_prior

Author(s)

Richèl J.C. Bilderbeek

See Also

An alignment ID can be extracted from its FASTA filename using [get_alignment_id](#)

Examples

```

if (is_on_ci()) {

  bd_tree_prior <- create_bd_tree_prior()

  beast2_input_file <- get_beautier_tempfilename()
  create_beast2_input_file(
    input_filename = get_fasta_filename(),
    beast2_input_file,
    tree_prior = bd_tree_prior
  )
  file.remove(beast2_input_file)

  remove_beautier_folder()
}

```

```
create_beast2_beast_xml
```

Create the <beast ...> XML

Description

The <beast ...> XML is the XML at the start of a BEAST2 XML input file, directly after the general XML declaration (as created by [create_xml_declaration](#)).

Usage

```
create_beast2_beast_xml(beauti_options)
```

Arguments

beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

the XML

Author(s)

Richèl J.C. Bilderbeek

Examples

```

remove_beautier_folder()

create_beast2_beast_xml(
  beauti_options = create_beauti_options_v2_6()
)

check_empty_beautier_folder()

```

create_beast2_input	Create a BEAST2 XML input text
---------------------	--------------------------------

Description

Create a BEAST2 XML input text

Usage

```
create_beast2_input(
  input_filename,
  tipdates_filename = NA,
  site_model = create_jc69_site_model(),
  clock_model = create_strict_clock_model(),
  tree_prior = create_yule_tree_prior(),
  mrca_prior = NA,
  mcmc = create_mcmc(),
  beauti_options = create_beauti_options()
)
```

Arguments

input_filename	A FASTA filename. Use get_fasta_filename to obtain a testing FASTA filename.
tipdates_filename	name of the file containing the tip dates. This file is assumed to have two columns, separated by a tab. The first column contains the taxa names, the second column contains the date.
site_model	a site model, as returned by create_site_model
clock_model	a clock model, as returned by create_clock_model
tree_prior	a tree priors, as returned by create_tree_prior
mrca_prior	a Most Recent Common Ancestor prior, as returned by create_mrca_prior
mcmc	one MCMC. Use create_mcmc to create an MCMC. Use create_ns_mcmc to create an MCMC for a Nested Sampling run. Use check_mcmc to check if an MCMC is valid. Use rename_mcmc_filenames to rename the filenames in an MCMC.
beauti_options	one BEAUti options object, as returned by create_beauti_options

Value

a character vector of XML strings

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_beast2_input_from_model](#) to create the BEAST2 XML input text from an inference model. Use [create_beast2_input_file](#) to also save it to file.

[create_beast2_input_file](#) shows more examples

Examples

```
if (is_on_ci()) {
  create_beast2_input(
    input_filename = get_fasta_filename()
  )
}
```

```
create_beast2_input_beast
```

Creates the XML text for the beast tag of a BEAST2 parameter file.

Description

Creates the XML text for the beast tag of a BEAST2 parameter file, which is directly after the XML declaration (created by [create_xml_declaration](#)).

Usage

```
create_beast2_input_beast(
  input_filename,
  inference_model = create_inference_model()
)
```

Arguments

input_filename A FASTA filename. Use [get_fasta_filename](#) to obtain a testing FASTA filename.

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Details

The beast tag has these elements:

```
<beast[...]>
  <data
  [...]
  </data>
  [map names]
  <run[...]>
  [...]
  </run>
</beast>
```

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_beast2_input_from_model](#) to create the complete XML text. Use [create_beast2_input_data](#) to create the XML text for the data tag only. Use [create_beast2_input_map](#) to create the XML text for the [map names] part. Use [create_beast2_input_run](#) to create the XML text for the run tag only.

create_beast2_input_data

Creates the data section of a BEAST2 XML parameter file

Description

Creates the data section of a BEAST2 XML parameter file

Usage

```
create_beast2_input_data(
  input_filename,
  beaوتي_options = create_beaوتي_options()
)
```

Arguments

input_filename A FASTA filename. Use [get_fasta_filename](#) to obtain a testing FASTA filename.

beaوتي_options one BEAUi options object, as returned by [create_beaوتي_options](#)

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

create_beast2_input_data(
  input_filename = get_fasta_filename(),
  beauti_options = create_beauti_options_v2_4()
)

check_empty_beautier_folder()
```

```
create_beast2_input_data_sequences
```

Creates the data section of a BEAST2 XML parameter file

Description

Creates the data section of a BEAST2 XML parameter file

Usage

```
create_beast2_input_data_sequences(
  input_fasta_filename,
  beauti_options = create_beauti_options()
)
```

Arguments

`input_fasta_filename` one FASTA filename

`beauti_options` one BEAUti options object, as returned by [create_beauti_options](#)

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

`create_beast2_input_distr`*Creates the distribution section of a BEAST2 XML parameter file.*

Description

Creates the distribution section of a BEAST2 XML parameter file.

Usage

```
create_beast2_input_distr(inference_model)
```

Arguments

`inference_model`

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

lines of XML text

Note

this function is not intended for regular use, thus its long name length is accepted

Author(s)

Richèl J.C. Bilderbeek

See Also

[create_beast2_input](#)

Examples

```
check_empty_beautier_folder()

inference_model <- init_inference_model(
  input_filename = get_fasta_filename(),
  inference_model = create_inference_model(
    beauti_options = create_beauti_options_v2_4()
  )
)
create_beast2_input_distr(
  inference_model = inference_model
```

```

)
# <distribution id="posterior" spec="util.CompoundDistribution">
#   <distribution id="prior" spec="util.CompoundDistribution">
#     HERE, where the ID of the distribution is 'prior'
#   </distribution>
#   <distribution id="likelihood" ...>
#   </distribution>
# </distribution>

check_empty_beautier_folder()

```

```
create_beast2_input_distr_lh
```

Creates the XML text for the distribution tag with the likelihood ID, of a BEAST2 parameter file.

Description

Creates the XML text for the distribution tag with the likelihood ID, of a BEAST2 parameter file, in an unindented form

Usage

```
create_beast2_input_distr_lh(inference_model)
```

Arguments

`inference_model`

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Details

The distribution tag (with ID equals likelihood) has these elements:

```

<distribution id="likelihood" [...]>
  <distribution id="treeLikelihood" [...]>
    [...]
  </distribution>
</distribution>

```

The distribution section with ID `treeLikelihood` is created by [create_tree_likelihood_distr_xml](#).

Zooming out:


```
<beast[...]>
  <run[...]>
    <distribution id="posterior"[...]>
      <distribution id="likelihood"[...]>
        [this section]
      </distribution>
    </distribution>
  </run>
</beast>
```

Value

lines of XML text

Note

this function is not intended for regular use, thus its long name length is accepted

Author(s)

Richèl J.C. Bilderbeek

See Also

this function is called by create_beast2_input_distr, together with create_beast2_input_distr_prior

create_beast2_input_distr_prior

Creates the prior section in the distribution section of a BEAST2 XML parameter file

Description

Creates the prior section in the distribution section of a BEAST2 XML parameter file

Usage

```
create_beast2_input_distr_prior(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

lines of XML text

Note

this function is not intended for regular use, thus its long name length is accepted

Author(s)

Richèl J.C. Bilderbeek

See Also

this function is called by create_beast2_input_distr, together with create_beast2_input_distr_lh

Examples

```
check_empty_beautier_folder()

# <distribution id="posterior" spec="util.CompoundDistribution">
#   <distribution id="prior" spec="util.CompoundDistribution">
#     HERE, where the ID of the distribution is 'prior'
#   </distribution>
#   <distribution id="likelihood" ...>
#     </distribution>
# </distribution>

check_empty_beautier_folder()
```

create_beast2_input_file

Create a BEAST2 input file

Description

Create a BEAST2 input file

Usage

```
create_beast2_input_file(
  input_filename,
  output_filename,
  site_model = create_jc69_site_model(),
  clock_model = create_strict_clock_model(),
  tree_prior = create_yule_tree_prior(),
  mrca_prior = NA,
  mcmc = create_mcmc(),
  beauti_options = create_beauti_options(),
  tipdates_filename = NA
)
```

Arguments

input_filename	A FASTA filename. Use get_fasta_filename to obtain a testing FASTA filename.
output_filename	Name of the XML parameter file created by this function. BEAST2 uses this file as input.
site_model	a site model, as returned by create_site_model
clock_model	a clock model, as returned by create_clock_model
tree_prior	a tree priors, as returned by create_tree_prior
mrca_prior	a Most Recent Common Ancestor prior, as returned by create_mrca_prior
mcmc	one MCMC. Use create_mcmc to create an MCMC. Use create_ns_mcmc to create an MCMC for a Nested Sampling run. Use check_mcmc to check if an MCMC is valid. Use rename_mcmc_filenames to rename the filenames in an MCMC.
beauti_options	one BEAUti options object, as returned by create_beauti_options
tipdates_filename	name of the file containing the tip dates. This file is assumed to have two columns, separated by a tab. The first column contains the taxa names, the second column contains the date.

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_beast2_input_file_from_model](#) to do the same with an inference model. See [create_site_model](#) for examples with different site models. See [create_clock_model](#) for examples with clock models. See [create_tree_prior](#) for examples with different tree priors. See [create_mcmc](#) for examples with a different MCMC setup.

Examples

```
if (is_on_ci()) {

  check_empty_beautier_folder()

  # Get an example FASTA file
  input_filename <- get_fasta_filename()

  # The file created by beautier, a BEAST2 input file
  output_filename <- get_beautier_tempfilename()

  create_beast2_input_file(
```

```

        input_filename,
        output_filename
    )
    file.remove(output_filename)

    remove_beautier_folder()
    check_empty_beautier_folder()
}

```

```
create_beast2_input_file_from_model
```

Create a BEAST2 input file from an inference model

Description

Create a BEAST2 input file from an inference model

Usage

```

create_beast2_input_file_from_model(
  input_filename,
  output_filename,
  inference_model = create_inference_model()
)

```

Arguments

input_filename	A FASTA filename. Use get_fasta_filename to obtain a testing FASTA filename.
output_filename	Name of the XML parameter file created by this function. BEAST2 uses this file as input.
inference_model	a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use create_inference_model to create an inference model. Use check_inference_model to check if an inference model is valid. Use rename_inference_model_filenames to rename the files in an inference model.

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

See Also

use [create_beast2_input_from_model](#) to get the BEAST2 input file as text

See [create_site_model](#) for examples with different site models. See [create_clock_model](#) for examples with clock models. See [create_tree_prior](#) for examples with different tree priors. See [create_mcmc](#) for examples with a different MCMC setup. Use [create_beast2_input_file](#) to do the same with the elements of an inference model.

Examples

```
if (is_on_ci()) {
  check_empty_beautier_folder()

  output_filename <- get_beautier_tempfilename()
  create_beast2_input_file_from_model(
    input_filename = get_fasta_filename(),
    output_filename = output_filename,
    inference_model = create_inference_model()
  )
  file.remove(output_filename)

  remove_beautier_folder()
  check_empty_beautier_folder()
}
```

```
create_beast2_input_from_model
```

Create a BEAST2 XML input text from an inference model

Description

The main two XML tags are these:

```
<?xml[...]?><beast[...]>
[...]
</beast>
```

Usage

```
create_beast2_input_from_model(input_filename, inference_model)
```

Arguments

input_filename A FASTA filename. Use [get_fasta_filename](#) to obtain a testing FASTA filename.

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

a character vector of XML strings

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_beast2_input_file_from_model](#) to also save it to file. Use [create_xml_declaration](#) to create the XML text of the XML declaration. Use [create_beast2_input_beast](#) to create the XML text of the beast tag.

Examples

```
if (is_on_ci()) {

  check_empty_beautier_folder()

  text <- create_beast2_input_from_model(
    input_filename = get_fasta_filename(),
    inference_model = create_inference_model()
  )

  check_empty_beautier_folder()
}
```

```
create_beast2_input_init
```

Creates the init section of a BEAST2 XML parameter file

Description

Creates the init section of a BEAST2 XML parameter file

Usage

```
create_beast2_input_init(inference_model)
```

Arguments

`inference_model`

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

inference_model <- init_inference_model(
  input_filename = get_fasta_filename(),
  inference_model = create_test_inference_model()
)
xml <- create_beast2_input_init(
  inference_model = inference_model
)

check_empty_beautier_folder()
```

```
create_beast2_input_map
```

Creates the map section of a BEAST2 XML parameter file

Description

Creates the map section of a BEAST2 XML parameter file

Usage

```
create_beast2_input_map(beauti_options)
```

Arguments

beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

```
create_beast2_input_operators
```

Creates the operators section of a BEAST2 XML parameter file

Description

Creates the operators section of a BEAST2 XML parameter file

Usage

```
create_beast2_input_operators(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

```
create_beast2_input_run
```

Creates the 'run' section of a BEAST2 XML parameter file

Description

Creates the 'run' section of a BEAST2 XML parameter file, without being indented.

Usage

```
create_beast2_input_run(
  input_filename,
  inference_model = create_inference_model()
)
```


Arguments

- `input_filename` A FASTA filename. Use [get_fasta_filename](#) to obtain a testing FASTA filename.
- `inference_model` a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Details

The run tag has these elements:

```
<run[...]>
  <state[...]>
  [...]
</state>
  <init[...]>
  [...]
</init>
  <distribution[...]>
  [...]
</distribution>
  [operator ids]
  [loggers]
</run>
```

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_beast2_input_state](#) to create the XML text of the state tag. Use [create_beast2_input_init](#) to create the XML text of the init tag. Use [create_beast2_input_distr](#) to create the XML text of the distribution tag. Use [create_beast2_input_operators](#) to create the XML text of the [operator ids] section. Use [create_loggers_xml](#) to create the XML text of the [loggers] part.

`create_beast2_input_state`*Creates the 'state' section of a BEAST2 XML parameter file*

Description

Creates the 'state' section of a BEAST2 XML parameter file, without being indented.

Usage

```
create_beast2_input_state(inference_model)
```

Arguments

`inference_model`

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Details

The state tag has these elements:

```
<state[...]>
  <tree[...]>
  [...]
</tree>
  [parameters]
</run>
```

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_beast2_input_state](#) to create the XML text of the tree tag. to create the XML text of the [parameters] section.

```
create_beautier_tempfolder
```

Create the default 'beautier' temporary folder

Description

Create the default 'beautier' temporary folder

Usage

```
create_beautier_tempfolder()
```

Value

nothing

Author(s)

Richèl J.C. Bilderbeek

Examples

```
create_beautier_tempfolder()

remove_beautier_folder()

check_empty_beautier_folder()
```

```
create_beauti_options
```

Function to create a set of 'BEAUi' options.

Description

'BEAUi' options are settings that differ between 'BEAUi' version. The use of these options is mostly for testing older versions. Whatever option chosen here, the created XML file will be valid.

Usage

```
create_beauti_options(
  capitalize_first_char_id = FALSE,
  nucleotides_uppercase = FALSE,
  beast2_version = "2.4",
  required = "",
  sequence_indent = 20,
  status = "",
  namespace = get_default_beast_namespace_v2_4()
)
```

Arguments

capitalize_first_char_id	must the ID of alignment start with a capital? TRUE if yes, FALSE if it can be left lower case (if it is lowercase)
nucleotides_uppercase	must the nucleotides of the DNA sequence be in uppercase?
beast2_version	the BEAST2 version
required	things that may be required, for example BEAST v2.5.0
sequence_indent	the number of spaces the XML sequence lines are indented
status	the BEAUti status
namespace	the 'namespace' XML element in the 'beast' XML tag.

Details

Available BEAUti options are:

* [create_beauti_options_v2_4](#) * [create_beauti_options_v2_6](#)

'beautier' uses v2.4 by default, as this is when the first tests were written.

Value

a BEAUti options structure

Author(s)

Richèl J.C. Bilderbeek

Examples

```
if (is_on_ci()) {

  check_empty_beautier_folder()

  beauti_options <- create_beauti_options_v2_4()
  xml <- create_beast2_input(
    get_fasta_filename(),
    beauti_options = beauti_options
  )

  check_empty_beautier_folder()
}
```

`create_beauti_options_v2_4`*Function to create the BEAUti options for version 2.4.*

Description

Function to create the BEAUti options for version 2.4, by calling [create_beauti_options](#).

Usage

```
create_beauti_options_v2_4()
```

Value

a BEAUti options structure

Author(s)

Richèl J.C. Bilderbeek

Examples

```
if (is_on_ci()) {  
  check_empty_beautier_folder()  
  
  beauti_options <- create_beauti_options_v2_4()  
  xml <- create_beast2_input(  
    get_fasta_filename(),  
    beauti_options = beauti_options  
  )  
  
  check_empty_beautier_folder()  
}
```

`create_beauti_options_v2_6`*Function to create the BEAUti options for version 2.6.*

Description

Function to create the BEAUti options for version 2.6, by calling [create_beauti_options](#).

Usage

```
create_beauti_options_v2_6(
  beast2_version = "2.6",
  sequence_indent = 8,
  nucleotides_uppercase = FALSE,
  status = "",
  namespace = get_default_beast_namespace_v2_6(),
  required = ""
)
```

Arguments

beast2_version	the BEAST2 version
sequence_indent	the number of spaces the XML sequence lines are indented
nucleotides_uppercase	must the nucleotides of the DNA sequence be in uppercase?
status	the BEAUti status
namespace	the 'namespace' XML element in the 'beast' XML tag.
required	things that may be required, for example BEAST v2.5.0

Value

a BEAUti options structure

Author(s)

Richèl J.C. Bilderbeek

See Also

see [create_beauti_options_v2_4](#) for using the older v2.4

Examples

```
if (is_on_ci()) {
  check_empty_beautier_folder()

  beauti_options <- create_beauti_options_v2_6()
  xml <- create_beast2_input(
    get_fasta_filename(),
    beauti_options = beauti_options
  )

  check_empty_beautier_folder()
}
```

create_beta_distr	Create a beta distribution
-------------------	----------------------------

Description

Create a beta distribution

Usage

```
create_beta_distr(  
  id = NA,  
  alpha = 0,  
  beta = 1,  
  value = NA,  
  lower = NA,  
  upper = NA  
)
```

Arguments

id	the distribution's ID
alpha	the alpha shape parameter, a numeric value. The value of alpha must be at least 0.0. For advanced usage, use the structure as returned by create_alpha_param .
beta	the beta shape parameter, a numeric value. The value of beta must be at least 1.0. For advanced usage, use the structure as returned by create_beta_param .
value	the initial value for the MCMC
lower	the lower bound, the lowest possible value
upper	an upper limit of the uniform distribution. If the upper limits needs to be infinity, set upper to Inf.

Value

a beta distribution

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_distr](#) shows an overview of all supported distributions

Examples

```

if (is_on_ci()) {

  beta_distr <- create_beta_distr()

  beast2_input_file <- get_beautier_tempfilename()
  create_beast2_input_file(
    input_filename = get_fasta_filename(),
    beast2_input_file,
    tree_prior = create_yule_tree_prior(
      birth_rate_distr = beta_distr
    )
  )
  file.remove(beast2_input_file)

  remove_beautier_folder()
}

```

create_beta_param	<i>Create a parameter called beta</i>
-------------------	---------------------------------------

Description

Create a parameter called beta

Usage

```
create_beta_param(id = NA, value = 1)
```

Arguments

id	the parameter's ID
value	value of the parameter

Value

a parameter called beta

Note

this parameter is used in a beta distribution (as returned by [create_beta_distr](#)) and gamma distribution (as returned by [create_gamma_distr](#)) and inverse-gamma distribution (as returned by [create_inv_gamma_distr](#)). It cannot be estimated (as a hyper parameter) yet.

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_param](#) contains a list of all parameters that can be created

Examples

```
if (is_on_ci()) {  
  
  # Create the parameter  
  beta_param <- create_beta_param()  
  
  # Use the parameter in a distribution  
  gamma_distr <- create_gamma_distr(  
    beta = beta_param  
  )  
  
  # Use the distribution to create a BEAST2 input file  
  beast2_input_file <- get_beautier_tempfilename()  
  create_beast2_input_file(  
    input_filename = get_fasta_filename(),  
    beast2_input_file,  
    tree_prior = create_yule_tree_prior(  
      birth_rate_distr = gamma_distr  
    )  
  )  
  file.remove(beast2_input_file)  
  
  remove_beautier_folder()  
}
```

create_branch_rate_model_xml

Internal function to create the branchRateModel section of the XML as text.

Description

Creates the branchRateModel section of the XML as text.

Usage

```
create_branch_rate_model_xml(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Details

The distribution tag (with ID equals treeLikelihood) has these elements:

```
<branchRateModel[...]>
  [...]
</branchRateModel>
```

When there is a strict clock, [create_strict_clock_branch_rate_model_xml](#) is called. When there is an RLN clock, [create_rln_clock_branch_rate_model_xml](#) is called.

Zooming out:

```
<beast[...]>
  <run[...]>
    <distribution id="posterior"[...]>
      <distribution id="likelihood"[...]>
        <distribution id="treeLikelihood"[...]>
          [...]

          [this section]
        </distribution>
      </distribution>
    </distribution>
  </run>
</beast>
```

Value

a character vector of XML strings

Author(s)

Richèl J.C. Bilderbeek

create_b_pop_sizes_param

Create a parameter called 'b_pop_sizes'.

Description

Create a parameter called 'b_pop_sizes'.

Usage

```
create_b_pop_sizes_param(id = NA, value = 1, upper = "380000.0")
```

Arguments

id	the parameter's ID
value	value of the parameter
upper	upper value of the parameter

Value

a parameter called b_pop_sizes

Note

this parameter is used in a CBS model, as created by [create_cbs_tree_prior](#)

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_param](#) contains a list of all parameters that can be created

Examples

```
# Create the parameter
b_pop_sizes_param <- create_b_pop_sizes_param()
```

`create_cbs_tree_prior` *Create a Coalescent Bayesian Skyline tree prior*

Description

Create a Coalescent Bayesian Skyline tree prior

Usage

```
create_cbs_tree_prior(
  id = NA,
  group_sizes_dimension = 5,
  b_pop_sizes_param = create_b_pop_sizes_param(),
  pop_sizes_scaler_scale_factor = ""
)
```

Arguments

- `id` an alignment's IDs. An ID can be extracted from its FASTA filename with [get_alignment_ids_from_fasta_filenames](#))
- `group_sizes_dimension` the group sizes' dimension, as used by the CBS tree prior (see [create_cbs_tree_prior](#))
- `b_pop_sizes_param` a Bayesian population size parameter, as created by [create_b_pop_sizes_param](#)
- `pop_sizes_scaler_scale_factor` the scale factor used by the population sizes scaler operator

Value

a Coalescent Bayesian Skyline tree_prior

Author(s)

Richèl J.C. Bilderbeek

See Also

An alignment ID can be extracted from its FASTA filename using [get_alignment_id](#)

Examples

```
if (is_on_ci()) {

  cbs_tree_prior <- create_cbs_tree_prior()

  beast2_input_file <- get_beautier_tempfilename()
  create_beast2_input_file(
    input_filename = get_beautier_path("test_output_6.fas"),
    beast2_input_file,
    tree_prior = cbs_tree_prior
  )
  file.remove(beast2_input_file)

  remove_beautier_folder()
}
```

`create_ccp_tree_prior` *Create a Coalescent Constant Population tree prior*

Description

Create a Coalescent Constant Population tree prior

Usage

```
create_ccp_tree_prior(  
  id = NA,  
  pop_size_distr = create_one_div_x_distr(value = 0.3)  
)
```

Arguments

`id` the ID of the alignment

`pop_size_distr` the population distribution, as created by a [create_distr](#) function

Value

a Coalescent Constant Population tree_prior

Author(s)

Richèl J.C. Bilderbeek

See Also

An alignment ID can be extracted from its FASTA filename using [get_alignment_id](#)

Examples

```
if (is_on_ci()) {  
  
  ccp_tree_prior <- create_ccp_tree_prior()  
  
  beast2_input_file <- get_beautier_tempfilename()  
  create_beast2_input_file(  
    input_filename = get_fasta_filename(),  
    beast2_input_file,  
    tree_prior = ccp_tree_prior  
  )  
  file.remove(beast2_input_file)  
  
  remove_beautier_folder()  
}
```

`create_cep_tree_prior` *Create a Coalescent Exponential Population tree prior*

Description

Create a Coalescent Exponential Population tree prior

Usage

```
create_cep_tree_prior(  
  id = NA,  
  pop_size_distr = create_one_div_x_distr(),  
  growth_rate_distr = create_laplace_distr()  
)
```

Arguments

`id` the ID of the alignment

`pop_size_distr` the population distribution, as created by a [create_distr](#) function

`growth_rate_distr` the growth rate distribution, as created by a [create_distr](#) function

Value

a Coalescent Exponential Population tree_prior

Author(s)

Richèl J.C. Bilderbeek

See Also

An alignment ID can be extracted from its FASTA filename using [get_alignment_id](#)

Examples

```
if (is_on_ci()) {  
  
  cep_tree_prior <- create_cep_tree_prior()  
  
  beast2_input_file <- get_beautier_tempfilename()  
  create_beast2_input_file(  
    input_filename = get_fasta_filename(),  
    beast2_input_file,  
    tree_prior = cep_tree_prior  
  )  
  file.remove(beast2_input_file)  
  
  remove_beautier_folder()  
}
```

create_clock_model	<i>General function to create a clock model</i>
--------------------	---

Description

General function to create a clock model

Usage

```
create_clock_model(name, id, ...)
```

Arguments

name	the clock model name. Valid names can be found in <code>get_clock_model_names</code>
id	a clock model's ID
...	specific clock model parameters

Value

a valid clock model

Note

Prefer using the named function [create_rln_clock_model](#) and [create_strict_clock_model](#)

Author(s)

Richèl J.C. Bilderbeek

See Also

An alignment ID can be extracted from its FASTA filename using [get_alignment_id](#). For more examples about creating a relaxed log-normal clock model, see [create_rln_clock_model](#). For more examples about creating a strict clock model, see [create_strict_clock_model](#).

Examples

```
if (is_on_ci()) {  
  # Can use any of these models  
  strict_clock_model <- create_strict_clock_model()  
  rln_clock_model <- create_rln_clock_model()  
  
  beast2_input_file <- get_beautier_tempfilename()  
  create_beast2_input_file(  
    get_fasta_filename(),  
    beast2_input_file,  
    clock_model = strict_clock_model  
  )  
}
```

```
file.remove(beast2_input_file)

remove_beautier_folder()
}
```

create_clock_models	<i>Creates all supported clock models, which is a list of the types returned by create_rln_clock_model, and create_strict_clock_model</i>
---------------------	---

Description

Creates all supported clock models, which is a list of the types returned by [create_rln_clock_model](#), and [create_strict_clock_model](#)

Usage

```
create_clock_models()
```

Value

a list of site_models

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_clock_model](#) to create a clock model

Examples

```
check_empty_beautier_folder()

clock_models <- create_clock_models()
is_rln_clock_model(clock_models[[1]])
is_strict_clock_model(clock_models[[2]])

check_empty_beautier_folder()
```

`create_clock_models_from_names`*Create clock models from their names*

Description

Create clock models from their names

Usage

```
create_clock_models_from_names(clock_model_names)
```

Arguments

`clock_model_names`

one or more names of a clock model, must be name among those returned by [get_clock_model_names](#)

Value

a list of one or more clock models

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_clock_models](#) to get all clock models

Examples

```
check_empty_beautier_folder()
```

```
create_clock_models_from_names(get_clock_model_names())
```

```
check_empty_beautier_folder()
```

`create_clock_model_from_name`*Create a clock model from name*

Description

Create a clock model from name

Usage

```
create_clock_model_from_name(clock_model_name)
```

Arguments

`clock_model_name`

name of a clock model, must be a name as returned by [get_clock_model_names](#)

Value

a clock model, as can be created by [create_clock_model](#)

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_clock_model](#) to create a clock model

Examples

```
check_empty_beautier_folder()
```

```
create_clock_model_from_name(get_clock_model_names()[1])
```

```
check_empty_beautier_folder()
```

`create_clock_rate_param`*Create a parameter called clock_rate, as needed by
[create_strict_clock_model](#)*

Description

Create a parameter called clock_rate, as needed by [create_strict_clock_model](#)

Usage

```
create_clock_rate_param(value = "1.0", estimate = FALSE, id = NA)
```

Arguments

value	value of the parameter
estimate	TRUE if this parameter is to be estimated by BEAST2, FALSE otherwise
id	the parameter's ID

Value

a parameter called rate

Note

It cannot be estimated (as a hyper parameter) yet.

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_param](#) contains a list of all parameters that can be created

Examples

```
if (is_on_ci()) {  
  
  clock_rate_param <- create_clock_rate_param(  
    id = "anthus_aco", value = 1.0  
  )  
  
  # Use the parameter in a clock model  
  strict_clock_model <- create_strict_clock_model(  
    clock_rate_param = clock_rate_param  
  )  
}
```

```

# Use the distribution to create a BEAST2 input file
beast2_input_file <- get_beautier_tempfilename()
create_beast2_input_file(
  input_filename = get_fasta_filename(),
  beast2_input_file,
  clock_model = strict_clock_model
)
file.remove(beast2_input_file)

remove_beautier_folder()
}

```

```
create_clock_rate_state_node_parameter_xml
```

Internal function

Description

Creates the clockRate parameter with the name stateNode, such as: `<parameter id="ucldStdev.c:[id]" [...] name="stateNode">0.1</parameter>`

Usage

```
create_clock_rate_state_node_parameter_xml(inference_model)
```

Arguments

`inference_model`

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

the following XML: `<parameter id="ucldStdev.c:[id]" lower="0.0" name="stateNode"> 0.1 </parameter>`

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

create_ucld_stdev_state_node_param_xml(
  create_inference_model(
    clock_model = create_rln_clock_model(id = 314)
  )
)

check_empty_beautier_folder()
```

create_data_xml	Create the <data ..> XML
-----------------	--------------------------

Description

Create the <data ..> XML

Usage

```
create_data_xml(id, beast2_version)
```

Arguments

id an alignment's IDs. An ID can be extracted from its FASTA filename with [get_alignment_ids_from_fasta_filenames](#))

beast2_version BEAST2 version, for example, "2.5"

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

create_distr	<i>General function to create a distribution.</i>
--------------	---

Description

General function to create a distribution.

Usage

```
create_distr(name, id, value = NA, lower = NA, upper = NA, ...)
```

Arguments

name	the distribution name. Valid names can be found in <code>get_distr_names</code>
id	the distribution's ID
value	the initial value for the MCMC
lower	the lower bound, the lowest possible value
upper	an upper limit of the uniform distribution. If the upper limits needs to be infinity, set upper to Inf.
...	specific distribution parameters

Value

a distribution

Note

Prefer using the named functions `create_beta_distr`, `create_exp_distr`, `create_gamma_distr`, `create_inv_gamma_distr`, `create_laplace_distr`, `create_log_normal_distr`, `create_normal_distr`, `create_one_div_x_distr`, `create_poisson_distr` and `create_uniform_distr`

See `create_beta_distr`, `create_exp_distr`, `create_gamma_distr`, `create_inv_gamma_distr`, `create_laplace_distr`, `create_log_normal_distr`, `create_normal_distr`, `create_one_div_x_distr`, `create_poisson_distr` and `create_uniform_distr` for examples how to use those distributions

Author(s)

Richèl J.C. Bilderbeek

Examples

```
if (is_on_ci()) {

  # Use any distribution
  distr <- create_beta_distr()

  beast2_input_file <- get_beautier_tempfilename()
```

```
create_beast2_input_file(  
  input_filename = get_fasta_filename(),  
  beast2_input_file,  
  tree_prior = create_yule_tree_prior(  
    birth_rate_distr = distr  
  )  
)  
file.remove(beast2_input_file)  
  
remove_beautier_folder()  
}
```

create_exp_distr	Create an exponential distribution
------------------	------------------------------------

Description

Create an exponential distribution

Usage

```
create_exp_distr(id = NA, mean = 1, value = NA, lower = NA, upper = NA)
```

Arguments

id	the distribution's ID
mean	the mean parameter, a numeric value. For advanced usage, use the structure as returned by create_mean_param
value	the initial value for the MCMC
lower	the lower bound, the lowest possible value
upper	an upper limit of the uniform distribution. If the upper limits needs to be infinity, set upper to Inf.

Value

an exponential distribution

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_distr](#) shows an overview of all supported distributions

Examples

```

if (is_on_ci()) {

  exp_distr <- create_exp_distr()

  beast2_input_file <- get_beautier_tempfilename()
  create_beast2_input_file(
    input_filename = get_fasta_filename(),
    beast2_input_file,
    tree_prior = create_yule_tree_prior(
      birth_rate_distr = exp_distr
    )
  )
  file.remove(beast2_input_file)

  remove_beautier_folder()
}

```

create_freq_param	<i>Create a parameter called freq</i>
-------------------	---------------------------------------

Description

Create a parameter called freq

Usage

```

create_freq_param(
  id = NA,
  lower = "0.0",
  upper = "1.0",
  value = "0.25",
  estimate = TRUE,
  dimension = 4
)

```

Arguments

id	the parameter's ID
lower	lowest possible value of the parameter. If the parameter is estimated, lower must be less than value
upper	upper value of the parameter
value	value of the parameter
estimate	TRUE if this parameter is to be estimated by BEAST2, FALSE otherwise
dimension	the number of dimensions, for example, as used in create_freq_param

Value

a parameter called freq

Author(s)

Richèl J.C. Bilderbeek

create_gamma_distr	Create a gamma distribution
--------------------	-----------------------------

Description

Create a gamma distribution

Usage

```
create_gamma_distr(  
  id = NA,  
  alpha = 0.5396,  
  beta = 0.3819,  
  value = NA,  
  lower = NA,  
  upper = NA  
)
```

Arguments

id	the distribution's ID
alpha	the alpha shape parameter, a numeric value. For advanced usage, use the structure as returned by create_alpha_param
beta	the beta shape parameter, a numeric value. For advanced usage, use the structure as returned by create_beta_param
value	the initial value for the MCMC
lower	the lower bound, the lowest possible value
upper	an upper limit of the uniform distribution. If the upper limits needs to be infinity, set upper to Inf.

Value

a gamma distribution

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_distr](#) shows an overview of all supported distributions

Examples

```
if (is_on_ci()) {  
  
  gamma_distr <- create_gamma_distr(  
    alpha = 0.05,  
    beta = 10.0  
  )  
  
  gtr_site_model <- create_gtr_site_model(  
    rate_ac_prior_distr = gamma_distr  
  )  
  
  beast2_input_file <- get_beautier_tempfilename()  
  create_beast2_input_file(  
    input_filename = get_fasta_filename(),  
    beast2_input_file,  
    site_model = gtr_site_model  
  )  
  file.remove(beast2_input_file)  
  
  remove_beautier_folder()  
}
```

create_gamma_site_model

Create a gamma site model, part of a site model

Description

Create a gamma site model, part of a site model

Usage

```
create_gamma_site_model(  
  gamma_cat_count = "0",  
  gamma_shape = "1.0",  
  prop_invariant = "0.0",  
  gamma_shape_prior_distr = NA,  
  freq_equilibrium = "estimated",  
  freq_prior_uniform_distr_id = 1000  
)
```

Arguments

- `gamma_cat_count` the number of gamma categories, must be an integer with value zero or more
- `gamma_shape` gamma curve shape parameter
- `prop_invariant` the proportion invariant, must be a value from 0.0 to 1.0
- `gamma_shape_prior_distr` the distribution of the gamma shape prior. `gamma_shape_prior_distr` must be NA for a `gamma_cat_count` of zero or one. For a `gamma_cat_count` of two or more, leaving `gamma_shape_prior_distr` equal to its default value of NA, a default distribution is used. Else `gamma_shape_prior_distr` must be a distribution, as can be created by [create_distr](#)
- `freq_equilibrium` the frequency in which the rates are at equilibrium are either estimated, empirical or all_equal. `get_freq_equilibrium_names` returns the possible values for `freq_equilibrium`
- `freq_prior_uniform_distr_id` the ID of the ‘FrequenciesPrior’'s uniform distribution

Value

a gamma site model

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_gamma_site_model](#) to create a gamma site model

Examples

```
if (is_on_ci()) {

  gamma_site_model <- create_gamma_site_model(prop_invariant = 0.5)

  site_model <- create_hky_site_model(gamma_site_model = gamma_site_model)

  beast2_input_file <- get_beautier_tempfilename()
  create_beast2_input_file(
    get_fasta_filename(),
    beast2_input_file,
    site_model = site_model
  )
  file.remove(beast2_input_file)

  remove_beautier_folder()
}
```

create_gtr_site_model *Create a GTR site model*

Description

Create a GTR site model

Usage

```
create_gtr_site_model(
  id = NA,
  gamma_site_model = create_gamma_site_model(),
  rate_ac_prior_distr = create_gamma_distr(alpha = 0.05, beta = create_beta_param(value =
    "10.0")),
  rate_ag_prior_distr = create_gamma_distr(alpha = 0.05, beta = create_beta_param(value =
    "20.0")),
  rate_at_prior_distr = create_gamma_distr(alpha = 0.05, beta = create_beta_param(value =
    "10.0")),
  rate_cg_prior_distr = create_gamma_distr(alpha = 0.05, beta = create_beta_param(value =
    "10.0")),
  rate_gt_prior_distr = create_gamma_distr(alpha = 0.05, beta = create_beta_param(value =
    "10.0")),
  rate_ac_param = create_rate_ac_param(),
  rate_ag_param = create_rate_ag_param(),
  rate_at_param = create_rate_at_param(),
  rate_cg_param = create_rate_cg_param(),
  rate_ct_param = create_rate_ct_param(),
  rate_gt_param = create_rate_gt_param(),
  freq_equilibrium = "estimated",
  freq_param = create_freq_param()
)
```

Arguments

id the IDs of the alignment (can be extracted from the FASTA filename using [get_alignment_id](#))

gamma_site_model a gamma site model, as created by [create_gamma_site_model](#)

rate_ac_prior_distr the AC rate prior distribution, as returned by [create_distr](#)

rate_ag_prior_distr the AG rate prior distribution, as returned by [create_distr](#)

rate_at_prior_distr the AT rate prior distribution, as returned by [create_distr](#)

rate_cg_prior_distr the CG rate prior distribution, as returned by [create_distr](#)

rate_gt_prior_distr	the GT rate prior distribution, as returned by create_distr
rate_ac_param	the 'rate AC' parameter, a numeric value. For advanced usage, use the structure as returned by create_rate_ac_param
rate_ag_param	the 'rate AG' parameter, a numeric value. For advanced usage, use the structure as returned by create_rate_ag_param
rate_at_param	the 'rate AT' parameter, a numeric value. For advanced usage, use the structure as returned by create_rate_at_param
rate_cg_param	the 'rate CG' parameter, a numeric value. For advanced usage, use the structure as returned by create_rate_cg_param
rate_ct_param	the 'rate CT' parameter, a numeric value. For advanced usage, use the structure as returned by create_rate_ct_param
rate_gt_param	the 'rate GT' parameter, a numeric value. For advanced usage, use the structure as returned by create_rate_gt_param
freq_equilibrium	the frequency in which the rates are at equilibrium are either estimated, empirical or all_equal. <code>get_freq_equilibrium_names</code> returns the possible values for <code>freq_equilibrium</code>
freq_param	a 'freq' parameter, as created by create_freq_param

Value

a GTR site_model

Author(s)

Richèl J.C. Bilderbeek

Examples

```
if (is_on_ci()) {

  gtr_site_model <- create_gtr_site_model(
    rate_ac_param = 1.2,
    rate_ag_param = 2.3,
    rate_at_param = 3.4,
    rate_cg_param = 4.5,
    rate_ct_param = 5.6,
    rate_gt_param = 6.7
  )

  beast2_input_file <- get_beautier_tempfilename()
  create_beast2_input_file(
    input_filename = get_fasta_filename(),
    beast2_input_file,
    site_model = gtr_site_model
  )
  file.remove(beast2_input_file)
```

```

    remove_beautier_folder()
}

```

```
create_gtr_subst_model_xml
```

Converts a GTR site model to XML, used in the substModel section

Description

Converts a GTR site model to XML, used in the substModel section

Usage

```
create_gtr_subst_model_xml(site_model)
```

Arguments

site_model a site model, as returned by [create_site_model](#)

Value

the site model as XML text

Author(s)

Richèl J.C. Bilderbeek

```
create_hky_site_model
```

Create an HKY site model

Description

Create an HKY site model

Usage

```

create_hky_site_model(
  id = NA,
  kappa = "obsolete",
  kappa_param = create_kappa_param(value = "2.0"),
  gamma_site_model = create_gamma_site_model(),
  kappa_prior_distr = create_log_normal_distr(m = create_m_param(value = "1.0"), s =
    1.25),
  freq_equilibrium = "estimated",
  freq_param = create_freq_param()
)

```

Arguments

id	the IDs of the alignment (can be extracted from the FASTA filename using get_alignment_id)
kappa	obsoleted parameter. It is the value in the ‘kappa_param’ argument
kappa_param	a ‘kappa’ parameter, as created by create_kappa_param
gamma_site_model	a gamma site model, as created by create_gamma_site_model
kappa_prior_distr	the distribution of the kappa prior, which is a log-normal distribution (as created by create_log_normal_distr) by default
freq_equilibrium	the frequency in which the rates are at equilibrium are either estimated, empirical or all_equal. get_freq_equilibrium_names returns the possible values for freq_equilibrium
freq_param	a ‘freq’ parameter, as created by create_freq_param

Value

an HKY site_model

Author(s)

Richèl J.C. Bilderbeek

Examples

```
if (is_on_ci()) {

  hky_site_model <- create_hky_site_model()
  output_filename <- get_beautier_tempfilename()
  create_beast2_input_file(
    input_filename = get_fasta_filename(),
    output_filename = output_filename,
    site_model = hky_site_model
  )
  file.remove(output_filename)

  remove_beautier_folder()
}
```

```
create_hky_subst_model_xml
```

Converts a site model to XML, used in the substModel section

Description

Converts a site model to XML, used in the substModel section

Usage

```
create_hky_subst_model_xml(site_model)
```

Arguments

site_model a site model, as returned by [create_site_model](#)

Value

the site model as XML text

Author(s)

Richèl J.C. Bilderbeek

```
create_inference_model
```

Create a Bayesian phylogenetic inference model.

Description

Create a Bayesian phylogenetic inference model, as can be done by BEAUti.

Usage

```
create_inference_model(
  site_model = create_jc69_site_model(),
  clock_model = create_strict_clock_model(),
  tree_prior = create_yule_tree_prior(),
  mrca_prior = NA,
  mcmc = create_mcmc(),
  beauti_options = create_beauti_options(),
  tipdates_filename = NA
)
```

Arguments

site_model a site model, as returned by [create_site_model](#)

clock_model a clock model, as returned by [create_clock_model](#)

tree_prior a tree priors, as returned by [create_tree_prior](#)

mrca_prior a Most Recent Common Ancestor prior, as returned by [create_mrca_prior](#)

mcmc one MCMC. Use [create_mcmc](#) to create an MCMC. Use [create_ns_mcmc](#) to create an MCMC for a Nested Sampling run. Use [check_mcmc](#) to check if an MCMC is valid. Use [rename_mcmc_filenames](#) to rename the filenames in an MCMC.

beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

tipdates_filename

name of the file containing the tip dates. This file is assumed to have two columns, separated by a tab. The first column contains the taxa names, the second column contains the date.

Value

an inference model

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_test_inference_model](#) to create an inference model with a short MCMC, to be used in testing. Use [create_ns_inference_model](#) to create an inference model to estimate the marginal likelihood (aka evidence) using a nested sampling approach.

Examples

```
if (is_on_ci()) {

  check_empty_beautier_folder()

  # Create an MCMC chain with 50 states
  inference_model <- create_inference_model(
    mcmc = create_mcmc(chain_length = 50000, store_every = 1000)
  )

  output_filename <- get_beautier_tempfilename()
  create_beast2_input_file_from_model(
    input_filename = get_fasta_filename(),
    output_filename = output_filename,
    inference_model = inference_model
  )
  file.remove(output_filename)

  remove_beautier_folder()
  check_empty_beautier_folder()
}
```

create_inv_gamma_distr

Create an inverse-gamma distribution

Description

Create an inverse-gamma distribution

Usage

```
create_inv_gamma_distr(
  id = NA,
  alpha = 0,
  beta = 1,
  value = NA,
  lower = NA,
  upper = NA
)
```

Arguments

id	the distribution's ID
alpha	the alpha shape parameter, a numeric value. For advanced usage, use the structure as returned by create_alpha_param
beta	the beta shape parameter, a numeric value. For advanced usage, use the structure as returned by create_beta_param
value	the initial value for the MCMC
lower	the lower bound, the lowest possible value
upper	an upper limit of the uniform distribution. If the upper limits needs to be infinity, set upper to Inf.

Value

an inverse-gamma distribution

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_distr](#) shows an overview of all supported distributions

Examples

```
if (is_on_ci()) {

  inv_gamma_distr <- create_inv_gamma_distr()

  beast2_input_file <- get_beautier_tempfilename()
  create_beast2_input_file(
    input_filename = get_fasta_filename(),
    beast2_input_file,
    tree_prior = create_yule_tree_prior(
      birth_rate_distr = inv_gamma_distr
    )
  )
  file.remove(beast2_input_file)
```

```
    remove_beautier_folder()
  }
```

```
create_jc69_site_model
```

Create a JC69 site model

Description

Create a JC69 site model

Usage

```
create_jc69_site_model(id = NA, gamma_site_model = create_gamma_site_model())
```

Arguments

id the IDs of the alignment (can be extracted from the FASTA filename using [get_alignment_id](#))

gamma_site_model a gamma site model, as created by [create_gamma_site_model](#)

Value

a JC69 site_model

Author(s)

Richèl J.C. Bilderbeek

Examples

```
if (is_on_ci()) {

  jc69_site_model <- create_jc69_site_model()

  output_filename <- get_beautier_tempfilename()
  create_beast2_input_file(
    input_filename = get_fasta_filename(),
    output_filename = output_filename,
    site_model = jc69_site_model
  )
  file.remove(output_filename)

  remove_beautier_folder()
}
```

create_jc69_subst_model_xml	<i>Converts a JC69 site model to XML, used in the substModel section</i>
-----------------------------	--

Description

Converts a JC69 site model to XML, used in the substModel section

Usage

create_jc69_subst_model_xml(site_model)

Arguments

site_model a site model, as returned by [create_site_model](#)

Value

the site model as XML text

Author(s)

Richèl J.C. Bilderbeek

create_kappa_1_param	<i>Create a parameter called kappa 1</i>
----------------------	--

Description

Create a parameter called kappa 1

Usage

create_kappa_1_param(id = NA, lower = "0.0", value = "2.0", estimate = TRUE)

Arguments

id	the parameter's ID
lower	lowest possible value of the parameter. If the parameter is estimated, lower must be less than value
value	value of the parameter
estimate	TRUE if this parameter is to be estimated by BEAST2, FALSE otherwise

Value

a parameter called kappa 1

Author(s)

Richèl J.C. Bilderbeek

create_kappa_2_param *Create a parameter called kappa 2*

Description

Create a parameter called kappa 2

Usage

```
create_kappa_2_param(id = NA, lower = "0.0", value = "2.0", estimate = TRUE)
```

Arguments

id	the parameter's ID
lower	lowest possible value of the parameter. If the parameter is estimated, lower must be less than value
value	value of the parameter
estimate	TRUE if this parameter is to be estimated by BEAST2, FALSE otherwise

Value

a parameter called kappa 2

Author(s)

Richèl J.C. Bilderbeek

create_kappa_param *Create a parameter called kappa*

Description

Create a parameter called kappa

Usage

```
create_kappa_param(id = NA, lower = "0.0", value = "2.0", estimate = TRUE)
```

Arguments

id	the parameter's ID
lower	lowest possible value of the parameter. If the parameter is estimated, lower must be less than value
value	value of the parameter
estimate	TRUE if this parameter is to be estimated by BEAST2, FALSE otherwise

Value

a parameter called kappa

Author(s)

Richèl J.C. Bilderbeek

create_lambda_param	<i>Create a parameter called lambda</i>
---------------------	---

Description

Create a parameter called lambda

Usage

```
create_lambda_param(id = NA, value = 0)
```

Arguments

id	the parameter's ID
value	value of the parameter

Value

a parameter called lambda

Note

this parameter is used in a Poisson distribution (as returned by [create_poisson_distr](#))

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_param](#) contains a list of all parameters that can be created

Examples

```
if (is_on_ci()) {  
  
  # Create the parameter  
  lambda_param <- create_lambda_param()  
  
  # Use the parameter in a distribution  
  poisson_distr <- create_poisson_distr(  
    lambda = lambda_param  
  )  
  
  # Use the distribution to create a BEAST2 input file  
  beast2_input_file <- get_beautier_tempfilename()  
  create_beast2_input_file(  
    input_filename = get_fasta_filename(),  
    beast2_input_file,  
    tree_prior = create_yule_tree_prior(  
      birth_rate_distr = poisson_distr  
    )  
  )  
  file.remove(beast2_input_file)  
  
  remove_beautier_folder()  
}
```

create_laplace_distr	Create a Laplace distribution
----------------------	-------------------------------

Description

Create a Laplace distribution

Usage

```
create_laplace_distr(  
  id = NA,  
  mu = 0,  
  scale = 1,  
  value = NA,  
  lower = NA,  
  upper = NA  
)
```

Arguments

id	the distribution's ID
mu	the mu parameter, a numeric value. For advanced usage, use the structure as returned by create_mu_param

scale	the scale parameter, a numeric value. For advanced usage, use the structure as returned by create_scale_param
value	the initial value for the MCMC
lower	the lower bound, the lowest possible value
upper	an upper limit of the uniform distribution. If the upper limits needs to be infinity, set upper to Inf.

Value

a Laplace distribution

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_distr](#) shows an overview of all supported distributions

Examples

```
if (is_on_ci()) {
  laplace_distr <- create_laplace_distr()

  beast2_input_file <- get_beautier_tempfilename()
  create_beast2_input_file(
    input_filename = get_fasta_filename(),
    beast2_input_file,
    tree_prior = create_yule_tree_prior(
      birth_rate_distr = laplace_distr
    )
  )
  file.remove(beast2_input_file)

  remove_beautier_folder()
}
```

create_loggers_xml	<i>Creates the three logger sections of a BEAST2 XML parameter file</i>
--------------------	---

Description

The logger section has these elements:


```

<logger id="tracelog" [...]>
  [...]
</logger>
<logger id="screenlog" [...]>
  [...]
</logger>
<logger id="treelog.t:[alignment ID]" [...]>
  [...]
</logger>

```

Usage

```
create_loggers_xml(input_filename, inference_model)
```

Arguments

`input_filename` A FASTA filename. Use [get_fasta_filename](#) to obtain a testing FASTA filename.

`inference_model` a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_tracelog_xml](#) to create the XML text of the logger with the tracelog ID. Use [create_screenlog_xml](#) to create the XML text of the logger with the screenlog ID. Use [create_treelog_xml](#) to create the XML text of the loggers with the treelog ID.

```
create_log_normal_distr
```

Create a log-normal distribution

Description

Create a log-normal distribution

Usage

```
create_log_normal_distr(
  id = NA,
  m = 0,
  s = 0,
  value = NA,
  lower = NA,
  upper = NA
)
```

Arguments

id	the distribution's ID
m	the m parameter, a numeric value. For advanced usage, use the structure as returned by create_m_param
s	the s parameter, a numeric value. For advanced usage, use the structure as returned by create_s_param
value	the initial value for the MCMC
lower	the lower bound, the lowest possible value
upper	an upper limit of the uniform distribution. If the upper limits needs to be infinity, set upper to Inf.

Value

a log-normal distribution

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_distr](#) shows an overview of all supported distributions

Examples

```
if (is_on_ci()) {

  log_normal_distr <- create_log_normal_distr()

  beast2_input_file <- get_beautier_tempfilename()
  create_beast2_input_file(
    input_filename = get_fasta_filename(),
    beast2_input_file,
    tree_prior = create_yule_tree_prior(
      birth_rate_distr = log_normal_distr
    )
  )
  file.remove(beast2_input_file)
```

```

    remove_beautier_folder()
}

```

create_mcmc	<i>Create an MCMC configuration.</i>
-------------	--------------------------------------

Description

Create an MCMC configuration, as in the BEAUti MCMC tab.

Usage

```

create_mcmc(
  chain_length = 1e+07,
  store_every = -1,
  pre_burnin = 0,
  n_init_attempts = 10,
  sample_from_prior = FALSE,
  tracelog = create_tracelog(),
  screenlog = create_screenlog(),
  treelog = create_treelog()
)

```

Arguments

chain_length	length of the MCMC chain
store_every	number of states the MCMC will process before the posterior's state will be saved to file. Use -1 or NA to use the default frequency.
pre_burnin	number of burn in samples taken before entering the main loop
n_init_attempts	number of initialization attempts before failing
sample_from_prior	set to TRUE to sample from the prior
tracelog	a tracelog, as created by create_tracelog
screenlog	a screenlog, as created by create_screenlog
treelog	a treelog, as created by create_treelog

Details

There are four things that can be saved: * store_every: saves the state of the MCMC to file, as a .state.xml file * tracelog: stores the trace of the state of the MCMC to file. See create_tracelog how to specify the filename * screenlog: stores the screen output to file. See create_screenlog how to specify the filename * treelog: stores the estimated phylogenies to file. See create_treelog how to specify the filename

Value

an MCMC configuration

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_test_mcmc](#) to create a short regular MCMC, that can be used for testing runs. Use [create_ns_mcmc](#) to create an MCMC for a Nested Sampling run. Use [check_mcmc](#) to check if an MCMC is valid. Use [rename_mcmc_filenames](#) to rename the filenames in an MCMC.

Examples

```
if (is_on_ci()) {

  # Create an MCMC chain with 50 states
  mcmc <- create_mcmc(chain_length = 50000, store_every = 1000)

  beast2_input_file <- get_beautier_tempfilename()
  create_beast2_input_file(
    get_fasta_filename(),
    beast2_input_file,
    mcmc = mcmc
  )
  file.remove(beast2_input_file)

  remove_beautier_folder()
}
```

create_mean_param	<i>Create a parameter called mean</i>
-------------------	---------------------------------------

Description

Create a parameter called mean

Usage

```
create_mean_param(id = NA, value = 0)
```

Arguments

id	the parameter's ID
value	value of the parameter

Value

a parameter called mean

Note

this parameter is used in an exponential distribution (as returned by [create_exp_distr](#)) and normal distribution (as returned by [create_normal_distr](#)). It cannot be estimated (as a hyper parameter) yet.

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_param](#) contains a list of all parameters that can be created

Examples

```
if (is_on_ci()) {  
  
  # Create the parameter  
  mean_param <- create_mean_param(value = 1.0)  
  
  # Use the parameter in a distribution  
  exp_distr <- create_exp_distr(  
    mean = mean_param  
  )  
  
  # Use the distribution to create a BEAST2 input file  
  beast2_input_file <- get_beautier_tempfilename()  
  create_beast2_input_file(  
    input_filename = get_fasta_filename(),  
    beast2_input_file,  
    tree_prior = create_yule_tree_prior(  
      birth_rate_distr = exp_distr  
    )  
  )  
  file.remove(beast2_input_file)  
  
  remove_beautier_folder()  
}
```

create_mrca_prior

Create a Most Recent Common Ancestor prior

Description

Create a Most Recent Common Ancestor prior

Usage

```
create_mrca_prior(
  alignment_id = NA,
  taxa_names = NA,
  is_monophyletic = FALSE,
  mrca_distr = NA,
  name = NA,
  clock_prior_distr_id = NA
)
```

Arguments

<code>alignment_id</code>	ID of the alignment, as returned by get_alignment_id . Keep at NA to have it initialized automatically
<code>taxa_names</code>	names of the taxa, as returned by get_taxa_names . Keep at NA to have it initialized automatically, using all taxa in the alignment
<code>is_monophyletic</code>	boolean to indicate monophyly is assumed in a Most Recent Common Ancestor prior, as returned by create_mrca_prior
<code>mrca_distr</code>	the distribution used by the MRCA prior. Can be NA (the default) or any distribution returned by create_distr
<code>name</code>	the unique name of the MRCA prior, for example a genus, family, order or even class name. Leave at NA to have it named automatically.
<code>clock_prior_distr_id</code>	ID of an MRCA clock model's distribution. Keep at NA to have it initialized automatically

Value

an MRCA prior

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

fasta_filename <- get_beautier_path("anthus_aco.fas")

# The first two taxa are sister species
mrca_prior <- create_mrca_prior(
  taxa_names = get_taxa_names(filename = fasta_filename)[1:2]
)

# The taxa are monophyletic
mrca_prior <- create_mrca_prior(
```

```

    taxa_names = get_taxa_names(filename = fasta_filename),
    is_monophyletic = TRUE
  )

  # Set the crown age to 10
  mrca_prior <- create_mrca_prior(
    taxa_names = get_taxa_names(fasta_filename),
    mrca_distr = create_normal_distr(mean = 10, sigma = 0.1)
  )

  check_empty_beautier_folder()

```

create_mu_param	<i>Create a parameter called mu</i>
-----------------	-------------------------------------

Description

Create a parameter called mu

Usage

```
create_mu_param(id = NA, value = 0)
```

Arguments

id	the parameter's ID
value	value of the parameter

Value

a parameter called mu

Note

this parameter is used in a Laplace distribution (as returned by [create_laplace_distr](#)). It cannot be estimated (as a hyper parameter) yet.

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_param](#) contains a list of all parameters that can be created

Examples

```

if (is_on_ci()) {

  # Create the parameter
  mu_param <- create_mu_param()

  # Use the parameter in a distribution
  laplace_distr <- create_laplace_distr(
    mu = mu_param
  )

  # Use the distribution to create a BEAST2 input file
  beast2_input_file <- get_beautier_tempfilename()
  create_beast2_input_file(
    input_filename = get_fasta_filename(),
    beast2_input_file,
    tree_prior = create_yule_tree_prior(
      birth_rate_distr = laplace_distr
    )
  )
  file.remove(beast2_input_file)

  remove_beautier_folder()
}

```

create_m_param	<i>Create a parameter called m</i>
----------------	------------------------------------

Description

Create a parameter called m

Usage

```
create_m_param(id = NA, estimate = FALSE, lower = NA, upper = NA, value = 0)
```

Arguments

id	the parameter's ID
estimate	TRUE if this parameter is to be estimated by BEAST2, FALSE otherwise
lower	lowest possible value of the parameter. If the parameter is estimated, lower must be less than value
upper	upper value of the parameter
value	value of the parameter

Value

a parameter called m

Note

this parameter is used in a log-normal distribution (as returned by [create_log_normal_distr](#)) It cannot be estimated (as a hyper parameter) yet.

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_param](#) contains a list of all parameters that can be created

Examples

```
if (is_on_ci()) {  
  
  # Create the parameter  
  m_param <- create_m_param()  
  
  # Use the parameter in a distribution  
  log_normal_distr <- create_log_normal_distr(  
    m = m_param  
  )  
  
  # Use the distribution to create a BEAST2 input file  
  beast2_input_file <- get_beautier_tempfilename()  
  create_beast2_input_file(  
    input_filename = get_fasta_filename(),  
    beast2_input_file,  
    tree_prior = create_yule_tree_prior(  
      birth_rate_distr = log_normal_distr  
    )  
  )  
  file.remove(beast2_input_file)  
  
  remove_beautier_folder()  
  
}
```

create_normal_distr	Create an normal distribution
---------------------	-------------------------------

Description

Create an normal distribution

Usage

```
create_normal_distr(  
  id = NA,  
  mean = 0,  
  sigma = 1,  
  value = NA,  
  lower = NA,  
  upper = NA  
)
```

Arguments

id	the distribution's ID
mean	the mean parameter, a numeric value. For advanced usage, use the structure as returned by create_mean_param
sigma	the sigma parameter, a numeric value. For advanced usage, use the structure as returned by create_sigma_param
value	the initial value for the MCMC
lower	the lower bound, the lowest possible value
upper	an upper limit of the uniform distribution. If the upper limits needs to be infinity, set upper to Inf.

Value

a normal distribution

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_distr](#) shows an overview of all supported distributions

Examples

```
if (is_on_ci()) {  
  
  normal_distr <- create_normal_distr()  
  
  beast2_input_file <- get_beautier_tempfilename()  
  create_beast2_input_file(  
    input_filename = get_fasta_filename(),  
    beast2_input_file,  
    tree_prior = create_yule_tree_prior(  
      birth_rate_distr = normal_distr  
    )  
  )  
  file.remove(beast2_input_file)
```

```
    remove_beautier_folder()
}
```

```
create_ns_inference_model
```

Create an inference model to measure the evidence of.

Description

Create an inference model to measure the evidence of. To do so, the inference model is created as usual (see [create_inference_model](#)), except for using a Nested Sampling MCMC (see [create_ns_mcmc](#))

Usage

```
create_ns_inference_model(
  site_model = create_jc69_site_model(),
  clock_model = create_strict_clock_model(),
  tree_prior = create_yule_tree_prior(),
  mcmc = create_ns_mcmc()
)
```

Arguments

site_model	a site model, as returned by create_site_model
clock_model	a clock model, as returned by create_clock_model
tree_prior	a tree priors, as returned by create_tree_prior
mcmc	one MCMC. Use create_mcmc to create an MCMC. Use create_ns_mcmc to create an MCMC for a Nested Sampling run. Use check_mcmc to check if an MCMC is valid. Use rename_mcmc_filenames to rename the filenames in an MCMC.

Value

an inference model

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_inference_model](#) to create a regular inference model. Use [create_test_ns_inference_model](#) to create an inference model to estimate the marginal likelihood with a short MCMC, to be used in testing.

Examples

```

check_empty_beautier_folder()

inference_model <- create_ns_inference_model()

check_empty_beautier_folder()

```

create_ns_mcmc	<i>Create an MCMC object to estimate the marginal likelihood using Nested Sampling.</i>
----------------	---

Description

This will result in a BEAST run that estimates the marginal likelihood until convergence is achieved. In this context, chain_length is only an upper bound to the length of that run.

Usage

```

create_ns_mcmc(
  chain_length = 1e+07,
  store_every = -1,
  pre_burnin = 0,
  n_init_attempts = 3,
  particle_count = 1,
  sub_chain_length = 5000,
  epsilon = "1e-12",
  tracelog = create_tracelog(),
  screenlog = create_screenlog(),
  treelog = create_treelog()
)

```

Arguments

chain_length	upper bound to the length of the MCMC chain
store_every	number of states the MCMC will process before the posterior's state will be saved to file. Use -1 or NA to use the default frequency.
pre_burnin	number of burn in samples taken before entering the main loop
n_init_attempts	number of initialization attempts before failing
particle_count	number of particles
sub_chain_length	sub-chain length
epsilon	epsilon
tracelog	a tracelog, as created by create_tracelog
screenlog	a screenlog, as created by create_screenlog
treelog	a treelog, as created by create_treelog

Value

an MCMC object

Author(s)

Richèl J.C. Bilderbeek

References

* [1] Patricio Maturana Russel, Brendon J Brewer, Steffen Klaere, Remco R Bouckaert; Model Selection and Parameter Inference in Phylogenetics Using Nested Sampling, Systematic Biology, 2018, syy050, <https://doi.org/10.1093/sysbio/syy050>

See Also

Use [create_mcmc](#) to create a regular MCMC. Use [create_test_ns_mcmc](#) to create an NS MCMC for testing, with, among others, a short MCMC chain length. Use [check_ns_mcmc](#) to check that an NS MCMC object is valid.

Examples

```
if (is_on_ci()) {  
  
  mcmc <- create_ns_mcmc(  
    chain_length = 1e7,  
    store_every = 1000,  
    particle_count = 1,  
    sub_chain_length = 1000,  
    epsilon = 1e-12  
  )  
  
  beast2_input_file <- get_beautier_tempfilename()  
  create_beast2_input_file(  
    get_fasta_filename(),  
    beast2_input_file,  
    mcmc = mcmc  
  )  
  file.remove(beast2_input_file)  
  
  remove_beautier_folder()  
}
```

create_one_div_x_distr

Create a 1/x distribution

Description

Create a 1/x distribution

Usage

```
create_one_div_x_distr(id = NA, value = NA, lower = NA, upper = NA)
```

Arguments

<code>id</code>	the distribution's ID
<code>value</code>	the initial value for the MCMC
<code>lower</code>	the lower bound, the lowest possible value
<code>upper</code>	an upper limit of the uniform distribution. If the upper limits needs to be infinity, set upper to Inf.

Value

a 1/x distribution

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_distr](#) shows an overview of all supported distributions

Examples

```
if (is_on_ci()) {  
  
  one_div_x_distr <- create_one_div_x_distr()  
  
  beast2_input_file <- get_beautier_tempfilename()  
  create_beast2_input_file(  
    input_filename = get_fasta_filename(),  
    beast2_input_file,  
    tree_prior = create_yule_tree_prior(  
      birth_rate_distr = one_div_x_distr  
    )  
  )  
  file.remove(beast2_input_file)  
  
  remove_beautier_folder()  
}
```

create_param	<i>General function to create a parameter.</i>
--------------	--

Description

General function to create a parameter.

Usage

```
create_param(name, id, value, ...)
```

Arguments

name	the parameters' name. Valid names can be found in <code>get_param_names</code>
id	the parameter's ID
value	value of the parameter
...	specific parameter parameters

Value

a parameter

Note

Prefer using the named functions `create_alpha_param`, `create_beta_param`, `create_clock_rate_param`, `create_kappa_1_param`, `create_kappa_2_param`, `create_lambda_param`, `create_m_param`, `create_mean_param`, `create_mu_param`, `create_rate_ac_param`, `create_rate_ag_param`, `create_rate_at_param`, `create_rate_cg_param`, `create_rate_ct_param`, `create_rate_gt_param`, `create_s_param`, `create_scale_param`, and `create_sigma_param`

Author(s)

Richèl J.C. Bilderbeek

Examples

```
if (is_on_ci()) {  
  
  # Create an alpha parameter  
  alpha_param <- create_alpha_param()  
  
  # Use the parameter in a distribution  
  beta_distr <- create_beta_distr(  
    alpha = alpha_param  
  )  
  
  # Use the distribution to create a BEAST2 input file  
  beast2_input_file <- get_beautier_tempfilename()
```

```

create_beast2_input_file(
  input_filename = get_fasta_filename(),
  beast2_input_file,
  tree_prior = create_yule_tree_prior(
    birth_rate_distr = beta_distr
  )
)
file.remove(beast2_input_file)

remove_beautier_folder()
}

```

create_poisson_distr *Create a Poisson distribution*

Description

Create a Poisson distribution

Usage

```
create_poisson_distr(id = NA, lambda = 0, value = NA, lower = NA, upper = NA)
```

Arguments

id	the distribution's ID
lambda	the lambda parameter, a numeric value. For advanced usage, use the structure as returned by create_lambda_param
value	the initial value for the MCMC
lower	the lower bound, the lowest possible value
upper	an upper limit of the uniform distribution. If the upper limits needs to be infinity, set upper to Inf.

Value

a Poisson distribution

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_distr](#) shows an overview of all supported distributions

Examples

```

if (is_on_ci()) {

  poisson_distr <- create_poisson_distr()

  beast2_input_file <- get_beautier_tempfilename()
  create_beast2_input_file(
    input_filename = get_fasta_filename(),
    beast2_input_file,
    tree_prior = create_yule_tree_prior(
      birth_rate_distr = poisson_distr
    )
  )
  file.remove(beast2_input_file)

  remove_beautier_folder()
}

```

create_rate_ac_param *Create a parameter called 'rate AC'*

Description

Create a parameter called 'rate AC'

Usage

```
create_rate_ac_param(id = NA, estimate = TRUE, value = "1.0", lower = "0.0")
```

Arguments

id	the parameter's ID
estimate	TRUE if this parameter is to be estimated by BEAST2, FALSE otherwise
value	value of the parameter
lower	lowest possible value of the parameter. If the parameter is estimated, lower must be less than value

Value

a parameter called 'rate AC'

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_param](#) contains a list of all parameters that can be created

Examples

```

if (is_on_ci()) {

  # Create parameter
  rate_ac_param <- create_rate_ac_param(value = 1, estimate = FALSE)

  # Use the parameter to create a BEAST2 input file
  beast2_input_file <- get_beautier_tempfilename()
  create_beast2_input_file(
    input_filename = get_fasta_filename(),
    beast2_input_file,
    site_model = create_gtr_site_model(
      rate_ac_param = rate_ac_param
    )
  )
  file.remove(beast2_input_file)

  remove_beautier_folder()
}

```

create_rate_ag_param *Create a parameter called 'rate AG'*

Description

Create a parameter called 'rate AG'

Usage

```
create_rate_ag_param(id = NA, estimate = TRUE, value = "1.0", lower = "0.0")
```

Arguments

id	the parameter's ID
estimate	TRUE if this parameter is to be estimated by BEAST2, FALSE otherwise
value	value of the parameter
lower	lowest possible value of the parameter. If the parameter is estimated, lower must be less than value

Value

a parameter called 'rate AG'

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_param](#) contains a list of all parameters that can be created

Examples

```
if (is_on_ci()) {
  # Create parameter
  rate_ag_param <- create_rate_ag_param(value = 1, estimate = FALSE)

  # Use the parameter to create a BEAST2 input file
  beast2_input_file <- get_beautier_tempfilename()
  create_beast2_input_file(
    input_filename = get_fasta_filename(),
    beast2_input_file,
    site_model = create_gtr_site_model(
      rate_ag_param = rate_ag_param
    )
  )
  file.remove(beast2_input_file)

  remove_beautier_folder()
}
```

create_rate_at_param *Create a parameter called 'rate AT'*

Description

Create a parameter called 'rate AT'

Usage

```
create_rate_at_param(id = NA, estimate = TRUE, value = "1.0", lower = "0.0")
```

Arguments

id	the parameter's ID
estimate	TRUE if this parameter is to be estimated by BEAST2, FALSE otherwise
value	value of the parameter
lower	lowest possible value of the parameter. If the parameter is estimated, lower must be less than value

Value

a parameter called 'rate AT'

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_param](#) contains a list of all parameters that can be created

Examples

```
if (is_on_ci()) {

  # Create parameter
  rate_at_param <- create_rate_at_param(value = 1, estimate = FALSE)

  # Use the parameter to create a BEAST2 input file
  beast2_input_file <- get_beautier_tempfilename()
  create_beast2_input_file(
    input_filename = get_fasta_filename(),
    beast2_input_file,
    site_model = create_gtr_site_model(
      rate_at_param = rate_at_param
    )
  )
  file.remove(beast2_input_file)

  remove_beautier_folder()
}
```

create_rate_categories_state_node_xml

Internal function

Description

Creates the rateCategories state node, such as: "<stateNode id=\"rateCategories.c:[id]\" spec=\"parameter.IntegerParameter\" dimension=\"[dimension]\"> 1 </stateNode>"

Usage

```
create_rate_categories_state_node_xml(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

the following XML: "<stateNode id=\"rateCategories.c:[id]\" spec=\"parameter.IntegerParameter\" dimension=\"[dimension]\"> 1 </stateNode>"

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

create_rate_categories_state_node_xml(
  create_inference_model(
    clock_model = create_rln_clock_model(
      id = 314,
      dimension = 1
    )
  )
)

check_empty_beautier_folder()
```

create_rate_cg_param *Create a parameter called 'rate CG'*

Description

Create a parameter called 'rate CG'

Usage

```
create_rate_cg_param(id = NA, estimate = TRUE, value = "1.0", lower = "0.0")
```

Arguments

id	the parameter's ID
estimate	TRUE if this parameter is to be estimated by BEAST2, FALSE otherwise
value	value of the parameter
lower	lowest possible value of the parameter. If the parameter is estimated, lower must be less than value

Value

a parameter called 'rate CG'

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_param](#) contains a list of all parameters that can be created

Examples

```
if (is_on_ci()) {

  # Create parameter
  rate_cg_param <- create_rate_cg_param(value = 1, estimate = FALSE)

  # Use the parameter to create a BEAST2 input file
  beast2_input_file <- get_beautier_tempfilename()
  create_beast2_input_file(
    input_filename = get_fasta_filename(),
    beast2_input_file,
    site_model = create_gtr_site_model(
      rate_cg_param = rate_cg_param
    )
  )
  file.remove(beast2_input_file)

  remove_beautier_folder()
}
```

create_rate_ct_param *Create a parameter called 'rate CT'*

Description

Create a parameter called 'rate CT'

Usage

```
create_rate_ct_param(id = NA, value = "1.0", lower = "0.0")
```

Arguments

id	the parameter's ID
value	value of the parameter
lower	lowest possible value of the parameter. If the parameter is estimated, lower must be less than value

Value

a parameter called 'rate CT'

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_param](#) contains a list of all parameters that can be created

Examples

```
if (is_on_ci()) {

  # Create parameter
  rate_ct_param <- create_rate_ct_param(value = 1)

  # Use the parameter to create a BEAST2 input file
  beast2_input_file <- get_beautier_tempfilename()
  create_beast2_input_file(
    input_filename = get_fasta_filename(),
    beast2_input_file,
    site_model = create_gtr_site_model(
      rate_ct_param = rate_ct_param
    )
  )
  file.remove(beast2_input_file)

  remove_beautier_folder()
}
```

create_rate_gt_param *Create a parameter called 'rate GT'*

Description

Create a parameter called 'rate GT'

Usage

```
create_rate_gt_param(id = NA, estimate = TRUE, value = "1.0", lower = "0.0")
```

Arguments

id	the parameter's ID
estimate	TRUE if this parameter is to be estimated by BEAST2, FALSE otherwise
value	value of the parameter
lower	lowest possible value of the parameter. If the parameter is estimated, lower must be less than value

Value

a parameter called 'rate GT'

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_param](#) contains a list of all parameters that can be created

Examples

```
if (is_on_ci()) {  
  
  # Create parameter  
  rate_gt_param <- create_rate_gt_param(value = 1, estimate = FALSE)  
  
  # Use the parameter to create a BEAST2 input file  
  beast2_input_file <- get_beautier_tempfilename()  
  create_beast2_input_file(  
    input_filename = get_fasta_filename(),  
    beast2_input_file,  
    site_model = create_gtr_site_model(  
      rate_gt_param = rate_gt_param  
    )  
  )  
  file.remove(beast2_input_file)  
  
  remove_beautier_folder()  
}
```

create_rln_clock_branch_rate_model_xml

Internal function

Description

Internal function to call [create_branch_rate_model_xml](#) for a relaxed log-normal clock.

Usage

```
create_rln_clock_branch_rate_model_xml(inference_model)
```


Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

a character vector of XML strings

Author(s)

Richèl J.C. Bilderbeek

 create_rln_clock_model

Create a relaxed log-normal clock model

Description

Create a relaxed log-normal clock model

Usage

```
create_rln_clock_model(
  id = NA,
  mean_rate_prior_distr = create_uniform_distr(),
  ucldstdev_distr = create_gamma_distr(),
  mparam_id = NA,
  mean_clock_rate = "1.0",
  n_rate_categories = -1,
  normalize_mean_clock_rate = FALSE,
  dimension = NA,
  rate_scaler_factor = 0.75
)
```

Arguments

id an alignment's IDs. An ID can be extracted from its FASTA filename with [get_alignment_ids_from_fasta_filenames](#)

mean_rate_prior_distr the mean clock rate prior distribution, as created by a [create_distr](#) function

ucldstdev_distr the standard deviation of the uncorrelated log-normal distribution, as created by a [create_distr](#) function

mparam_id	the ID of the M parameter in the branchRateModel, set to NA to have it initialized
mean_clock_rate	the mean clock rate, 1.0 by default (is called uclsd_stdev in XML, where uclsd_stdev is always 0.1)
n_rate_categories	the number of rate categories. -1 is default, 0 denotes as much rates as branches
normalize_mean_clock_rate	normalize the mean clock rate
dimension	the dimensionality of the relaxed clock model. Leave NA to let beautier calculate it. Else, the dimensionality of the clock equals twice the number of taxa minus two.
rate_scaler_factor	the strict clock model's operator scaler for the rate. Use an empty string to indicate the default.

Value

a relaxed log-normal clock_model

Author(s)

Richèl J.C. Bilderbeek

Examples

```
if (is_on_ci()) {
  rln_clock_model <- create_rln_clock_model()

  beast2_input_file <- get_beautier_tempfilename()

  create_beast2_input_file(
    get_fasta_filename(),
    beast2_input_file,
    clock_model = rln_clock_model
  )
  file.remove(beast2_input_file)

  remove_beautier_folder()
}
```

create_scale_param	<i>Create a parameter called scale</i>
--------------------	--

Description

Create a parameter called scale

Usage

```
create_scale_param(id = NA, value = 0)
```

Arguments

id	the parameter's ID
value	value of the parameter

Value

a parameter called scale

Note

this parameter is used in a Laplace distribution (as returned by [create_laplace_distr](#))

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_param](#) contains a list of all parameters that can be created

Examples

```
if (is_on_ci()) {  
  # Create the parameter  
  scale_param <- create_scale_param()  
  
  # Use the parameter in a distribution  
  laplace_distr <- create_laplace_distr(  
    scale = scale_param  
  )  
  
  # Use the distribution to create a BEAST2 input file  
  beast2_input_file <- get_beautier_tempfilename()  
  create_beast2_input_file(  
    input_filename = get_fasta_filename(),  
    beast2_input_file,  
    tree_prior = create_yule_tree_prior(  
      birth_rate_distr = laplace_distr  
    )  
  )  
  file.remove(beast2_input_file)  
  
  remove_beautier_folder()  
}
```

create_screenlog	Create a screenlog object
------------------	---------------------------

Description

Create a screenlog object

Usage

```
create_screenlog(  
  filename = "",  
  log_every = 1000,  
  mode = "autodetect",  
  sanitise_headers = FALSE,  
  sort = "none"  
)
```

Arguments

filename	name of the file to store the posterior screens phylogenies to. By default, this is <code>\$(screen).screens</code>
log_every	number of MCMC states between writing to file
mode	mode how to log. Valid values are the ones returned by get_log_modes
sanitise_headers	set to TRUE to sanitise the headers of the log file
sort	how to sort the log. Valid values are the ones returned by get_log_sorts

Value

a screenlog object

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()  
  
create_screenlog()  
  
check_empty_beautier_folder()
```

create_screenlog_xml	<i>Creates the screenlog section of the logger section of a BEAST2 XML parameter file</i>
----------------------	---

Description

Creates the screenlog section of the logger section of a BEAST2 XML parameter file

Usage

```
create_screenlog_xml(inference_model = create_inference_model())
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

the XML text

Author(s)

Richèl J.C. Bilderbeek

create_sigma_param	<i>Create a parameter called sigma</i>
--------------------	--

Description

Create a parameter called sigma

Usage

```
create_sigma_param(id = NA, value = 1)
```

Arguments

id	the parameter's ID
value	value of the parameter

Value

a parameter called sigma

Note

this parameter is used in a normal distribution (as returned by [create_normal_distr](#))

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_param](#) contains a list of all parameters that can be created

Examples

```
if (is_on_ci()) {  
  
  # Create the parameter  
  sigma_param <- create_sigma_param()  
  
  # Use the parameter in a distribution  
  normal_distr <- create_normal_distr(  
    sigma = sigma_param  
  )  
  
  # Use the distribution to create a BEAST2 input file  
  beast2_input_file <- get_beautier_tempfilename()  
  create_beast2_input_file(  
    input_filename = get_fasta_filename(),  
    beast2_input_file,  
    tree_prior = create_yule_tree_prior(  
      birth_rate_distr = normal_distr  
    )  
  )  
  file.remove(beast2_input_file)  
  
  remove_beautier_folder()  
}
```

create_site_model

General function to create a site model.

Description

General function to create a site model.

Usage

```
create_site_model(name, id, gamma_site_model = create_gamma_site_model(), ...)
```

Arguments

name	the site model name. Valid names can be found in <code>get_site_model_names</code>
id	the IDs of the alignment (can be extracted from the FASTA filename using get_alignment_id)
gamma_site_model	a gamma site model, as created by create_gamma_site_model
...	specific site model parameters

Value

a `site_model`

Note

Prefer using the named functions [create_gtr_site_model](#), [create_hky_site_model](#), [create_jc69_site_model](#), and [create_tn93_site_model](#)

Author(s)

Richèl J.C. Bilderbeek

See Also

See [create_gtr_site_model](#) for more examples with a GTR site model. See [create_hky_site_model](#) for more examples with an HKY site model. See [create_jc69_site_model](#) for more examples with a JC69 site model. See [create_tn93_site_model](#) for more examples with a TN93 site model

Examples

```
if (is_on_ci()) {  
  
  check_empty_beautier_folder()  
  
  input_filename <- get_fasta_filename()  
  gtr_site_model <- create_gtr_site_model()  
  hk_site_model <- create_hky_site_model()  
  jc69_site_model <- create_jc69_site_model()  
  tn93_site_model <- create_tn93_site_model()  
  
  # Can use any site model  
  output_filename <- get_beautier_tempfilename()  
  create_beast2_input_file(  
    input_filename = input_filename,  
    output_filename = output_filename,  
    site_model = jc69_site_model  
  )  
}
```

```

file.remove(output_filename)

remove_beautier_folder()
check_empty_beautier_folder()
}

```

create_site_models	<i>Creates all supported site models which is a list of the types returned by create_gtr_site_model, create_hky_site_model, create_jc69_site_model and create_tn93_site_model</i>
--------------------	---

Description

Creates all supported site models which is a list of the types returned by [create_gtr_site_model](#), [create_hky_site_model](#), [create_jc69_site_model](#) and [create_tn93_site_model](#)

Usage

```
create_site_models()
```

Value

a list of site_models

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_site_model](#) to create a site model

Examples

```

check_empty_beautier_folder()

# All created site models are a kind of site model
site_models <- create_site_models()

# TRUE
is_gtr_site_model(site_models[[1]])
is_hky_site_model(site_models[[2]])
is_jc69_site_model(site_models[[3]])
is_tn93_site_model(site_models[[4]])

check_empty_beautier_folder()

```

`create_site_models_from_names`*Create site models from their names*

Description

Create site models from their names

Usage

```
create_site_models_from_names(site_model_names)
```

Arguments

`site_model_names`

one or more names of a site model, must be name among those returned by [get_site_model_names](#)

Value

one or more site models

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_site_model](#) to create a site model

Examples

```
check_empty_beautier_folder()

create_site_models_from_names(get_site_model_names())

check_empty_beautier_folder()
```

```
create_site_model_from_name
```

Create a site model from name

Description

Create a site model from name

Usage

```
create_site_model_from_name(site_model_name)
```

Arguments

site_model_name
name of a site model, must be a name as returned by [get_site_model_names](#)

Value

a site model

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_site_model](#) to create a site model

Examples

```
check_empty_beautier_folder()

site_model <- create_site_model_from_name(get_site_model_names()[1])

check_empty_beautier_folder()
```

`create_site_model_parameters_xml`

Internal function to creates the XML text for the parameters within the siteModel section of a BEAST2 parameter file.

Description

Internal function to creates the XML text for the parameters within the siteModel section, which is part of the siteModel section of a BEAST2 parameter file.

Usage

```
create_site_model_parameters_xml(inference_model)
```

Arguments

`inference_model`

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Details

The parameters sections has these elements:

```
[parameters]
```

[parameters] can be a combination of these:

```
<parameter id="mutationRate.s[...]>  
<parameter id="gammaShape.s[...]>  
<parameter id="proportionInvariant.s[...]>
```

Value

the site model as XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()
```

`create_site_model_xml` *Internal function to creates the XML text for the siteModel tag of a BEAST2 parameter file.*

Description

Creates the XML text for the siteModel tag of a BEAST2 parameter file, which is part of the distribution node for the treeLikelihood ID.

Usage

```
create_site_model_xml(inference_model)
```

Arguments

`inference_model`

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Details

The siteModel tag has these elements:

```
<siteModel[...]>
  [parameters]
  <substModel[...]>
    [...]
  </substModel>
</siteModel>
```

The parameter section is created by [create_site_model_parameters_xml](#) The substModel section is created by [create_subst_model_xml](#)

Value

the site model as XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()
# <distribution id="posterior"[...]>
#   <distribution id="likelihood" [...]>
#     <siteModel...>
#       [parameters]
#     </siteModel>
#   </distribution>
# </distribution>

check_empty_beautier_folder()
```

create_strict_clock_branch_rate_model_xml

Internal function.

Description

Internal function to create the branchRateModel section of the XML as text, for a strict clock model

Usage

```
create_strict_clock_branch_rate_model_xml(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

a character vector of XML strings

Author(s)

Richèl J.C. Bilderbeek

`create_strict_clock_model`*Create a strict clock model*

Description

Create a strict clock model

Usage

```
create_strict_clock_model(  
  id = NA,  
  clock_rate_param = create_clock_rate_param(),  
  clock_rate_distr = create_uniform_distr(),  
  rate_scaler_factor = 0.75  
)
```

Arguments

`id` an alignment's IDs. An ID can be extracted from its FASTA filename with [get_alignment_ids_from_fasta_filenames](#))

`clock_rate_param` the clock rate's parameter, a numeric value. For advanced usage, use the structure as created by the [create_clock_rate_param](#) function

`clock_rate_distr` the clock rate's distribution, as created by a [create_distr](#) function

`rate_scaler_factor` the strict clock model's operator scaler for the rate. Use an empty string to indicate the default.

Value

a strict clock_model

Note

I am unsure about the relationship between 'clock_rate_param' and 'clock_rate_distr'. Please contact me if you know the most natural architecture

Author(s)

Richèl J.C. Bilderbeek

Examples

```
if (is_on_ci()) {  
  strict_clock_model <- create_strict_clock_model(  
    clock_rate_param = 1.0,  
    clock_rate_distr = create_uniform_distr()  
  )  
  
  beast2_input_file <- get_beautier_tempfilename()  
  create_beast2_input_file(  
    get_fasta_filename(),  
    beast2_input_file,  
    clock_model = strict_clock_model  
  )  
  file.remove(beast2_input_file)  
  
  remove_beautier_folder()  
}
```

create_strict_clock_rate_scaler_operator_xml

Internal function

Description

Creates the StrictClockRateScaler operator such as: ...

Usage

```
create_strict_clock_rate_scaler_operator_xml(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

the following XML: ...

Author(s)

Richèl J.C. Bilderbeek

Examples

```

check_empty_beautier_folder()

create_strict_clock_rate_scaler_operator_xml(
  create_inference_model(
    clock_model = create_strict_clock_model(id = 314)
  )
)

check_empty_beautier_folder()

```

```
create_subst_model_xml
```

Internal function to create the substModel section

Description

Internal function to create the substModel section

Usage

```
create_subst_model_xml(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

the substModel section as XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```

check_empty_beautier_folder()

# Inference model must be initialized
inference_model <- create_inference_model(
  site_model = create_jc69_site_model(id = 123)
)
create_subst_model_xml(

```



```
    inference_model = inference_model
  )

  check_empty_beautier_folder()
```

create_s_param	<i>Create a parameter called s</i>
----------------	------------------------------------

Description

Create a parameter called s

Usage

```
create_s_param(id = NA, value = 0, lower = 0, upper = Inf)
```

Arguments

id	the parameter's ID
value	value of the parameter
lower	lowest possible value of the parameter. If the parameter is estimated, lower must be less than value
upper	upper value of the parameter

Value

a parameter called s

Note

this parameter is used in a log-normal distribution (as returned by [create_log_normal_distr](#))

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_param](#) contains a list of all parameters that can be created

Examples

```
if (is_on_ci()) {  
  
  # Create the parameter  
  s_param <- create_s_param()  
  
  # Use the parameter in a distribution  
  log_normal_distr <- create_log_normal_distr(  
    s = s_param  
  )  
  
  # Use the distribution to create a BEAST2 input file  
  beast2_input_file <- get_beautier_tempfilename()  
  create_beast2_input_file(  
    input_filename = get_fasta_filename(),  
    beast2_input_file,  
    tree_prior = create_yule_tree_prior(  
      birth_rate_distr = log_normal_distr  
    )  
  )  
  file.remove(beast2_input_file)  
  
  remove_beautier_folder()  
}
```

create_temp_screenlog_filename

Create a filename for a temporary 'screenlog' file

Description

Create a filename for a temporary 'screenlog' file

Usage

```
create_temp_screenlog_filename()
```

Value

a filename for a temporary 'screenlog' file

Author(s)

Richèl J.C. Bilderbeek

See Also

use [create_screenlog](#) to create a screenlog.

Examples

```
check_empty_beautier_folder()

create_temp_screenlog_filename()

check_empty_beautier_folder()
```

```
create_temp_tracelog_filename
```

Create a filename for a temporary 'tracelog' file

Description

Create a filename for a temporary 'tracelog' file

Usage

```
create_temp_tracelog_filename()
```

Value

a filename for a temporary 'tracelog' file

Author(s)

Richèl J.C. Bilderbeek

See Also

use [create_tracelog](#) to create a tracelog.

Examples

```
check_empty_beautier_folder()

create_temp_tracelog_filename()

check_empty_beautier_folder()
```

`create_temp_treelog_filename`*Create a filename for a temporary 'treelog' file*

Description

Create a filename for a temporary 'treelog' file

Usage

```
create_temp_treelog_filename()
```

Value

a filename for a temporary 'treelog' file

Author(s)

Richèl J.C. Bilderbeek

See Also

use [create_treelog](#) to create a treelog.

Examples

```
check_empty_beautier_folder()
create_temp_treelog_filename()
check_empty_beautier_folder()
```

`create_test_inference_model`*Create a testing inference model.*

Description

Creates a simple inference model with a short MCMC chain, to be used in testing.

Usage

```
create_test_inference_model(
  site_model = create_jc69_site_model(),
  clock_model = create_strict_clock_model(),
  tree_prior = create_yule_tree_prior(),
  mrca_prior = NA,
  mcmc = create_test_mcmc(),
  beauti_options = create_beauti_options(),
  tipdates_filename = NA
)
```

Arguments

site_model	a site model, as returned by create_site_model
clock_model	a clock model, as returned by create_clock_model
tree_prior	a tree priors, as returned by create_tree_prior
mrca_prior	a Most Recent Common Ancestor prior, as returned by create_mrca_prior
mcmc	one MCMC. Use create_mcmc to create an MCMC. Use create_ns_mcmc to create an MCMC for a Nested Sampling run. Use check_mcmc to check if an MCMC is valid. Use rename_mcmc_filenames to rename the filenames in an MCMC.
beauti_options	one BEAUti options object, as returned by create_beauti_options
tipdates_filename	name of the file containing the tip dates. This file is assumed to have two columns, separated by a tab. The first column contains the taxa names, the second column contains the date.

Value

an inference model

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_inference_model](#) to create a regular inference model. Use [create_test_ns_inference_model](#) to create an inference model to estimate the marginal likelihood with a short MCMC, to be used in testing

Examples

```
if (is_on_ci()) {
  check_empty_beautier_folder()

  inference_model <- create_test_inference_model()
```

```

beast2_input_file <- get_beautier_tempfilename()
create_beast2_input_file_from_model(
  get_fasta_filename(),
  beast2_input_file,
  inference_model = inference_model
)
file.remove(beast2_input_file)

remove_beautier_folder()
check_empty_beautier_folder()
}

```

create_test_mcmc

Create an MCMC configuration for testing.

Description

Create an MCMC configuration for testing.

Usage

```

create_test_mcmc(
  chain_length = 3000,
  store_every = 1000,
  pre_burnin = 0,
  n_init_attempts = 10,
  sample_from_prior = FALSE,
  tracelog = create_test_tracelog(),
  screenlog = create_test_screenlog(),
  treelog = create_test_treelog()
)

```

Arguments

chain_length	length of the MCMC chain
store_every	number of states the MCMC will process before the posterior's state will be saved to file. Use -1 or NA to use the default frequency.
pre_burnin	number of burn in samples taken before entering the main loop
n_init_attempts	number of initialization attempts before failing
sample_from_prior	set to TRUE to sample from the prior
tracelog	a tracelog, as created by create_tracelog
screenlog	a screenlog, as created by create_screenlog
treelog	a treelog, as created by create_treelog

Value

an MCMC configuration

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_mcmc](#) to create a default BEAST2 MCMC

Examples

```
if (is_on_ci()) {  
  
  # Create an MCMC chain with 50 states  
  mcmc <- create_test_mcmc()  
  
  beast2_input_file <- get_beautier_tempfilename()  
  create_beast2_input_file(  
    get_fasta_filename(),  
    beast2_input_file,  
    mcmc = mcmc  
  )  
  file.remove(beast2_input_file)  
  
  remove_beautier_folder()  
}
```

create_test_ns_inference_model

Create an inference model to be tested by Nested Sampling

Description

Create an inference model to be tested by Nested Sampling

Usage

```
create_test_ns_inference_model(  
  site_model = create_jc69_site_model(),  
  clock_model = create_strict_clock_model(),  
  tree_prior = create_yule_tree_prior(),  
  mcmc = create_test_ns_mcmc()  
)
```

Arguments

site_model	a site model, as returned by create_site_model
clock_model	a clock model, as returned by create_clock_model
tree_prior	a tree priors, as returned by create_tree_prior
mcmc	one MCMC. Use create_mcmc to create an MCMC. Use create_ns_mcmc to create an MCMC for a Nested Sampling run. Use check_mcmc to check if an MCMC is valid. Use rename_mcmc_filenames to rename the filenames in an MCMC.

Value

an inference model

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_test_inference_model](#) to create a regular inference model with a short MCMC, to be used in testing. Use [create_ns_inference_model](#) to create an inference model to estimate the marginal likelihood.

Examples

```
check_empty_beautier_folder()

inference_model <- create_test_ns_inference_model()

check_empty_beautier_folder()
```

create_test_ns_mcmc	<i>Create an NS MCMC object for testing</i>
---------------------	---

Description

Create an NS MCMC object for testing

Usage

```
create_test_ns_mcmc(
  chain_length = 2000,
  store_every = 1000,
  pre_burnin = 0,
  n_init_attempts = 3,
  particle_count = 1,
  sub_chain_length = 500,
```



```

    epsilon = 1e-12,
    tracelog = create_test_tracelog(),
    screenlog = create_test_screenlog(),
    treelog = create_test_treelog()
  )

```

Arguments

chain_length	upper bound to the length of the MCMC chain
store_every	number of states the MCMC will process before the posterior's state will be saved to file. Use -1 or NA to use the default frequency.
pre_burnin	number of burn in samples taken before entering the main loop
n_init_attempts	number of initialization attempts before failing
particle_count	number of particles
sub_chain_length	sub-chain length
epsilon	epsilon
tracelog	a tracelog, as created by create_tracelog
screenlog	a screenlog, as created by create_screenlog
treelog	a treelog, as created by create_treelog

Value

an MCMC object

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_ns_mcmc](#) to create a default nested sampling MCMC

Examples

```

if (is_on_ci()) {

  mcmc <- create_test_ns_mcmc()
  beast2_input_file <- get_beautier_tempfilename()
  create_beast2_input_file(
    get_fasta_filename(),
    beast2_input_file,
    mcmc = mcmc
  )
  file.remove(beast2_input_file)

  remove_beautier_folder()
}

```

`create_test_screenlog` *Create a screenlog object, to be used in testing*

Description

Create a screenlog object, to be used in testing

Usage

```
create_test_screenlog(  
  filename = create_temp_screenlog_filename(),  
  log_every = 1000,  
  mode = "autodetect",  
  sanitise_headers = FALSE,  
  sort = "none"  
)
```

Arguments

<code>filename</code>	name of the file to store the posterior screens phylogenies to. By default, this is <code>\$(screen).screens</code>
<code>log_every</code>	number of MCMC states between writing to file
<code>mode</code>	mode how to log. Valid values are the ones returned by get_log_modes
<code>sanitise_headers</code>	set to TRUE to sanitise the headers of the log file
<code>sort</code>	how to sort the log. Valid values are the ones returned by get_log_sorts

Value

a screenlog object

Author(s)

Richèl J.C. Bilderbeek

Examples

```
create_test_screenlog()
```

create_test_tracelog *Create a tracelog object, as used for testing*

Description

Create a tracelog object, as used for testing

Usage

```
create_test_tracelog(  
  filename = create_temp_tracelog_filename(),  
  log_every = 1000,  
  mode = "autodetect",  
  sanitise_headers = TRUE,  
  sort = "smart"  
)
```

Arguments

filename	name of the file to store the posterior traces. Use NA to use the filename <code>[alignment_id].log</code> , where <code>alignment_id</code> is obtained using get_alignment_id
log_every	number of MCMC states between writing to file
mode	mode how to log. Valid values are the ones returned by get_log_modes
sanitise_headers	set to TRUE to sanitise the headers of the log file
sort	how to sort the log. Valid values are the ones returned by get_log_sorts

Value

a tracelog object

Author(s)

Richèl J.C. Bilderbeek

Examples

```
create_test_tracelog()
```

create_test_treelog	Create a treelog object to be used in testing
---------------------	---

Description

Create a treelog object to be used in testing

Usage

```
create_test_treelog(  
  filename = create_temp_treelog_filename(),  
  log_every = 1000,  
  mode = "tree",  
  sanitise_headers = FALSE,  
  sort = "none"  
)
```

Arguments

filename	name of the file to store the posterior trees
log_every	number of MCMC states between writing to file
mode	mode how to log. Valid values are the ones returned by get_log_modes
sanitise_headers	set to TRUE to sanitise the headers of the log file
sort	how to sort the log. Valid values are the ones returned by get_log_sorts

Value

a treelog object

Author(s)

Richèl J.C. Bilderbeek

Examples

```
create_test_treelog()
```

```
create_tn93_site_model
```

Create a TN93 site model

Description

Create a TN93 site model

Usage

```
create_tn93_site_model(
  id = NA,
  gamma_site_model = create_gamma_site_model(),
  kappa_1_param = create_kappa_1_param(),
  kappa_2_param = create_kappa_2_param(),
  kappa_1_prior_distr = create_log_normal_distr(m = 1, s = 1.25),
  kappa_2_prior_distr = create_log_normal_distr(m = 1, s = 1.25),
  freq_equilibrium = "estimated",
  freq_param = create_freq_param()
)
```

Arguments

<code>id</code>	the IDs of the alignment (can be extracted from the FASTA filename using get_alignment_id)
<code>gamma_site_model</code>	a gamma site model, as created by create_gamma_site_model
<code>kappa_1_param</code>	the 'kappa 1' parameter, a numeric value. For advanced usage, use the structure as returned by create_kappa_1_param
<code>kappa_2_param</code>	the 'kappa 2' parameter, a numeric value. For advanced usage, use the structure as returned by create_kappa_2_param
<code>kappa_1_prior_distr</code>	the distribution of the kappa 1 prior, which is a log-normal distribution (as created by create_log_normal_distr) by default
<code>kappa_2_prior_distr</code>	the distribution of the kappa 2 prior, which is a log-normal distribution (as created by create_log_normal_distr) by default
<code>freq_equilibrium</code>	the frequency in which the rates are at equilibrium are either estimated, empirical or all_equal. get_freq_equilibrium_names returns the possible values for <code>freq_equilibrium</code>
<code>freq_param</code>	a 'freq' parameter, as created by create_freq_param

Value

a TN93 site_model

Author(s)

Richèl J.C. Bilderbeek

Examples

```
if (is_on_ci()) {  
  
  tn93_site_model <- create_tn93_site_model(  
    kappa_1_param = 2.0,  
    kappa_2_param = 2.0  
  )  
  
  output_filename <- get_beautier_tempfilename()  
  create_beast2_input_file(  
    input_filename = get_fasta_filename(),  
    output_filename = output_filename,  
    site_model = tn93_site_model  
  )  
  file.remove(output_filename)  
  
  remove_beautier_folder()  
}
```

create_tn93_subst_model_xml

Converts a TN93 site model to XML, used in the substModel section

Description

Converts a TN93 site model to XML, used in the substModel section

Usage

```
create_tn93_subst_model_xml(site_model)
```

Arguments

site_model a site model, as returned by [create_site_model](#)

Value

the site model as XML text

Author(s)

Richèl J.C. Bilderbeek

create_tracelog	Create a tracelog object
-----------------	--------------------------

Description

Create a tracelog object

Usage

```
create_tracelog(  
  filename = NA,  
  log_every = 1000,  
  mode = "autodetect",  
  sanitise_headers = TRUE,  
  sort = "smart"  
)
```

Arguments

filename	name of the file to store the posterior traces. Use NA to use the filename <code>[alignment_id].log</code> , where <code>alignment_id</code> is obtained using get_alignment_id
log_every	number of MCMC states between writing to file
mode	mode how to log. Valid values are the ones returned by get_log_modes
sanitise_headers	set to TRUE to sanitise the headers of the log file
sort	how to sort the log. Valid values are the ones returned by get_log_sorts

Value

a tracelog object

Author(s)

Richèl J.C. Bilderbeek

Examples

```
create_tracelog()
```

create_tracelog_xml	<i>Internal function</i>
---------------------	--------------------------

Description

Creates the tracelog section of the logger section of a BEAST2 XML parameter file

Usage

```
create_tracelog_xml(input_filename, inference_model)
```

Arguments

`input_filename` A FASTA filename. Use [get_fasta_filename](#) to obtain a testing FASTA filename.

`inference_model` a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

create_trait_set_string	<i>Create a trait set string.</i>
-------------------------	-----------------------------------

Description

For example, a data frame with row A 1 and another row B 2, the trait set string will be A=1,B=2

Usage

```
create_trait_set_string(df)
```

Arguments

`df` a data frame with two columns

Value

the trait set string

Author(s)

Richèl J.C. Bilderbeek

create_treelog	Create a treelog object
----------------	-------------------------

Description

Create a treelog object

Usage

```
create_treelog(  
  filename = "${tree}.trees",  
  log_every = 1000,  
  mode = "tree",  
  sanitise_headers = FALSE,  
  sort = "none"  
)
```

Arguments

filename	name of the file to store the posterior trees
log_every	number of MCMC states between writing to file
mode	mode how to log. Valid values are the ones returned by get_log_modes
sanitise_headers	set to TRUE to sanitise the headers of the log file
sort	how to sort the log. Valid values are the ones returned by get_log_sorts

Value

a 'treelog', as can be checked by [check_treelog](#)

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()  
  
create_treelog()  
  
check_empty_beautier_folder()
```

create_treelog_xml	<i>Creates the XML text for the ‘logger’ tag with ID ‘treelog’. This section has these elements: ““ <logger id="treelog.t:test_output_0" spec="Logger" fileName="my_treelog.trees" logEvery="345000" mode="tree" sanitiseHeaders="true" sort="smart"> # nolint indeed long <log id="TreeWithMetaDataLogger.t:test_output_0" spec="beast.evolution.tree.TreeWithMetaDataLogger" tree="@Tree.t:test_output_0"/> # nolint indeed long </logger> ““</i>
--------------------	---

Description

Creates the XML text for the ‘logger’ tag with ID ‘treelog’. This section has these elements: ““ <logger id="treelog.t:test_output_0" spec="Logger" fileName="my_treelog.trees" logEvery="345000" mode="tree" sanitiseHeaders="true" sort="smart"> # nolint indeed long <log id="TreeWithMetaDataLogger.t:test_output_0" spec="beast.evolution.tree.TreeWithMetaDataLogger" tree="@Tree.t:test_output_0"/> # nolint indeed long </logger> ““

Usage

```
create_treelog_xml(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

```
create_tree_likelihood_distr_xml
```

Creates the XML text for the distribution tag with the treeLikelihood ID, of a BEAST2 parameter file.

Description

Creates the XML text for the distribution tag with the treeLikelihood ID, of a BEAST2 parameter file, in an unindented form

Usage

```
create_tree_likelihood_distr_xml(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Details

The distribution tag (with ID equals treeLikelihood) has these elements:

```
<distribution id="treeLikelihood" [...]>
  <siteModel [...]>
    [...]
  </siteModel>
  <branchRateModel [...]>
    [...]
  </branchRateModel>
</distribution>
```

The siteModel section is created by [create_site_model_xml](#). The branchRateModel section is created by [create_branch_rate_model_xml](#).

Zooming out:

```
<beast [...]>
  <run [...]>
    <distribution id="posterior" [...]>
      <distribution id="likelihood" [...]>
        [this section]
      </distribution>
    </distribution>
  </run>
</beast>
```

Value

lines of XML text

Note

this function is not intended for regular use, thus its long name length is accepted

Author(s)

Richèl J.C. Bilderbeek

See Also

this function is called by `create_beast2_input_distr`, together with `create_beast2_input_distr_prior`

<code>create_tree_prior</code>	<i>Internal function to create a tree prior</i>
--------------------------------	---

Description

Internal function to create a tree prior

Usage

```
create_tree_prior(name, id, ...)
```

Arguments

<code>name</code>	the tree prior name. Can be any name in <code>get_tree_prior_names</code>
<code>id</code>	the ID of the alignment
<code>...</code>	specific tree prior parameters

Value

a `tree_prior`

Note

Prefer the use the named functions `create_bd_tree_prior`, `create_cbs_tree_prior`, `create_ccp_tree_prior`, `create_cep_tree_prior` and `create_yule_tree_prior` instead

Author(s)

Richèl J.C. Bilderbeek

See Also

See [create_bd_tree_prior](#), [create_cbs_tree_prior](#), [create_ccp_tree_prior](#), [create_cep_tree_prior](#) and [create_yule_tree_prior](#) for more examples using those functions

Examples

```
if (is_on_ci()) {

  check_empty_beautier_folder()

  beast2_input_file <- get_beautier_tempfilename()

  bd_tree_prior <- create_bd_tree_prior()
  cbs_tree_prior <- create_cbs_tree_prior()
  ccp_tree_prior <- create_ccp_tree_prior()
  cep_tree_prior <- create_cep_tree_prior()
  yule_tree_prior <- create_yule_tree_prior()

  # Use any of the above tree priors
  create_beast2_input_file(
    input_filename = get_fasta_filename(),
    beast2_input_file,
    tree_prior = bd_tree_prior
  )
  file.remove(beast2_input_file)

  remove_beautier_folder()
  check_empty_beautier_folder()
}
```

create_tree_priors	<i>Creates all supported tree priors, which is a list of the types returned by create_bd_tree_prior, create_cbs_tree_prior, create_ccp_tree_prior, create_cep_tree_prior and create_yule_tree_prior</i>
--------------------	---

Description

Creates all supported tree priors, which is a list of the types returned by [create_bd_tree_prior](#), [create_cbs_tree_prior](#), [create_ccp_tree_prior](#), [create_cep_tree_prior](#) and [create_yule_tree_prior](#)

Usage

```
create_tree_priors()
```

Value

a list of tree_priors

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

tree_priors <- create_tree_priors()
# TRUE
is_bd_tree_prior(tree_priors[[1]])
is_cbs_tree_prior(tree_priors[[2]])
is_ccp_tree_prior(tree_priors[[3]])
is_cep_tree_prior(tree_priors[[4]])
is_yule_tree_prior(tree_priors[[5]])

check_empty_beautier_folder()
```

```
create_ucld_mean_state_node_param_xml
```

Internal function

Description

Creates the ucldMean.c parameter with the name stateNode, such as: `<parameter id=\"ucldMean.c:[id]\" spec=\"parameter.RealParameter\" name=\"stateNode\">1.0</parameter>`

Usage

```
create_ucld_mean_state_node_param_xml(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

the XML `<parameter id=\"ucldMean.c:[id]\" spec=\"parameter.RealParameter\" name=\"stateNode\">1.0</parameter>`

Author(s)

Richèl J.C. Bilderbeek

Examples

```

check_empty_beautier_folder()

create_ucld_mean_state_node_param_xml(
  create_inference_model(
    clock_model = create_rln_clock_model(id = 314),
    beauti_options = create_beauti_options_v2_6()
  )
)

check_empty_beautier_folder()

```

```

create_ucld_stdev_state_node_param_xml
      Internal function

```

Description

Creates the ucldStdev parameter with the name stateNode, such as: <parameter id="ucldStdev.c:[id]" [...] name="stateNode">0.1</parameter>

Usage

```
create_ucld_stdev_state_node_param_xml(inference_model)
```

Arguments

`inference_model`
 a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

the following XML: <parameter id="ucldStdev.c:[id]" lower="0.0" name="stateNode"> 0.1 </parameter>

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

create_ucld_stdev_state_node_param_xml(
  create_inference_model(
    clock_model = create_rln_clock_model(id = 314)
  )
)

check_empty_beautier_folder()
```

create_uniform_distr *Create a uniform distribution*

Description

Create a uniform distribution

Usage

```
create_uniform_distr(id = NA, value = NA, lower = NA, upper = Inf)
```

Arguments

id	the distribution's ID
value	the initial value for the MCMC
lower	the lower bound, the lowest possible value
upper	an upper limit of the uniform distribution. If the upper limits needs to be infinity, set upper to Inf.

Value

a uniform distribution

Author(s)

Richèl J.C. Bilderbeek

See Also

the function [create_distr](#) shows an overview of all supported distributions

Examples

```
if (is_on_ci()) {  
  
  uniform_distr <- create_uniform_distr()  
  
  beast2_input_file <- get_beautier_tempfilename()  
  create_beast2_input_file(  
    input_filename = get_fasta_filename(),  
    beast2_input_file,  
    tree_prior = create_yule_tree_prior(  
      birth_rate_distr = uniform_distr  
    )  
  )  
  file.remove(beast2_input_file)  
  
  remove_beautier_folder()  
}
```

create_xml_declaration

Create the XML declaration of the BEAST2 XML input file

Description

Create the XML declaration of the BEAST2 XML input file

Usage

```
create_xml_declaration()
```

Value

one line of XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()  
  
create_xml_declaration()  
  
check_empty_beautier_folder()
```

`create_yule_tree_prior`*Create a Yule tree prior*

Description

Create a Yule tree prior

Usage

```
create_yule_tree_prior(  
  id = NA,  
  birth_rate_distr = create_uniform_distr()  
)
```

Arguments

`id` the ID of the alignment
`birth_rate_distr` the birth rate distribution, as created by a [create_distr](#) function

Value

a Yule tree_prior

Author(s)

Richèl J.C. Bilderbeek

See Also

An alignment ID can be extracted from its FASTA filename using [get_alignment_id](#)

Examples

```
if (is_on_ci()) {  
  
  yule_tree_prior <- create_yule_tree_prior()  
  
  beast2_input_file <- get_beautier_tempfilename()  
  create_beast2_input_file(  
    input_filename = get_fasta_filename(),  
    beast2_input_file,  
    tree_prior = yule_tree_prior  
  )  
  file.remove(beast2_input_file)  
  
  remove_beautier_folder()  
}
```

`default_parameters_doc`

Documentation of parameters (for example, `create_param`. This function does nothing. It is intended to inherit documentation from.

Description

Documentation of parameters (for example, `create_param`. This function does nothing. It is intended to inherit documentation from.

Usage

```
default_parameters_doc(dimension, estimate, id, lower, name, upper, value, ...)
```

Arguments

<code>dimension</code>	the number of dimensions, for example, as used in create_freq_param
<code>estimate</code>	TRUE if this parameter is to be estimated by BEAST2, FALSE otherwise
<code>id</code>	the parameter's ID
<code>lower</code>	lowest possible value of the parameter. If the parameter is estimated, lower must be less than value
<code>name</code>	the parameters' name. Valid names can be found in <code>get_param_names</code>
<code>upper</code>	upper value of the parameter
<code>value</code>	value of the parameter
<code>...</code>	specific parameter parameters

Note

This is an internal function, so it should be marked with `@export`. This is not done, as this will disallow all functions to find the documentation parameters

Author(s)

Richèl J.C. Bilderbeek

default_params_doc	<i>Documentation of general function arguments. This function does nothing. It is intended to inherit function argument documentation.</i>
--------------------	--

Description

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

Usage

```
default_params_doc(
  alignment_id,
  allow_empty_str,
  allow_na,
  alpha_parameter,
  b_pop_sizes_param,
  b_pop_sizes_parameter,
  bd_tree_prior,
  beautier_folder,
  cbs_tree_prior,
  beast2_version,
  beauti_options,
  beta_parameter,
  ccp_tree_prior,
  cep_tree_prior,
  chain_length,
  clock_model,
  clock_model_name,
  clock_model_names,
  clock_models,
  clock_prior_distr_id,
  clock_rate_param,
  crown_age,
  crown_ages,
  distr_id,
  fasta_filename,
  fasta_filenames,
  filename,
  fixed_crown_age,
  fixed_crown_ages,
  freq_param,
  gamma_distr,
  gamma_site_model,
  group_sizes_dimension,
  gtr_site_model,
  has_non_strict_clock_model,
```

has_tip_dating,
hky_site_model,
id,
ids,
inference_model,
inference_models,
initial_phylogenies,
input_filename,
input_filenames,
is_monophyletic,
jc69_site_model,
kappa_param,
log_every,
m_param,
mcmc,
mode,
mrca_prior,
mrca_priors,
mrca_prior_name,
n_init_attempts,
output_filename,
param,
param_id,
phylogeny,
pop_sizes_scaler_scale_factor,
pre_burnin,
rate_scaler_factor,
rename_fun,
rln_clock_model,
sample_from_prior,
sanitise_headers,
screenlog,
sequence_length,
site_model,
site_model_name,
site_model_names,
site_models,
sort,
store_every,
strict_clock_model,
taxa_names,
tipdates_filename,
tn93_site_model,
tracelog,
treelog,
tree_prior,
tree_prior_name,
tree_prior_names,

```

    tree_priors,
    verbose,
    yule_tree_prior
)

```

Arguments

alignment_id ID of the alignment, as returned by [get_alignment_id](#). Keep at NA to have it initialized automatically

allow_empty_str allow a string to be empty

allow_na allow [NA](#)

alpha_parameter an alpha parameter, as created by [create_alpha_param](#)

b_pop_sizes_param a Bayesian population size parameter, as created by [create_b_pop_sizes_param](#)

b_pop_sizes_parameter a Bayesian population size parameter, as created by [create_b_pop_sizes_param](#)

bd_tree_prior a Birth-Death tree prior, as created by [create_bd_tree_prior](#)

beautier_folder the path to the [beautier](#) temporary files folder

cbs_tree_prior a Coalescent Bayesian Skyline tree prior, as returned by [create_cbs_tree_prior](#)

beast2_version BEAST2 version, for example, "2.5"

beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

beta_parameter a beta parameter, as created by [create_beta_param](#)

ccp_tree_prior a Coalescent Constant Population tree prior, as returned by [create_ccp_tree_prior](#)

cep_tree_prior a Coalescent Exponential Population tree prior, as returned by [create_cep_tree_prior](#)

chain_length length of the MCMC chain

clock_model a clock model, as returned by [create_clock_model](#)

clock_model_name name of a clock model, must be a name as returned by [get_clock_model_names](#)

clock_model_names one or more names of a clock model, must be name among those returned by [get_clock_model_names](#)

clock_models a list of one or more clock models, as returned by [create_clock_model](#)

clock_prior_distr_id ID of an MRCA clock model's distribution. Keep at NA to have it initialized automatically

clock_rate_param a clockRate parameter, a numeric value, as created by [create_clock_rate_param](#)

crown_age the crown age of the phylogeny

crown_ages the crown ages of the phylogenies. Set to NA if the crown age needs to be estimated

distr_id	a distributions' ID
fasta_filename	a FASTA filename. Use get_fasta_filename to obtain a testing FASTA filename. Note that BEAST2 also supports missing data, by using a dash (-) or question mark (?) as a sequence.
fasta_filenames	One or more FASTA filenames. Use get_fasta_filename to obtain a testing FASTA filename.
filename	a filename, as can be checked by check_filename
fixed_crown_age	determines if the phylogeny's crown age is fixed. If FALSE, crown age is estimated by BEAST2. If TRUE, the crown age is fixed to the crown age of the initial phylogeny.
fixed_crown_ages	one or more booleans to determine if the phylogenies' crown ages are fixed. If FALSE, crown age is estimated by BEAST2. If TRUE, the crown age is fixed to the crown age of the initial phylogeny.
freq_param	a 'freq' parameter, as created by create_freq_param
gamma_distr	a gamma distribution, as created by create_gamma_distr
gamma_site_model	a site model's gamma site model, as returned by create_gamma_site_model
group_sizes_dimension	the group sizes' dimension, as used by the CBS tree prior (see create_cbs_tree_prior)
gtr_site_model	a GTR site model, as returned by create_gtr_site_model
has_non_strict_clock_model	boolean to indicate that there is already at least one non-strict (i.e. relaxed log-normal) clock model
has_tip_dating	TRUE if the user has supplied tip dates, FALSE otherwise
hky_site_model	an HKY site model, as returned by create_hky_site_model
id	an alignment's IDs. An ID can be extracted from its FASTA filename with get_alignment_ids_from_fasta_filenames
ids	one or more alignments' IDs. IDs can be extracted from their FASTA filenames with get_alignment_ids_from_fasta_filenames
inference_model	a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use create_inference_model to create an inference model. Use check_inference_model to check if an inference model is valid. Use rename_inference_model_filenames to rename the files in an inference model.
inference_models	a list of one or more inference models, as can be created by create_inference_model
initial_phylogenies	one or more MCMC chain's initial phylogenies. Each one set to NA will result in BEAST2 using a random phylogeny. Else the phylogeny is assumed to be of class phylo from the ape package

input_filename	A FASTA filename. Use get_fasta_filename to obtain a testing FASTA filename.
input_filenames	One or more FASTA filenames. Use get_fasta_filename to obtain a testing FASTA filename.
is_monophyletic	boolean to indicate monophyly is assumed in a Most Recent Common Ancestor prior, as returned by create_mrca_prior
jc69_site_model	a JC69 site model, as returned by create_jc69_site_model
kappa_param	a kappa parameter, as created by create_kappa_param
log_every	number of MCMC states between writing to file
m_param	an m parameter, as created by create_m_param
mcmc	one MCMC. Use create_mcmc to create an MCMC. Use create_ns_mcmc to create an MCMC for a Nested Sampling run. Use check_mcmc to check if an MCMC is valid. Use rename_mcmc_filenames to rename the filenames in an MCMC.
mode	mode how to log. Valid values are the ones returned by get_log_modes
mrca_prior	a Most Recent Common Ancestor prior, as returned by create_mrca_prior
mrca_priors	a list of one or more Most Recent Common Ancestor priors, as returned by create_mrca_prior
mrca_prior_name	the unique name of the MRCA prior, for example a genus, family, order or even class name. Leave at NA to have it named automatically.
n_init_attempts	number of initialization attempts before failing
output_filename	Name of the XML parameter file created by this function. BEAST2 uses this file as input.
param	a parameter, as can be created by create_param .
param_id	a parameter's ID
phylogeny	a phylogeny of type phylo from the ape package
pop_sizes_scaler_scale_factor	the scale factor used by the population sizes scaler operator
pre_burnin	number of burn in samples taken before entering the main loop
rate_scaler_factor	the strict clock model's operator scaler for the rate. Use an empty string to indicate the default.
rename_fun	a function to rename a filename, as can be checked by check_rename_fun . This function should have one argument, which will be a filename or NA . The function should return one filename (when passed one filename) or one NA (when passed one NA). Example rename functions are: • get_remove_dir_fun get a function that removes the directory paths from the filenames, in effect turning these into local files

- [get_replace_dir_fun](#) get a function that replaces the directory paths from the filenames
- [get_remove_hex_fun](#) get a function that removes the hex string from filenames. For example, `tracelog_82c1a522040.log` becomes `tracelog.log`

<code>rln_clock_model</code>	a Relaxed Log-Normal clock model, as returned by create_rln_clock_model
<code>sample_from_prior</code>	set to TRUE to sample from the prior
<code>sanitise_headers</code>	set to TRUE to sanitise the headers of the log file
<code>screenlog</code>	a screenlog, as created by create_screenlog
<code>sequence_length</code>	a DNA sequence length, in base pairs
<code>site_model</code>	a site model, as returned by create_site_model
<code>site_model_name</code>	name of a site model, must be a name as returned by get_site_model_names
<code>site_model_names</code>	one or more names of a site model, must be name among those returned by get_site_model_names
<code>site_models</code>	one or more site models, as returned by create_site_model
<code>sort</code>	how to sort the log. Valid values are the ones returned by get_log_sorts
<code>store_every</code>	number of states the MCMC will process before the posterior's state will be saved to file. Use -1 or NA to use the default frequency.
<code>strict_clock_model</code>	a strict clock model, as returned by create_strict_clock_model
<code>taxa_names</code>	names of the taxa, as returned by get_taxa_names . Keep at NA to have it initialized automatically, using all taxa in the alignment
<code>tipdates_filename</code>	name of the file containing the tip dates. This file is assumed to have two columns, separated by a tab. The first column contains the taxa names, the second column contains the date.
<code>tn93_site_model</code>	a TN93 site model, as returned by create_tn93_site_model
<code>tracelog</code>	a tracelog, as created by create_tracelog
<code>treelog</code>	a treelog, as created by create_treelog
<code>tree_prior</code>	a tree priors, as returned by create_tree_prior
<code>tree_prior_name</code>	name of a tree prior, must be a name as returned by get_tree_prior_names
<code>tree_prior_names</code>	one or more names of a tree prior, must be a name among those returned by get_tree_prior_names
<code>tree_priors</code>	one or more tree priors, as returned by create_tree_prior
<code>verbose</code>	if TRUE , additional information is displayed, that is potentially useful in debugging
<code>yule_tree_prior</code>	a Yule tree_prior, as created by create_yule_tree_prior

Note

This is an internal function, so it should be marked with `@export`. This is not done, as this will disallow all functions to find the documentation parameters

Author(s)

Richèl J.C. Bilderbeek

distr_to_xml

Internal function

Description

Converts a distribution to XML

Usage

```
distr_to_xml(distr, beauti_options)
```

Arguments

distr a distribution, as created by [create_distr](#))

beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

the distribution as XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

distr_to_xml(
  create_uniform_distr(id = 1),
  beauti_options = create_beauti_options()
)

check_empty_beautier_folder()
```

distr_to_xml_beta	<i>Internal function</i>
-------------------	--------------------------

Description

Converts a beta distribution to XML

Usage

```
distr_to_xml_beta(distr, beauti_options)
```

Arguments

distr a beta distribution, as created by [create_beta_distr](#))
beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

the distribution as XML text

Author(s)

Richèl J.C. Bilderbeek

distr_to_xml_exp	<i>Internal function</i>
------------------	--------------------------

Description

Converts an exponential distribution to XML

Usage

```
distr_to_xml_exp(distr, beauti_options)
```

Arguments

distr an exponential distribution, as created by [create_exp_distr](#))
beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

the distribution as XML text

Author(s)

Richèl J.C. Bilderbeek

`distr_to_xml_inv_gamma`*Internal function*

Description

Converts an inverse-gamma distribution to XML

Usage

```
distr_to_xml_inv_gamma(distr, beauti_options)
```

Arguments

`distr` an inverse-gamma distribution, as created by [create_inv_gamma_distr](#)
`beauti_options` one BEAUti options object, as returned by [create_beauti_options](#)

Value

the distribution as XML text

Author(s)

Richèl J.C. Bilderbeek

`distr_to_xml_laplace` *Internal function*

Description

Converts a Laplace distribution to XML

Usage

```
distr_to_xml_laplace(distr, beauti_options)
```

Arguments

`distr` a Laplace distribution as created by [create_laplace_distr](#)
`beauti_options` one BEAUti options object, as returned by [create_beauti_options](#)

Value

the distribution as XML text

Author(s)

Richèl J.C. Bilderbeek

`distr_to_xml_log_normal`*Internal function*

Description

Converts a log-normal distribution to XML

Usage

```
distr_to_xml_log_normal(distr, beauti_options)
```

Arguments

`distr` a log-normal distribution, as created by [create_log_normal_distr](#)
`beauti_options` one BEAUti options object, as returned by [create_beauti_options](#)

Value

the distribution as XML text

Author(s)

Richèl J.C. Bilderbeek

`distr_to_xml_normal` *Internal function*

Description

Converts a normal distribution to XML

Usage

```
distr_to_xml_normal(distr, beauti_options)
```

Arguments

`distr` a normal distribution, as created by [create_normal_distr](#)
`beauti_options` one BEAUti options object, as returned by [create_beauti_options](#)

Value

the distribution as XML text

Author(s)

Richèl J.C. Bilderbeek

`distr_to_xml_one_div_x`*Internal function*

Description

Converts a $1/x$ distribution to XML

Usage

```
distr_to_xml_one_div_x(distr, beauti_options)
```

Arguments

`distr` a $1/x$ distribution, as created by [create_one_div_x_distr](#)
`beauti_options` one BEAUti options object, as returned by [create_beauti_options](#)

Value

the distribution as XML text

Author(s)

Richèl J.C. Bilderbeek

`distr_to_xml_poisson` *Internal function*

Description

Converts a Poisson distribution to XML

Usage

```
distr_to_xml_poisson(distr, beauti_options)
```

Arguments

`distr` a Poisson distribution, as created by [create_poisson_distr](#)
`beauti_options` one BEAUti options object, as returned by [create_beauti_options](#)

Value

the distribution as XML text

Author(s)

Richèl J.C. Bilderbeek

distr_to_xml_uniform *Internal function*

Description

Converts a uniform distribution to XML

Usage

```
distr_to_xml_uniform(distr, beauti_options)
```

Arguments

distr a uniform distribution, as created by [create_uniform_distr](#))
beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

the distribution as XML text

Author(s)

Richèl J.C. Bilderbeek

extract_xml_loggers_from_lines
 Extract everything between first loggers and last loggers line

Description

Extract everything between first loggers and last loggers line

Usage

```
extract_xml_loggers_from_lines(lines)
```

Arguments

lines lines of text

Value

lines of text from the first to and including the last operators line

Author(s)

Richèl J.C. Bilderbeek

`extract_xml_operators_from_lines`*Extract everything between first operators and last operators line*

Description

Extract everything between first operators and last operators line

Usage

```
extract_xml_operators_from_lines(lines)
```

Arguments

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

Value

lines of text from the first to and including the last operators line

Author(s)

Richèl J.C. Bilderbeek

`extract_xml_section_from_lines`*Get the lines of an XML section, including the section tags*

Description

Get the lines of an XML section, including the section tags

Usage

```
extract_xml_section_from_lines(lines, section)
```

Arguments

lines	lines of the XML text
section	the XML section name

Value

the section's lines of XML text, including the tags

Author(s)

Richèl J.C. Bilderbeek

`fasta_file_to_sequences`*Convert a FASTA file to a table of sequences*

Description

Convert a FASTA file to a table of sequences

Usage

```
fasta_file_to_sequences(fasta_filename)
```

Arguments

`fasta_filename` One existing FASTA filenames

Value

a table of sequences

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

fasta_file_to_sequences(fasta_filename = get_fasta_filename())

check_empty_beautier_folder()
```

`find_clock_model`*Finds a clock model with a certain ID*

Description

Finds a clock model with a certain ID

Usage

```
find_clock_model(clock_models, id)
```

Arguments

`clock_models` a list of one or more clock models, as returned by [create_clock_model](#)
`id` the ID of the clock model

Value

the clock models with the desired ID, NULL if such a clock model is absent

Author(s)

Richèl J.C. Bilderbeek

<code>find_first_regex_line</code>	<i>Find the first line that satisfies a regex</i>
------------------------------------	---

Description

Find the first line that satisfies a regex

Usage

```
find_first_regex_line(lines, regex)
```

Arguments

<code>lines</code>	lines of text
<code>regex</code>	the regex as text

Value

index of the line

Author(s)

Richèl J.C. Bilderbeek

<code>find_first_xml_opening_tag_line</code>	<i>Find the line number of the first section's opening tag</i>
--	--

Description

Find the line number of the first section's opening tag

Usage

```
find_first_xml_opening_tag_line(lines, section)
```

Arguments

lines	the lines of an XML text
section	the name of the XML section

Value

the line number's index (which is 1 for the first line) if the opening tag is found, else NA

Author(s)

Richèl J.C. Bilderbeek

find_last_regex_line	<i>Find the index of the last line that matches a regex</i>
----------------------	---

Description

Find the index of the last line that matches a regex

Usage

```
find_last_regex_line(lines, regex)
```

Arguments

lines	lines of text
regex	regex string

Value

index of the line

Author(s)

Richèl J.C. Bilderbeek

```
find_last_xml_closing_tag_line
```

Find the highest line number of a section's closing tag

Description

Find the highest line number of a section's closing tag

Usage

```
find_last_xml_closing_tag_line(lines, section)
```

Arguments

lines	the lines of an XML text
section	the name of the XML section

Value

the line number's index (which is 1 for the first line) if the opening tag is found, else NA

Author(s)

Richèl J.C. Bilderbeek

```
freq_equilibrium_to_xml
```

Creates the freq_equilibrium as XML

Description

Creates the freq_equilibrium as XML

Usage

```
freq_equilibrium_to_xml(freq_equilibrium, id)
```

Arguments

freq_equilibrium	a freq_equilibrium name
id	a site model's name

Value

the freq_equilibrium as XML

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

freq_equilibrium_to_xml(freq_equilibrium = "estimated", id = "my_id")

check_empty_beautier_folder()
```

freq_param_to_xml	<i>Internal function</i>
-------------------	--------------------------

Description

Converts a ‘freq’ parameter to XML

Usage

```
freq_param_to_xml(freq_param, beauti_options = create_beauti_options())
```

Arguments

freq_param a ‘freq’ parameter, as created by [create_freq_param](#)
beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

the parameter as XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# The freq parameter must be initialized, i.e. have an ID
freq_param_to_xml(freq_param = create_freq_param(id = "1"))

check_empty_beautier_folder()
```

gamma_distr_to_xml	<i>Internal function</i>
--------------------	--------------------------

Description

Converts a gamma distribution to XML

Usage

```
gamma_distr_to_xml(gamma_distr, beauti_options = create_beauti_options())
```

Arguments

gamma_distr a gamma distribution, as created by [create_gamma_distr](#))

beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

the distribution as XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# gamma distribution must be initialized
gamma_distr_to_xml(
  gamma_distr = create_gamma_distr(
    id = "0",
    alpha = create_alpha_param(id = "2", value = "0.5396"),
    beta = create_beta_param(id = "3", value = "0.3819")
  )
)

check_empty_beautier_folder()
```

gamma_site_models_to_xml_prior_distr
Deprecated function

Description

Internal function to creates the gamma site models section in the distribution section of a BEAST2 XML parameter file

Usage

```
gamma_site_models_to_xml_prior_distr(  
  site_models,  
  beauti_options = create_beauti_options()  
)
```

Arguments

site_models one or more site models, as returned by [create_site_model](#)
beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

gamma_site_model_to_xml_prior_distr
Internal function.

Description

Creates the gamma site models section in the distribution section of a BEAST2 XML parameter file

Usage

```
gamma_site_model_to_xml_prior_distr(inference_model)
```

Arguments

`inference_model`
a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

<code>gamma_site_model_to_xml_state</code>
<i>Converts a gamma site model to XML, used in the state section</i>

Description

Converts a gamma site model to XML, used in the state section

Usage

```
gamma_site_model_to_xml_state(gamma_site_model, id)
```

Arguments

`gamma_site_model`
a gamma site model, as created by [create_gamma_site_model](#))
`id`
the site model's ID

Value

the gamma_site model as XML text

Author(s)

Richèl J.C. Bilderbeek

get_alignment_id	<i>Conclude the ID from a FASTA filename.</i>
------------------	---

Description

This is done in the same way as BEAST2 will do so.

Usage

```
get_alignment_id(fasta_filename, capitalize_first_char_id = FALSE)
```

Arguments

`fasta_filename` a FASTA filename. Use [get_fasta_filename](#) to obtain a testing FASTA filename. Note that BEAST2 also supports missing data, by using a dash (-) or question mark (?) as a sequence.

`capitalize_first_char_id`
if TRUE, the first character will be capitalized

Value

an alignment's ID

Author(s)

Rich  l J.C. Bilderbeek

See Also

Use [check_alignment_id](#) to check if an alignment ID is valid.

Examples

```
check_empty_beautier_folder()

# Path need not exist, use UNIX path as example
# anthus_aco_sub
alignment_id <- get_alignment_id("/home/homer/anthus_aco_sub.fas")
check_alignment_id(alignment_id)

check_empty_beautier_folder()
```

get_alignment_ids	<i>Get the alignment IDs from one or more files.</i>
-------------------	--

Description

This is done in the same way as BEAST2 does by default The file extension will be used to determine which type of file is worked on.

Usage

```
get_alignment_ids(filenamees)
```

Arguments

filenamees	names of the files to be checked
------------	----------------------------------

Value

the IDs extracted from the one or more files

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [get_alignment_ids_from_fasta_filenames](#) to get the alignment IDs from files known to be FASTA files

Examples

```
check_empty_beautier_folder()

get_alignment_ids(
  get_beautier_paths(c("anthus_aco.fas", "anthus_nd2.fas"))
)

check_empty_beautier_folder()
```

`get_alignment_ids_from_fasta_filenames`*Get the alignment ID from one or more FASTA filenames.*

Description

This is done in the same way as BEAST2 does by default. The files are assumed to be FASTA. If this is not the case, there may be any kind of error message when calling this function.

Usage

```
get_alignment_ids_from_fasta_filenames(fasta_filenames)
```

Arguments

`fasta_filenames`

One or more FASTA filenames. Use [get_fasta_filename](#) to obtain a testing FASTA filename.

Value

the IDs from one or more FASTA files

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [get_alignment_ids](#) to get the alignment IDs from multiple kinds of files. Use [are_fasta_filenames](#) to see if the filenames all have a common FASTA filename extension.

Examples

```
check_empty_beautier_folder()

get_alignment_ids_from_fasta_filenames(
  get_beautier_paths(c("anthus_aco.fas", "anthus_nd2.fas"))
)

check_empty_beautier_folder()
```

get_beautier_folder	<i>Get the path to the beautier temporary files folder</i>
---------------------	---

Description

Get the path to the **beautier** temporary files folder

Usage

```
get_beautier_folder()
```

Value

the path to the **beautier** temporary files folder

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

get_beautier_folder()

check_empty_beautier_folder()
```

get_beautier_path	<i>Get the full path of a file in the inst/extdata folder</i>
-------------------	---

Description

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

Usage

```
get_beautier_path(filename)
```

Arguments

filename	the file's name, without the path
----------	-----------------------------------

Value

the full path of the filename

Author(s)

Richèl J.C. Bilderbeek

See Also

for more files, use [get_beautier_paths](#)

Examples

```
check_empty_beautier_folder()

get_beautier_path("test_output_0.fas")
get_beautier_path("anthus_aco.fas")
get_beautier_path("anthus_nd2.fas")

check_empty_beautier_folder()
```

get_beautier_paths	<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_beautier_paths(filenamees)
```

Arguments

filenamees the files' names, without the path

Value

the filenamees' full paths

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [get_beautier_path](#) to get the path of one file
for one file, use [get_beautier_path](#)

Examples

```

check_empty_beautier_folder()

get_beautier_paths(
  c("test_output_0.fas", "anthus_aco.fas", "anthus_nd2.fas")
)

check_empty_beautier_folder()

```

```
get_beautier_tempfilename
```

Get a temporary filename

Description

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

Usage

```
get_beautier_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

```
get_clock_models_ids
```

Collect the IDs of the list of clock models

Description

Collect the IDs of the list of clock models

Usage

```
get_clock_models_ids(clock_models)
```

Arguments

clock_models a list of one or more clock models, as returned by [create_clock_model](#)

Value

IDs of the clock models

Author(s)

Richèl J.C. Bilderbeek

get_clock_model_name *Get the BEAUti name for a clock model*

Description

Will [stop](#) if the clock model is an invalid clock model

Usage

```
get_clock_model_name(clock_model)
```

Arguments

clock_model a clock model, as returned by [create_clock_model](#)

Value

name of the clock model

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# StrictClock
get_clock_model_name(create_strict_clock_model())

# RelaxedClock
get_clock_model_name(create_rln_clock_model())

check_empty_beautier_folder()
```

get_clock_model_names *Get the clock model names*

Description

Get the clock model names

Usage

```
get_clock_model_names()
```

Value

the clock model names

Author(s)

Rich  l J.C. Bilderbeek

See Also

Use [create_clock_models](#) to create a list with all clock models

Examples

```
check_empty_beautier_folder()
```

```
get_clock_model_names()
```

```
check_empty_beautier_folder()
```

get_crown_age *Obtain the crown age of a phylogeny.*

Description

The crown age of a phylogeny is the time between the present and the moment of at which the first diversification (resulting in two lineages) happened.

Usage

```
get_crown_age(phylogeny)
```

Arguments

phylogeny The phylogeny to obtain the crown age of

Value

the crown age of the phylogeny

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

phylogeny <- ape::read.tree(text = "(a:15,b:15):1;")
get_crown_age(phylogeny = phylogeny)

check_empty_beautier_folder()
```

get_default_beast_namespace

Get the default 'namespace' element value of the 'beast' XML tag.

Description

Get the default 'namespace' element value of the 'beast' XML tag.

Usage

```
get_default_beast_namespace()
```

Value

the default 'namespace' element value of the 'beast' XML tag.

Author(s)

Richèl J.C. Bilderbeek

See Also

* For BEAST2 v2.4, use [get_default_beast_namespace_v2_4](#) * For BEAST2 v2.6, use [get_default_beast_namespace_v2_6](#)

Examples

```
get_default_beast_namespace()
```

```
get_default_beast_namespace_v2_4
```

*Get the default 'namespace' element value of the 'beast' XML tag for
BEAST 2.4*

Description

Get the default 'namespace' element value of the 'beast' XML tag for BEAST 2.4

Usage

```
get_default_beast_namespace_v2_4()
```

Value

the default 'namespace' element value of the 'beast' XML tag for BEAST 2.4

Author(s)

Richèl J.C. Bilderbeek

Examples

```
get_default_beast_namespace_v2_4()
```

```
get_default_beast_namespace_v2_6
```

*Get the default 'namespace' element value of the 'beast' XML tag for
BEAST 2.6*

Description

Get the default 'namespace' element value of the 'beast' XML tag for BEAST 2.6

Usage

```
get_default_beast_namespace_v2_6()
```

Value

the default 'namespace' element value of the 'beast' XML tag for BEAST 2.6

Author(s)

Richèl J.C. Bilderbeek

Examples

```
get_default_beast_namespace_v2_6()
```

get_distr_names	<i>Get the distribution names</i>
-----------------	-----------------------------------

Description

Get the distribution names

Usage

```
get_distr_names()
```

Value

the distribution names

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

get_distr_names()

check_empty_beautier_folder()
```

get_distr_n_params	<i>Get the number of parameters a distribution uses</i>
--------------------	---

Description

Get the number of parameters a distribution uses

Usage

```
get_distr_n_params(distr)
```

Arguments

distr a distribution, as created by [create_distr](#) or (preferable) its named functions

Value

the number of parameters that distribution uses

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

get_distr_n_params(create_beta_distr())
get_distr_n_params(create_exp_distr())
get_distr_n_params(create_gamma_distr())
get_distr_n_params(create_inv_gamma_distr())
get_distr_n_params(create_laplace_distr())
get_distr_n_params(create_log_normal_distr())
get_distr_n_params(create_normal_distr())
get_distr_n_params(create_one_div_x_distr())
get_distr_n_params(create_poisson_distr())
get_distr_n_params(create_uniform_distr())

check_empty_beautier_folder()
```

get_fasta_filename	<i>Get the path of a FASTA file used in testing</i>
--------------------	---

Description

Get the path of a FASTA file used in testing

Usage

```
get_fasta_filename()
```

Value

the path of a FASTA file used in testing

Author(s)

Richèl J.C. Bilderbeek

Examples

```
if (is_on_ci()) {

  input_filename <- get_fasta_filename()
  output_filename <- get_beautier_tempfilename()

  create_beast2_input_file(
    input_filename = input_filename,
    output_filename = output_filename
```

```
)  
file.remove(output_filename)  
  
remove_beautier_folder()  
}
```

`get_file_base_sans_ext`*Get the base of the filename base without extension*

Description

The path need not to actually exist

Usage

```
get_file_base_sans_ext(filename)
```

Arguments

filename	A filename
----------	------------

Value

That filename without its full path and extension

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()  
  
# Path need not exist, use UNIX path as example  
# test  
get_file_base_sans_ext("/home/homer/test.txt")  
  
check_empty_beautier_folder()
```

`get_freq_equilibrium_names`*Returns valid values for the freq_equilibrium argument*

Description

Returns valid values for the freq_equilibrium argument

Usage

```
get_freq_equilibrium_names()
```

Value

the valid values for the freq_equilibrium argument

Author(s)

Richèl J.C. Bilderbeek

See Also

the freq_equilibrium argument is used in [create_gtr_site_model](#), [create_hky_site_model](#), and [create_tn93_site_model](#)

Examples

```
check_empty_beautier_folder()
```

```
get_freq_equilibrium_names()
```

```
check_empty_beautier_folder()
```

`get_gamma_site_model_n_distrs`*Get the number of distributions in a gamma site model*

Description

Get the number of distributions in a gamma site model

Usage

```
get_gamma_site_model_n_distrs(gamma_site_model)
```

Arguments

`gamma_site_model`
a site model's gamma site model, as returned by [create_gamma_site_model](#)

Value

the number of distributions a gamma site model has

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_gamma_site_model](#) to create a gamma site model

Examples

```
check_empty_beautier_folder()

# zero distributions
gamma_site_model <- create_gamma_site_model()
get_gamma_site_model_n_distrs(
  gamma_site_model
)

gamma_site_model <- create_gamma_site_model(
  gamma_cat_count = 2,
  gamma_shape_prior_distr = create_exp_distr()
)

# one distribution
get_gamma_site_model_n_distrs(gamma_site_model)

check_empty_beautier_folder()
```

`get_gamma_site_model_n_params`

Get the number of distributions a site model has

Description

Get the number of distributions a site model has

Usage

```
get_gamma_site_model_n_params(gamma_site_model)
```

Arguments

`gamma_site_model`

a site model's gamma site model, as returned by [create_gamma_site_model](#)

Value

the number of parameters a site model has

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# 0 parameters
get_gamma_site_model_n_params(
  create_gamma_site_model(gamma_cat_count = 0)
)

# 0 parameters
get_gamma_site_model_n_params(
  create_gamma_site_model(gamma_cat_count = 1)
)

# 1 parameter
get_gamma_site_model_n_params(
  create_gamma_site_model(
    gamma_cat_count = 2,
    gamma_shape_prior_distr = create_exp_distr()
  )
)

check_empty_beautier_folder()
```

`get_has_non_strict_clock_model`

Determines if there is at least one non-strict clock model in the list of one or more clock models

Description

Determines if there is at least one non-strict clock model in the list of one or more clock models

Usage

```
get_has_non_strict_clock_model(clock_models)
```


Arguments

clock_models a list of one or more clock models, as returned by [create_clock_model](#)

Value

TRUE if there is at least one non-strict clock model

Author(s)

Richèl J.C. Bilderbeek

get_inference_model_filenames

Get the filenames stored in an inference model.

Description

If there is no name for a tipdates file specified (as done by setting inference_model\$tipdates_filename to [NA](#), there will be one filename less returned

Usage

```
get_inference_model_filenames(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

the filenames stored in an inference model

Examples

```
check_empty_beautier_folder()

inference_model <- create_inference_model()
filenames <- get_inference_model_filenames(inference_model)

check_empty_beautier_folder()
```

get_log_modes	<i>Get the possible log modes</i>
---------------	-----------------------------------

Description

Get the possible log modes

Usage

```
get_log_modes()
```

Value

the possible log modes

Author(s)

Richèl J.C. Bilderbeek

Examples

```
get_log_modes()
```

get_log_sorts	<i>Get the possible log sorts</i>
---------------	-----------------------------------

Description

Get the possible log sorts

Usage

```
get_log_sorts()
```

Value

the possible log sorts

Author(s)

Richèl J.C. Bilderbeek

Examples

```
get_log_sorts()
```

get_mcmc_filenames	<i>Get the filenames stored in an MCMC.</i>
--------------------	---

Description

If a filename is set to an empty string, to indicate a certain log file need not be created, this (non-)filename will not be returned.

Usage

```
get_mcmc_filenames(mcmc)
```

Arguments

mcmc	one MCMC. Use create_mcmc to create an MCMC. Use create_ns_mcmc to create an MCMC for a Nested Sampling run. Use check_mcmc to check if an MCMC is valid. Use rename_mcmc_filenames to rename the filenames in an MCMC.
------	---

Value

the filenames stored in an MCMC

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

mcmc <- create_mcmc()
mcmc$tracelog$filename <- "/home/john/trace.log"
mcmc$screenlog$filename <- "/home/john/screen.log"
mcmc$treelog$filename <- "/home/john/tree.log"

# 3 filenames
filenames <- get_mcmc_filenames(mcmc)

# If there is no need to write to the screenlog file ...
mcmc$screenlog$filename <- ""

# 2 filenames
# ... one file less will be created
filenames <- get_mcmc_filenames(mcmc)

check_empty_beautier_folder()
```

get_n_taxa	<i>Extract the number of taxa from a file</i>
------------	---

Description

Extract the number of taxa from a file

Usage

```
get_n_taxa(filename)
```

Arguments

filename	name of a FASTA file
----------	----------------------

Value

the number of taxa

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

fasta_filename <- get_beautier_path("test_output_5.fas")
# 5
get_n_taxa(fasta_filename)

check_empty_beautier_folder()
```

get_operator_id_pre	<i>Get the prefix of operator IDs</i>
---------------------	---------------------------------------

Description

Get the prefix of operator IDs

Usage

```
get_operator_id_pre(tree_prior)
```

Arguments

tree_prior	a tree priors, as returned by create_tree_prior
------------	---

Value

the prefix of operator IDs, similar to the name of a tree prior

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# BirthDeath
get_operator_id_pre(
  tree_prior = create_bd_tree_prior()
)

check_empty_beautier_folder()
```

get_param_names	<i>Get the parameter names</i>
-----------------	--------------------------------

Description

Get the parameter names

Usage

```
get_param_names()
```

Value

the parameter names

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

names <- get_param_names()

check_empty_beautier_folder()
```

get_remove_dir_fun	<i>Get a function that, from a filename, returns the part without the directory.</i>
--------------------	--

Description

Or: get a function that returns the local version of a filename. Also, the function will return [NA](#) if the filename is [NA](#)

Usage

```
get_remove_dir_fun()
```

Value

a function to remove the folder name from a path

Author(s)

Rich  l J.C. Bilderbeek

See Also

see [check_rename_fun](#) for an overview of file renaming functions

get_remove_hex_fun	<i>Get a function that removes the hex string from filenames.</i>
--------------------	---

Description

The default filenames created by [beautier](#) are temporary files, such as /home/john/.cache/trace_log_82c5888db98.log (on Linux), where /home/john/.cache is the location to a temporary folder (on Linux) and trace_log_82c5888db98.log the filename. The filename ends with a hex string (as is common for temporary files, as [tempfile](#) does so). Because [beautier](#) puts an underscore between the filename description (trace_log) and the hex string, this function removes both.

Usage

```
get_remove_hex_fun()
```

Value

a function to remove the hex string from filenames

Author(s)

Rich  l J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

f <- get_remove_hex_fun()
# /home/john/beast2.xml.state
f("/home/john/beast2_186c7404208c.xml.state")

# beast2.xml.state
f("beast2_186c7404208c.xml.state")

# NA
f(NA)

check_empty_beautier_folder()
```

get_replace_dir_fun	<i>Get a function to replace the directory of a filename</i>
---------------------	--

Description

Get a function to replace the directory of a filename

Usage

```
get_replace_dir_fun(new_dir_name = "")
```

Arguments

new_dir_name the new directory name

Value

a function to replace the directory of a filename

Author(s)

Richèl J.C. Bilderbeek

`get_site_models_n_distrs`*Get the number of distributions a site model has*

Description

Get the number of distributions a site model has

Usage

```
get_site_models_n_distrs(site_models)
```

Arguments

`site_models` one or more site models, as returned by [create_site_model](#)

Value

the number of distributions the site models have

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# 5
get_site_models_n_distrs(list(create_gtr_site_model()))
# 1
get_site_models_n_distrs(list(create_hky_site_model()))
# 0
get_site_models_n_distrs(list(create_jc69_site_model()))
# 2
get_site_models_n_distrs(list(create_tn93_site_model()))

check_empty_beautier_folder()
```

`get_site_models_n_params`*Get the number of distributions one or more site models have*

Description

Get the number of distributions one or more site models have

Usage

```
get_site_models_n_params(site_models)
```

Arguments

`site_models` one or more site models, as returned by [create_site_model](#)

Value

the number of parameters the site models have

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# Ten
get_site_models_n_params(list(create_gtr_site_model()))

# Two
get_site_models_n_params(list(create_hky_site_model()))

# Zero
get_site_models_n_params(list(create_jc69_site_model()))

# Four
get_site_models_n_params(list(create_tn93_site_model()))

check_empty_beautier_folder()
```

get_site_model_names *Get the site models' names*

Description

Get the site models' names

Usage

```
get_site_model_names()
```

Value

the site model names

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_site_models](#) to get all site models

Examples

```
check_empty_beautier_folder()
```

```
get_site_model_names()
```

```
check_empty_beautier_folder()
```

get_site_model_n_distrs

Get the number of distributions a site model has

Description

Get the number of distributions a site model has

Usage

```
get_site_model_n_distrs(site_model)
```

Arguments

site_model a site model, as returned by [create_site_model](#)

Value

the number of distributions a site model has

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# 5: rates AC, AG, AT, CG and GT
get_site_model_n_distrs(create_gtr_site_model())

# 1: kappa
get_site_model_n_distrs(create_hky_site_model())

# 0: npne
get_site_model_n_distrs(create_jc69_site_model())

# 2: kappa 1 and kappa 2
get_site_model_n_distrs(create_tn93_site_model())

check_empty_beautier_folder()
```

```
get_site_model_n_params
```

Get the number of distributions a site model has

Description

Get the number of distributions a site model has

Usage

```
get_site_model_n_params(site_model)
```

Arguments

site_model a site model, as returned by [create_site_model](#)

Value

the number of parameters a site model has

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# Ten
get_site_model_n_params(create_gtr_site_model())

# Two
get_site_model_n_params(create_hky_site_model())

# Zero
get_site_model_n_params(create_jc69_site_model())

# Four
get_site_model_n_params(create_tn93_site_model())

check_empty_beautier_folder()
```

get_taxa_names	<i>Extract the names of taxa from a file</i>
----------------	--

Description

Extract the names of taxa from a file

Usage

```
get_taxa_names(filename)
```

Arguments

filename	name of a FASTA file
----------	----------------------

Value

the taxa names

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

get_taxa_names(get_beautier_path("anthus_aco_sub.fas"))

check_empty_beautier_folder()
```

`get_tree_priors_n_distrs`*Get the number of distributions a tree prior has*

Description

Get the number of distributions a tree prior has

Usage

```
get_tree_priors_n_distrs(tree_priors)
```

Arguments

`tree_priors` one or more tree priors, as returned by [create_tree_prior](#)

Value

the number of distributions a tree prior has

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# Three distributions
get_tree_priors_n_distrs(
  list(
    create_bd_tree_prior(), # has two distributions
    create_ccp_tree_prior() # has one distribution
  )
)

check_empty_beautier_folder()
```

`get_tree_priors_n_params`*Get the number of parameters a list of tree priors has*

Description

Get the number of parameters a list of tree priors has

Usage

```
get_tree_priors_n_params(tree_priors)
```

Arguments

tree_priors one or more tree priors, as returned by [create_tree_prior](#)

Value

the number of parameters the tree priors have

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# Two
get_tree_priors_n_params(
  list(
    create_bd_tree_prior(), # zero
    create_cep_tree_prior() # two
  )
)

check_empty_beautier_folder()
```

get_tree_prior_names *Get the tree prior names*

Description

Get the tree prior names

Usage

```
get_tree_prior_names()
```

Value

the tree prior names

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_tree_priors](#) to get all tree priors

Examples

```
check_empty_beautier_folder()

get_tree_prior_names()

check_empty_beautier_folder()
```

`get_tree_prior_n_distrs`

Get the number of distributions a tree prior has

Description

Get the number of distributions a tree prior has

Usage

```
get_tree_prior_n_distrs(tree_prior)
```

Arguments

`tree_prior` a tree priors, as returned by [create_tree_prior](#)

Value

the number of distributions a tree prior has

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# 2: birth_rate_distr and death_rate_distr
get_tree_prior_n_distrs(create_bd_tree_prior())

# 0: none
get_tree_prior_n_distrs(create_cbs_tree_prior())

# 1: pop_size_distr
get_tree_prior_n_distrs(create_ccp_tree_prior())

# 2: pop_size_distr and growth_rate_distr
```

```
get_tree_prior_n_distrs(create_cep_tree_prior())

# 1: birth_rate_distr
get_tree_prior_n_distrs(create_yule_tree_prior())

check_empty_beautier_folder()
```

get_tree_prior_n_params

Get the number of parameters a tree prior has

Description

Get the number of parameters a tree prior has

Usage

```
get_tree_prior_n_params(tree_prior)
```

Arguments

tree_prior a tree_prior, as created by [create_tree_prior](#)

Value

the number of parameters a tree prior has

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# birth_rate_distr is uniform, which has zero parameters
# death_rate_distr is uniform, which has zero parameters
get_tree_prior_n_params(create_bd_tree_prior())

# no distributions, no parameters
get_tree_prior_n_params(create_cbs_tree_prior())

# pop_size_distr is 1/x, which has zero parameters
get_tree_prior_n_params(create_ccp_tree_prior())

# pop_size_distr is 1/x, which has zero parameters
# growth_rate_distr is Laplace, which has two parameters
get_tree_prior_n_params(create_cep_tree_prior())

# birth_rate_distr is uniform, which has zero parameters
```



```
get_tree_prior_n_params(create_yule_tree_prior())  
check_empty_beautier_folder()
```

get_xml_closing_tag	<i>Get the XML closing tag</i>
---------------------	--------------------------------

Description

Get the XML closing tag

Usage

```
get_xml_closing_tag(text)
```

Arguments

text	lines of XML to extract the XML closing tag from
------	--

Value

the closing tag if found, else NA

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()  
  
# my_tag  
get_xml_closing_tag("<my_tag text=something></my_tag>")  
  
# Will return NA  
get_xml_closing_tag("<my_tag text=something/>")  
get_xml_closing_tag("no_xml")  
  
check_empty_beautier_folder()
```

get_xml_opening_tag *Get the XML opening tag*

Description

Get the XML opening tag

Usage

```
get_xml_opening_tag(text)
```

Arguments

text text to be determined to be valid

Value

the opening tag if found, else NA

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# my_tag
get_xml_opening_tag("<my_tag text=something/>")

# NA when there is no opening tag
get_xml_opening_tag("no_xml")

check_empty_beautier_folder()
```

gtr_site_model_to_xml_prior_distr
Internal function

Description

Converts a GTR site model to XML, used in the prior section

Usage

```
gtr_site_model_to_xml_prior_distr(site_model, beauti_options)
```

Arguments

site_model a site model, as returned by [create_site_model](#)
beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

the site model as XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
gtr_site_model_to_xml_prior_distr(  
  site_model = create_gtr_site_model(  
    id = 1,  
    rate_ac_prior_distr = create_uniform_distr(id = 2),  
    rate_ag_prior_distr = create_uniform_distr(id = 3),  
    rate_at_prior_distr = create_uniform_distr(id = 4),  
    rate_cg_prior_distr = create_uniform_distr(id = 5),  
    rate_gt_prior_distr = create_uniform_distr(id = 6)  
  ),  
  beauti_options = create_beauti_options()  
)
```

gtr_site_model_to_xml_state

Converts a site model to XML, used in the state section

Description

Converts a site model to XML, used in the state section

Usage

```
gtr_site_model_to_xml_state(  
  site_model,  
  beauti_options = create_beauti_options()  
)
```

Arguments

site_model a site model, as returned by [create_site_model](#)
beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

the site model as XML text

Author(s)

Richèl J.C. Bilderbeek

has_mrca_prior	<i>Determines if the inference model has an MRCA prior.</i>
----------------	---

Description

Will [stop](#) if the inference model is invalid

Usage

```
has_mrca_prior(inference_model)
```

Arguments

inference_model
a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

TRUE if the inference model has an MRCA prior, FALSE otherwise

Note

MRCA: 'Most Recent Common Ancestor'

Author(s)

Richèl J.C. Bilderbeek

See Also

- [create_inference_model](#): create an inference model
- [create_mrca_prior](#): create an MRCA prior

Examples

```
check_empty_beautier_folder()

# No MRCA prior
inference_model <- create_inference_model(
  mrca_prior = NA
)
has_mrca_prior(inference_model) # Returns FALSE

# A default MRCA prior
inference_model <- create_inference_model(
  mrca_prior = create_mrca_prior()
)
has_mrca_prior(inference_model) # Returns TRUE

check_empty_beautier_folder()
```

has_mrca_prior_with_distr

See if the inference model has one MRCA prior with a distribution

Description

See if the inference model has one MRCA prior with a distribution

Usage

```
has_mrca_prior_with_distr(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

TRUE if the inference model has one MRCA prior with a distribution, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

has_rln_clock_model	<i>Determine if the inference_model uses a relaxed log-normal clock model.</i>
---------------------	--

Description

Determine if the inference_model uses a relaxed log-normal clock model.

Usage

```
has_rln_clock_model(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

TRUE if the inference_model uses a relaxed log-normal clock model, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
if (is_on_ci()) {
  check_empty_beautier_folder()

  # Yes, has a RLN clock model
  has_rln_clock_model(
    create_inference_model(clock_model = create_rln_clock_model())
  )

  # No RLN clock model
  has_rln_clock_model(
    create_inference_model(clock_model = create_strict_clock_model())
  )

  check_empty_beautier_folder()
}
```

`has_strict_clock_model`*Determine if the inference_model uses a strict clock model.*

Description

Determine if the inference_model uses a strict clock model

Usage

```
has_strict_clock_model(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

TRUE if the inference_model uses a strict clock model, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# Yes, has a strict clock model
has_strict_clock_model(
  create_inference_model(clock_model = create_strict_clock_model())
)

# No strict clock model
has_strict_clock_model(
  create_inference_model(clock_model = create_rln_clock_model())
)

check_empty_beautier_folder()
```

has_tip_dating	<i>Determine if the inference_model uses tip dating.</i>
----------------	--

Description

Determine if the inference_model uses tip dating

Usage

```
has_tip_dating(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

TRUE if the inference_model uses tip dating, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# Yes, has tip dating
has_strict_clock_model(
  create_inference_model(
    tipdates_filename = get_beautier_path("test_output_0_tipdates.tsv")
  )
)

# No tip dating
has_strict_clock_model(
  create_inference_model()
)

check_empty_beautier_folder()
```

has_xml_closing_tag	<i>Is an XML closing tag with the value of section present among the lines of the text?</i>
---------------------	---

Description

Is an XML closing tag with the value of section present among the lines of the text?

Usage

```
has_xml_closing_tag(lines, section)
```

Arguments

lines	lines of the XML text
section	the XML section

Value

TRUE if there is an XML closing tag with the value of section present. FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

has_xml_opening_tag	<i>Is an XML opening tag with value 'section' present among the lines of the text?</i>
---------------------	--

Description

Is an XML opening tag with value 'section' present among the lines of the text?

Usage

```
has_xml_opening_tag(lines, section = NA)
```

Arguments

lines	lines of an XML text
section	if NA, this function returns TRUE if there is any XML opening tag. If section is set to a certain word, this function returns TRUE if that tag matches section

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

has_xml_short_closing_tag

Is an XML closing tag with short closing text in one of the lines of the text?

Description

Is an XML closing tag with short closing text in one of the lines of the text?

Usage

```
has_xml_short_closing_tag(lines)
```

Arguments

lines lines of an XML text

Value

TRUE if there is an XML tag that also closes present in the lines of text, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# TRUE
has_xml_short_closing_tag("<my_tag id=1/>")
# FALSE
has_xml_short_closing_tag("<my_tag id=1>text</my_tag>")

check_empty_beautier_folder()
```

hky_site_model_to_xml_prior_distr
Internal function

Description

Converts an HKY site model to XML, used in the prior section

Usage

```
hky_site_model_to_xml_prior_distr(site_model, beauti_options)
```

Arguments

site_model a site model, as returned by [create_site_model](#)
beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

the site model as XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
hky_site_model_to_xml_prior_distr(  
  site_model = create_hky_site_model(  
    id = 1,  
    kappa_prior_distr = create_uniform_distr(id = 2)  
  ),  
  beauti_options = create_beauti_options()  
)
```

hky_site_model_to_xml_state
Converts a site model to XML, used in the state section

Description

Converts a site model to XML, used in the state section

Usage

```
hky_site_model_to_xml_state(  
  site_model,  
  beauti_options = create_beauti_options()  
)
```

Arguments

`site_model` a site model, as returned by [create_site_model](#)
`beauti_options` one BEAUi options object, as returned by [create_beauti_options](#)

Value

the site model as XML text

Author(s)

Richèl J.C. Bilderbeek

indent	<i>Indent text for a certain number of spaces. If the text is only whitespace, leave it as such</i>
--------	---

Description

Indent text for a certain number of spaces. If the text is only whitespace, leave it as such

Usage

```
indent(text, n_spaces = 4)
```

Arguments

`text` the text to indent
`n_spaces` the number of spaces to add before the text. BEAUi uses four spaces by default

Value

the indented text

Author(s)

Richèl J.C. Bilderbeek

init_bd_tree_prior	<i>Initializes a Birth-Death tree prior</i>
--------------------	---

Description

Initializes a Birth-Death tree prior

Usage

```
init_bd_tree_prior(bd_tree_prior, distr_id, param_id)
```

Arguments

bd_tree_prior	a Birth-Death tree prior, as created by create_bd_tree_prior
distr_id	a distributions' ID
param_id	a parameter's ID

Value

an initialized Birth-Death tree prior

Author(s)

Richèl J.C. Bilderbeek

init_beta_distr	<i>Initializes a beta distribution</i>
-----------------	--

Description

Initializes a beta distribution

Usage

```
init_beta_distr(beta_distr, distr_id = 0, param_id = 0)
```

Arguments

beta_distr	a beta distribution, using create_beta_distr
distr_id	the first distribution's ID
param_id	the first parameter's ID

Value

an initialized beta distribution

Author(s)

Richèl J.C. Bilderbeek

init_ccp_tree_prior	<i>Initializes a Coalescent Constant Population tree prior</i>
---------------------	--

Description

Initializes a Coalescent Constant Population tree prior

Usage

```
init_ccp_tree_prior(ccp_tree_prior, distr_id, param_id)
```

Arguments

ccp_tree_prior	a Coalescent Constant Population tree prior, as returned by create_ccp_tree_prior
distr_id	a distributions' ID
param_id	a parameter's ID

Value

an initialized Coalescent Constant Population tree prior

Author(s)

Richèl J.C. Bilderbeek

init_cep_tree_prior	<i>Initializes a Coalescent Exponential Population tree prior</i>
---------------------	---

Description

Initializes a Coalescent Exponential Population tree prior

Usage

```
init_cep_tree_prior(cep_tree_prior, distr_id, param_id)
```

Arguments

cep_tree_prior	a Coalescent Exponential Population tree prior, as returned by create_cep_tree_prior
distr_id	a distributions' ID
param_id	a parameter's ID

Value

an initialized Coalescent Exponential Population tree prior

Author(s)

Richèl J.C. Bilderbeek

init_clock_models	<i>Initializes all clock models</i>
-------------------	-------------------------------------

Description

Initializes all clock models

Usage

```
init_clock_models(fasta_filenames, clock_models, distr_id = 0, param_id = 0)
```

Arguments

fasta_filenames	One or more FASTA filenames. Use get_fasta_filename to obtain a testing FASTA filename.
clock_models	a list of one or more clock models, as returned by create_clock_model
distr_id	the first distributions' ID
param_id	the first parameter's ID

Value

a list of initialized clock models

Author(s)

Richèl J.C. Bilderbeek

init_distr	<i>Initializes a distribution</i>
------------	-----------------------------------

Description

Initializes a distribution

Usage

```
init_distr(distr, distr_id = 0, param_id = 0)
```

Arguments

distr	a distribution, using create_distr
distr_id	the first distribution's ID
param_id	the first parameter's ID

Value

an initialized distribution

Author(s)

Richèl J.C. Bilderbeek

init_exp_distr	<i>Initializes an exponential distribution</i>
----------------	--

Description

Initializes an exponential distribution

Usage

```
init_exp_distr(exp_distr, distr_id = 0, param_id = 0)
```

Arguments

exp_distr	a exponential distribution, using create_exp_distr
distr_id	the first distribution's ID
param_id	the first parameter's ID

Value

an initialized exponential distribution

Author(s)

Richèl J.C. Bilderbeek

init_gamma_distr	<i>Initializes a gamma distribution</i>
------------------	---

Description

Initializes a gamma distribution

Usage

```
init_gamma_distr(gamma_distr, distr_id = 0, param_id = 0)
```

Arguments

gamma_distr	a gamma distribution, using create_gamma_distr
distr_id	the first distribution's ID
param_id	the first parameter's ID

Value

an initialized gamma distribution

Author(s)

Richèl J.C. Bilderbeek

init_gamma_site_model	<i>Initializes a gamma site model</i>
-----------------------	---------------------------------------

Description

Initializes a gamma site model

Usage

```
init_gamma_site_model(gamma_site_model, distr_id = 0, param_id = 0)
```

Arguments

gamma_site_model	a site model's gamma site model, as returned by create_gamma_site_model
distr_id	the first distributions' ID
param_id	the first parameter's ID

Value

an initialized gamma site model

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

gamma_site_model <- create_gamma_site_model(
  gamma_cat_count = 2,
  gamma_shape_prior_distr = create_one_div_x_distr(id = NA)
)
# FALSE: not yet initialized
is_init_gamma_site_model(gamma_site_model)
gamma_site_model <- init_gamma_site_model(gamma_site_model)
# TRUE: now it is initialized
is_init_gamma_site_model(gamma_site_model)

check_empty_beautier_folder()
```

init_gtr_site_model	<i>Initializes a GTR site model</i>
---------------------	-------------------------------------

Description

Initializes a GTR site model

Usage

```
init_gtr_site_model(gtr_site_model, distr_id = 0, param_id = 0)
```

Arguments

gtr_site_model	a GTR site model, as returned by create_gtr_site_model
distr_id	a distributions' ID
param_id	a parameter's ID

Value

an initialized GTR site model

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

gtr_site_model <- create_gtr_site_model()
# FALSE
is_init_gtr_site_model(gtr_site_model)
gtr_site_model <- init_gtr_site_model(gtr_site_model)
# TRUE
is_init_gtr_site_model(gtr_site_model)

check_empty_beautier_folder()
```

init_hky_site_model	<i>Initializes an HKY site model</i>
---------------------	--------------------------------------

Description

Initializes an HKY site model

Usage

```
init_hky_site_model(hky_site_model, distr_id = 0, param_id = 0)
```

Arguments

hky_site_model	an HKY site model, as returned by create_hky_site_model
distr_id	a distributions' ID
param_id	a parameter's ID

Value

an initialized HKY site model

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

hky_site_model <- create_hky_site_model()
is_init_hky_site_model(hky_site_model)
hky_site_model <- init_hky_site_model(hky_site_model)
is_init_hky_site_model(hky_site_model)

check_empty_beautier_folder()
```

`init_inference_model` *Initialize an inference model*

Description

Initialize an inference model

Usage

```
init_inference_model(input_filename, inference_model)
```

Arguments

`input_filename` A FASTA filename. Use [get_fasta_filename](#) to obtain a testing FASTA filename.

`inference_model` a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

an initialized inference model

Author(s)

Rich  l J.C. Bilderbeek

`init_inv_gamma_distr` *Initializes an inverse gamma distribution*

Description

Initializes an inverse gamma distribution

Usage

```
init_inv_gamma_distr(inv_gamma_distr, distr_id = 0, param_id = 0)
```

Arguments

`inv_gamma_distr` an inverse gamma distribution, using [create_inv_gamma_distr](#)

`distr_id` the first distribution's ID

`param_id` the first parameter's ID

Value

an initialized inverse gamma distribution

Author(s)

Richèl J.C. Bilderbeek

init_jc69_site_model *Initializes a JC69 site model*

Description

Initializes a JC69 site model

Usage

```
init_jc69_site_model(jc69_site_model, distr_id = 0, param_id = 0)
```

Arguments

jc69_site_model	a JC69 site model, as returned by create_jc69_site_model
distr_id	a distributions' ID
param_id	a parameter's ID

Value

an initialized HKY site model

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

hky_site_model <- create_hky_site_model()
is_init_hky_site_model(hky_site_model)
hky_site_model <- init_hky_site_model(hky_site_model)
is_init_hky_site_model(hky_site_model)

check_empty_beautier_folder()
```

init_laplace_distr	<i>Initializes an Laplace distribution</i>
--------------------	--

Description

Initializes an Laplace distribution

Usage

```
init_laplace_distr(laplace_distr, distr_id = 0, param_id = 0)
```

Arguments

laplace_distr	a Laplace distribution, using create_laplace_distr
distr_id	the first distribution's ID
param_id	the first parameter's ID

Value

an initialized Laplace distribution

Author(s)

Richèl J.C. Bilderbeek

init_log_normal_distr	<i>Initializes an log-normal distribution</i>
-----------------------	---

Description

Initializes an log-normal distribution

Usage

```
init_log_normal_distr(log_normal_distr, distr_id = 0, param_id = 0)
```

Arguments

log_normal_distr	a log-normal distribution, using create_log_normal_distr
distr_id	the first distribution's ID
param_id	the first parameter's ID

Value

an initialized log-normal distribution

Author(s)

Richèl J.C. Bilderbeek

init_mrca_prior	<i>Initialize the MRCA prior.</i>
-----------------	-----------------------------------

Description

Initialized by

- if no alignment ID is set, it is set by reading it from the alignment file
- if no taxa names are set, these are set by reading these from the alignment file

Usage

```
init_mrca_prior(input_filename, inference_model)
```

Arguments

input_filename A FASTA filename. Use [get_fasta_filename](#) to obtain a testing FASTA filename.

inference_model a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

an initialized MRCA prior

Author(s)

Richèl J.C. Bilderbeek

init_mrca_priors	<i>Initializes all MRCA priors</i>
------------------	------------------------------------

Description

Initializes all MRCA priors

Usage

```
init_mrca_priors(mrca_priors, distr_id = 0, param_id = 0, beauti_options)
```

Arguments

mrca_priors	a list of one or more Most Recent Common Ancestor priors, as returned by create_mrca_prior
distr_id	the first distributions' ID
param_id	the first parameter's ID
beauti_options	one BEAUti options object, as returned by create_beauti_options

Value

a list of initialized MRCA priors

Author(s)

Richèl J.C. Bilderbeek

init_normal_distr	<i>Initializes an normal distribution</i>
-------------------	---

Description

Initializes an normal distribution

Usage

```
init_normal_distr(normal_distr, distr_id = 0, param_id = 0)
```

Arguments

normal_distr	a normal distribution, using create_normal_distr
distr_id	the first distribution's ID
param_id	the first parameter's ID

Value

an initialized normal distribution

Author(s)

Richèl J.C. Bilderbeek

init_one_div_x_distr	<i>Initializes an one-divided-by-x distribution</i>
----------------------	---

Description

Initializes an one-divided-by-x distribution

Usage

```
init_one_div_x_distr(one_div_x_distr, distr_id = 0)
```

Arguments

one_div_x_distr	a one-divided-by-x distribution, using create_one_div_x_distr
distr_id	the first distribution's ID

Value

an initialized one-divided-by-x distribution

Author(s)

Richèl J.C. Bilderbeek

init_param	<i>Initializes a parameter</i>
------------	--------------------------------

Description

Initializes a parameter

Usage

```
init_param(param, id)
```

Arguments

param	a parameter, using create_param
id	the parameter's ID. Will be ignored if the parameter already has an ID

Value

an initialized parameter

Author(s)

Richèl J.C. Bilderbeek

init_poisson_distr	<i>Initializes an Poisson distribution</i>
--------------------	--

Description

Initializes an Poisson distribution

Usage

```
init_poisson_distr(poisson_distr, distr_id = 0, param_id = 0)
```

Arguments

poisson_distr	a Poisson distribution, using create_poisson_distr
distr_id	the first distribution's ID
param_id	the first parameter's ID

Value

an initialized Poisson distribution

Author(s)

Richèl J.C. Bilderbeek

init_rln_clock_model *Initializes a Relaxed Log-Normal clock model*

Description

Initializes a Relaxed Log-Normal clock model

Usage

```
init_rln_clock_model(rln_clock_model, distr_id = 0, param_id = 0)
```

Arguments

rln_clock_model	a Relaxed Log-Normal clock model, as returned by create_rln_clock_model
distr_id	a distributions' ID
param_id	a parameter's ID

Value

an initialized Relaxed Log-Normal clock model

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

rln_clock_model <- create_rln_clock_model()
# FALSE: not yet initialized
is_init_rln_clock_model(rln_clock_model)
rln_clock_model <- init_rln_clock_model(rln_clock_model)
# Dimension is set to NA by default, for unknown reasons.
# Because 'init_rln_clock_model' does not initialize it (for
# unknown reasons), set it manually
rln_clock_model$dimension <- 42
# TRUE: now it is initialized
is_init_rln_clock_model(rln_clock_model)

check_empty_beautier_folder()
```

init_site_models	<i>Initializes all site models</i>
------------------	------------------------------------

Description

Initializes all site models

Usage

```
init_site_models(site_models, ids, distr_id = 0, param_id = 0)
```

Arguments

site_models	one or more site models, as returned by create_site_model
ids	one or more alignments' IDs. IDs can be extracted from their FASTA filenames with get_alignment_ids_from_fasta_filenames
distr_id	the first distributions' ID
param_id	the first parameter's ID

Value

a list of initialized site models

Author(s)

Richèl J.C. Bilderbeek

init_strict_clock_model	<i>Initializes a strict clock model</i>
-------------------------	---

Description

Initializes a strict clock model

Usage

```
init_strict_clock_model(strict_clock_model, distr_id = 0, param_id = 0)
```

Arguments

strict_clock_model	a strict clock model, as returned by create_strict_clock_model
distr_id	a distributions' ID
param_id	a parameter's ID

Value

an initialized strict clock model

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

strict_clock_model <- create_strict_clock_model()
# FALSE: not yet initialized
is_init_strict_clock_model(strict_clock_model)
strict_clock_model <- init_strict_clock_model(strict_clock_model)
# TRUE: initialized
is_init_strict_clock_model(strict_clock_model)

check_empty_beautier_folder()
```

init_tn93_site_model *Initializes a TN93 site model*

Description

Initializes a TN93 site model

Usage

```
init_tn93_site_model(tn93_site_model, distr_id = 0, param_id = 0)
```

Arguments

tn93_site_model	a TN93 site model, as returned by create_tn93_site_model
distr_id	a distributions' ID
param_id	a parameter's ID

Value

an initialized TN93 site model

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

tn93_site_model <- create_tn93_site_model()
is_init_tn93_site_model(tn93_site_model)
tn93_site_model <- init_tn93_site_model(tn93_site_model)
is_init_tn93_site_model(tn93_site_model)

check_empty_beautier_folder()
```

init_tree_priors	<i>Initializes all tree priors</i>
------------------	------------------------------------

Description

Initializes all tree priors

Usage

```
init_tree_priors(tree_priors, ids, distr_id = 0, param_id = 0)
```

Arguments

tree_priors	one or more tree priors, as returned by create_tree_prior
ids	one or more alignments' IDs. IDs can be extracted from their FASTA filenames with get_alignment_ids_from_fasta_filenames)
distr_id	the first distributions' ID
param_id	the first parameter's ID

Value

a list of initialized tree priors

Author(s)

Richèl J.C. Bilderbeek

init_uniform_distr	<i>Initializes a uniform distribution</i>
--------------------	---

Description

Initializes a uniform distribution

Usage

```
init_uniform_distr(uniform_distr, distr_id = 0)
```

Arguments

uniform_distr	a uniform distribution, using create_uniform_distr
distr_id	the first distribution's ID

Value

an initialized uniform distribution

Author(s)

Rich  l J.C. Bilderbeek

init_yule_tree_prior	<i>Initializes a Yule tree prior</i>
----------------------	--------------------------------------

Description

Initializes a Yule tree prior

Usage

```
init_yule_tree_prior(yule_tree_prior, distr_id, param_id)
```

Arguments

yule_tree_prior	a Yule tree_prior, as created by create_yule_tree_prior
distr_id	a distributions' ID
param_id	a parameter's ID

Value

an initialized Yule tree prior

Author(s)

Richèl J.C. Bilderbeek

interspace	<i>Puts spaces in between the lines</i>
------------	---

Description

Puts spaces in between the lines

Usage

interspace(lines)

Arguments

lines lines of text

Value

interspaced lines of text

Author(s)

Richèl J.C. Bilderbeek

is_alpha_param	<i>Determine if the object is a valid alpha parameter</i>
----------------	---

Description

Determine if the object is a valid alpha parameter

Usage

is_alpha_param(x)

Arguments

x an object, to be determined if it is a valid alpha parameter

Value

TRUE if x is a valid alpha parameter, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

is_alpha_param(create_alpha_param())
is_alpha_param(create_beta_param())
is_alpha_param(create_clock_rate_param())
is_alpha_param(create_kappa_1_param())
is_alpha_param(create_kappa_2_param())
is_alpha_param(create_lambda_param())
is_alpha_param(create_m_param())
is_alpha_param(create_mean_param())
is_alpha_param(create_mu_param())
is_alpha_param(create_rate_ac_param())
is_alpha_param(create_rate_ag_param())
is_alpha_param(create_rate_at_param())
is_alpha_param(create_rate_cg_param())
is_alpha_param(create_rate_ct_param())
is_alpha_param(create_rate_gt_param())
is_alpha_param(create_s_param())
is_alpha_param(create_scale_param())
is_alpha_param(create_sigma_param())

is_alpha_param(NA)
is_alpha_param(NULL)
is_alpha_param("nonsense")
is_alpha_param(create_jc69_site_model())
is_alpha_param(create_strict_clock_model())
is_alpha_param(create_yule_tree_prior())
is_alpha_param(create_mcmc())

check_empty_beautier_folder()
```

is_bd_tree_prior

Determine if the object is a valid Birth Death tree prior

Description

Determine if the object is a valid Birth Death tree prior

Usage

```
is_bd_tree_prior(x)
```

Arguments

x an object, to be determined if it is a valid birth death tree prior

Value

TRUE if x is a valid birth death tree prior, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_bd_tree_prior](#) to create a valid Birth-Death tree prior

Examples

```
check_empty_beautier_folder()

is_bd_tree_prior(create_bd_tree_prior())
!is_bd_tree_prior(create_cbs_tree_prior())
!is_bd_tree_prior(create_ccp_tree_prior())
!is_bd_tree_prior(create_cep_tree_prior())
!is_bd_tree_prior(create_yule_tree_prior())

check_empty_beautier_folder()
```

is_beauti_options	<i>Determine if the object is a valid beauti_options</i>
-------------------	--

Description

Determine if the object is a valid beauti_options

Usage

```
is_beauti_options(x)
```

Arguments

x an object, to be determined if it is a beauti_options

Value

TRUE if the object is a valid beauti_options, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

use [create_beauti_options](#) to create a valid beauti_options object

Examples

```
check_empty_beautier_folder()

# TRUE
is_beauti_options(create_beauti_options())

# FALSE
is_beauti_options("nonsense")
is_beauti_options(NA)
is_beauti_options(NULL)
is_beauti_options("")
is_beauti_options(c())

check_empty_beautier_folder()
```

is_beta_distr	<i>Determine if the object is a valid beta distribution, as created by create_beta_distr</i>
---------------	--

Description

Determine if the object is a valid beta distribution, as created by [create_beta_distr](#)

Usage

```
is_beta_distr(x)
```

Arguments

x an object, to be determined if it is a valid beta distribution,

Value

TRUE if x is a valid beta distribution, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

use [is_distr](#) to see if x is any distribution

Examples

```

check_empty_beautier_folder()

# TRUE
is_beta_distr(create_beta_distr())
# FALSE
is_beta_distr(create_exp_distr())
is_beta_distr(NA)
is_beta_distr(NULL)
is_beta_distr("nonsense")

check_empty_beautier_folder()

```

is_beta_param	<i>Determine if the object is a valid beta parameter</i>
---------------	--

Description

Determine if the object is a valid beta parameter

Usage

```
is_beta_param(x)
```

Arguments

x an object, to be determined if it is a valid beta parameter

Value

TRUE if x is a valid beta parameter, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```

check_empty_beautier_folder()

is_beta_param(create_alpha_param())
is_beta_param(create_beta_param())
is_beta_param(create_clock_rate_param())
is_beta_param(create_kappa_1_param())
is_beta_param(create_kappa_2_param())
is_beta_param(create_lambda_param())
is_beta_param(create_m_param())
is_beta_param(create_mean_param())
is_beta_param(create_mu_param())

```

```

is_beta_param(create_rate_ac_param())
is_beta_param(create_rate_ag_param())
is_beta_param(create_rate_at_param())
is_beta_param(create_rate_cg_param())
is_beta_param(create_rate_ct_param())
is_beta_param(create_rate_gt_param())
is_beta_param(create_s_param())
is_beta_param(create_scale_param())
is_beta_param(create_sigma_param())

is_beta_param(NA)
is_beta_param(NULL)
is_beta_param("nonsense")
is_beta_param(create_jc69_site_model())
is_beta_param(create_strict_clock_model())
is_beta_param(create_yule_tree_prior())
is_beta_param(create_mcmc())

check_empty_beautier_folder()

```

is_b_pop_sizes_param *Determine if the object is a valid b_pop_sizes parameter*

Description

Determine if the object is a valid b_pop_sizes parameter

Usage

```
is_b_pop_sizes_param(x)
```

Arguments

x an object, to be determined if it is a valid b_pop_sizes parameter

Value

TRUE if x is a valid b_pop_sizes parameter, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```

check_empty_beautier_folder()

is_b_pop_sizes_param(create_alpha_param())
is_b_pop_sizes_param(create_b_pop_sizes_param())
is_b_pop_sizes_param(create_beta_param())

```

```
is_b_pop_sizes_param(create_clock_rate_param())
is_b_pop_sizes_param(create_kappa_1_param())
is_b_pop_sizes_param(create_kappa_2_param())
is_b_pop_sizes_param(create_lambda_param())
is_b_pop_sizes_param(create_m_param())
is_b_pop_sizes_param(create_mean_param())
is_b_pop_sizes_param(create_mu_param())
is_b_pop_sizes_param(create_rate_ac_param())
is_b_pop_sizes_param(create_rate_ag_param())
is_b_pop_sizes_param(create_rate_at_param())
is_b_pop_sizes_param(create_rate_cg_param())
is_b_pop_sizes_param(create_rate_ct_param())
is_b_pop_sizes_param(create_rate_gt_param())
is_b_pop_sizes_param(create_s_param())
is_b_pop_sizes_param(create_scale_param())
is_b_pop_sizes_param(create_sigma_param())

is_b_pop_sizes_param(NA)
is_b_pop_sizes_param(NULL)
is_b_pop_sizes_param("nonsense")
is_b_pop_sizes_param(create_jc69_site_model())
is_b_pop_sizes_param(create_strict_clock_model())
is_b_pop_sizes_param(create_yule_tree_prior())
is_b_pop_sizes_param(create_mcmc())

check_empty_beautier_folder()
```

is_cbs_tree_prior	<i>Determine if the object is a valid constant coalescent Bayesian skyline prior</i>
-------------------	--

Description

Determine if the object is a valid constant coalescent Bayesian skyline prior

Usage

```
is_cbs_tree_prior(x)
```

Arguments

x an object, to be determined if it is a valid constant coalescent Bayesian skyline prior

Value

‘TRUE’ if ‘x’ is a valid constant coalescent Bayesian skyline prior, ‘FALSE’ otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_cbs_tree_prior](#) to create a valid coalescent Bayes skyline tree prior

Examples

```
check_empty_beautier_folder()

# TRUE
is_cbs_tree_prior(create_cbs_tree_prior())

# FALSE
is_cbs_tree_prior(create_bd_tree_prior())
is_cbs_tree_prior(create_ccp_tree_prior())
is_cbs_tree_prior(create_cep_tree_prior())
is_cbs_tree_prior(create_yule_tree_prior())

check_empty_beautier_folder()
```

is_ccp_tree_prior	<i>Determine if the object is a valid constant coalescence population tree prior</i>
-------------------	--

Description

Determine if the object is a valid constant coalescence population tree prior

Usage

```
is_ccp_tree_prior(x)
```

Arguments

x	an object, to be determined if it is a valid constant coalescence population tree prior
---	---

Value

TRUE if x is a valid constant coalescence population tree prior, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_ccp_tree_prior](#) to create a valid constant coalescence population tree prior

Examples

```
check_empty_beautier_folder()
!is_ccp_tree_prior(create_bd_tree_prior())
!is_ccp_tree_prior(create_cbs_tree_prior())
is_ccp_tree_prior(create_ccp_tree_prior())
!is_ccp_tree_prior(create_cep_tree_prior())
!is_ccp_tree_prior(create_yule_tree_prior())
check_empty_beautier_folder()
```

is_cep_tree_prior	<i>Determine if the object is a valid coalescent exponential population tree prior</i>
-------------------	--

Description

Determine if the object is a valid coalescent exponential population tree prior

Usage

```
is_cep_tree_prior(x)
```

Arguments

x	an object, to be determined if it is a valid constant coalescent exponential population tree prior
---	--

Value

TRUE if x is a valid coalescent exponential population tree prior, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_cep_tree_prior](#) to create a valid coalescent exponential population tree prior

Examples

```

check_empty_beautier_folder()

!is_cep_tree_prior(create_bd_tree_prior())
!is_cep_tree_prior(create_cbs_tree_prior())
!is_cep_tree_prior(create_ccp_tree_prior())
is_cep_tree_prior(create_cep_tree_prior())
!is_cep_tree_prior(create_yule_tree_prior())

check_empty_beautier_folder()

```

is_clock_model	<i>Determine if the object is a valid clock_model</i>
----------------	---

Description

Determine if the object is a valid clock_model

Usage

```
is_clock_model(x)
```

Arguments

x an object, to be determined if it is a clock_model

Value

TRUE if the clock_model is a valid clock_model, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

see [create_clock_model](#) for an overview of functions to create valid clock model

Examples

```

check_empty_beautier_folder()

# TRUE
is_clock_model(create_strict_clock_model())
is_clock_model(create_rln_clock_model())

# FALSE
is_clock_model(NA)
is_clock_model(NULL)

```

```
is_clock_model("nonsense")
is_clock_model(create_jc69_site_model())
is_clock_model(create_mcmc())

check_empty_beautier_folder()
```

is_clock_model_name	<i>Determines if the name is a valid clock model name</i>
---------------------	---

Description

Determines if the name is a valid clock model name

Usage

```
is_clock_model_name(name)
```

Arguments

name	the name to be tested
------	-----------------------

Value

TRUE if the name is a valid clock_model name, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# TRUE
is_clock_model_name("relaxed_log_normal")
is_clock_model_name("strict")

check_empty_beautier_folder()
```

is_clock_rate_param	<i>Determine if the object is a valid clock_rate parameter</i>
---------------------	--

Description

Determine if the object is a valid clock_rate parameter

Usage

```
is_clock_rate_param(x)
```

Arguments

x an object, to be determined if it is a valid clock_rate parameter

Value

TRUE if x is a valid clock_rate parameter, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

is_clock_rate_param(create_alpha_param())
is_clock_rate_param(create_beta_param())
is_clock_rate_param(create_clock_rate_param())
is_clock_rate_param(create_kappa_1_param())
is_clock_rate_param(create_kappa_2_param())
is_clock_rate_param(create_lambda_param())
is_clock_rate_param(create_m_param())
is_clock_rate_param(create_mean_param())
is_clock_rate_param(create_mu_param())
is_clock_rate_param(create_rate_ac_param())
is_clock_rate_param(create_rate_ag_param())
is_clock_rate_param(create_rate_at_param())
is_clock_rate_param(create_rate_cg_param())
is_clock_rate_param(create_rate_ct_param())
is_clock_rate_param(create_rate_gt_param())
is_clock_rate_param(create_s_param())
is_clock_rate_param(create_scale_param())
is_clock_rate_param(create_sigma_param())

is_clock_rate_param(NA)
is_clock_rate_param(NULL)
is_clock_rate_param("nonsense")
is_clock_rate_param(create_jc69_site_model())
```

```

is_clock_rate_param(create_strict_clock_model())
is_clock_rate_param(create_yule_tree_prior())
is_clock_rate_param(create_mcmc())

check_empty_beautier_folder()

```

is_default_mcmc	<i>Determine if the MCMC is a default MCMC</i>
-----------------	--

Description

Determine if the MCMC is a default MCMC

Usage

```
is_default_mcmc(mcmc)
```

Arguments

mcmc	one MCMC. Use create_mcmc to create an MCMC. Use create_ns_mcmc to create an MCMC for a Nested Sampling run. Use check_mcmc to check if an MCMC is valid. Use rename_mcmc_filenames to rename the filenames in an MCMC.
------	---

Value

TRUE if the MCMC is a default MCMC

Author(s)

Richèl J.C. Bilderbeek

Examples

```

if (is_on_ci()) {

  check_empty_beautier_folder()

  # TRUE: An MCMC created by 'create_mcmc' is default.
  is_default_mcmc(create_mcmc())

  # FALSE: An MCMC created by 'create_ns_mcmc' is not
  is_default_mcmc(create_ns_mcmc())

  check_empty_beautier_folder()
}

```

is_distr	<i>Determine if the object is a valid distribution</i>
----------	--

Description

Determine if the object is a valid distribution

Usage

```
is_distr(x)
```

Arguments

x an object, to be determined if it is a valid distribution

Value

TRUE if x is a valid distribution, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

use [is_beta_distr](#), [is_exp_distr](#), [is_gamma_distr](#), [is_inv_gamma_distr](#), [is_laplace_distr](#), [is_log_normal_distr](#), [is_normal_distr](#), [is_one_div_x_distr](#), [is_poisson_distr](#), or [is_uniform_distr](#), to check for more specific distribution

Examples

```
check_empty_beautier_folder()

# TRUE
is_distr(create_beta_distr())
is_distr(create_exp_distr())
is_distr(create_gamma_distr())
is_distr(create_inv_gamma_distr())
is_distr(create_laplace_distr())
is_distr(create_log_normal_distr())
is_distr(create_normal_distr())
is_distr(create_one_div_x_distr())
is_distr(create_poisson_distr())
is_distr(create_uniform_distr())

# FALSE
is_distr(NA)
is_distr(NULL)
is_distr("nonsense")
```

```
check_empty_beautier_folder()
```

is_distr_name	<i>Determines if the name is a valid distribution name</i>
---------------	--

Description

Determines if the name is a valid distribution name

Usage

```
is_distr_name(name)
```

Arguments

name the name to be tested

Value

TRUE if the name is a valid distribution name, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# TRUE
is_distr_name("uniform")
is_distr_name("normal")
is_distr_name("one_div_x")
is_distr_name("log_normal")
is_distr_name("exponential")
is_distr_name("gamma")
is_distr_name("beta")
is_distr_name("laplace")
is_distr_name("inv_gamma")
is_distr_name("poisson")
# FALSE
is_distr_name("nonsense")

check_empty_beautier_folder()
```

is_exp_distr	<i>Determine if the object is a valid exponential distribution as created by create_exp_distr</i>
--------------	---

Description

Determine if the object is a valid exponential distribution as created by [create_exp_distr](#)

Usage

```
is_exp_distr(x)
```

Arguments

x an object, to be determined if it is a valid exponential distribution

Value

TRUE if x is a valid exponential distribution, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

use [is_distr](#) to see if x is any distribution

Examples

```
check_empty_beautier_folder()

# TRUE
is_exp_distr(create_exp_distr())
# FALSE
is_exp_distr(create_gamma_distr())
is_exp_distr(NA)
is_exp_distr(NULL)
is_exp_distr("nonsense")

check_empty_beautier_folder()
```

`is_freq_equilibrium_name`*Checks if name is a valid freq_equilibrium argument value*

Description

Checks if name is a valid freq_equilibrium argument value

Usage

```
is_freq_equilibrium_name(name)
```

Arguments

name the name to check if it is a valid freq_equilibrium argument value

Value

TRUE if the name is a valid freq_equilibrium value

Author(s)

Richèl J.C. Bilderbeek

See Also

the freq_equilibrium argument is used by [create_gtr_site_model](#), [create_hky_site_model](#),
and [create_tn93_site_model](#)

Examples

```
check_empty_beautier_folder()

# TRUE
is_freq_equilibrium_name("estimated")
is_freq_equilibrium_name("empirical")
is_freq_equilibrium_name("all_equal")
# FALSE
is_freq_equilibrium_name("nonsense")

check_empty_beautier_folder()
```

is_freq_param	<i>Determine if the object is a valid freq parameter</i>
---------------	--

Description

Determine if the object is a valid freq parameter

Usage

```
is_freq_param(x)
```

Arguments

x an object, to be determined if it is a valid freq parameter

Value

TRUE if x is a valid freq parameter, FALSE otherwise

Author(s)

Rich  l J.C. Bilderbeek

See Also

freq parameters are returned by [create_freq_param](#)

Examples

```
check_empty_beautier_folder()

is_freq_param(create_alpha_param())
is_freq_param(create_beta_param())
is_freq_param(create_clock_rate_param())
is_freq_param(create_freq_param())
is_freq_param(create_freq_param())
is_freq_param(create_kappa_param())
is_freq_param(create_kappa_1_param())
is_freq_param(create_kappa_2_param())
is_freq_param(create_lambda_param())
is_freq_param(create_m_param())
is_freq_param(create_mean_param())
is_freq_param(create_mu_param())
is_freq_param(create_rate_ac_param())
is_freq_param(create_rate_ag_param())
is_freq_param(create_rate_at_param())
is_freq_param(create_rate_cg_param())
is_freq_param(create_rate_ct_param())
is_freq_param(create_rate_gt_param())
```

```

is_freq_param(create_s_param())
is_freq_param(create_scale_param())
is_freq_param(create_sigma_param())

is_freq_param(NA)
is_freq_param(NULL)
is_freq_param("nonsense")
is_freq_param(create_jc69_site_model())
is_freq_param(create_strict_clock_model())
is_freq_param(create_yule_tree_prior())
is_freq_param(create_mcmc())

check_empty_beautier_folder()

```

is_gamma_distr	<i>Determine if the object is a valid gamma distribution, as created by create_gamma_distr</i>
----------------	--

Description

Determine if the object is a valid gamma distribution, as created by [create_gamma_distr](#)

Usage

```
is_gamma_distr(x)
```

Arguments

x an object, to be determined if it is a valid gamma distribution

Value

TRUE if x is a valid gamma distribution, FALSE otherwise

Author(s)

Rich  l J.C. Bilderbeek

See Also

use [is_distr](#) to see if x is any distribution

Examples

```

check_empty_beautier_folder()

# TRUE
is_gamma_distr(create_gamma_distr())
# FALSE
is_gamma_distr(create_inv_gamma_distr())

```

```
is_gamma_distr(NA)
is_gamma_distr(NULL)
is_gamma_distr("nonsense")

check_empty_beautier_folder()
```

is_gamma_site_model	<i>Is object x a gamma site model?</i>
---------------------	--

Description

Is object x a gamma site model?

Usage

```
is_gamma_site_model(x)
```

Arguments

x the object to be determined if it is a valid gamma site object

Value

TRUE if x is a valid gamma site object, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# TRUE
is_gamma_site_model(create_gamma_site_model())

# FALSE
is_gamma_site_model("nonsense")
is_gamma_site_model(NA)
is_gamma_site_model(NULL)
is_gamma_site_model("")
is_gamma_site_model(c())

check_empty_beautier_folder()
```

is_gtr_site_model	<i>Determine if the object is a valid GTR site model, as created by create_gtr_site_model</i>
-------------------	---

Description

Determine if the object is a valid GTR site model, as created by [create_gtr_site_model](#)

Usage

```
is_gtr_site_model(x)
```

Arguments

x an object, to be determined if it is a valid GTR site model

Value

TRUE if x is a valid GTR site model, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# site models
is_gtr_site_model(create_gtr_site_model())
is_gtr_site_model(create_hky_site_model())
is_gtr_site_model(create_jc69_site_model())
is_gtr_site_model(create_tn93_site_model())

# other models
is_gtr_site_model(NA)
is_gtr_site_model(NULL)
is_gtr_site_model("nonsense")
is_gtr_site_model(create_strict_clock_model())
is_gtr_site_model(create_bd_tree_prior())
is_gtr_site_model(create_mcmc())

check_empty_beautier_folder()
```

is_hky_site_model	<i>Determine if the object is a valid HKY site model, as created by create_hky_site_model</i>
-------------------	---

Description

Determine if the object is a valid HKY site model, as created by [create_hky_site_model](#)

Usage

```
is_hky_site_model(x)
```

Arguments

x an object, to be determined if it is a valid HKY site model

Value

TRUE if x is a valid HKY site model, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# site models
is_hky_site_model(create_hky_site_model())
is_hky_site_model(create_gtr_site_model())
is_hky_site_model(create_jc69_site_model())
is_hky_site_model(create_tn93_site_model())

# other models
is_hky_site_model(NA)
is_hky_site_model(NULL)
is_hky_site_model("nonsense")
is_hky_site_model(create_strict_clock_model())
is_hky_site_model(create_bd_tree_prior())
is_hky_site_model(create_mcmc())

check_empty_beautier_folder()
```

`is_id`*Determine if the object is a valid ID*

Description

Determine if the object is a valid ID

Usage

```
is_id(x)
```

Arguments

`x` an object, to be determined if it is a valid ID

Value

TRUE if `x` is a valid ID, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

to check multiple IDs, use [are_ids](#)

Examples

```
check_empty_beautier_folder()

# TRUE
is_id("anthus_aco")
is_id(3)

# FALSE
is_id(ape::rcoal(3))
is_id(NULL)
is_id(NA)

check_empty_beautier_folder()
```

is_inference_model	<i>Determine if the input is an inference model</i>
--------------------	---

Description

Determine if the input is an inference model

Usage

```
is_inference_model(x)
```

Arguments

x	object to be determined of if it is an inference model
---	--

Value

TRUE if the object is an inference model

is_init_bd_tree_prior	<i>Determine if x is an initialized Birth-Death tree_prior object</i>
-----------------------	---

Description

Determine if x is an initialized Birth-Death tree_prior object

Usage

```
is_init_bd_tree_prior(x)
```

Arguments

x	the object to check if it is an initialized Birth-Death tree prior object
---	---

Value

TRUE if x is an initialized Birth-Death tree_prior object

Author(s)

Richèl J.C. Bilderbeek

is_init_beta_distr	<i>Determine if x is an initialized beta distribution object as created by create_beta_distr</i>
--------------------	--

Description

Determine if x is an initialized beta distribution object as created by [create_beta_distr](#)

Usage

```
is_init_beta_distr(x)
```

Arguments

x	the object to check if it is an initialized beta distribution object
---	--

Value

TRUE if x is an initialized beta distribution object

Author(s)

Richèl J.C. Bilderbeek

is_init_cbs_tree_prior	<i>Determine if x is an initialized Coalescent Bayesian Skyline tree_prior object</i>
------------------------	---

Description

Determine if x is an initialized Coalescent Bayesian Skyline tree_prior object

Usage

```
is_init_cbs_tree_prior(x)
```

Arguments

x	the object to check if it is an initialized Coalescent Bayesian Skyline tree prior object
---	---

Value

TRUE if x is an initialized Coalescent Bayesian Skyline tree prior object

Author(s)

Richèl J.C. Bilderbeek

`is_init_ccp_tree_prior`*Determine if x is an initialized Coalescent Constant Population tree_prior object*

Description

Determine if x is an initialized Coalescent Constant Population tree_prior object

Usage`is_init_ccp_tree_prior(x)`**Arguments**

x	the object to check if it is an initialized Coalescent Constant Population tree prior object
---	--

Value

TRUE if x is an initialized Coalescent Constant Population tree prior object

Author(s)

Richèl J.C. Bilderbeek

`is_init_cep_tree_prior`*Determine if x is an initialized Coalescent Exponential Population tree_prior object*

Description

Determine if x is an initialized Coalescent Exponential Population tree_prior object

Usage`is_init_cep_tree_prior(x)`**Arguments**

x	the object to check if it is an initialized Coalescent Exponential Population tree prior object
---	---

Value

TRUE if x is an initialized Coalescent Exponential Population tree prior object

Author(s)

Richèl J.C. Bilderbeek

is_init_clock_model	<i>Determine if x is an initialized clock_model object, as created by create_clock_model</i>
---------------------	--

Description

Determine if x is an initialized clock_model object, as created by [create_clock_model](#)

Usage

```
is_init_clock_model(x)
```

Arguments

x the object to check if it is an initialized clock_models object

Value

TRUE if x is an initialized clock_model object

Author(s)

Richèl J.C. Bilderbeek

is_init_distr	<i>Determine if x is an initialized distribution object as created by create_distr</i>
---------------	--

Description

Determine if x is an initialized distribution object as created by [create_distr](#)

Usage

```
is_init_distr(x)
```

Arguments

x the object to check if it is an initialized distribution object

Value

TRUE if x is an initialized distribution object

Author(s)

Richèl J.C. Bilderbeek

is_init_exp_distr	<i>Determine if x is an initialized exponential distribution object as created by create_exp_distr</i>
-------------------	--

Description

Determine if x is an initialized exponential distribution object as created by [create_exp_distr](#)

Usage

```
is_init_exp_distr(x)
```

Arguments

x the object to check if it is an initialized exponential distribution object

Value

TRUE if x is an initialized exponential distribution object

Author(s)

Richèl J.C. Bilderbeek

is_init_gamma_distr	<i>Determine if x is an initialized gamma distribution object</i>
---------------------	---

Description

Determine if x is an initialized gamma distribution object

Usage

```
is_init_gamma_distr(x)
```

Arguments

x the object to check if it is an initialized gamma distribution object

Value

TRUE if x is an initialized gamma distribution object

Author(s)

Richèl J.C. Bilderbeek

is_init_gamma_site_model

Determine if x is an initialized gamma site model, as created by [create_gamma_site_model](#)

Description

Determine if x is an initialized gamma site model, as created by [create_gamma_site_model](#)

Usage

```
is_init_gamma_site_model(x)
```

Arguments

x the object to check if it is an initialized gamma site_models object

Value

TRUE if x is an initialized gamma site model

Author(s)

Richèl J.C. Bilderbeek

is_init_gtr_site_model

Determine if x is an initialized GTR site model as created by [create_gtr_site_model](#)

Description

Determine if x is an initialized GTR site model as created by [create_gtr_site_model](#)

Usage

```
is_init_gtr_site_model(x)
```

Arguments

x the object to check if it is an initialized GTR site model

Value

TRUE if x is an initialized GTR site model

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

gtr_site_model <- create_gtr_site_model()
# FALSE: not yet initialized
is_init_gtr_site_model(gtr_site_model)
gtr_site_model <- init_gtr_site_model(gtr_site_model)
# TRUE: now it is initialized
is_init_gtr_site_model(gtr_site_model)

check_empty_beautier_folder()
```

is_init_hky_site_model

*Determine if x is an initialized HKY site model as created by
[create_hky_site_model](#)*

Description

Determine if x is an initialized HKY site model as created by [create_hky_site_model](#)

Usage

```
is_init_hky_site_model(x)
```

Arguments

x the object to check if it is an initialized HKY site model

Value

TRUE if x is an initialized HKY site model

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

hky_site_model <- create_hky_site_model()
# FALSE: not yet initialized
is_init_hky_site_model(hky_site_model)
hky_site_model <- init_hky_site_model(hky_site_model)
# TRUE: now it is initialized
is_init_hky_site_model(hky_site_model)

check_empty_beautier_folder()
```

```
is_init_inv_gamma_distr
```

Determine if x is an initialized inverse-gamma distribution as created by [create_inv_gamma_distr](#)

Description

Determine if x is an initialized inverse-gamma distribution as created by [create_inv_gamma_distr](#)

Usage

```
is_init_inv_gamma_distr(x)
```

Arguments

x the object to check if it is an initialized inverse-gamma distribution

Value

TRUE if x is an initialized inverse-gamma distribution

Author(s)

Richèl J.C. Bilderbeek

`is_init_jc69_site_model`

Determine if x is an initialized JC69 site model as created by [create_jc69_site_model](#)

Description

Determine if x is an initialized JC69 site model as created by [create_jc69_site_model](#)

Usage

```
is_init_jc69_site_model(x)
```

Arguments

x the object to check if it is an initialized JC69 site model

Value

TRUE if x is an initialized JC69 site model

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

jc69_site_model <- create_jc69_site_model(
  gamma_site_model = create_gamma_site_model(
    gamma_cat_count = 2,
    gamma_shape_prior_distr = create_normal_distr()
  )
)
# FALSE: not yet initialized
is_init_jc69_site_model(jc69_site_model)
jc69_site_model <- init_jc69_site_model(jc69_site_model)
# TRUE: now it is initialized
is_init_jc69_site_model(jc69_site_model)

check_empty_beautier_folder()
```

`is_init_laplace_distr` *Determine if x is an initialized Laplace distribution as created by [create_laplace_distr](#)*

Description

Determine if x is an initialized Laplace distribution as created by [create_laplace_distr](#)

Usage

```
is_init_laplace_distr(x)
```

Arguments

x the object to check if it is an initialized Laplace distribution

Value

TRUE if x is an initialized Laplace distribution

Author(s)

Richèl J.C. Bilderbeek

`is_init_log_normal_distr` *Determine if x is an initialized log_normal distribution object as created by [create_log_normal_distr](#)*

Description

Determine if x is an initialized log_normal distribution object as created by [create_log_normal_distr](#)

Usage

```
is_init_log_normal_distr(x)
```

Arguments

x the object to check if it is an initialized log_normal distribution object

Value

TRUE if x is an initialized log_normal distribution object

Author(s)

Richèl J.C. Bilderbeek

is_init_mrca_prior	<i>Determine if x is an initialized MRCA prior</i>
--------------------	--

Description

Determine if x is an initialized MRCA prior

Usage

```
is_init_mrca_prior(x)
```

Arguments

x	the object to check if it is an initialized MRCA prior
---	--

Value

TRUE if x is an initialized MRCA prior

Author(s)

Richèl J.C. Bilderbeek

is_init_normal_distr	<i>Determine if x is an initialized normal distribution object as created by create_normal_distr</i>
----------------------	--

Description

Determine if x is an initialized normal distribution object as created by [create_normal_distr](#)

Usage

```
is_init_normal_distr(x)
```

Arguments

x	the object to check if it is an initialized normal distribution object
---	--

Value

TRUE if x is an initialized normal distribution object

Author(s)

Richèl J.C. Bilderbeek

is_init_one_div_x_distr

Determine if x is an initialized one_div_x distribution object as created by [create_one_div_x_distr](#)

Description

Determine if x is an initialized one_div_x distribution object as created by [create_one_div_x_distr](#)

Usage

```
is_init_one_div_x_distr(x)
```

Arguments

x the object to check if it is an initialized one_div_x distribution object

Value

TRUE if x is an initialized one_div_x distribution object

Author(s)

Richèl J.C. Bilderbeek

is_init_param

Determine if x is an initialized parameter, as created by [create_param](#)

Description

Determine if x is an initialized parameter, as created by [create_param](#)

Usage

```
is_init_param(x)
```

Arguments

x the object to check if it is an initialized parameter

Value

[TRUE](#) if x is an initialized parameter, [FALSE](#) otherwise

Author(s)

Richèl J.C. Bilderbeek

`is_init_poisson_distr` *Determine if x is an initialized Poisson distribution object as created by [create_poisson_distr](#)*

Description

Determine if x is an initialized Poisson distribution object as created by [create_poisson_distr](#)

Usage

```
is_init_poisson_distr(x)
```

Arguments

x the object to check if it is an initialized Poisson distribution object

Value

TRUE if x is an initialized Poisson distribution object

Author(s)

Richèl J.C. Bilderbeek

`is_init_rln_clock_model` *Determine if x is an initialized relaxed log-normal clock_model object*

Description

Determine if x is an initialized relaxed log-normal clock_model object

Usage

```
is_init_rln_clock_model(rln_clock_model)
```

Arguments

`rln_clock_model`
a Relaxed Log-Normal clock model, as returned by [create_rln_clock_model](#)

Value

TRUE if x is an initialized relaxed log-normal clock_model object, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

is_init_site_model	<i>Determine if x is an initialized site model, as created by create_site_model</i>
--------------------	---

Description

Determine if x is an initialized site model, as created by [create_site_model](#)

Usage

```
is_init_site_model(x)
```

Arguments

x the object to check if it is an initialized site_models object

Value

TRUE if x is an initialized site model

Author(s)

Richèl J.C. Bilderbeek

is_init_strict_clock_model	<i>Determine if x is an initialized strict clock_model object</i>
----------------------------	---

Description

Determine if x is an initialized strict clock_model object

Usage

```
is_init_strict_clock_model(strict_clock_model)
```

Arguments

strict_clock_model
a strict clock model, as returned by [create_strict_clock_model](#)

Value

TRUE if x is an initialized strict clock_model object

Author(s)

Richèl J.C. Bilderbeek

```
is_init_tn93_site_model
```

Determine if x is an initialized tn93 site model as created by [create_tn93_site_model](#)

Description

Determine if x is an initialized tn93 site model as created by [create_tn93_site_model](#)

Usage

```
is_init_tn93_site_model(x)
```

Arguments

x the object to check if it is an initialized TN93 site model

Value

TRUE if x is an initialized TN93 site model

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

tn93_site_model <- create_tn93_site_model()
# FALSE: not yet initialized
is_init_tn93_site_model(tn93_site_model)
tn93_site_model <- init_tn93_site_model(tn93_site_model)
# TRUE: now it is initialized
is_init_tn93_site_model(tn93_site_model)

check_empty_beautier_folder()
```

```
is_init_tree_prior      Determine if x is an initialized tree_prior objects
```

Description

Determine if x is an initialized tree_prior objects

Usage

```
is_init_tree_prior(x)
```

Arguments

x the object to check if it is an initialized tree_priors object

Value

TRUE if x is an initialized tree_prior object

Author(s)

Richèl J.C. Bilderbeek

is_init_uniform_distr *Determine if x is an initialized uniform distribution object as created by [create_uniform_distr](#)*

Description

Determine if x is an initialized uniform distribution object as created by [create_uniform_distr](#)

Usage

```
is_init_uniform_distr(x)
```

Arguments

x the object to check if it is an initialized uniform distribution object

Value

TRUE if x is an initialized uniform distribution object

Author(s)

Richèl J.C. Bilderbeek

`is_init_yule_tree_prior`*Determine if x is an initialized Yule tree_prior object*

Description

Determine if x is an initialized Yule tree_prior object

Usage

```
is_init_yule_tree_prior(x)
```

Arguments

x the object to check if it is an initialized Yule tree prior object

Value

TRUE if x is an initialized Yule tree_prior object

Author(s)

Richèl J.C. Bilderbeek

`is_inv_gamma_distr`*Determine if the object is a valid inverse-gamma distribution as created by [create_inv_gamma_distr](#)*

Description

Determine if the object is a valid inverse-gamma distribution as created by [create_inv_gamma_distr](#)

Usage

```
is_inv_gamma_distr(x)
```

Arguments

x an object, to be determined if it is a valid inverse-gamma distribution

Value

TRUE if x is a valid inverse-gamma distribution, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

use `is_distr` to see if x is any distribution

Examples

```
check_empty_beautier_folder()

# TRUE
is_inv_gamma_distr(create_inv_gamma_distr())
# FALSE
is_inv_gamma_distr(create_laplace_distr())
is_inv_gamma_distr(NA)
is_inv_gamma_distr(NULL)
is_inv_gamma_distr("nonsense")

check_empty_beautier_folder()
```

is_in_patterns	<i>Is there at least one regular expression having a match with the line?</i>
----------------	---

Description

Is there at least one regular expression having a match with the line?

Usage

```
is_in_patterns(line, patterns)
```

Arguments

line	a line of text
patterns	one or more regular expression patterns

Value

TRUE if there is at least one match found

Author(s)

Richèl J.C. Bilderbeek

is_jc69_site_model	<i>Determine if the object is a valid JC69 site model</i>
--------------------	---

Description

Determine if the object is a valid JC69 site model

Usage

```
is_jc69_site_model(x)
```

Arguments

x an object, to be determined if it is a valid JC69 site model

Value

TRUE if x is a valid JC69 site model, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# site models
is_jc69_site_model(create_gtr_site_model())
is_jc69_site_model(create_hky_site_model())
is_jc69_site_model(create_jc69_site_model())
is_jc69_site_model(create_tn93_site_model())

# other models
is_jc69_site_model(NA)
is_jc69_site_model(NULL)
is_jc69_site_model("nonsense")
is_jc69_site_model(create_strict_clock_model())
is_jc69_site_model(create_bd_tree_prior())
is_jc69_site_model(create_mcmc())

check_empty_beautier_folder()
```

is_kappa_1_param	<i>Determine if the object is a valid kappa 1 parameter</i>
------------------	---

Description

Determine if the object is a valid kappa 1 parameter

Usage

```
is_kappa_1_param(x)
```

Arguments

x an object, to be determined if it is a valid kappa 1 parameter

Value

TRUE if x is a valid kappa 1 parameter, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

kappa 1 parameters are returned by [create_kappa_1_param](#)

Examples

```
check_empty_beautier_folder()

is_kappa_1_param(create_alpha_param())
is_kappa_1_param(create_beta_param())
is_kappa_1_param(create_clock_rate_param())
is_kappa_1_param(create_kappa_param())
is_kappa_1_param(create_kappa_1_param())
is_kappa_1_param(create_kappa_2_param())
is_kappa_1_param(create_lambda_param())
is_kappa_1_param(create_m_param())
is_kappa_1_param(create_mean_param())
is_kappa_1_param(create_mu_param())
is_kappa_1_param(create_rate_ac_param())
is_kappa_1_param(create_rate_ag_param())
is_kappa_1_param(create_rate_at_param())
is_kappa_1_param(create_rate_cg_param())
is_kappa_1_param(create_rate_ct_param())
is_kappa_1_param(create_rate_gt_param())
is_kappa_1_param(create_s_param())
is_kappa_1_param(create_scale_param())
```

```

is_kappa_1_param(create_sigma_param())

is_kappa_1_param(NA)
is_kappa_1_param(NULL)
is_kappa_1_param("nonsense")
is_kappa_1_param(create_jc69_site_model())
is_kappa_1_param(create_strict_clock_model())
is_kappa_1_param(create_yule_tree_prior())
is_kappa_1_param(create_mcmc())

check_empty_beautier_folder()

```

is_kappa_2_param	<i>Determine if the object is a valid kappa 2 parameter</i>
------------------	---

Description

Determine if the object is a valid kappa 2 parameter

Usage

```
is_kappa_2_param(x)
```

Arguments

x an object, to be determined if it is a valid kappa 2 parameter

Value

TRUE if x is a valid kappa_2 parameter, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

kappa 2 parameters are returned by [create_kappa_2_param](#)

Examples

```

check_empty_beautier_folder()

is_kappa_2_param(create_alpha_param())
is_kappa_2_param(create_beta_param())
is_kappa_2_param(create_clock_rate_param())
is_kappa_2_param(create_kappa_1_param())
is_kappa_2_param(create_kappa_2_param())
is_kappa_2_param(create_lambda_param())
is_kappa_2_param(create_m_param())

```

```

is_kappa_2_param(create_mean_param())
is_kappa_2_param(create_mu_param())
is_kappa_2_param(create_rate_ac_param())
is_kappa_2_param(create_rate_ag_param())
is_kappa_2_param(create_rate_at_param())
is_kappa_2_param(create_rate_cg_param())
is_kappa_2_param(create_rate_ct_param())
is_kappa_2_param(create_rate_gt_param())
is_kappa_2_param(create_s_param())
is_kappa_2_param(create_scale_param())
is_kappa_2_param(create_sigma_param())

is_kappa_2_param(NA)
is_kappa_2_param(NULL)
is_kappa_2_param("nonsense")
is_kappa_2_param(create_jc69_site_model())
is_kappa_2_param(create_strict_clock_model())
is_kappa_2_param(create_yule_tree_prior())
is_kappa_2_param(create_mcmc())

check_empty_beautier_folder()

```

is_kappa_param	<i>Determine if the object is a valid kappa parameter</i>
----------------	---

Description

Determine if the object is a valid kappa parameter

Usage

```
is_kappa_param(x)
```

Arguments

x an object, to be determined if it is a valid kappa parameter

Value

TRUE if x is a valid kappa parameter, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

kappa parameters are returned by [create_kappa_param](#)

Examples

```

check_empty_beautier_folder()

is_kappa_param(create_alpha_param())
is_kappa_param(create_beta_param())
is_kappa_param(create_clock_rate_param())
is_kappa_param(create_kappa_param())
is_kappa_param(create_kappa_1_param())
is_kappa_param(create_kappa_2_param())
is_kappa_param(create_lambda_param())
is_kappa_param(create_m_param())
is_kappa_param(create_mean_param())
is_kappa_param(create_mu_param())
is_kappa_param(create_rate_ac_param())
is_kappa_param(create_rate_ag_param())
is_kappa_param(create_rate_at_param())
is_kappa_param(create_rate_cg_param())
is_kappa_param(create_rate_ct_param())
is_kappa_param(create_rate_gt_param())
is_kappa_param(create_s_param())
is_kappa_param(create_scale_param())
is_kappa_param(create_sigma_param())

is_kappa_param(NA)
is_kappa_param(NULL)
is_kappa_param("nonsense")
is_kappa_param(create_jc69_site_model())
is_kappa_param(create_strict_clock_model())
is_kappa_param(create_yule_tree_prior())
is_kappa_param(create_mcmc())

check_empty_beautier_folder()

```

is_lambda_param	<i>Determine if the object is a valid lambda parameter</i>
-----------------	--

Description

Determine if the object is a valid lambda parameter

Usage

```
is_lambda_param(x)
```

Arguments

x an object, to be determined if it is a valid lambda parameter

Value

TRUE if x is a valid lambda parameter, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

lambda parameters are returned by [create_lambda_param](#)

Examples

```
check_empty_beautier_folder()

is_lambda_param(create_alpha_param())
is_lambda_param(create_beta_param())
is_lambda_param(create_clock_rate_param())
is_lambda_param(create_kappa_1_param())
is_lambda_param(create_kappa_2_param())
is_lambda_param(create_lambda_param())
is_lambda_param(create_m_param())
is_lambda_param(create_mean_param())
is_lambda_param(create_mu_param())
is_lambda_param(create_rate_ac_param())
is_lambda_param(create_rate_ag_param())
is_lambda_param(create_rate_at_param())
is_lambda_param(create_rate_cg_param())
is_lambda_param(create_rate_ct_param())
is_lambda_param(create_rate_gt_param())
is_lambda_param(create_s_param())
is_lambda_param(create_scale_param())
is_lambda_param(create_sigma_param())

is_lambda_param(NA)
is_lambda_param(NULL)
is_lambda_param("nonsense")
is_lambda_param(create_jc69_site_model())
is_lambda_param(create_strict_clock_model())
is_lambda_param(create_yule_tree_prior())
is_lambda_param(create_mcmc())

check_empty_beautier_folder()
```

is_laplace_distr

Determine if the object is a valid Laplace distribution, as created by
[create_laplace_distr](#)

Description

Determine if the object is a valid Laplace distribution, as created by [create_laplace_distr](#)

Usage

```
is_laplace_distr(x)
```

Arguments

x an object, to be determined if it is a valid Laplace distribution

Value

TRUE if x is a valid Laplace distribution, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

use [is_distr](#) to see if x is any distribution

Examples

```
# TRUE
is_laplace_distr(create_laplace_distr())
# FALSE
is_laplace_distr(create_log_normal_distr())
is_laplace_distr(NA)
is_laplace_distr(NULL)
is_laplace_distr("nonsense")
```

is_log_normal_distr	<i>Determine if the object is a valid log-normal distribution, as created by create_log_normal_distr</i>
---------------------	--

Description

Determine if the object is a valid log-normal distribution, as created by [create_log_normal_distr](#)

Usage

```
is_log_normal_distr(x)
```

Arguments

x an object, to be determined if it is a valid log-normal distribution

Value

TRUE if x is a valid log-normal distribution, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

use `is_distr` to see if x is any distribution

Examples

```
check_empty_beautier_folder()

# TRUE
is_log_normal_distr(create_log_normal_distr())
# FALSE
is_log_normal_distr(create_normal_distr())
is_distr(NA)
is_distr(NULL)
is_distr("nonsense")

check_empty_beautier_folder()
```

`is_mcmc`*Determine if the object is a valid MCMC*

Description

Determine if the object is a valid MCMC

Usage

```
is_mcmc(x)
```

Arguments

x an object, to be determined if it is a valid MCMC

Value

TRUE if x is a valid MCMC, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

Use `create_mcmc` to create an MCMC

Examples

```
if (is_on_ci()) {  
  check_empty_beautier_folder()  
  
  # Returns TRUE  
  is_mcmc(create_mcmc())  
  is_mcmc(create_ns_mcmc())  
  
  # Returns FALSE  
  is_mcmc("nonsense")  
  is_mcmc(NULL)  
  is_mcmc(NA)  
  is_mcmc("")  
  is_mcmc(c())  
  
  check_empty_beautier_folder()  
}
```

`is_mcmc_nested_sampling`

Determine if the object is a valid Nested-Sampling MCMC, as used in [1]

Description

Determine if the object is a valid Nested-Sampling MCMC, as used in [1]

Usage

```
is_mcmc_nested_sampling(x)
```

Arguments

`x` an object, to be determined if it is a valid MCMC

Value

TRUE if `x` is a valid Nested-Sampling MCMC, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

References

* [1] Patricio Maturana Russel, Brendon J Brewer, Steffen Klaere, Remco R Bouckaert; Model Selection and Parameter Inference in Phylogenetics Using Nested Sampling, Systematic Biology, 2018, syy050, <https://doi.org/10.1093/sysbio/syy050>

See Also

Use [create_ns_mcmc](#) to create an NS MCMC

Examples

```
if (is_on_ci()) {
  check_empty_beautier_folder()

  # TRUE
  is_nested_sampling_mcmc(create_ns_mcmc())
  # FALSE
  is_nested_sampling_mcmc(create_mcmc())
  is_nested_sampling_mcmc("nonsense")

  check_empty_beautier_folder()
}
```

is_mean_param

Determine if the object is a valid mean parameter

Description

Determine if the object is a valid mean parameter

Usage

```
is_mean_param(x)
```

Arguments

x an object, to be determined if it is a valid mean parameter, as created by [create_mean_param](#))

Value

TRUE if x is a valid mean parameter, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```

check_empty_beautier_folder()

is_mean_param(create_alpha_param())
is_mean_param(create_beta_param())
is_mean_param(create_clock_rate_param())
is_mean_param(create_kappa_1_param())
is_mean_param(create_kappa_2_param())
is_mean_param(create_lambda_param())
is_mean_param(create_m_param())
is_mean_param(create_mean_param())
is_mean_param(create_mu_param())
is_mean_param(create_rate_ac_param())
is_mean_param(create_rate_ag_param())
is_mean_param(create_rate_at_param())
is_mean_param(create_rate_cg_param())
is_mean_param(create_rate_ct_param())
is_mean_param(create_rate_gt_param())
is_mean_param(create_s_param())
is_mean_param(create_scale_param())
is_mean_param(create_sigma_param())

is_mean_param(NA)
is_mean_param(NULL)
is_mean_param("nonsense")
is_mean_param(create_jc69_site_model())
is_mean_param(create_strict_clock_model())
is_mean_param(create_yule_tree_prior())
is_mean_param(create_mcmc())

check_empty_beautier_folder()

```

```
is_mrca_align_ids_in_fastas
```

Determine if an MRCA prior's alignment IDs are present in the FASTA files

Description

Determine if an MRCA prior's alignment IDs are present in the FASTA files

Usage

```
is_mrca_align_ids_in_fastas(mrca_prior, fasta_filenames)
```

Arguments

`mrca_prior` a Most Recent Common Ancestor prior, as returned by [create_mrca_prior](#)

fasta_filenames

One or more FASTA filenames. Use [get_fasta_filename](#) to obtain a testing FASTA filename.

Value

TRUE if the MRCA prior's alignment IDs is present in the FASTA files. Returns FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

is_mrca_align_id_in_fasta

Determine if an MRCA prior's alignment IDs is present in the FASTA file

Description

Determine if an MRCA prior's alignment IDs is present in the FASTA file

Usage

```
is_mrca_align_id_in_fasta(mrca_prior, fasta_filename)
```

Arguments

mrca_prior a Most Recent Common Ancestor prior, as returned by [create_mrca_prior](#)

fasta_filename a FASTA filename. Use [get_fasta_filename](#) to obtain a testing FASTA filename. Note that BEAST2 also supports missing data, by using a dash (-) or question mark (?) as a sequence.

Value

TRUE if the MRCA prior's alignment IDs is present in the FASTA file. Returns FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

is_mrca_prior	<i>Determine of the object is an empty (NA) or valid MRCA prior.</i>
---------------	--

Description

Determine of the object is an empty (NA) or valid MRCA prior.

Usage

```
is_mrca_prior(mrca_prior)
```

Arguments

mrca_prior a Most Recent Common Ancestor prior, as returned by [create_mrca_prior](#)

Value

TRUE if x is an MRCA prior, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# TRUE
is_mrca_prior(create_mrca_prior())
# Also 'NA' is a valid MRCA prior,
# denoting that there no MRCA priors
is_mrca_prior(NA)

# FALSE
is_mrca_prior(NULL)
is_mrca_prior("nonsense")

check_empty_beautier_folder()
```

`is_mrca_prior_with_distr`*See if x is one MRCA prior with a distribution*

Description

See if x is one MRCA prior with a distribution

Usage

```
is_mrca_prior_with_distr(x)
```

Arguments

x the object to be tested

Value

TRUE if x is one MRCA prior with a distribution, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

`is_mu_param`*Determine if the object is a valid mu parameter*

Description

Determine if the object is a valid mu parameter

Usage

```
is_mu_param(x)
```

Arguments

x an object, to be determined if it is a valid mu parameter

Value

TRUE if x is a valid mu parameter, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

[create_mu_param](#) creates a mu parameter

Examples

```
check_empty_beautier_folder()

is_mu_param(create_alpha_param())
is_mu_param(create_beta_param())
is_mu_param(create_clock_rate_param())
is_mu_param(create_kappa_1_param())
is_mu_param(create_kappa_2_param())
is_mu_param(create_lambda_param())
is_mu_param(create_m_param())
is_mu_param(create_mean_param())
is_mu_param(create_mu_param())
is_mu_param(create_rate_ac_param())
is_mu_param(create_rate_ag_param())
is_mu_param(create_rate_at_param())
is_mu_param(create_rate_cg_param())
is_mu_param(create_rate_ct_param())
is_mu_param(create_rate_gt_param())
is_mu_param(create_s_param())
is_mu_param(create_scale_param())
is_mu_param(create_sigma_param())

is_mu_param(NA)
is_mu_param(NULL)
is_mu_param("nonsense")
is_mu_param(create_jc69_site_model())
is_mu_param(create_strict_clock_model())
is_mu_param(create_yule_tree_prior())
is_mu_param(create_mcmc())

check_empty_beautier_folder()
```

is_m_param

Determine if the object is a valid m parameter

Description

Determine if the object is a valid m parameter

Usage

```
is_m_param(m_param)
```

Arguments

m_param an m parameter, as created by [create_m_param](#)

Value

TRUE if x is a valid m parameter, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

is_m_param(create_alpha_param())
is_m_param(create_beta_param())
is_m_param(create_clock_rate_param())
is_m_param(create_kappa_1_param())
is_m_param(create_kappa_2_param())
is_m_param(create_lambda_param())
is_m_param(create_m_param())
is_m_param(create_mean_param())
is_m_param(create_mu_param())
is_m_param(create_rate_ac_param())
is_m_param(create_rate_ag_param())
is_m_param(create_rate_at_param())
is_m_param(create_rate_cg_param())
is_m_param(create_rate_ct_param())
is_m_param(create_rate_gt_param())
is_m_param(create_s_param())
is_m_param(create_scale_param())
is_m_param(create_sigma_param())

is_m_param(NA)
is_m_param(NULL)
is_m_param("nonsense")
is_m_param(create_jc69_site_model())
is_m_param(create_strict_clock_model())
is_m_param(create_yule_tree_prior())
is_m_param(create_mcmc())

check_empty_beautier_folder()
```

is_normal_distr	<i>Determine if the object is a valid normal distribution as created by</i> create_normal_distr
-----------------	--

Description

Determine if the object is a valid normal distribution as created by [create_normal_distr](#)

Value

TRUE if the argument is one boolean, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# TRUE
is_one_bool(TRUE)
is_one_bool(FALSE)

# FALSE
is_one_bool(NULL)
is_one_bool(NA)
is_one_bool(c())
is_one_bool("nonsense")
is_one_bool(is_one_bool)
is_one_bool(c(TRUE, FALSE))

check_empty_beautier_folder()
```

is_one_div_x_distr	<i>Determine if the object is a valid 1/x distribution, as created by create_one_div_x_distr</i>
--------------------	--

Description

Determine if the object is a valid 1/x distribution, as created by [create_one_div_x_distr](#)

Usage

```
is_one_div_x_distr(x)
```

Arguments

x an object, to be determined if it is a valid 1/x distribution

Value

TRUE if x is a valid 1/x distribution, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

use `is_distr` to see if x is any distribution

Examples

```
check_empty_beautier_folder()

# TRUE
is_one_div_x_distr(create_one_div_x_distr())
# FALSE
is_one_div_x_distr(create_poisson_distr())
is_one_div_x_distr(NA)
is_one_div_x_distr(NULL)
is_one_div_x_distr("nonsense")

check_empty_beautier_folder()
```

is_one_double	<i>Determines if the argument is a double</i>
---------------	---

Description

Determines if the argument is a double

Usage

```
is_one_double(x)
```

Arguments

x the object to be determined of if it is one double

Value

TRUE if the argument is one floating point value, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# TRUE
is_one_double(314)
is_one_double(0)
is_one_double(-314)
is_one_double(3.14)
```

```
# FALSE
is_one_double(NULL)
is_one_double(NA)
is_one_double(Inf)
is_one_double("nonsense")
is_one_double(is_one_double)
is_one_double(c())
is_one_double(c(1, 2))

check_empty_beautier_folder()
```

is_one_empty_string	<i>Determine if an object is one empty string</i>
---------------------	---

Description

Determine if an object is one empty string

Usage

```
is_one_empty_string(x)
```

Arguments

x the object that may be one string that may be empty

Value

TRUE is 'x' is one string that is empty

Author(s)

Richèl J.C. Bilderbeek

Examples

```
# TRUE
is_one_empty_string("")

# FALSE
is_one_empty_string("3.14")
is_one_empty_string(c("", ""))
is_one_empty_string(42)
is_one_empty_string("nonsense")
```

`is_one_int`*Determines if the argument is a whole number*

Description

Determines if the argument is a whole number

Usage

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

Arguments

<code>x</code>	the object to be determined of if it is one integer
<code>tolerance</code>	tolerance to rounding errors

Value

TRUE if the argument is one int, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# TRUE
is_one_int(314)
is_one_int(0)
is_one_int(-314)
# FALSE
is_one_int(3.14)
is_one_int(NULL)
is_one_int(NA)
is_one_int(Inf)
is_one_int("nonsense")
is_one_int(c())
is_one_int(c(1, 2))

check_empty_beautier_folder()
```

is_one_na	<i>Determines if x is one NA</i>
-----------	----------------------------------

Description

Determines if x is one NA

Usage

```
is_one_na(x)
```

Arguments

x the object to be determined if it is one NA

Value

TRUE if x is one NA, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()
```

```
check_empty_beautier_folder()
```

is_one_string	<i>Determines if the argument is one string</i>
---------------	---

Description

Determines if the argument is one string

Usage

```
is_one_string(x)
```

Arguments

x the object to be determined of if it is one string

Value

TRUE if the argument is one string, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# TRUE
is_one_string("This is one string")

# FALSE
is_one_string(NULL)
is_one_string(NA)
is_one_string(Inf)
is_one_string(314)
is_one_string(0)
is_one_string(-314)
is_one_string(3.14)
is_one_string(c("a", "b"))
is_one_string(is_one_string)
is_one_string(c())
is_one_string(c(1, 2))

check_empty_beautier_folder()
```

is_one_string_that_is_a_number

General function to create a distribution.

Description

General function to create a distribution.

Usage

```
is_one_string_that_is_a_number(x)
```

Arguments

x the object that may be one string that may be a number

Value

TRUE is 'x' is one string that is a number

Author(s)

Richèl J.C. Bilderbeek

Examples

```
# TRUE
is_one_string_that_is_a_number("3.14")

# FALSE
is_one_string_that_is_a_number(c("3.14", "42"))
is_one_string_that_is_a_number("")
is_one_string_that_is_a_number(42)
is_one_string_that_is_a_number("nonsense")
```

is_on_appveyor	<i>Determines if the environment is AppVeyor</i>
----------------	--

Description

Determines if the environment is AppVeyor

Usage

```
is_on_appveyor()
```

Value

TRUE if run on AppVeyor, **FALSE** otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

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

`is_on_ci`*Determines if the environment is a continuous integration service*

Description

Determines if the environment is a continuous integration service

Usage

```
is_on_ci()
```

Value

TRUE if run on AppVeyor or Travis CI, **FALSE** otherwise

Note

It is possible to fake being on continuous integration service, in this case GitHub Actions, using:

```
““r Sys.setenv(GITHUB_ACTIONS = "I fake being on GitHub Actions") is_on_ci() # Will be true  
““
```

To undo this, do

```
““r Sys.setenv(GITHUB_ACTIONS = "") is_on_ci() # Will be false  
““
```

Author(s)

Richèl J.C. Bilderbeek

Examples

```
is_on_ci()
```

`is_on_github_actions`*Determines if the environment is GitHub Actions*

Description

Determines if the environment is GitHub Actions

Usage

```
is_on_github_actions()
```

Value

TRUE if run on GitHub Actions, **FALSE** otherwise

Note

It is possible to fake being on GitHub Actions, using:

```
““r Sys.setenv(GITHUB_ACTIONS = "I fake being on GitHub Actions") is_on_github_actions() #  
Will be true ““
```

To undo this, do

```
““r Sys.setenv(GITHUB_ACTIONS = "") is_on_github_actions() # Will be false ““
```

Author(s)

Richèl J.C. Bilderbeek

Examples

```
if (is_on_github_actions()) {  
  message("Running on GitHub Actions")  
}
```

is_on_travis

Determines if the environment is Travis CI

Description

Determines if the environment is Travis CI

Usage

```
is_on_travis()
```

Value

TRUE if run on Travis CI, **FALSE** otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
if (is_on_ci()) {  
  message("Running on Travis CI")  
}
```

is_param	<i>Determine if the object is a valid parameter</i>
----------	---

Description

Determine if the object is a valid parameter

Usage

```
is_param(x)
```

Arguments

x an object, to be determined if it is a valid parameter, as created by [create_param](#))

Value

TRUE if x is a valid parameter, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# TRUE
is_param(create_alpha_param())
is_param(create_beta_param())
is_param(create_clock_rate_param())
is_param(create_kappa_1_param())
is_param(create_kappa_2_param())
is_param(create_lambda_param())
is_param(create_m_param())
is_param(create_mean_param())
is_param(create_mu_param())
is_param(create_rate_ac_param())
is_param(create_rate_ag_param())
is_param(create_rate_at_param())
is_param(create_rate_cg_param())
is_param(create_rate_ct_param())
is_param(create_rate_gt_param())
is_param(create_s_param())
is_param(create_scale_param())
is_param(create_sigma_param())

# FALSE
is_param(NA)
is_param(NULL)
```

```

is_param("nonsense")
is_param(create_jc69_site_model())
is_param(create_strict_clock_model())
is_param(create_yule_tree_prior())
is_param(create_mcmc())

check_empty_beautier_folder()

```

is_param_name

Determines if the name is a valid parameter name

Description

Determines if the name is a valid parameter name

Usage

```
is_param_name(name)
```

Arguments

name the name to be tested

Value

TRUE if the name is a valid parameter name, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```

check_empty_beautier_folder()

# TRUE
is_param_name("alpha")
is_param_name("beta")
is_param_name("clock_rate")
is_param_name("kappa_1")
is_param_name("kappa_2")
is_param_name("lambda")
is_param_name("m")
is_param_name("mean")
is_param_name("mu")
is_param_name("rate_ac")
is_param_name("rate_ag")
is_param_name("rate_at")
is_param_name("rate_cg")
is_param_name("rate_ct")

```

```
is_param_name("rate_gt")
is_param_name("s")
is_param_name("scale")
is_param_name("sigma")

# FALSE
is_param_name("nonsense")
is_param_name(NA)
is_param_name(NULL)
is_param_name("")
is_param_name(c())

check_empty_beautier_folder()
```

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

Description

Checks if the input is a phylogeny

Usage

```
is_phylo(x)
```

Arguments

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

Value

TRUE or FALSE

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [check_phylogeny](#) to check for a phylogeny

Examples

```
check_empty_beautier_folder()

# TRUE
phylogeny <- ape::read.tree(text = "(a:15,b:15):1;")
is_phylo(phylogeny)

# FALSE
```

```
is_phylo("nonsense")
is_phylo(NA)
is_phylo(NULL)

check_empty_beautier_folder()
```

is_poisson_distr	<i>Determine if the object is a valid Poisson distribution as created by create_poisson_distr</i>
------------------	---

Description

Determine if the object is a valid Poisson distribution as created by [create_poisson_distr](#)

Usage

```
is_poisson_distr(x)
```

Arguments

x an object, to be determined if it is a valid Poisson distribution

Value

TRUE if x is a valid Poisson distribution, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

use [is_distr](#) to see if x is any distribution

Examples

```
check_empty_beautier_folder()

# TRUE
is_poisson_distr(create_poisson_distr())
# FALSE
is_poisson_distr(create_uniform_distr())
is_distr(NA)
is_distr(NULL)
is_distr("nonsense")

check_empty_beautier_folder()
```

is_rate_ac_param	<i>Determine if the object is a valid 'rate AC' parameter</i>
------------------	---

Description

Determine if the object is a valid 'rate AC' parameter

Usage

```
is_rate_ac_param(x)
```

Arguments

x an object, to be determined if it is a valid 'rate AC' parameter

Value

TRUE if x is a valid 'rate AC' parameter, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

[create_rate_ac_param](#) creates a 'rate AC' parameter

Examples

```
check_empty_beautier_folder()

is_rate_ac_param(create_alpha_param())
is_rate_ac_param(create_beta_param())
is_rate_ac_param(create_clock_rate_param())
is_rate_ac_param(create_kappa_1_param())
is_rate_ac_param(create_kappa_2_param())
is_rate_ac_param(create_lambda_param())
is_rate_ac_param(create_m_param())
is_rate_ac_param(create_mean_param())
is_rate_ac_param(create_mu_param())
is_rate_ac_param(create_rate_ac_param())
is_rate_ac_param(create_rate_ag_param())
is_rate_ac_param(create_rate_at_param())
is_rate_ac_param(create_rate_cg_param())
is_rate_ac_param(create_rate_ct_param())
is_rate_ac_param(create_rate_gt_param())
is_rate_ac_param(create_s_param())
is_rate_ac_param(create_scale_param())
is_rate_ac_param(create_sigma_param())
```

```

is_rate_ac_param(NA)
is_rate_ac_param(NULL)
is_rate_ac_param("nonsense")
is_rate_ac_param(create_jc69_site_model())
is_rate_ac_param(create_strict_clock_model())
is_rate_ac_param(create_yule_tree_prior())
is_rate_ac_param(create_mcmc())

check_empty_beautier_folder()

```

is_rate_ag_param	<i>Determine if the object is a valid 'rate AG' parameter</i>
------------------	---

Description

Determine if the object is a valid 'rate AG' parameter

Usage

```
is_rate_ag_param(x)
```

Arguments

x an object, to be determined if it is a valid 'rate AG' parameter

Value

TRUE if x is a valid 'rate AG' parameter, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

[create_rate_ag_param](#) creates a 'rate AG' parameter

Examples

```

check_empty_beautier_folder()

is_rate_ag_param(create_alpha_param())
is_rate_ag_param(create_beta_param())
is_rate_ag_param(create_clock_rate_param())
is_rate_ag_param(create_kappa_1_param())
is_rate_ag_param(create_kappa_2_param())
is_rate_ag_param(create_lambda_param())
is_rate_ag_param(create_m_param())
is_rate_ag_param(create_mean_param())

```



```

is_rate_ag_param(create_mu_param())
is_rate_ag_param(create_rate_ac_param())
is_rate_ag_param(create_rate_ag_param())
is_rate_ag_param(create_rate_at_param())
is_rate_ag_param(create_rate_cg_param())
is_rate_ag_param(create_rate_ct_param())
is_rate_ag_param(create_rate_gt_param())
is_rate_ag_param(create_s_param())
is_rate_ag_param(create_scale_param())
is_rate_ag_param(create_sigma_param())

is_rate_ag_param(NA)
is_rate_ag_param(NULL)
is_rate_ag_param("nonsense")
is_rate_ag_param(create_jc69_site_model())
is_rate_ag_param(create_strict_clock_model())
is_rate_ag_param(create_yule_tree_prior())
is_rate_ag_param(create_mcmc())

check_empty_beautier_folder()

```

is_rate_at_param	<i>Determine if the object is a valid 'rate AT' parameter</i>
------------------	---

Description

Determine if the object is a valid 'rate AT' parameter

Usage

```
is_rate_at_param(x)
```

Arguments

x an object, to be determined if it is a valid 'rate AT' parameter

Value

TRUE if x is a valid 'rate AT' parameter, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

[create_rate_at_param](#) creates a 'rate AT' parameter

Examples

```
check_empty_beautier_folder()

is_rate_at_param(create_alpha_param())
is_rate_at_param(create_beta_param())
is_rate_at_param(create_clock_rate_param())
is_rate_at_param(create_kappa_1_param())
is_rate_at_param(create_kappa_2_param())
is_rate_at_param(create_lambda_param())
is_rate_at_param(create_m_param())
is_rate_at_param(create_mean_param())
is_rate_at_param(create_mu_param())
is_rate_at_param(create_rate_ac_param())
is_rate_at_param(create_rate_ag_param())
is_rate_at_param(create_rate_at_param())
is_rate_at_param(create_rate_cg_param())
is_rate_at_param(create_rate_ct_param())
is_rate_at_param(create_rate_gt_param())
is_rate_at_param(create_s_param())
is_rate_at_param(create_scale_param())
is_rate_at_param(create_sigma_param())

is_rate_at_param(NA)
is_rate_at_param(NULL)
is_rate_at_param("nonsense")
is_rate_at_param(create_jc69_site_model())
is_rate_at_param(create_strict_clock_model())
is_rate_at_param(create_yule_tree_prior())
is_rate_at_param(create_mcmc())

check_empty_beautier_folder()
```

is_rate_cg_param	Determine if the object is a valid 'rate CG' parameter
------------------	--

Description

Determine if the object is a valid 'rate CG' parameter

Usage

```
is_rate_cg_param(x)
```

Arguments

x an object, to be determined if it is a valid 'rate CG' parameter

Value

TRUE if x is a valid 'rate CG' parameter, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

[create_rate_cg_param](#) creates a 'rate CG' parameter

Examples

```
check_empty_beautier_folder()

is_rate_cg_param(create_alpha_param())
is_rate_cg_param(create_beta_param())
is_rate_cg_param(create_clock_rate_param())
is_rate_cg_param(create_kappa_1_param())
is_rate_cg_param(create_kappa_2_param())
is_rate_cg_param(create_lambda_param())
is_rate_cg_param(create_m_param())
is_rate_cg_param(create_mean_param())
is_rate_cg_param(create_mu_param())
is_rate_cg_param(create_rate_ac_param())
is_rate_cg_param(create_rate_ag_param())
is_rate_cg_param(create_rate_at_param())
is_rate_cg_param(create_rate_cg_param())
is_rate_cg_param(create_rate_ct_param())
is_rate_cg_param(create_rate_gt_param())
is_rate_cg_param(create_s_param())
is_rate_cg_param(create_scale_param())
is_rate_cg_param(create_sigma_param())

is_rate_cg_param(NA)
is_rate_cg_param(NULL)
is_rate_cg_param("nonsense")
is_rate_cg_param(create_jc69_site_model())
is_rate_cg_param(create_strict_clock_model())
is_rate_cg_param(create_yule_tree_prior())
is_rate_cg_param(create_mcmc())

check_empty_beautier_folder()
```

is_rate_ct_param	<i>Determine if the object is a valid 'rate CT' parameter</i>
------------------	---

Description

Determine if the object is a valid 'rate CT' parameter

Usage

```
is_rate_ct_param(x)
```

Arguments

`x` an object, to be determined if it is a valid 'rate CT' parameter

Value

TRUE if `x` is a valid 'rate CG' parameter, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

[create_rate_ct_param](#) creates a 'rate CT' parameter

Examples

```
check_empty_beautier_folder()

is_rate_ct_param(create_alpha_param())
is_rate_ct_param(create_beta_param())
is_rate_ct_param(create_clock_rate_param())
is_rate_ct_param(create_kappa_1_param())
is_rate_ct_param(create_kappa_2_param())
is_rate_ct_param(create_lambda_param())
is_rate_ct_param(create_m_param())
is_rate_ct_param(create_mean_param())
is_rate_ct_param(create_mu_param())
is_rate_ct_param(create_rate_ac_param())
is_rate_ct_param(create_rate_ag_param())
is_rate_ct_param(create_rate_at_param())
is_rate_ct_param(create_rate_cg_param())
is_rate_ct_param(create_rate_ct_param())
is_rate_ct_param(create_rate_gt_param())
is_rate_ct_param(create_s_param())
is_rate_ct_param(create_scale_param())
is_rate_ct_param(create_sigma_param())

is_rate_ct_param(NA)
is_rate_ct_param(NULL)
is_rate_ct_param("nonsense")
is_rate_ct_param(create_jc69_site_model())
is_rate_ct_param(create_strict_clock_model())
is_rate_ct_param(create_yule_tree_prior())
is_rate_ct_param(create_mcmc())

check_empty_beautier_folder()
```

is_rate_gt_param	<i>Determine if the object is a valid 'rate GT' parameter</i>
------------------	---

Description

Determine if the object is a valid 'rate GT' parameter

Usage

```
is_rate_gt_param(x)
```

Arguments

x an object, to be determined if it is a valid 'rate GT' parameter

Value

TRUE if x is a valid 'rate GT' parameter, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

[create_rate_gt_param](#) creates a 'rate GT' parameter

Examples

```
check_empty_beautier_folder()

is_rate_gt_param(create_alpha_param())
is_rate_gt_param(create_beta_param())
is_rate_gt_param(create_clock_rate_param())
is_rate_gt_param(create_kappa_1_param())
is_rate_gt_param(create_kappa_2_param())
is_rate_gt_param(create_lambda_param())
is_rate_gt_param(create_m_param())
is_rate_gt_param(create_mean_param())
is_rate_gt_param(create_mu_param())
is_rate_gt_param(create_rate_ac_param())
is_rate_gt_param(create_rate_ag_param())
is_rate_gt_param(create_rate_at_param())
is_rate_gt_param(create_rate_cg_param())
is_rate_gt_param(create_rate_ct_param())
is_rate_gt_param(create_rate_gt_param())
is_rate_gt_param(create_s_param())
is_rate_gt_param(create_scale_param())
is_rate_gt_param(create_sigma_param())
```

```

is_rate_gt_param(NA)
is_rate_gt_param(NULL)
is_rate_gt_param("nonsense")
is_rate_gt_param(create_jc69_site_model())
is_rate_gt_param(create_strict_clock_model())
is_rate_gt_param(create_yule_tree_prior())
is_rate_gt_param(create_mcmc())

check_empty_beautier_folder()

```

is_rln_clock_model	<i>Determine if the object is a valid relaxed log normal clock model</i>
--------------------	--

Description

Determine if the object is a valid relaxed log normal clock model

Usage

```
is_rln_clock_model(x)
```

Arguments

x	an object, to be determined if it is a valid relaxed log normal clock model, as created by create_rln_clock_model)
---	---

Value

TRUE if x is a valid relaxed log normal clock model, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

[create_clock_model](#) shows an overview of functions to create a clock model

Examples

```

check_empty_beautier_folder()

is_rln_clock_model(create_strict_clock_model())
is_rln_clock_model(create_rln_clock_model())

is_rln_clock_model(NA)
is_rln_clock_model(NULL)
is_rln_clock_model("nonsense")
is_rln_clock_model(create_jc69_site_model())

```

```
is_rln_clock_model(create_mcmc())
check_empty_beautier_folder()
```

is_scale_param	<i>Determine if the object is a valid scale parameter</i>
----------------	---

Description

Determine if the object is a valid scale parameter

Usage

```
is_scale_param(x)
```

Arguments

x an object, to be determined if it is a valid scale parameter

Value

TRUE if x is a valid scale parameter, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

is_scale_param(create_alpha_param())
is_scale_param(create_beta_param())
is_scale_param(create_clock_rate_param())
is_scale_param(create_kappa_1_param())
is_scale_param(create_kappa_2_param())
is_scale_param(create_lambda_param())
is_scale_param(create_m_param())
is_scale_param(create_mean_param())
is_scale_param(create_mu_param())
is_scale_param(create_rate_ac_param())
is_scale_param(create_rate_ag_param())
is_scale_param(create_rate_at_param())
is_scale_param(create_rate_cg_param())
is_scale_param(create_rate_ct_param())
is_scale_param(create_rate_gt_param())
is_scale_param(create_s_param())
is_scale_param(create_scale_param())
is_scale_param(create_sigma_param())
```

```

is_scale_param(NA)
is_scale_param(NULL)
is_scale_param("nonsense")
is_scale_param(create_jc69_site_model())
is_scale_param(create_strict_clock_model())
is_scale_param(create_yule_tree_prior())
is_scale_param(create_mcmc())

check_empty_beautier_folder()

```

is_sigma_param	<i>Determine if the object is a valid sigma parameter</i>
----------------	---

Description

Determine if the object is a valid sigma parameter

Usage

```
is_sigma_param(x)
```

Arguments

x an object, to be determined if it is a valid sigma parameter

Value

TRUE if x is a valid sigma parameter, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```

check_empty_beautier_folder()

is_sigma_param(create_alpha_param())
is_sigma_param(create_beta_param())
is_sigma_param(create_clock_rate_param())
is_sigma_param(create_kappa_1_param())
is_sigma_param(create_kappa_2_param())
is_sigma_param(create_lambda_param())
is_sigma_param(create_m_param())
is_sigma_param(create_mean_param())
is_sigma_param(create_mu_param())
is_sigma_param(create_rate_ac_param())
is_sigma_param(create_rate_ag_param())
is_sigma_param(create_rate_at_param())
is_sigma_param(create_rate_cg_param())

```



```

is_sigma_param(create_rate_ct_param())
is_sigma_param(create_rate_gt_param())
is_sigma_param(create_s_param())
is_sigma_param(create_scale_param())
is_sigma_param(create_sigma_param())

is_sigma_param(NA)
is_sigma_param(NULL)
is_sigma_param("nonsense")
is_sigma_param(create_jc69_site_model())
is_sigma_param(create_strict_clock_model())
is_sigma_param(create_yule_tree_prior())
is_sigma_param(create_mcmc())

check_empty_beautier_folder()

```

is_site_model	<i>Determine if the object is a valid site_model</i>
---------------	--

Description

Determine if the object is a valid site_model

Usage

```
is_site_model(x)
```

Arguments

x an object, to be determined if it is a site_model

Value

TRUE if the site_model is a valid site_model, FALSE otherwise

See Also

A site model can be created using [create_site_model](#)

Examples

```

check_empty_beautier_folder()

# TRUE
is_site_model(create_gtr_site_model())
is_site_model(create_hky_site_model())
is_site_model(create_jc69_site_model())
is_site_model(create_tn93_site_model())

# FALSE

```

```

is_site_model(NA)
is_site_model(NULL)
is_site_model("nonsense")
is_site_model(create_strict_clock_model())
is_site_model(create_bd_tree_prior())
is_site_model(create_mcmc())

check_empty_beautier_folder()

```

is_site_model_name	<i>Determines if the name is a valid site_model name</i>
--------------------	--

Description

Determines if the name is a valid site_model name

Usage

```
is_site_model_name(name)
```

Arguments

name	the name to be tested
------	-----------------------

Value

TRUE if the name is a valid site_model name, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```

check_empty_beautier_folder()

# TRUE
is_site_model_name("JC69")
is_site_model_name("HKY")
is_site_model_name("TN93")
is_site_model_name("GTR")
# FALSE
is_site_model_name("nonsense")

check_empty_beautier_folder()

```

`is_strict_clock_model` *Determine if the object is a valid strict clock model, as returned by [create_strict_clock_model](#)*

Description

Determine if the object is a valid strict clock model, as returned by [create_strict_clock_model](#)

Usage

```
is_strict_clock_model(x)
```

Arguments

`x` an object, to be determined if it is a valid strict clock model

Value

TRUE if `x` is a valid strict clock model, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

[create_clock_model](#) shows an overview of functions to create a clock model

Examples

```
check_empty_beautier_folder()

is_strict_clock_model(create_strict_clock_model())
is_strict_clock_model(create_rln_clock_model())

is_strict_clock_model(NA)
is_strict_clock_model(NULL)
is_strict_clock_model("nonsense")
is_strict_clock_model(create_jc69_site_model())
is_strict_clock_model(create_mcmc())

check_empty_beautier_folder()
```

is_s_param	<i>Determine if the object is a valid s parameter</i>
------------	---

Description

Determine if the object is a valid s parameter

Usage

```
is_s_param(x)
```

Arguments

x an object, to be determined if it is a valid s parameter

Value

TRUE if x is a valid s parameter, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

is_s_param(create_alpha_param())
is_s_param(create_beta_param())
is_s_param(create_clock_rate_param())
is_s_param(create_kappa_1_param())
is_s_param(create_kappa_2_param())
is_s_param(create_lambda_param())
is_s_param(create_m_param())
is_s_param(create_mean_param())
is_s_param(create_mu_param())
is_s_param(create_rate_ac_param())
is_s_param(create_rate_ag_param())
is_s_param(create_rate_at_param())
is_s_param(create_rate_cg_param())
is_s_param(create_rate_ct_param())
is_s_param(create_rate_gt_param())
is_s_param(create_s_param())
is_s_param(create_scale_param())
is_s_param(create_sigma_param())

is_s_param(NA)
is_s_param(NULL)
is_s_param("nonsense")
is_s_param(create_jc69_site_model())
```

```

is_s_param(create_strict_clock_model())
is_s_param(create_yule_tree_prior())
is_s_param(create_mcmc())

check_empty_beautier_folder()

```

is_tn93_site_model	<i>Determine if the object is a valid TN93 site model,</i>
--------------------	--

Description

Determine if the object is a valid TN93 site model,

Usage

```
is_tn93_site_model(x)
```

Arguments

x	an object, to be determined if it is a valid TN93 site model, as created by create_tn93_site_model
---	--

Value

TRUE if x is a valid TN93 site model, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```

check_empty_beautier_folder()

# site models
is_tn93_site_model(create_gtr_site_model())
is_tn93_site_model(create_hky_site_model())
is_tn93_site_model(create_jc69_site_model())
is_tn93_site_model(create_tn93_site_model())

# other models
is_tn93_site_model(NA)
is_tn93_site_model(NULL)
is_tn93_site_model("nonsense")
is_tn93_site_model("")
is_tn93_site_model(c())
is_tn93_site_model(create_strict_clock_model())
is_tn93_site_model(create_bd_tree_prior())
is_tn93_site_model(create_mcmc())

check_empty_beautier_folder()

```

is_tree_prior	<i>Determine if an object is a valid tree prior</i>
---------------	---

Description

Determine if an object is a valid tree prior

Usage

```
is_tree_prior(x)
```

Arguments

x	an object
---	-----------

Value

TRUE if x is a valid tree_prior, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

tree priors can be created by [create_tree_prior](#)

Examples

```
check_empty_beautier_folder()

is_tree_prior(create_bd_tree_prior())
is_tree_prior(create_yule_tree_prior())
!is_tree_prior("nonsense")

check_empty_beautier_folder()
```

is_tree_prior_name	<i>Determines if the name is a valid tree prior name</i>
--------------------	--

Description

Determines if the name is a valid tree prior name

Usage

```
is_tree_prior_name(name)
```

Arguments

name	the name to be tested
------	-----------------------

Value

TRUE if the name is a valid tree_prior name, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# TRUE
is_tree_prior_name("birth_death")
is_tree_prior_name("coalescent_bayesian_skylines")
is_tree_prior_name("coalescent_constant_population")
is_tree_prior_name("coalescent_exp_population")
is_tree_prior_name("yule")
# FALSE
is_tree_prior_name("nonsense")

check_empty_beautier_folder()
```

is_uniform_distr	<i>Determine if the object is a valid uniform distribution as created by create_uniform_distr</i>
------------------	---

Description

Determine if the object is a valid uniform distribution as created by [create_uniform_distr](#)

Usage

```
is_uniform_distr(x)
```

Arguments

x an object, to be determined if it is a valid uniform distribution

Value

TRUE if x is a valid uniform distribution, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

use [is_distr](#) to see if x is any distribution

Examples

```
check_empty_beautier_folder()

# TRUE
is_uniform_distr(create_uniform_distr())
# FALSE
is_uniform_distr(create_beta_distr())
is_uniform_distr(NA)
is_uniform_distr(NULL)
is_uniform_distr("nonsense")

check_empty_beautier_folder()
```

is_xml	<i>Checks if the text is a valid XML node, that is, it has a opening and matching closing tag</i>
--------	---

Description

Checks if the text is a valid XML node, that is, it has a opening and matching closing tag

Usage

```
is_xml(text)
```

Arguments

text text to be determined to be valid

Value

TRUE if the text is valid XML, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

is_yule_tree_prior	<i>Determine if the object is a valid Yule tree prior,</i>
--------------------	--

Description

Determine if the object is a valid Yule tree prior,

Usage

```
is_yule_tree_prior(x)
```

Arguments

x an object, to be determined if it is a valid Yule tree prior

Value

TRUE if x is a valid Yule tree prior, FALSE otherwise

Author(s)

Richèl J.C. Bilderbeek

See Also

Use [create_yule_tree_prior](#) to create a valid Yule tree prior

Examples

```
check_empty_beautier_folder()

# TRUE
is_yule_tree_prior(create_yule_tree_prior())

# FALSE
is_yule_tree_prior(create_bd_tree_prior())
is_yule_tree_prior(create_cbs_tree_prior())
is_yule_tree_prior(create_ccp_tree_prior())
is_yule_tree_prior(create_cep_tree_prior())

check_empty_beautier_folder()
```

```
jc69_site_model_to_xml_state
```

Converts a site model to XML, used in the state section

Description

Converts a site model to XML, used in the state section

Usage

```
jc69_site_model_to_xml_state(  
  site_model,  
  beauti_options = create_beauti_options()  
)
```

Arguments

`site_model` a site model, as returned by [create_site_model](#)
`beauti_options` one BEAUti options object, as returned by [create_beauti_options](#)

Value

the site model as XML text

Author(s)

Richèl J.C. Bilderbeek

```
kappa_param_to_xml
```

Internal function

Description

Converts an kappa parameter to XML

Usage

```
kappa_param_to_xml(kappa_param, beauti_options = create_beauti_options())
```

Arguments

`kappa_param` a kappa parameter, as created by [create_kappa_param](#)
`beauti_options` one BEAUti options object, as returned by [create_beauti_options](#)

Value

the parameter as XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# The kappa parameter must be initialized, i.e. have an ID
kappa_param_to_xml(kappa_param = create_kappa_param(id = "1"))

check_empty_beautier_folder()
```

mcmc_to_xml_run

Converts an MCMC object to the run section's XML

Description

Converts an MCMC object to the run section's XML

Usage

```
mcmc_to_xml_run(mcmc)
```

Arguments

mcmc	one MCMC. Use create_mcmc to create an MCMC. Use create_ns_mcmc to create an MCMC for a Nested Sampling run. Use check_mcmc to check if an MCMC is valid. Use rename_mcmc_filenames to rename the filenames in an MCMC.
------	---

Value

the XML as text

Author(s)

Richèl J.C. Bilderbeek

Examples

```

if (is_on_ci()) {

  check_empty_beautier_folder()

  # <run id=\"mcmc\" spec=\"MCMC\" chainLength=\"1e+07\">
  mcmc_to_xml_run(create_mcmc())

  check_empty_beautier_folder()
}

```

mcmc_to_xml_run_default

Converts an MCMC object to the run section's XML for a default MCMC

Description

Converts an MCMC object to the run section's XML for a default MCMC

Usage

```
mcmc_to_xml_run_default(mcmc)
```

Arguments

mcmc	one MCMC. Use create_mcmc to create an MCMC. Use create_ns_mcmc to create an MCMC for a Nested Sampling run. Use check_mcmc to check if an MCMC is valid. Use rename_mcmc_filenames to rename the filenames in an MCMC.
------	---

Value

the XML as text

Author(s)

Richèl J.C. Bilderbeek

Examples

```

check_empty_beautier_folder()

# <run id=\"mcmc\" spec=\"MCMC\" chainLength=\"1e+07\">
xml <- mcmc_to_xml_run_default(create_mcmc())

check_empty_beautier_folder()

```

mcmc_to_xml_run_nested_sampling

Converts an MCMC object to the run section's XML for a Nested-Sampling MCMC

Description

Converts an MCMC object to the run section's XML for a Nested-Sampling MCMC

Usage

```
mcmc_to_xml_run_nested_sampling(mcmc)
```

Arguments

mcmc	one MCMC. Use create_mcmc to create an MCMC. Use create_ns_mcmc to create an MCMC for a Nested Sampling run. Use check_mcmc to check if an MCMC is valid. Use rename_mcmc_filenames to rename the filenames in an MCMC.
------	---

Value

the XML as text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# "<run id=\"mcmc\" spec=\"beast.gss.NS\" chainLength=\"1e+07\" \"
# \"particleCount=\"1\" subChainLength=\"5000\" epsilon=\"1e-12\">\"
mcmc_to_xml_run_nested_sampling(create_ns_mcmc())

check_empty_beautier_folder()
```

```
mrca_priors_to_xml_prior_distr
```

Creates the the distribution's prior section (which is part of a posterior distribution section) of a BEAST2 XML parameter file.

Description

These lines start with '<distribution id="prior"'

Usage

```
mrca_priors_to_xml_prior_distr(inference_model)
```

Arguments

```
inference_model
```

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Details

```
<distribution id="posterior" spec="util.CompoundDistribution"> <distribution id="prior"
spec="util.CompoundDistribution"> HERE, where the ID of the distribution is 'prior' </distribution>
<distribution id="likelihood" ...> </distribution> </distribution>
```

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

```
mrca_prior_to_xml_prior_distr
```

Creates the distribution section in the prior section of the distribution section of a BEAST2 XML parameter file.

Description

These lines start with '<distribution id='

Usage

```
mrca_prior_to_xml_prior_distr(inference_model)
```

Arguments

```
inference_model
```

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

```
lines of XML text
```

Author(s)

```
Richèl J.C. Bilderbeek
```

Examples

```
check_empty_beautier_folder()

# <distribution id="posterior" spec="util.CompoundDistribution">
#   <distribution id="prior" spec="util.CompoundDistribution">
#     HERE, where the ID of the distribution is 'prior'
#   </distribution>
#   <distribution id="likelihood" ...>
#     </distribution>
# </distribution>

check_empty_beautier_folder()
```

```
mrca_prior_to_xml_state
```

Internal function to create the XML of an MRCA prior, as used in the state section

Description

Internal function to create the XML of an MRCA prior, as used in the state section

Usage

```
mrca_prior_to_xml_state(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

the tree prior as XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

mrca_prior_to_xml_state(
  inference_model = create_inference_model(
    mrca_prior = create_mrca_prior(
      alignment_id = "test_output_0",
      mrca_distr = create_normal_distr(id = 42)
    ),
    clock_model = create_strict_clock_model()
  )
)

check_empty_beautier_folder()
```

mrca_prior_to_xml_taxonset

Creates the taxonset section in the prior section of the distribution section of a BEAST2 XML parameter file.

Description

Creates the taxonset section in the prior section of the distribution section of a BEAST2 XML parameter file.

Usage

```
mrca_prior_to_xml_taxonset(mrca_prior, taxa_names_with_ids = NULL)
```


Arguments

mrca_prior a Most Recent Common Ancestor prior, as returned by [create_mrca_prior](#)
 taxa_names_with_ids
 taxa names that already have received an ID. Causes the XML to idref these

Details

```
<taxonset id="all" spec="TaxonSet"> <taxon id="626029_aco" spec="Taxon"/> <taxon id="630116_aco"
spec="Taxon"/> <taxon id="630210_aco" spec="Taxon"/> <taxon id="B25702_aco" spec="Taxon"/>
<taxon id="61430_aco" spec="Taxon"/> </taxonset>
```

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

mrca_prior_to_xml_tracelog

Internal function

Description

Internal function to creates the MRCA prior's XML for the tracelog section.

Usage

```
mrca_prior_to_xml_tracelog(inference_model)
```

Arguments

inference_model
 a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Details

```
<logger id="tracelog" ...> # Here </logger>
```

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

m_param_to_xml	<i>Internal function</i>
----------------	--------------------------

Description

Converts an m parameter to XML

Usage

```
m_param_to_xml(m_param, beauti_options = create_beauti_options())
```

Arguments

m_param an m parameter, as created by [create_m_param](#)
 beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

the parameter as XML text

Author(s)

Richèl J.C. Bilderbeek

no_taxa_to_xml_tree	<i>Internal function</i>
---------------------	--------------------------

Description

Creates the 'tree' section of a BEAST2 XML parameter file, which is part of a 'state' section, without being indented, when there is no tip-dating

Usage

```
no_taxa_to_xml_tree(inference_model)
```

Arguments

inference_model
 a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Details

The tree tag has these elements:

```
<tree[...]>
  <taxonset[...]>
    [...]
  </taxonset>
</run>
```

Value

the random phylogeny as XML text

Author(s)

Richèl J.C. Bilderbeek

parameter_to_xml	<i>Internal function</i>
------------------	--------------------------

Description

Converts a parameter to XML

Usage

```
parameter_to_xml(parameter, beauti_options)
```

Arguments

parameter a parameter, as created by [create_param](#))
beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

the parameter as XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

parameter_to_xml(
  create_alpha_param(id = 1),
  beauti_options = create_beauti_options()
)

check_empty_beautier_folder()
```

parameter_to_xml_kappa_1

Internal function

Description

Converts a kappa 1 parameter to XML

Usage

```
parameter_to_xml_kappa_1(parameter, beauti_options = create_beauti_options())
```

Arguments

parameter a kappa 1 parameter, a numeric value. For advanced usage, use the structure as created by [create_kappa_1_param](#))

beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

the parameter as XML text

Author(s)

Richèl J.C. Bilderbeek

`parameter_to_xml_kappa_2`*Internal function*

Description

Converts a kappa 2 parameter to XML

Usage

```
parameter_to_xml_kappa_2(parameter, beauti_options = create_beauti_options())
```

Arguments

`parameter` a kappa 2 parameter, a numeric value. For advanced usage, use the structure as created by [create_kappa_2_param](#))

`beauti_options` one BEAUti options object, as returned by [create_beauti_options](#)

Value

the parameter as XML text

Author(s)

Richèl J.C. Bilderbeek

`parameter_to_xml_lambda`*Internal function*

Description

Converts a lambda parameter to XML

Usage

```
parameter_to_xml_lambda(parameter, beauti_options = create_beauti_options())
```

Arguments

`parameter` a lambda parameter, a numeric value. For advanced usage, use the structure as created by [create_lambda_param](#))

`beauti_options` one BEAUti options object, as returned by [create_beauti_options](#)

Value

the parameter as XML text

Author(s)

Richèl J.C. Bilderbeek

parameter_to_xml_mean *Internal function*

Description

Converts a mean parameter to XML

Usage

```
parameter_to_xml_mean(parameter, beauti_options = create_beauti_options())
```

Arguments

parameter a mean parameter, a numeric value. For advanced usage, use the structure as created by [create_mean_param](#))

beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

the parameter as XML text

Author(s)

Richèl J.C. Bilderbeek

parameter_to_xml_mu *Internal function*

Description

Converts a mu parameter to XML

Usage

```
parameter_to_xml_mu(parameter, beauti_options = create_beauti_options())
```

Arguments

`parameter` a mu parameter, a numeric value. For advanced usage, use the structure as created by [create_mu_param](#))

`beauti_options` one BEAUti options object, as returned by [create_beauti_options](#)

Value

the parameter as XML text

Author(s)

Richèl J.C. Bilderbeek

parameter_to_xml_rate_ac

Internal function

Description

Converts a 'rate AC' parameter to XML

Usage

```
parameter_to_xml_rate_ac(
  parameter,
  beauti_options = create_beauti_options(),
  which_name = "state_node"
)
```

Arguments

`parameter` a 'rate AC' parameter, a numeric value. For advanced usage, use the structure as created by [create_rate_ac_param](#))

`beauti_options` one BEAUti options object, as returned by [create_beauti_options](#)

`which_name` the name, can be state_node or rate_name

Value

the parameter as XML text

Author(s)

Richèl J.C. Bilderbeek

parameter_to_xml_rate_ag
Internal function

Description

Converts a 'rate AG' parameter to XML

Usage

```
parameter_to_xml_rate_ag(  
  parameter,  
  beauti_options = create_beauti_options(),  
  which_name = "state_node"  
)
```

Arguments

parameter	a 'rate AG' parameter, a numeric value. For advanced usage, use the structure as created by create_rate_ag_param)
beauti_options	one BEAUti options object, as returned by create_beauti_options
which_name	the name, can be state_node or rate_name

Value

the parameter as XML text

Author(s)

Richèl J.C. Bilderbeek

parameter_to_xml_rate_at
Internal function

Description

Converts a 'rate AT' parameter to XML

Usage

```
parameter_to_xml_rate_at(  
  parameter,  
  beauti_options = create_beauti_options(),  
  which_name = "state_node"  
)
```


Arguments

parameter a 'rate AT' parameter, a numeric value. For advanced usage, use the structure as created by [create_rate_at_param](#))

beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

which_name the name, can be state_node or rate_name

Value

the parameter as XML text

Author(s)

Richèl J.C. Bilderbeek

parameter_to_xml_rate_cg
Internal function

Description

Converts a 'rate CG' parameter to XML

Usage

```
parameter_to_xml_rate_cg(
  parameter,
  beauti_options = create_beauti_options(),
  which_name = "state_node"
)
```

Arguments

parameter a 'rate CG' parameter, a numeric value. For advanced usage, use the structure as created by [create_rate_cg_param](#))

beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

which_name the name, can be state_node or rate_name

Value

the parameter as XML text

Author(s)

Richèl J.C. Bilderbeek

parameter_to_xml_rate_ct
Internal function

Description

Converts a 'rate CT' parameter to XML

Usage

```
parameter_to_xml_rate_ct(  
  parameter,  
  beauti_options = create_beauti_options(),  
  which_name = "state_node"  
)
```

Arguments

parameter	a 'rate CT' parameter, a numeric value. For advanced usage, use the structure as created by create_rate_ct_param)
beauti_options	one BEAUti options object, as returned by create_beauti_options
which_name	the name, can be state_node or rate_name

Value

the parameter as XML text

Author(s)

Richèl J.C. Bilderbeek

parameter_to_xml_rate_gt
Internal function

Description

Converts a 'rate GT' parameter to XML

Usage

```
parameter_to_xml_rate_gt(  
  parameter,  
  beauti_options = create_beauti_options(),  
  which_name = "state_node"  
)
```

Arguments

- parameter a 'rate GT' parameter, a numeric value. For advanced usage, use the structure as created by [create_rate_gt_param](#))
- beauti_options one BEAUti options object, as returned by [create_beauti_options](#)
- which_name the name, can be state_node or rate_name

Value

the parameter as XML text

Author(s)

Richèl J.C. Bilderbeek

parameter_to_xml_scale

Internal function

Description

Converts a scale parameter to XML

Usage

```
parameter_to_xml_scale(parameter, beauti_options = create_beauti_options())
```

Arguments

- parameter a scale parameter, a numeric value. For advanced usage, use the structure as created by [create_scale_param](#))
- beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

the parameter as XML text

Author(s)

Richèl J.C. Bilderbeek

`parameter_to_xml_sigma`*Internal function*

Description

Converts a sigma parameter to XML

Usage

```
parameter_to_xml_sigma(parameter, beauti_options = create_beauti_options())
```

Arguments

`parameter` a sigma parameter, a numeric value. For advanced usage, use the structure as created by [create_sigma_param](#))

`beauti_options` one BEAUti options object, as returned by [create_beauti_options](#)

Value

the parameter as XML text

Author(s)

Richèl J.C. Bilderbeek

`remove_beautier_folder`*Check there are no files in the default [beautier](#) folder*

Description

Check there are no files in the default [beautier](#) folder. The goal is to make sure no temporary files are left undeleted. Will [stop](#) if there are files in the [beautier](#) folder.

Usage

```
remove_beautier_folder()
```

Value

No return value, called for side effects.

Author(s)

Richèl J.C. Bilderbeek

See Also

use [remove_beautier_folder](#) to remove the default ‘beautier’ folder

Examples

```
check_empty_beautier_folder()
```

```
remove_beautier_folder()
```

```
check_empty_beautier_folder()
```

remove_empty_lines	<i>Remove all lines that are only whitespace</i>
--------------------	--

Description

Remove all lines that are only whitespace

Usage

```
remove_empty_lines(lines, trim = FALSE)
```

Arguments

lines character vector with text

trim FALSE if indentation must be preserved, TRUE will remove all surrounding whitespace

Value

the lines with text

Author(s)

Richèl J.C. Bilderbeek

remove_multiline	<i>Remove consecutive lines</i>
------------------	---------------------------------

Description

Remove consecutive lines

Usage

```
remove_multiline(text, lines_to_remove)
```

Arguments

text	lines of characters
lines_to_remove	lines of character that need to be removed from text

Value

lines of text

Author(s)

Richèl J.C. Bilderbeek

rename_inference_model_filenames	<i>Rename the filenames in an inference model</i>
----------------------------------	---

Description

Rename the filenames in an inference model

Usage

```
rename_inference_model_filenames(inference_model, rename_fun)
```

Arguments

inference_model	a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use create_inference_model to create an inference model. Use check_inference_model to check if an inference model is valid. Use rename_inference_model_filenames to rename the files in an inference model.
-----------------	--

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

- [get_remove_dir_fun](#) get a function that removes the directory paths from the filenames, in effect turning these into local files
- [get_replace_dir_fun](#) get a function that replaces the directory paths from the filenames
- [get_remove_hex_fun](#) get a function that removes the hex string from filenames. For example, `tracelog_82c1a522040.log` becomes `tracelog.log`

Value

an inference model with the renamed filenames

Examples

```
check_empty_beautier_folder()

inference_model <- create_inference_model()
inference_model$mcmc$tracelog$filename <- "trace.log"
inference_model$mcmc$screenlog$filename <- "screen.log"
inference_model$mcmc$treelog$filename <- "tree.log"
inference_model$tipdates$filename <- "tipdates.csv"

# Nah, put the files in a folder
inference_model <- rename_inference_model_filenames(
  inference_model = inference_model,
  rename_fun = get_replace_dir_fun("/home/john")
)

# Nah, put the files in anoth folder
inference_model <- rename_inference_model_filenames(
  inference_model = inference_model,
  rename_fun = get_replace_dir_fun("/home/doe")
)

# Nah, store the files locally
rename_inference_model_filenames(
  inference_model = inference_model,
  rename_fun = get_remove_dir_fun()
)

check_empty_beautier_folder()
```

Description

Rename the filenames within an MCMC

Usage

```
rename_mcmc_filenames(mcmc, rename_fun)
```

Arguments

- | | |
|------------|---|
| mcmc | one MCMC. Use create_mcmc to create an MCMC. Use create_ns_mcmc to create an MCMC for a Nested Sampling run. Use check_mcmc to check if an MCMC is valid. Use rename_mcmc_filenames to rename the filenames in an MCMC. |
| rename_fun | a function to rename a filename, as can be checked by check_rename_fun . This function should have one argument, which will be a filename or <code>NA</code> . The function should return one filename (when passed one filename) or one <code>NA</code> (when passed one <code>NA</code>). Example rename functions are: <ul style="list-style-type: none"> • get_remove_dir_fun get a function that removes the directory paths from the filenames, in effect turning these into local files • get_replace_dir_fun get a function that replaces the directory paths from the filenames • get_remove_hex_fun get a function that removes the hex string from filenames. For example, <code>tracelog_82c1a522040.log</code> becomes <code>tracelog.log</code> |

Value

an 'mcmc' (see [create_mcmc](#)) with renamed filenames

Examples

```
check_empty_beautier_folder()

# Create an MCMC with local filenames
mcmc <- create_mcmc()
mcmc$tracelog$filename <- "trace.log"
mcmc$screenlog$filename <- "screen.log"
mcmc$treelog$filename <- "tree.log"

# Nah, files should be put in '/home/john' folder
mcmc <- rename_mcmc_filenames(
  mcmc = mcmc,
  rename_fun = get_replace_dir_fun("/home/john")
)

# Nah, files should be put in '/home/doe' folder instead
mcmc <- rename_mcmc_filenames(
  mcmc = mcmc,
  rename_fun = get_replace_dir_fun("/home/doe")
)
```



```
# Nah, files should be put in local folder instead
mcmc <- rename_mcmc_filenames(
  mcmc = mcmc,
  rename_fun = get_remove_dir_fun()
)

check_empty_beautier_folder()
```

rln_clock_model_to_xml_mean_rate_prior

Internal function

Description

Internal function

Usage

```
rln_clock_model_to_xml_mean_rate_prior(rln_clock_model, beauti_options)
```

Arguments

rln_clock_model

a Relaxed Log-Normal clock model, as returned by [create_rln_clock_model](#)

beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

rln_clock_model_to_xml_operators

Internal function

Description

Converts an RLN clock model to the operators section of the XML as text

Usage

```
rln_clock_model_to_xml_operators(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

a character vector of XML strings

Author(s)

Richèl J.C. Bilderbeek

rln_clock_model_to_xml_prior_distr
Internal function

Description

Internal function to converts a relaxed log-normal clock model to the prior section of the XML as text

Usage

```
rln_clock_model_to_xml_prior_distr(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

a character vector of XML strings

Author(s)

Richèl J.C. Bilderbeek

Examples

```

check_empty_beautier_folder()

# <distribution id="posterior" spec="util.CompoundDistribution">
#   <distribution id="prior" spec="util.CompoundDistribution">
#     HERE, where the ID of the distribution is 'prior'
#   </distribution>
#   <distribution id="likelihood" ...>
#     </distribution>
# </distribution>

# Must be an initialized inference model
inference_model <- create_inference_model(
  clock_model = create_rln_clock_model(
    id = "test_output_0",
    ucldstdev_distr = create_gamma_distr(
      id = 0,
      alpha = create_alpha_param(id = 2, value = "0.5396"),
      beta = create_beta_param(id = 3, value = "0.3819")
    ),
    mean_rate_prior_distr = create_uniform_distr(id = 1),
    mparam_id = 1
  )
)

rln_clock_model_to_xml_prior_distr(inference_model)

check_empty_beautier_folder()

```

rln_clock_model_to_xml_state

Internal function

Description

Converts an RLN clock model to the ‘state’ section of the XML as text

Usage

```
rln_clock_model_to_xml_state(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

lines of XML text, without indentation nor state tags

Author(s)

Richèl J.C. Bilderbeek

rln_clock_model_to_xml_tracelog
Internal function

Description

Creates the RLN clock model's XML for the tracelog section

Usage

```
rln_clock_model_to_xml_tracelog(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

a character vector of XML strings

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# <logger id="tracelog" ...>
#'   # Here
# </logger>

check_empty_beautier_folder()
```

`rnd_phylo_to_xml_init` *Creates the XML of a random phylogeny, as used in the init section*

Description

Creates the XML text for the beast tag of a BEAST2 parameter file, which is directly after the XML declaration (created by [create_xml_declaration](#)).

Usage

```
rnd_phylo_to_xml_init(inference_model)
```

Arguments

`inference_model`

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Details

The init tag has these elements:

```
<init id=\"RandomTree.t:[...]>
  <populationModel[...]>
    [...]
  </populationModel>
</init>
```

Value

the phylogeny as XML text

Author(s)

Richèl J.C. Bilderbeek

`site_models_to_xml_operators`*Write the XML operators section from the site models.*

Description

Write the XML operators section from the site models.

Usage

```
site_models_to_xml_operators(site_models)
```

Arguments

`site_models` one or more site models, as returned by [create_site_model](#)

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

`site_models_to_xml_prior_distr`*Represent the site models as XML*

Description

Represent the site models as XML

Usage

```
site_models_to_xml_prior_distr(site_models, beauti_options)
```

Arguments

`site_models` one or more site models, as returned by [create_site_model](#)
`beauti_options` one BEAUti options object, as returned by [create_beauti_options](#)

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# <distribution id="posterior" spec="util.CompoundDistribution">
#   <distribution id="prior" spec="util.CompoundDistribution">
#     HERE, where the ID of the distribution is 'prior'
#   </distribution>
#   <distribution id="likelihood" ...>
#     </distribution>
# </distribution>

check_empty_beautier_folder()
```

site_models_to_xml_tracelog

Creates the site models' XML for the tracelog section

Description

Creates the site models' XML for the tracelog section

Usage

```
site_models_to_xml_tracelog(site_models)
```

Arguments

site_models one or more site models, as returned by [create_site_model](#)

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

See Also

the complete tracelog section is created by [create_tracelog_xml](#)

Examples

```

check_empty_beautier_folder()

# <logger id="tracelog" ...>
# '   # Here
# </logger>

check_empty_beautier_folder()

```

```
site_model_to_xml_operators
```

Converts a site model to XML, used in the operators section

Description

Converts a site model to XML, used in the operators section

Usage

```
site_model_to_xml_operators(site_model)
```

Arguments

site_model a site model, as returned by [create_site_model](#)

Value

the site model as XML text

Author(s)

Richèl J.C. Bilderbeek

```
site_model_to_xml_prior_distr
```

Internal function

Description

Converts a site model to XML, used in the prior section

Usage

```
site_model_to_xml_prior_distr(site_model, beauti_options)
```


Arguments

site_model a site model, as returned by [create_site_model](#)

beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

the site model as XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```

site_model_to_xml_prior_distr(
  site_model = create_jc69_site_model(id = 1),
  beauti_options = create_beauti_options()
)
site_model_to_xml_prior_distr(
  site_model = create_hky_site_model(
    id = 1,
    kappa_prior_distr = create_uniform_distr(id = 2)
  ),
  beauti_options = create_beauti_options()
)
site_model_to_xml_prior_distr(
  site_model = create_tn93_site_model(
    id = 1,
    kappa_1_prior_distr = create_uniform_distr(id = 2),
    kappa_2_prior_distr = create_uniform_distr(id = 3)
  ),
  beauti_options = create_beauti_options()
)
site_model_to_xml_prior_distr(
  site_model = create_gtr_site_model(
    id = 1,
    rate_ac_prior_distr = create_uniform_distr(id = 2),
    rate_ag_prior_distr = create_uniform_distr(id = 3),
    rate_at_prior_distr = create_uniform_distr(id = 4),
    rate_cg_prior_distr = create_uniform_distr(id = 5),
    rate_gt_prior_distr = create_uniform_distr(id = 6)
  ),
  beauti_options = create_beauti_options()
)

```

`site_model_to_xml_state`*Internal function to convert a site model to XML, used in the ‘state’ section*

Description

Internal function to convert a site model to XML, used in the ‘state’ section

Usage

```
site_model_to_xml_state(site_model, beauti_options = create_beauti_options())
```

Arguments

`site_model` a site model, as returned by [create_site_model](#)

`beauti_options` one BEAUti options object, as returned by [create_beauti_options](#)

Value

the site model as XML text

Author(s)

Richèl J.C. Bilderbeek

`site_model_to_xml_tracelog`*Creates the site model’s XML for the tracelog section*

Description

Creates the site model’s XML for the tracelog section

Usage

```
site_model_to_xml_tracelog(site_model)
```

Arguments

`site_model` a site model, as returned by [create_site_model](#)

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

See Also

all site models' tracelog section is created by [site_models_to_xml_tracelog](#)

Examples

```
check_empty_beautier_folder()

# <logger id="tracelog" ...>
#'   # Here
# </logger>

check_empty_beautier_folder()
```

```
strict_clock_model_to_xml_operators
```

Internal function

Description

Converts a clock model to the operators section of the XML as text

Usage

```
strict_clock_model_to_xml_operators(inference_model)
```

Arguments

`inference_model`
 a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

a character vector of XML strings

Author(s)

Richèl J.C. Bilderbeek

strict_clock_model_to_xml_prior_distr
Internal function

Description

Internal function to converts a strict clock model to the prior section of the XML as text

Usage

```
strict_clock_model_to_xml_prior_distr(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

a character vector of XML strings

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()
# <distribution id="posterior" spec="util.CompoundDistribution">
#   <distribution id="prior" spec="util.CompoundDistribution">
#     HERE, where the ID of the distribution is 'prior'
#   </distribution>
#   <distribution id="likelihood" ...>
#   </distribution>
# </distribution>
strict_clock_model_to_xml_prior_distr(
  inference_model = create_inference_model()
)
check_empty_beautier_folder()
```

strict_clock_model_to_xml_state
Internal function

Description

Converts a strict clock model to the ‘state’ section of the XML as text

Usage

```
strict_clock_model_to_xml_state(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

lines of XML text, without indentation nor state tags

Author(s)

Richèl J.C. Bilderbeek

strict_clock_model_to_xml_tracelog
Internal function

Description

Creates a strict clock model’s XML for the tracelog section

Usage

```
strict_clock_model_to_xml_tracelog(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

a character vector of XML strings

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# <logger id="tracelog" ...>
#'   # Here
# </logger>

check_empty_beautier_folder()
```

s_parameter_to_xml	<i>Internal function</i>
--------------------	--------------------------

Description

Converts an 's_param' to XML

Usage

```
s_parameter_to_xml(parameter, beauti_options)
```

Arguments

parameter a s parameter, a numeric value. For advanced usage, use the structure as created by [create_s_param](#))

beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

the parameter as XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
s_parameter_to_xml(
  create_s_param(id = 4, value = 1.25),
  beauti_options = create_beauti_options_v2_4()
)
s_parameter_to_xml(
  create_s_param(id = 4, value = 1.25),
  beauti_options = create_beauti_options_v2_6()
)
```

taxa_to_xml_tree	<i>Internal function</i>
------------------	--------------------------

Description

Internal function to creates the 'tree' section of a BEAST2 XML parameter file, which is part of a 'state' section, without being indented.

Usage

```
taxa_to_xml_tree(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Details

The tree tag has these elements:

```
<tree[...]>
  <taxonset[...]>
  [...]
</taxonset>
</run>
```

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

tipdate_taxa_to_xml_trait

Internal function

Description

Internal function to creates the 'trait' section of a BEAST2 XML parameter file, which is part of a 'tree' section, without being indented.

Usage

```
tipdate_taxa_to_xml_trait(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Details

The tree tag has these elements:

```
<run[...]>
  <state[...]>
    <tree[...]>
      <trait[...]>
        This part
      </trait>
    </tree>
  </run>
</state>
```

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

`tipdate_taxa_to_xml_tree`*Internal function*

Description

Creates the tree section (part of the state section) when there is tip-dating

Usage

```
tipdate_taxa_to_xml_tree(inference_model)
```

Arguments

`inference_model`

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

the random phylogeny as XML text

Author(s)

Richèl J.C. Bilderbeek

`tn93_site_model_to_xml_prior_distr`*Internal function*

Description

Converts a TN93 site model to XML, used in the prior section

Usage

```
tn93_site_model_to_xml_prior_distr(site_model, beauti_options)
```

Arguments

`site_model` a site model, as returned by [create_site_model](#)

`beauti_options` one BEAUti options object, as returned by [create_beauti_options](#)

Value

the site model as XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
tn93_site_model_to_xml_prior_distr(
  site_model = create_tn93_site_model(
    id = 1,
    kappa_1_prior_distr = create_uniform_distr(id = 2),
    kappa_2_prior_distr = create_uniform_distr(id = 3)
  ),
  beauti_options = create_beauti_options()
)
```

tn93_site_model_to_xml_state

Converts a site model to XML, used in the state section

Description

Converts a site model to XML, used in the state section

Usage

```
tn93_site_model_to_xml_state(
  site_model,
  beauti_options = create_beauti_options()
)
```

Arguments

site_model a site model, as returned by [create_site_model](#)
 beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

the site model as XML text

Author(s)

Richèl J.C. Bilderbeek

tree_model_to_tracelog_xml
Internal function

Description

Creates the tree models' XML for the tracelog section. That is, all XML tags that have the word 'tree' in them.

Usage

```
tree_model_to_tracelog_xml(inference_model)
```

Arguments

inference_model

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

lines of XML text

Note

use site_models just because it contains all IDs

Author(s)

Richèl J.C. Bilderbeek

See Also

the complete tracelog section is created by [create_tracelog_xml](#)

Examples

```
check_empty_beautier_folder()

# <logger id="tracelog" ...>
#'   # Here
# </logger>

check_empty_beautier_folder()
```

tree_priors_to_xml_prior_distr

Creates the distribution section in the prior section of the distribution section of a BEAST2 XML parameter file.

Description

These lines start with '<distribution id='

Usage

```
tree_priors_to_xml_prior_distr(tree_priors, beauti_options)
```

Arguments

tree_priors one or more tree priors, as returned by [create_tree_prior](#)

beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# <distribution id="posterior" spec="util.CompoundDistribution">
#   <distribution id="prior" spec="util.CompoundDistribution">
#     HERE, where the ID of the distribution is 'prior'
#   </distribution>
#   <distribution id="likelihood" ...>
#     </distribution>
# </distribution>

check_empty_beautier_folder()
```

`tree_priors_to_xml_tracelog`*Creates the tree priors' XML for the tracelog section*

Description

Creates the tree priors' XML for the tracelog section

Usage

```
tree_priors_to_xml_tracelog(tree_priors)
```

Arguments

`tree_priors` one or more tree priors, as returned by [create_tree_prior](#)

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

See Also

the complete tracelog section is created by [create_tracelog_xml](#)

Examples

```
check_empty_beautier_folder()

# <logger id="tracelog" ...>
# '   # Here
# </logger>

check_empty_beautier_folder()
```

```
tree_prior_to_xml_operators
```

Internal function

Description

Creates the XML of a tree prior, as used in the operators section

Usage

```
tree_prior_to_xml_operators(inference_model)
```

Arguments

`inference_model`
 a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

the tree prior as XML text

Author(s)

Richèl J.C. Bilderbeek

```
tree_prior_to_xml_prior_distr
```

Creates the distribution section in the prior section of the distribution section of a BEAST2 XML parameter file.

Description

These lines start with '<distribution id='

Usage

```
tree_prior_to_xml_prior_distr(tree_prior, beauti_options)
```

Arguments

`tree_prior` a tree priors, as returned by [create_tree_prior](#)
`beauti_options` one BEAUti options object, as returned by [create_beauti_options](#)

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# <distribution id="posterior" spec="util.CompoundDistribution">
#   <distribution id="prior" spec="util.CompoundDistribution">
#     HERE, where the ID of the distribution is 'prior'
#   </distribution>
#   <distribution id="likelihood" ...>
#   </distribution>
# </distribution>

check_empty_beautier_folder()
```

```
tree_prior_to_xml_state
```

Creates the XML of a tree prior, as used in the state section

Description

Creates the XML of a tree prior, as used in the state section

Usage

```
tree_prior_to_xml_state(inference_model)
```

Arguments

`inference_model`

a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

the tree prior as XML text

Author(s)

Richèl J.C. Bilderbeek

tree_prior_to_xml_tracelog

Creates the tree prior's XML for the tracelog section

Description

Creates the tree prior's XML for the tracelog section

Usage

```
tree_prior_to_xml_tracelog(tree_prior)
```

Arguments

tree_prior a tree priors, as returned by [create_tree_prior](#)

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

See Also

all tree priors' tracelog section is created by [tree_priors_to_xml_tracelog](#)

Examples

```
check_empty_beautier_folder()

# <logger id="tracelog" ...>
# '   # Here
# </logger>

check_empty_beautier_folder()
```

unindent	<i>Unindents text</i>
----------	-----------------------

Description

Unindents text

Usage

unindent(text)

Arguments

text one or more lines of text

Value

unindented lines of text

Author(s)

Richèl J.C. Bilderbeek

yule_tree_prior_to_xml_operators
<i>Internal function</i>

Description

Creates the XML of a Yule tree prior, as used in the operators section

Usage

yule_tree_prior_to_xml_operators(inference_model)

Arguments

inference_model
a Bayesian phylogenetic inference model. An inference model is the complete model setup in which a site model, clock model, tree prior and more are specified. Use [create_inference_model](#) to create an inference model. Use [check_inference_model](#) to check if an inference model is valid. Use [rename_inference_model_filenames](#) to rename the files in an inference model.

Value

the tree prior as XML text

Author(s)

Richèl J.C. Bilderbeek

yule_tree_prior_to_xml_prior_distr

Creates the prior section in the prior section of the prior section of the distribution section of a BEAST2 XML parameter file for a Yule tree prior

Description

Creates the prior section in the prior section of the prior section of the distribution section of a BEAST2 XML parameter file for a Yule tree prior

Usage

```
yule_tree_prior_to_xml_prior_distr(
  yule_tree_prior,
  beauti_options = create_beauti_options()
)
```

Arguments

yule_tree_prior a Yule tree_prior, as created by [create_yule_tree_prior](#)
 beauti_options one BEAUti options object, as returned by [create_beauti_options](#)

Value

lines of XML text

Author(s)

Richèl J.C. Bilderbeek

Examples

```
check_empty_beautier_folder()

# <distribution id="posterior" spec="util.CompoundDistribution">
#   <distribution id="prior" spec="util.CompoundDistribution">
#     HERE, where the ID of the distribution is 'prior'
#   </distribution>
#   <distribution id="likelihood" ...>
#   </distribution>
# </distribution>

check_empty_beautier_folder()
```

Index

alpha_parameter_to_xml, 12
are_clock_models, 13
are_equal_mcmcs, 14
are_equal_screenlogs, 15
are_equal_tracelogs, 16
are_equal_treelogs, 17
are_equal_xml_files, 18
are_equal_xml_lines, 19
are_equivalent_xml_files, 18, 20
are_equivalent_xml_lines, 21
are_equivalent_xml_lines_all, 21
are_equivalent_xml_lines_loggers, 22
are_equivalent_xml_lines_operators, 23
are_equivalent_xml_lines_section, 23
are_fasta_filenames, 24, 227
are_ids, 25, 310
are_init_clock_models, 26
are_init_mrca_priors, 26
are_init_site_models, 27
are_init_tree_priors, 27
are_mrca_align_ids_in_fasta, 28
are_mrca_priors, 28
are_mrca_taxon_names_in_fasta, 29
are_rln_clock_models, 30
are_site_models, 30
are_tree_priors, 31

b_pop_sizes_param_to_xml, 35
b_pop_sizes_parameter_to_xml, 34
bd_tree_prior_to_xml_prior_distr, 32
beautier, 42, 206, 228, 230, 246, 396
beta_parameter_to_xml, 33

cbs_tree_prior_to_xml_prior_distr, 35
ccp_tree_prior_to_xml_prior_distr, 36
ccp_tree_prior_to_xml_state, 37
cep_tree_prior_to_xml_prior_distr, 38
check_alignment_id, 39, 225
check_beauti_options, 40
check_clock_model, 40

check_clock_models, 41
check_empty_beautier_folder, 42
check_file_and_model_agree, 44
check_file_exists, 44
check_filename, 43, 43, 207
check_gamma_site_model, 45
check_gamma_site_model_names, 46
check_gtr_site_model, 46
check_gtr_site_model_names, 47
check_inference_model, 37, 44, 48, 48,
73–76, 84, 87–89, 92–94, 96–98,
105, 116, 137, 156, 161, 165,
171–173, 175, 176, 192, 194, 195,
198, 199, 207, 224, 241, 260–264,
276, 279, 382–386, 398, 402–405,
411–417, 419, 422, 423, 425
check_inference_models, 49
check_is_monophyletic, 50
check_log_mode, 50
check_log_sort, 51
check_mcmc, 51, 51, 52, 53, 56, 83, 91, 128,
140, 147, 181, 184, 208, 243, 300,
379–381, 400
check_mcmc_list_element_names, 52
check_mcmc_nested_sampling
(check_ns_mcmc), 56
check_mcmc_values, 53
check_mrca_prior, 53, 55
check_mrca_prior_name, 54
check_mrca_prior_names, 55
check_mrca_prior_taxa_names, 55
check_nested_sampling_mcmc
(check_ns_mcmc), 56
check_ns_mcmc, 56, 149
check_param, 56
check_param_names, 57
check_param_types, 58
check_phylogeny, 58, 357
check_rename_fun, 59, 59, 208, 246, 399, 400

- check_rln_clock_model, 60
- check_screenlog, 60
- check_screenlog_names, 61
- check_screenlog_values, 62
- check_site_model, 62
- check_site_model_names, 64
- check_site_model_types, 65
- check_site_models, 63
- check_store_every, 65
- check_strict_clock_model, 66
- check_tn93_site_model, 66
- check_tn93_site_model_names, 67
- check_tracelog, 68
- check_tracelog_names, 68
- check_tracelog_values, 69
- check_tree_prior, 71
- check_tree_priors, 72
- check_treelog, 69, 193
- check_treelog_names, 70
- check_treelog_values, 71
- clock_model_to_xml_operators, 73
- clock_model_to_xml_prior_distr, 74
- clock_model_to_xml_state, 75
- clock_model_to_xml_tracelog, 75
- clock_model_to_xml_treelogger, 76
- clock_rate_param_to_xml, 77
- compare_lines, 78
- count_trailing_spaces, 79
- create_alpha_param, 13, 80, 103, 121, 130, 151, 206
- create_b_pop_sizes_param, 34, 35, 106, 108, 206
- create_bd_tree_prior, 32, 81, 196, 197, 206, 269, 290
- create_beast2_beast_xml, 82
- create_beast2_input, 83, 87
- create_beast2_input_beast, 84, 94
- create_beast2_input_data, 85, 85
- create_beast2_input_data_sequences, 86
- create_beast2_input_distr, 87, 97
- create_beast2_input_distr_lh, 88
- create_beast2_input_distr_prior, 89
- create_beast2_input_file, 84, 90, 93
- create_beast2_input_file_from_model, 91, 92, 94
- create_beast2_input_from_model, 84, 85, 93, 93
- create_beast2_input_init, 94, 97
- create_beast2_input_map, 85, 95
- create_beast2_input_operators, 96, 97
- create_beast2_input_run, 85, 96
- create_beast2_input_state, 97, 98, 98
- create_beauti_options, 13, 32–36, 38, 40, 77, 82, 83, 85, 86, 91, 95, 99, 101, 128, 181, 206, 210–215, 221–223, 259, 267, 268, 280, 290, 378, 386–396, 401, 406, 409, 410, 414, 417, 418, 420, 422, 426
- create_beauti_options_v2_4, 100, 101, 102
- create_beauti_options_v2_6, 100, 101
- create_beautier_tempfolder, 99
- create_beta_distr, 80, 103, 104, 118, 211, 269, 291, 312
- create_beta_param, 33, 103, 104, 121, 130, 151, 206
- create_branch_rate_model_xml, 105, 160, 195
- create_cbs_tree_prior, 36, 107, 107, 108, 196, 197, 206, 207, 295
- create_ccp_tree_prior, 36, 108, 196, 197, 206, 270, 296
- create_cep_tree_prior, 38, 109, 196, 197, 206, 270, 296
- create_clock_model, 30, 41, 42, 60, 66, 76, 83, 91, 93, 111, 112, 114, 128, 147, 181, 184, 206, 217, 231, 241, 271, 297, 314, 366, 371
- create_clock_model_from_name, 114
- create_clock_model_rln
(create_rln_clock_model), 161
- create_clock_model_strict
(create_strict_clock_model), 174
- create_clock_models, 112, 113, 232
- create_clock_models_from_names, 113
- create_clock_rate_param, 77, 115, 151, 174, 206
- create_clock_rate_state_node_parameter_xml, 116
- create_data_xml, 117
- create_distr, 81, 103, 109, 110, 118, 119, 122–125, 130, 136, 138, 142, 146, 150, 152, 161, 174, 200, 202, 210, 235, 272, 314
- create_distr_beta (create_beta_distr),

- 103
- create_distr_exp (create_exp_distr), 119
- create_distr_gamma
(create_gamma_distr), 121
- create_distr_inv_gamma
(create_inv_gamma_distr), 129
- create_distr_laplace
(create_laplace_distr), 135
- create_distr_log_normal
(create_log_normal_distr), 137
- create_distr_normal
(create_normal_distr), 145
- create_distr_one_div_x
(create_one_div_x_distr), 149
- create_distr_poisson
(create_poisson_distr), 152
- create_distr_uniform
(create_uniform_distr), 200
- create_exp_distr, 118, 119, 141, 211, 272, 303, 315
- create_freq_param, 120, 120, 125, 127, 189, 203, 207, 221, 305
- create_gamma_distr, 80, 104, 118, 121, 207, 222, 273, 306
- create_gamma_site_model, 45, 46, 122, 123, 124, 127, 131, 167, 189, 207, 224, 239, 240, 273, 316
- create_gtr_site_model, 46, 47, 124, 167, 168, 207, 238, 274, 304, 308, 316
- create_gtr_subst_model_xml, 126
- create_hky_site_model, 126, 167, 168, 207, 238, 275, 304, 309, 317
- create_hky_subst_model_xml, 127
- create_inference_model, 37, 44, 48, 49, 73–76, 84, 87–89, 92–94, 96–98, 105, 116, 128, 137, 147, 156, 161, 165, 171–173, 175, 176, 181, 192, 194, 195, 198, 199, 207, 224, 241, 260–264, 276, 279, 382–386, 398, 402–405, 411–417, 419, 422, 423, 425
- create_inv_gamma_distr, 80, 104, 118, 129, 212, 276, 318, 327
- create_jc69_site_model, 131, 167, 168, 208, 277, 319
- create_jc69_subst_model_xml, 132
- create_kappa_1_param, 132, 151, 189, 330, 388
- create_kappa_2_param, 133, 151, 189, 331, 389
- create_kappa_param, 127, 133, 208, 332, 378
- create_lambda_param, 134, 151, 152, 334, 389
- create_laplace_distr, 118, 135, 143, 163, 212, 278, 320, 334, 335
- create_log_normal_distr, 118, 127, 137, 145, 177, 189, 213, 278, 320, 335
- create_loggers_xml, 97, 136
- create_m_param, 138, 144, 151, 208, 343, 386
- create_mcmc, 14, 51–53, 56, 83, 91, 93, 128, 139, 147, 149, 181, 183, 184, 208, 243, 300, 337, 379–381, 400
- create_mcmc_nested_sampling
(create_ns_mcmc), 148
- create_mean_param, 119, 140, 146, 151, 338, 390
- create_mrca_prior, 28, 29, 50, 53–55, 83, 91, 128, 141, 142, 181, 208, 260, 280, 339–341, 385
- create_mu_param, 135, 143, 151, 343, 391
- create_normal_distr, 118, 141, 145, 166, 213, 280, 321, 344
- create_ns_inference_model, 129, 147, 184
- create_ns_mcmc, 51–53, 56, 83, 91, 128, 140, 147, 148, 181, 184, 185, 208, 243, 300, 338, 379–381, 400
- create_one_div_x_distr, 118, 149, 214, 281, 322, 346
- create_param, 56–58, 80, 105, 107, 115, 134, 141, 143, 145, 151, 153, 155, 156, 158–160, 163, 166, 177, 208, 282, 322, 355, 387
- create_param_alpha
(create_alpha_param), 80
- create_param_b_pop_sizes
(create_b_pop_sizes_param), 106
- create_param_beta (create_beta_param), 104
- create_param_clock_rate
(create_clock_rate_param), 115
- create_param_freq (create_freq_param), 120
- create_param_kappa
(create_kappa_param), 133
- create_param_kappa_1

- (create_kappa_1_param), 132
- create_param_kappa_2
 - (create_kappa_2_param), 133
- create_param_lambda
 - (create_lambda_param), 134
- create_param_m(create_m_param), 144
- create_param_mean(create_mean_param), 140
- create_param_mu(create_mu_param), 143
- create_param_rate_ac
 - (create_rate_ac_param), 153
- create_param_rate_ag
 - (create_rate_ag_param), 154
- create_param_rate_at
 - (create_rate_at_param), 155
- create_param_rate_cg
 - (create_rate_cg_param), 157
- create_param_rate_ct
 - (create_rate_ct_param), 158
- create_param_rate_gt
 - (create_rate_gt_param), 159
- create_param_s(create_s_param), 177
- create_param_scale
 - (create_scale_param), 162
- create_param_sigma
 - (create_sigma_param), 165
- create_poisson_distr, 118, 134, 152, 214, 282, 323, 358
- create_rate_ac_param, 125, 151, 153, 359, 391
- create_rate_ag_param, 125, 151, 154, 360, 392
- create_rate_at_param, 125, 151, 155, 361, 393
- create_rate_categories_state_node_xml, 156
- create_rate_cg_param, 125, 151, 157, 363, 393
- create_rate_ct_param, 125, 151, 158, 364, 394
- create_rate_gt_param, 125, 151, 159, 365, 395
- create_rln_clock_branch_rate_model_xml, 106, 160
- create_rln_clock_model, 111, 112, 161, 209, 283, 323, 366, 401
- create_s_param, 138, 151, 177, 414
- create_scale_param, 136, 151, 162, 395
- create_screenlog, 15, 61, 62, 139, 148, 164, 178, 182, 185, 209
- create_screenlog_xml, 137, 165
- create_sigma_param, 146, 151, 165, 396
- create_site_model, 31, 62–65, 83, 91, 93, 126, 128, 132, 147, 166, 168–170, 181, 184, 190, 209, 223, 248–251, 259, 267, 268, 284, 324, 369, 378, 406–410, 417, 418
- create_site_model_from_name, 170
- create_site_model_gtr
 - (create_gtr_site_model), 124
- create_site_model_hky
 - (create_hky_site_model), 126
- create_site_model_jc69
 - (create_jc69_site_model), 131
- create_site_model_parameters_xml, 171, 172
- create_site_model_tn93
 - (create_tn93_site_model), 189
- create_site_model_xml, 172, 195
- create_site_models, 168, 250
- create_site_models_from_names, 169
- create_strict_clock_branch_rate_model_xml, 106, 173
- create_strict_clock_model, 111, 112, 115, 174, 209, 284, 324, 371
- create_strict_clock_rate_scaler_operator_xml, 175
- create_subst_model_xml, 172, 176
- create_temp_screenlog_filename, 178
- create_temp_tracelog_filename, 179
- create_temp_treelog_filename, 180
- create_test_inference_model, 129, 180, 184
- create_test_mcmc, 140, 182
- create_test_ns_inference_model, 147, 181, 183
- create_test_ns_mcmc, 149, 184
- create_test_screenlog, 186
- create_test_tracelog, 187
- create_test_treelog, 188
- create_tn93_site_model, 66, 67, 167, 168, 189, 209, 238, 285, 304, 325, 373
- create_tn93_subst_model_xml, 190
- create_tracelog, 16, 68, 69, 139, 148, 179, 182, 185, 191, 209
- create_tracelog_xml, 137, 192, 407, 419,

- 421
- create_trait_set_string, 192
- create_tree_likelihood_distr_xml, 88, 195
- create_tree_prior, 71, 72, 83, 91, 93, 128, 147, 181, 184, 196, 209, 244, 253–256, 286, 374, 420–422, 424
- create_tree_prior_bd
(create_bd_tree_prior), 81
- create_tree_prior_cbs
(create_cbs_tree_prior), 107
- create_tree_prior_ccp
(create_ccp_tree_prior), 108
- create_tree_prior_cep
(create_cep_tree_prior), 109
- create_tree_prior_yule
(create_yule_tree_prior), 202
- create_tree_priors, 197, 255
- create_treelog, 17, 69–71, 139, 148, 180, 182, 185, 193, 209
- create_treelog_xml, 137, 194
- create_uclid_mean_state_node_param_xml, 198
- create_uclid_stdev_state_node_param_xml, 199
- create_uniform_distr, 118, 200, 215, 287, 326, 375
- create_xml_declaration, 82, 84, 94, 201, 405
- create_yule_tree_prior, 31, 196, 197, 202, 209, 287, 377, 426
- default_parameters_doc, 203
- default_params_doc, 204
- distr_to_xml, 210
- distr_to_xml_beta, 211
- distr_to_xml_exp, 211
- distr_to_xml_inv_gamma, 212
- distr_to_xml_laplace, 212
- distr_to_xml_log_normal, 213
- distr_to_xml_normal, 213
- distr_to_xml_one_div_x, 214
- distr_to_xml_poisson, 214
- distr_to_xml_uniform, 215
- extract_xml_loggers_from_lines, 215
- extract_xml_operators_from_lines, 216
- extract_xml_section_from_lines, 216
- FALSE, 290, 322, 352–354
- fasta_file_to_sequences, 217
- find_clock_model, 217
- find_first_regex_line, 218
- find_first_xml_opening_tag_line, 218
- find_last_regex_line, 219
- find_last_xml_closing_tag_line, 220
- freq_equilibrium_to_xml, 220
- freq_param_to_xml, 221
- gamma_distr_to_xml, 222
- gamma_site_model_to_xml_prior_distr, 223
- gamma_site_model_to_xml_state, 224
- gamma_site_models_to_xml_prior_distr, 223
- get_alignment_id, 39, 81, 108–111, 124, 127, 131, 142, 167, 187, 189, 191, 202, 206, 225
- get_alignment_ids, 226, 227
- get_alignment_ids_from_fasta_filenames, 108, 117, 161, 174, 207, 226, 227, 284, 286
- get_beautier_folder, 228
- get_beautier_path, 228, 229
- get_beautier_paths, 229, 229
- get_beautier_tempfilename, 230
- get_clock_model_name, 231
- get_clock_model_names, 113, 114, 206, 232
- get_clock_models_ids, 230
- get_crown_age, 232
- get_default_beast_namespace, 233
- get_default_beast_namespace_v2_4, 233, 234
- get_default_beast_namespace_v2_6, 233, 234
- get_distr_n_params, 235
- get_distr_names, 235
- get_fasta_filename, 28, 29, 44, 83–85, 91–93, 97, 137, 192, 207, 208, 225, 227, 236, 271, 276, 279, 340
- get_file_base_sans_ext, 237
- get_freq_equilibrium_names, 238
- get_gamma_site_model_n_distrs, 238
- get_gamma_site_model_n_params, 239
- get_has_non_strict_clock_model, 240
- get_inference_model_filenames, 241
- get_log_modes, 164, 186–188, 191, 193, 208, 242

- get_log_sorts, [164](#), [186–188](#), [191](#), [193](#), [209](#), [242](#)
- get_mcmc_filenames, [243](#)
- get_n_taxa, [244](#)
- get_operator_id_pre, [244](#)
- get_param_names, [245](#)
- get_remove_dir_fun, [59](#), [208](#), [246](#), [399](#), [400](#)
- get_remove_hex_fun, [59](#), [209](#), [246](#), [399](#), [400](#)
- get_replace_dir_fun, [59](#), [209](#), [247](#), [399](#), [400](#)
- get_site_model_n_distrs, [250](#)
- get_site_model_n_params, [251](#)
- get_site_model_names, [169](#), [170](#), [209](#), [250](#)
- get_site_models_n_distrs, [248](#)
- get_site_models_n_params, [249](#)
- get_taxa_names, [55](#), [142](#), [209](#), [252](#)
- get_tree_prior_n_distrs, [255](#)
- get_tree_prior_n_params, [256](#)
- get_tree_prior_names, [209](#), [254](#)
- get_tree_priors_n_distrs, [253](#)
- get_tree_priors_n_params, [253](#)
- get_xml_closing_tag, [257](#)
- get_xml_opening_tag, [258](#)
- gtr_site_model_to_xml_prior_distr, [258](#)
- gtr_site_model_to_xml_state, [259](#)

- has_mrca_prior, [260](#)
- has_mrca_prior_with_distr, [261](#)
- has_rln_clock_model, [262](#)
- has_strict_clock_model, [263](#)
- has_tip_dating, [264](#)
- has_xml_closing_tag, [265](#)
- has_xml_opening_tag, [265](#)
- has_xml_short_closing_tag, [266](#)
- hky_site_model_to_xml_prior_distr, [267](#)
- hky_site_model_to_xml_state, [267](#)

- indent, [268](#)
- init_bd_tree_prior, [269](#)
- init_beta_distr, [269](#)
- init_ccp_tree_prior, [270](#)
- init_cep_tree_prior, [270](#)
- init_clock_models, [271](#)
- init_distr, [272](#)
- init_exp_distr, [272](#)
- init_gamma_distr, [273](#)
- init_gamma_site_model, [273](#)
- init_gtr_site_model, [274](#)
- init_hky_site_model, [275](#)
- init_inference_model, [276](#)
- init_inv_gamma_distr, [276](#)
- init_jc69_site_model, [277](#)
- init_laplace_distr, [278](#)
- init_log_normal_distr, [278](#)
- init_mrca_prior, [279](#)
- init_mrca_priors, [280](#)
- init_normal_distr, [280](#)
- init_one_div_x_distr, [281](#)
- init_param, [281](#)
- init_poisson_distr, [282](#)
- init_rln_clock_model, [283](#)
- init_site_models, [284](#)
- init_strict_clock_model, [284](#)
- init_tn93_site_model, [285](#)
- init_tree_priors, [286](#)
- init_uniform_distr, [287](#)
- init_yule_tree_prior, [287](#)
- interspace, [288](#)
- is_alpha_param, [288](#)
- is_b_pop_sizes_param, [293](#)
- is_bd_tree_prior, [289](#)
- is_beauti_options, [290](#)
- is_beta_distr, [291](#), [301](#)
- is_beta_param, [292](#)
- is_cbs_tree_prior, [294](#)
- is_ccp_tree_prior, [295](#)
- is_cep_tree_prior, [296](#)
- is_clock_model, [297](#)
- is_clock_model_name, [298](#)
- is_clock_rate_param, [299](#)
- is_default_mcmc, [300](#)
- is_distr, [291](#), [301](#), [303](#), [306](#), [328](#), [335](#), [336](#), [345](#), [347](#), [358](#), [376](#)
- is_distr_name, [302](#)
- is_exp_distr, [301](#), [303](#)
- is_freq_equilibrium_name, [304](#)
- is_freq_param, [305](#)
- is_gamma_distr, [301](#), [306](#)
- is_gamma_site_model, [307](#)
- is_gtr_site_model, [308](#)
- is_hky_site_model, [309](#)
- is_id, [25](#), [310](#)
- is_in_patterns, [328](#)
- is_inference_model, [311](#)
- is_init_bd_tree_prior, [311](#)
- is_init_beta_distr, [312](#)
- is_init_cbs_tree_prior, [312](#)

[is_init_ccp_tree_prior](#), 313
[is_init_cep_tree_prior](#), 313
[is_init_clock_model](#), 314
[is_init_distr](#), 314
[is_init_exp_distr](#), 315
[is_init_gamma_distr](#), 315
[is_init_gamma_site_model](#), 316
[is_init_gtr_site_model](#), 316
[is_init_hky_site_model](#), 317
[is_init_inv_gamma_distr](#), 318
[is_init_jc69_site_model](#), 319
[is_init_laplace_distr](#), 320
[is_init_log_normal_distr](#), 320
[is_init_mrca_prior](#), 321
[is_init_normal_distr](#), 321
[is_init_one_div_x_distr](#), 322
[is_init_param](#), 322
[is_init_poisson_distr](#), 323
[is_init_rln_clock_model](#), 323
[is_init_site_model](#), 324
[is_init_strict_clock_model](#), 324
[is_init_tn93_site_model](#), 325
[is_init_tree_prior](#), 325
[is_init_uniform_distr](#), 326
[is_init_yule_tree_prior](#), 327
[is_inv_gamma_distr](#), 301, 327
[is_jc69_site_model](#), 329
[is_kappa_1_param](#), 330
[is_kappa_2_param](#), 331
[is_kappa_param](#), 332
[is_lambda_param](#), 333
[is_laplace_distr](#), 301, 334
[is_log_normal_distr](#), 301, 335
[is_m_param](#), 343
[is_mcmc](#), 336
[is_mcmc_nested_sampling](#), 337
[is_mean_param](#), 338
[is_mrca_align_id_in_fasta](#), 340
[is_mrca_align_ids_in_fastas](#), 339
[is_mrca_prior](#), 341
[is_mrca_prior_with_distr](#), 342
[is_mu_param](#), 342
[is_nested_sampling_mcmc](#)
 ([is_mcmc_nested_sampling](#)), 337
[is_normal_distr](#), 301, 344
[is_on_appveyor](#), 352
[is_on_ci](#), 353
[is_on_github_actions](#), 353
[is_on_travis](#), 354
[is_one_bool](#), 345
[is_one_div_x_distr](#), 301, 346
[is_one_double](#), 347
[is_one_empty_string](#), 348
[is_one_int](#), 349
[is_one_na](#), 350
[is_one_string](#), 350
[is_one_string_that_is_a_number](#), 351
[is_param](#), 355
[is_param_name](#), 356
[is_phylo](#), 357
[is_poisson_distr](#), 301, 358
[is_rate_ac_param](#), 359
[is_rate_ag_param](#), 360
[is_rate_at_param](#), 361
[is_rate_cg_param](#), 362
[is_rate_ct_param](#), 363
[is_rate_gt_param](#), 365
[is_rln_clock_model](#), 366
[is_s_param](#), 372
[is_scale_param](#), 367
[is_sigma_param](#), 368
[is_site_model](#), 369
[is_site_model_name](#), 370
[is_strict_clock_model](#), 371
[is_tn93_site_model](#), 373
[is_tree_prior](#), 374
[is_tree_prior_name](#), 375
[is_uniform_distr](#), 301, 375
[is_xml](#), 376
[is_yule_tree_prior](#), 377

[jc69_site_model_to_xml_state](#), 378

[kappa_param_to_xml](#), 378

[m_param_to_xml](#), 386
[mcmc_to_xml_run](#), 379
[mcmc_to_xml_run_default](#), 380
[mcmc_to_xml_run_nested_sampling](#), 381
[mrca_prior_to_xml_prior_distr](#), 382
[mrca_prior_to_xml_state](#), 383
[mrca_prior_to_xml_taxonset](#), 384
[mrca_prior_to_xml_tracelog](#), 385
[mrca_priors_to_xml_prior_distr](#), 382

[NA](#), 43, 54, 59, 142, 187, 191, 206, 208, 241,
 246, 399, 400

- no_taxa_to_xml_tree, 386
- parameter_to_xml, 387
- parameter_to_xml_kappa_1, 388
- parameter_to_xml_kappa_2, 389
- parameter_to_xml_lambda, 389
- parameter_to_xml_mean, 390
- parameter_to_xml_mu, 390
- parameter_to_xml_rate_ac, 391
- parameter_to_xml_rate_ag, 392
- parameter_to_xml_rate_at, 392
- parameter_to_xml_rate_cg, 393
- parameter_to_xml_rate_ct, 394
- parameter_to_xml_rate_gt, 394
- parameter_to_xml_scale, 395
- parameter_to_xml_sigma, 396
- remove_beautier_folder, 42, 396, 397
- remove_empty_lines, 397
- remove_multiline, 398
- rename_inference_model_filenames, 37, 44, 48, 73–76, 84, 87–89, 92–94, 96–98, 105, 116, 137, 156, 161, 165, 171–173, 175, 176, 192, 194, 195, 198, 199, 207, 224, 241, 260–264, 276, 279, 382–386, 398, 398, 402–405, 411–417, 419, 422, 423, 425
- rename_mcmc_filenames, 51–53, 56, 83, 91, 128, 140, 147, 181, 184, 208, 243, 300, 379–381, 399, 400
- return, 59, 208, 399, 400
- rln_clock_model_to_xml_mean_rate_prior, 401
- rln_clock_model_to_xml_operators, 401
- rln_clock_model_to_xml_prior_distr, 402
- rln_clock_model_to_xml_state, 403
- rln_clock_model_to_xml_tracelog, 404
- rnd_phylo_to_xml_init, 405
- s_parameter_to_xml, 414
- site_model_to_xml_operators, 408
- site_model_to_xml_prior_distr, 408
- site_model_to_xml_state, 410
- site_model_to_xml_tracelog, 410
- site_models_to_xml_operators, 406
- site_models_to_xml_prior_distr, 406
- site_models_to_xml_tracelog, 407, 411
- stop, 14–17, 39, 41, 44, 50, 54–56, 59, 60, 63, 65, 68, 69, 72, 231, 260, 396
- strict_clock_model_to_xml_operators, 411
- strict_clock_model_to_xml_prior_distr, 412
- strict_clock_model_to_xml_state, 413
- strict_clock_model_to_xml_tracelog, 413
- taxa_to_xml_tree, 415
- tempfile, 230, 246
- tipdate_taxa_to_xml_trait, 416
- tipdate_taxa_to_xml_tree, 417
- tn93_site_model_to_xml_prior_distr, 417
- tn93_site_model_to_xml_state, 418
- tree_model_to_tracelog_xml, 419
- tree_prior_to_xml_operators, 422
- tree_prior_to_xml_prior_distr, 422
- tree_prior_to_xml_state, 423
- tree_prior_to_xml_tracelog, 424
- tree_priors_to_xml_prior_distr, 420
- tree_priors_to_xml_tracelog, 421, 424
- TRUE, 139, 164, 182, 186–188, 191, 193, 209, 290, 322, 352–354
- unindent, 425
- yule_tree_prior_to_xml_operators, 425
- yule_tree_prior_to_xml_prior_distr, 426