

Package ‘datelife’

June 21, 2022

Title Scientific Data on Time of Lineage Divergence for Your Taxa

Version 0.6.5

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Description Methods and workflows to get chronograms (i.e., phylogenetic trees with branch lengths proportional to time), using open, peer-reviewed, state-of-the-art scientific data on time of lineage divergence.

This package constitutes the main underlying code of the DateLife web service at <www.datelife.org>. To obtain a single summary chronogram from a group of relevant chronograms, we implement the Super Distance Matrix (SDM) method described in Criscuolo et al. (2006) <doi:10.1080/10635150600969872>.

To find the grove of chronograms with a sufficiently overlapping set of taxa for summarizing, we implement theorem 1.1. from Ané et al. (2009) <doi:10.1007/s00026-009-0017-x>.

A given phylogenetic tree can be dated using time of lineage divergence data as secondary calibrations (with caution, see Schenk (2016) <doi:10.1371/journal.pone.0148228>).

To obtain and apply secondary calibrations, the package implements the congruification method described in Eastman et al. (2013) <doi:10.1111/2041-210X.12051>. Tree dating can be performed with different methods including BLADJ (Webb et al. (2008) <doi:10.1093/bioinformatics/btn358>), PATHd8 (Britton et al. (2007) <doi:10.1080/10635150701613783>), mrBayes (Huelsenbeck and Ronquist (2001) <doi:10.1093/bioinformatics/17.8.754>), and treePL (Smith and O'Meara (2012) <doi:10.1093/bioinformatics/bts492>).

Depends R (>= 3.6.0)

biocViews Software

Imports ape, abind, bold, phangorn, phytools, ips, cluster, compare, geiger, stats, stringr, rotl, paleotree, knitcitations, phylobase, taxize, treebase, utils, httr, plyr, phylocomr, BiocManager, data.table

Suggests testthat, knitr, rmarkdown, usethis, devtools, covr, msa, Biostrings

LazyDataCompression xz

SystemRequirements PATHd8

URL <https://github.com/phyloTastic/datelife>,
<http://phyloTastic.org/datelife/>

License GPL (>= 2)

LazyData true

RoxygenNote 7.1.2

Encoding UTF-8

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

Date/Publication 2022-06-21 11:00:02 UTC

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<code>.get_ott_lineage</code>	<i>Get the lineage of a set of taxa. <code>.get_ott_lineage</code> uses <code>rotl::taxonomy_taxon_info()</code> with <code>include_lineage = TRUE</code>.</i>
-------------------------------	--

Description

Get the lineage of a set of taxa. `.get_ott_lineage` uses `rotl::taxonomy_taxon_info()` with `include_lineage = TRUE`.

Usage

```
.get_ott_lineage(input_ott_match)
```

Arguments

input_ott_match

An Output of check_ott_input function.

Value

A taxonomy_taxon_info object

birds_and_cats	<i>A multiPhylo object with trees resulting from a datelife search of some birds and cats species</i>
----------------	---

Description

A multiPhylo object with trees resulting from a datelife search of some birds and cats species

Usage

birds_and_cats

Format

A multiPhylo object

Details

Generated with: taxa <- c("Rhea americana", "Pterocnemia pennata", "Struthio camelus", "Gallus", "Felis") birds_and_cats <- datelife_search(input = taxa, summary_format = "phylo_all", get_spp_from_taxon = TRUE) usethis::use_data(birds_and_cats)

build_grove_list	<i>Build grove list</i>
------------------	-------------------------

Description

This function implements theorem 1.1 of Ané et al. (2009) [doi:10.1007/s000260090017x](https://doi.org/10.1007/s000260090017x) to find a grove for a given group of chronograms.

Usage

build_grove_list(datelife_result, n = 2)

Arguments

- `datelife_result`
A `datelifeResult` object.
- `n`
The degree of taxon name overlap among input chronograms. Defaults to `n = 2`, i.e., at least two overlapping taxon names.

Value

A list of vectors; each list element is a grove.

`build_grove_matrix` *Find the grove for a group of chronograms and build a matrix.*

Description

This function implements theorem 1.1 of Ané et al. (2009) [doi:10.1007/s000260090017x](https://doi.org/10.1007/s000260090017x) to find a grove for a given group of chronograms.

Usage

```
build_grove_matrix(datelife_result, n = 2)
```

Arguments

- `datelife_result`
A `datelifeResult` object.
- `n`
The degree of taxon name overlap among input chronograms. Defaults to `n = 2`, i.e., at least two overlapping taxon names.

Value

A matrix. Each cell shows whether `n`-overlap exists between a pair of inputs.

References

Ané, C., Eulenstein, O., Piaggio-Talice, R., & Sanderson, M. J. (2009). "Groves of phylogenetic trees". *Annals of Combinatorics*, 13(2), 139-167, [doi:10.1007/s000260090017x](https://doi.org/10.1007/s000260090017x).

check_conflicting_calibrations
Check for conflicting calibrations.

Description

check_conflicting_calibrations checks if calibrations are younger or older relative to descendants and ancestors, respectively.

Usage

```
check_conflicting_calibrations(phy, calibration_distribution)
```

Arguments

phy	A phylo object.
calibration_distribution	A list of node age distributions, named with phy's node numbers.

Details

It removes conflicting calibrations if needed, but BLADJ works as long as it has an age for the root.

check_ott_input *Check input for other functions*

Description

check_ott_input is currently used in functions [get_ott_clade\(\)](#), [get_ott_children\(\)](#), and [get_ott_synthetic_tree\(\)](#).

Usage

```
check_ott_input(input = NULL, ott_ids = NULL, ...)
```

Arguments

input	Optional. A character vector of names or a datelifeQuery object.
ott_ids	If not NULL, it takes this argument and ignores input. A numeric vector of ott ids obtained with rotl::taxonomy_taxon_info() or rotl::tnrs_match_names() or tnrs_match() .
...	Arguments passed on to make_datelife_query
use_tnrs	Whether to use Open Tree of Life's Taxonomic Name Resolution Service (TNRS) to process input taxon names. Default to TRUE, it corrects misspellings and taxonomic name variations with tnrs_match() , a wrapper of rotl::tnrs_match_names() .

`get_spp_from_taxon` Whether to search ages for all species belonging to a given taxon or not. Default to FALSE. If TRUE, it must have same length as input. If input is a newick string with some clades it will be converted to a phylo object, and the order of `get_spp_from_taxon` will match `phy$tip.label`.

`taxonomic_source` Used if `get_spp_from_taxon = TRUE`. A character vector with the desired taxonomic sources. Options are "ott", "ncbi", "gbif" or "irmng". The function defaults to "ott".

Details

By default, it uses the `ott_id` argument if it is not NULL.

Value

A named numeric vector of valid Open Tree Taxonomy (OTT) ids.

<code>choose_cluster</code>	<i>Choose an ultrametric phylo object from <code>cluster_patristicmatrix()</code> obtained with a particular clustering method, or the next best tree. If there are no ultrametric trees, it does not force them to be ultrametric.</i>
-----------------------------	---

Description

Choose an ultrametric phylo object from `cluster_patristicmatrix()` obtained with a particular clustering method, or the next best tree. If there are no ultrametric trees, it does not force them to be ultrametric.

Usage

```
choose_cluster(phycluster, clustering_method = "nj")
```

Arguments

`phycluster` An output from `cluster_patristicmatrix()`

`clustering_method` A character vector indicating the method to construct the tree. Options are:

- nj** Neighbor-Joining method applied with `ape::nj()`.
- upgma** Unweighted Pair Group Method with Arithmetic Mean method applied with `phangorn::upgma()`.
- bionj** An improved version of the Neighbor-Joining method applied with `ape::bionj()`.
- triangle** Triangles method applied with `ape::triangMtd()`
- mvr** Minimum Variance Reduction method applied with `ape::mvr()`.

Value

A phylo object or NA.

`classification_paths_from_taxonomy`*Gets classification paths for a vector of taxa*

Description

This uses the `taxize` package's wrapper of the Global Names Resolver to get taxonomic paths for the vector of taxa you pass in. Sources is a vector of source labels in order (though it works best if everything uses the same taxonomy, so we recommend doing just one source). You can see options by doing `taxize::gnr_datasources()`. Our default is Catalogue of Life

Usage

```
classification_paths_from_taxonomy(taxa, sources = "Catalogue of Life")
```

Arguments

<code>taxa</code>	Vector of taxon names
<code>sources</code>	Vector of names of preferred sources; see <code>taxize::gnr_datasources()</code> . Currently supports 100 taxonomic resources, see details.

Details

Taxonomies supported by `taxize::gnr_datasources()`

1. Catalogue of Life
2. Wikispecies
3. ITIS
4. NCBI
5. Index Fungorum
6. GRIN Taxonomy for Plants
7. Union 4
8. The Interim Register of Marine and Nonmarine Genera
9. World Register of Marine Species
10. Freebase
11. GBIF Backbone Taxonomy
12. EOL
13. Passiflora vernacular names
14. Inventory of Fish Species in the Wami River Basin
15. Pheasant Diversity and Conservation in the Mt. Gaoligongshan Region
16. Finding Species
17. Birds of Lindi Forests Plantation

18. Nemertea
19. Kihansi Gorge Amphibian Species Checklist
20. Mushroom Observer
21. TaxonConcept
22. Amphibia and Reptilia of Yunnan
23. Common names of Chilean Plants
24. Invasive Species of Belgium
25. ZooKeys
26. COA Wildlife Conservation List
27. AskNature
28. China: Yunnan, Southern Gaoligongshan, Rapid Biological Inventories Report No. 04
29. Native Orchids from Gaoligongshan Mountains, China
30. Illinois Wildflowers
31. Coleorrhyncha Species File
32. /home/dimus/files/dwca/zoological names.zip
33. Peces de la zona hidrogeográfica de la Amazonia, Colombia (Spreadsheet)
34. Eastern Mediterranean Syllidae
35. Gaoligong Shan Medicinal Plants Checklist
36. birds_of_tanzania
37. AmphibiaWeb
38. tanzania_plant_sepecimens
39. Papahānaumokuākea Marine National Monument
40. Taiwanese IUCN species list
41. BioPedia
42. AnAge
43. Embioptera Species File
44. Global Invasive Species Database
45. Sendoya S., Fernández F. AAT de hormigas (Hymenoptera: Formicidae) del Neotrópico 1.0 2004 (Spreadsheet)
46. Flora of Gaoligong Mountains
47. ARKive
48. True Fruit Flies (Diptera, Tephritidae) of the Afrotropical Region
49. 3i - Typhlocybinae Database
50. CATE Sphingidae
51. ZooBank
52. Diatoms
53. AntWeb

54. Endemic species in Taiwan
55. Dermaptera Species File
56. Mantodea Species File
57. Birds of the World: Recommended English Names
58. New Zealand Animalia
59. Blattodea Species File
60. Plecoptera Species File
61. /home/dimus/files/dwca/clemens.zip
62. Coreoidea Species File
63. Freshwater Animal Diversity Assessment - Normalized export
64. Catalogue of Vascular Plant Species of Central and Northeastern Brazil
65. Wikipedia in EOL
66. Database of Vascular Plants of Canada (VASCAN)
67. Phasmida Species File
68. OBIS
69. USDA NRCS PLANTS Database
70. Catalog of Fishes
71. Aphid Species File
72. The National Checklist of Taiwan
73. Psocodea Species File
74. FishBase
75. 3i - Typhlocybinae Database
76. Belgian Species List
77. EUNIS
78. CU*STAR
79. Orthoptera Species File
80. Bishop Museum
81. IUCN Red List of Threatened Species
82. BioLib.cz
83. Tropicos - Missouri Botanical Garden
84. nlbif
85. The International Plant Names Index
86. Index to Organism Names
87. uBio NameBank
88. Arctos
89. Checklist of Beetles (Coleoptera) of Canada and Alaska. Second Edition.
90. The Paleobiology Database

91. The Reptile Database
92. The Mammal Species of The World
93. BirdLife International
94. Checklist da Flora de Portugal (Continental, Açores e Madeira)
95. FishBase Cache
96. Silva
97. Open Tree of Life Reference Taxonomy
98. iNaturalist
99. The Interim Register of Marine and Nonmarine Genera
100. Gymno

Value

A list with resolved taxa (a tibble, from `taxize::gnr_resolve`) and a vector of taxa not resolved

`clean_ott_chronogram` *Clean up some issues with Open Tree of Life chronograms For now it 1) checks unmapped taxa and maps them with `tnrs_match.phylo`, 2) roots the chronogram if unrooted*

Description

Clean up some issues with Open Tree of Life chronograms For now it 1) checks unmapped taxa and maps them with `tnrs_match.phylo`, 2) roots the chronogram if unrooted

Usage

```
clean_ott_chronogram(phy)
```

Arguments

`phy` A phylo object.

Details

There is no limit to the number of names that can be queried and matched.

The output will preserve all elements from original input phylo object and will add

phy\$mapped A character vector indicating the state of mapping of `phy$tip.labels`:

original Tnrs matching was not attempted. Original labeling is preserved.

ott Matching was manually made by a curator in Open Tree of Life.

tnrs Tnrs matching was attempted and successful with no approximate matching. Original label is replaced by the matched name.

approximated Tnrs matching was attempted and successful but with approximate matching. Original labeling is preserved.

unmatched Tnrs matching was attempted and unsuccessful. Original labeling is preserved.

phy\$original.tip.label A character vector preserving all original labels.

phy\$ott_ids A numeric vector with ott id numbers of matched tips. Unmatched and original tips will be NaN.

if tips are duplicated, tnrs will only be run once (avoiding increases in function running time) but the result will be applied to all duplicated tip labels

Value

An object of class data frame or phylo, with the added class match_names.

NULL

NULL

clean_taxon_info_children

Identify, extract and clean taxonomic children names from a [taxonomy_taxon_info\(\)](#) output.

Description

clean_taxon_info_children eliminates all taxa that will give problems when trying to retrieve an induced subtree from Open Tree of Life.

Usage

```
clean_taxon_info_children(
  taxon_info,
  invalid = c("barren", "extinct", "uncultured", "major_rank_conflict",
             "incertae_sedis", "unplaced", "conflict", "environmental", "not_otu", "hidden",
             "hybrid")
)
```

Arguments

taxon_info	An output of rotl::taxonomy_taxon_info() .
invalid	A character vector of "flags", i.e., characteristics that are used by Open Tree of Life Taxonomy to detect invalid taxon names.

Value

A list with valid children unique OTT names, OTT ids and taxonomic ranks.

clean_tnrs	<i>Eliminates unmatched (NAs) and invalid taxa from a <code>rotl::tnrs_match_names()</code> or <code>tnrs_match()</code> output Useful to get ott ids to retrieve an induced synthetic Open Tree of Life. Needed because using <code>include_suppressed = FALSE</code> in <code>rotl::tnrs_match_names()</code> does not drop all invalid taxa.</i>
------------	---

Description

Eliminates unmatched (NAs) and invalid taxa from a `rotl::tnrs_match_names()` or `tnrs_match()` output Useful to get ott ids to retrieve an induced synthetic Open Tree of Life. Needed because using `include_suppressed = FALSE` in `rotl::tnrs_match_names()` does not drop all invalid taxa.

Usage

```
clean_tnrs(
  tnrs,
  invalid = c("barren", "extinct", "uncultured", "major_rank_conflict", "incertae",
             "unplaced", "conflict", "environmental", "not_otu"),
  remove_nonmatches = FALSE
)
```

Arguments

tnrs	A data frame, usually an output from <code>datelife::tnrs_match</code> or <code>rotl::tnrs_match_names</code> functions, but see details.
invalid	A character string with flags to be removed from final object.
remove_nonmatches	Boolean, whether to remove unsuccessfully matched names or not.

Details

Input can be any data frame or named list that relates taxa stored in an element named "unique" to a validity category stored in "flags".

Value

A data frame or named list (depending on the input) with valid taxa only.

cluster_patristicmatrix

Cluster a patristic matrix into a tree with various methods.

Description

Cluster a patristic matrix into a tree with various methods.

Usage

```
cluster_patristicmatrix(patristic_matrix, variance_matrix = NULL)
```

Arguments

patristic_matrix

A patristic matrix

variance_matrix

A variance matrix from a `datelifeResult` object, usually an output from `datelife_result_variance_`.
Only used if `clustering_method = "mvr"`.

Details

If clustering method fails, NA is returned.

Value

A list of trees obtained with clustering methods detailed in `patristic_matrix_to_phylo()`.

congruify_and_check *Congruify and Check.*

Description

Congruify and Check.

Usage

```
congruify_and_check(
  reference,
  target,
  taxonomy = NULL,
  tol = 0.01,
  option = 2,
  scale = "pathd8",
  attempt_fix = TRUE
)
```


Arguments

reference	an ultrametric tree used to time-scale the target
target	a phylogram that is sought to be ultrametricized based on the reference phylogeny
taxonomy	a linkage table between tips of the phylogeny and clades represented in the tree; rownames of 'taxonomy' should be tips found in the phylogeny
tol	branching time in reference above which secondary constraints will be applied to target
option	an integer (1 or 2; see details).
scale	NA, "PATHd8" or "treePL" (if PATHd8 or "treePL" are available in the R PATH)
attempt_fix	Default to TRUE. If congruification results in NA branch lengths, it will attempt to fix them.

congruify_and_mrca_multiPhylo

Congruify nodes of a tree topology to nodes from a source chronogram, and find the mrca nodes

Description

congruify_and_mrca_multiPhylo congruifies a target tree against all source chronograms in a multiPhylo object, and gets nodes of target tree that correspond to the most recent common ancestor (mrca) of taxon pairs in the congruified calibrations. It calls [congruify_and_mrca_phylo\(\)](#), and [phytools::findMRCA\(\)](#) to get mrca nodes.

Usage

```
congruify_and_mrca_multiPhylo(phy, source_chronograms)
```

Arguments

phy	A phylo object.
source_chronograms	A multiPhylo object, output of datelife_search() .

Value

a data.frame of node ages from source_chronograms and corresponding mrca nodes in target tree phy.

congruify_and_mrca_phylo

Congruify nodes of a tree topology to nodes from a source chronogram, and find the mrca nodes

Description

congruify_and_mrca congruifies a target tree against a single source chronogram, and gets nodes of target tree that correspond to the most recent common ancestor (mrca) of taxon pairs from the congruified calibrations. It uses `phytools::findMRCA()` to get mrca nodes.

Usage

```
congruify_and_mrca_phylo(phy, source_chronogram, reference)
```

Arguments

phy	A phylo object.
source_chronogram	A phylo object, output of <code>datelife_search()</code> .
reference	A character string indicating the study reference that the source_chronogram comes from.

Value

a data.frame of node ages from source_chronograms and corresponding mrca nodes in target tree phy.

contributor_cache	<i>Information on contributors, authors, study ids and clades from studies with chronograms in Open Tree of Life (Open Tree)</i>
-------------------	--

Description

Information on contributors, authors, study ids and clades from studies with chronograms in Open Tree of Life (Open Tree)

Usage

```
contributor_cache
```

Format

A list of five data sets.

author.pretty A character vector with the author names from studies with chronograms that are in Open Tree.

author.results A dataframe with three variables: authors, study ids and clades.

curator.pretty A character vector with the names of curators of chronograms that are in Open Tree.

curator.results A data.frame with three variables: curators, study ids and clades.

missed_doi A character vector with study ids whose "doi" could not be retrieved.

Details

Generated with `make_contributor_cache()`.

Source

<http://opentreeoflife.org>

datelife_authors_tabulate

Return the relevant authors for a set of studies.

Description

Return the relevant authors for a set of studies.

Usage

```
datelife_authors_tabulate(results.index, cache = "opentree_chronograms")
```

Arguments

`results.index` A vector from `datelife_result_study_index()` with the indices of the relevant studies.

`cache` The cached chronogram database.

Value

A vector with counts of each author, with names equal to author names.

datelife_result_median

Get a median summary chronogram from a datelifeResult object.

Description

Get a median summary chronogram from a datelifeResult object.

Usage

```
datelife_result_median(datelife_result, ...)
```

Arguments

datelife_result

A datelifeResult object, usually an output of [get_datelife_result\(\)](#).

...

Arguments passed on to [summary_matrix_to_phylo](#)

summ_matrix Any summary patristic distance matrix, such as the ones obtained with [datelife_result_sdm_matrix\(\)](#) or [datelife_result_median_matrix\(\)](#).

total_distance Whether the input summ_matrix stores total age distance (from tip to tip) or distance from node to tip. Default to TRUE, divides the matrix in half, if FALSE it will take it as is.

use A character vector indicating what type of age to use for summary tree. One of the following:

"mean" It will use the [mean\(\)](#) of the node ages in summ_matrix.

"median" It uses the [stats::median\(\)](#) age of node ages in summ_matrix.

"min" It will use the [min\(\)](#) age from node ages in summ_matrix.

"max" Choose this if you wanna be conservative; it will use the [max\(\)](#) age from node ages in summ_matrix.

"midpoint" It will use the mean of minimum age and maximum age.

target_tree A phylo object. Use this in case you want a specific backbone for the output tree.

datelife_query A datelifeQuery object, usually an output of [make_datelife_query\(\)](#).

Value

A phylo object.

`datelife_result_median_matrix`*Compute a median matrix of a datelifeResult object.*

Description

Compute a median matrix of a datelifeResult object.

Usage

```
datelife_result_median_matrix(datelife_result)
```

Arguments

`datelife_result`

A datelifeResult object, usually an output of [get_datelife_result\(\)](#).

Value

A patristic distance summary matrix from a datelifeResult object.

`datelife_result_MRCA` *Get a numeric vector of MRCAs from a datelifeResult object. Used in [summarize_datelife_result\(\)](#).*

Description

Get a numeric vector of MRCAs from a datelifeResult object. Used in [summarize_datelife_result\(\)](#).

Usage

```
datelife_result_MRCA(datelife_result, na_rm = TRUE)
```

Arguments

`datelife_result`

A datelifeResult object, usually an output of [get_datelife_result\(\)](#).

`na_rm`

If TRUE, it drops rows containing NAs from the datelifeResult patristic matrix; if FALSE, it returns NA where there are missing entries.

Value

A named numeric vector of MRCA ages for each element given in `datelife_result`.

datelife_result_sdm_matrix

Go from a datelifeResult object to a Super Distance Matrix (SDM) using weighting = "flat"

Description

Go from a datelifeResult object to a Super Distance Matrix (SDM) using weighting = "flat"

Usage

```
datelife_result_sdm_matrix(datelife_result)
```

Arguments

datelife_result

A datelifeResult object, usually an output of [get_datelife_result\(\)](#).

Value

A numeric matrix.

datelife_result_sdm_phylo

Reconstruct a supertree from a datelifeResult object using the Super Distance Matrix (SDM) method.

Description

Reconstruct a supertree from a datelifeResult object using the Super Distance Matrix (SDM) method.

Usage

```
datelife_result_sdm_phylo(datelife_result, weighting = "flat", ...)
```

Arguments

datelife_result

A datelifeResult object, usually an output of [get_datelife_result\(\)](#).

weighting

A character vector indicating how much weight to give to each tree in input during the SDM analysis. Options are:

weighting = "flat" All trees have equal weighting.

weighting = "taxa" Weight is proportional to number of taxa.

weighting = "inverse" Weight is proportional to 1 / number of taxa.

Defaults to `weighting = "flat"`.

... Arguments passed on to `summary_matrix_to_phylo`

`summ_matrix` Any summary patristic distance matrix, such as the ones obtained with `datelife_result_sdm_matrix()` or `datelife_result_median_matrix()`.

`total_distance` Whether the input `summ_matrix` stores total age distance (from tip to tip) or distance from node to tip. Default to `TRUE`, divides the matrix in half, if `FALSE` it will take it as is.

`use` A character vector indicating what type of age to use for summary tree. One of the following:

- "mean"** It will use the `mean()` of the node ages in `summ_matrix`.
- "median"** It uses the `stats::median()` age of node ages in `summ_matrix`.
- "min"** It will use the `min()` age from node ages in `summ_matrix`.
- "max"** Choose this if you wanna be conservative; it will use the `max()` age from node ages in `summ_matrix`.
- "midpoint"** It will use the mean of minimum age and maximum age.

`target_tree` A phylo object. Use this in case you want a specific backbone for the output tree.

`datelife_query` A `datelifeQuery` object, usually an output of `make_datelife_query()`.

Details

Chronograms given as input in `datelife_result` are summarized with the Super Distance Matrix (SDM) method described in Criscuolo et al. (2006) [doi:10.1080/10635150600969872](https://doi.org/10.1080/10635150600969872), implemented with the function `ape::SDM()`. The resulting summary SDM is clustered with `summary_matrix_to_phylo()`.

Value

A supertree with branch lengths proportional to time, obtained by summarizing individual chronograms given as input in `datelife_result`. It is returned as an object of class `datelifeSDM`, which is a phylo object with an additional `$data` element storing the input chronograms as a `datelifeResult` object, and a `$citation` element containing citations of studies from input chronograms.

References

Criscuolo A, Berry V, Douzery EJ, Gascuel O. (2006) "SDM: a fast distance-based approach for (super) tree building in phylogenomics" [doi:10.1080/10635150600969872](https://doi.org/10.1080/10635150600969872).

`datelife_result_study_index`

Find the index of relevant studies in a cached chronogram database.

Description

`datelife_result_study_index` is used in `summarize_datelife_result()`.

Usage

```
datelife_result_study_index(datelife_result, cache = "opentree_chronograms")
```

Arguments

`datelife_result`
A `datelifeResult` object, usually an output of `get_datelife_result()`.

`cache`
The cached chronogram database.

Value

A vector of indices of studies that have relevant information.

`datelife_result_variance_matrix`

Compute a variance matrix of a `datelifeResult` object.

Description

Compute a variance matrix of a `datelifeResult` object.

Usage

```
datelife_result_variance_matrix(datelife_result)
```

Arguments

`datelife_result`
A `datelifeResult` object, usually an output of `get_datelife_result()`.

Value

A variance matrix from a `datelifeResult` object.

datelife_search	<i>Get scientific, peer-reviewed information on time of lineage divergence openly available for a given set of taxon names</i>
-----------------	--

Description

datelife_search is the core DateLife function to find and get all openly available, peer-reviewed scientific information on time of lineage divergence for a set of input taxon names given as a character vector, a newick character string, a phylo or multiPhylo object or as a an already processed datelifeQuery object obtained with [make_datelife_query\(\)](#).

Usage

```
datelife_search(
  input = c("Rhea americana", "Pterocnemia pennata", "Struthio camelus"),
  use_tnrs = FALSE,
  get_spp_from_taxon = FALSE,
  partial = TRUE,
  cache = "opentree_chronograms",
  summary_format = "phylo_all",
  na_rm = FALSE,
  summary_print = c("citations", "taxa"),
  taxon_summary = c("none", "summary", "matrix"),
  criterion = "taxa"
)
```

Arguments

input	<p>One of the following:</p> <p>A character vector With taxon names as a single comma separated starting or concatenated with <code>c()</code>.</p> <p>A phylogenetic tree with taxon names as tip labels As a phylo or multiPhylo object, OR as a newick character string.</p> <p>A datelifeQuery object An output from make_datelife_query().</p>
use_tnrs	Whether to use Open Tree of Life's Taxonomic Name Resolution Service (TNRS) to process input taxon names. Default to TRUE, it corrects misspellings and taxonomic name variations with tnrs_match() , a wrapper of <code>rotl::tnrs_match_names()</code> .
get_spp_from_taxon	Whether to search ages for all species belonging to a given taxon or not. Default to FALSE. If TRUE, it must have same length as input. If input is a newick string with some clades it will be converted to a phylo object, and the order of get_spp_from_taxon will match phy\$tip.label.
partial	Whether to return or exclude partially matching source chronograms, i.e, those that match some and not all of taxa given in datelife_query. Options are TRUE or FALSE. Defaults to TRUE: return all matching source chronograms.

cache	A character vector of length one, with the name of the data object to cache. Default to "opentree_chronograms", a data object storing Open Tree of Life's database chronograms and other associated information.
summary_format	<p>A character vector of length one, indicating the output format for results of the DateLife search. Available output formats are:</p> <p>"citations" A character vector of references where chronograms with some or all of the target taxa are published (source chronograms).</p> <p>"mrca" A named numeric vector of most recent common ancestor (mrca) ages of target taxa defined in input, obtained from the source chronograms. Names of mrca vector are equal to citations.</p> <p>"newick_all" A named character vector of newick strings corresponding to target chronograms derived from source chronograms. Names of newick_all vector are equal to citations.</p> <p>"newick_sdm" Only if multiple source chronograms are available. A character vector with a single newick string corresponding to a target chronogram obtained with SDM supertree method (Criscuolo et al. 2006).</p> <p>"newick_median" Only if multiple source chronograms are available. A character vector with a single newick string corresponding to a target chronogram from the median of all source chronograms.</p> <p>"phylo_sdm" Only if multiple source chronograms are available. A phylo object with a single target chronogram obtained with SDM supertree method (Criscuolo et al. 2006).</p> <p>"phylo_median" Only if multiple source chronograms are available. A phylo object with a single target chronogram obtained from source chronograms with median method.</p> <p>"phylo_all" A named list of phylo objects corresponding to each target chronogram obtained from available source chronograms. Names of phylo_all list correspond to citations.</p> <p>"phylo_biggest" The chronogram with the most taxa. In the case of a tie, the chronogram with clade age closest to the median age of the equally large trees is returned.</p> <p>"html" A character vector with an html string that can be saved and then opened in any web browser. It contains a 4 column table with data on target taxa: mrca, number of taxa, citations of source chronogram and newick target chronogram.</p> <p>"data_frame" A 4 column data.frame with data on target taxa: mrca, number of taxa, citations of source chronograms and newick string.</p>
na_rm	If TRUE, it drops rows containing NAs from the datelifeResult patristic matrix; if FALSE, it returns NA where there are missing entries.
summary_print	<p>A character vector specifying the type of summary information to be printed to screen. Options are:</p> <p>"citations" Prints references of chronograms where target taxa are found.</p> <p>"taxa" Prints a summary of the number of chronograms where each target taxon is found.</p> <p>"none" Nothing is printed to screen.</p>

	Defaults to <code>c("citations", "taxa")</code> , which displays both.
<code>taxon_summary</code>	A character vector specifying if data on target taxa missing in source chronograms should be added to the output as a "summary" or as a presence/absence "matrix". Default to "none", no information on <code>taxon_summary</code> added to the output.
<code>criterion</code>	Defaults to <code>criterion = "taxa"</code> . Used for chronogram summarizing, i.e., obtaining a single summary chronogram from a group of input chronograms. For summarizing approaches that return a single summary tree from a group of phylogenetic trees, it is necessary that the latter form a grove, roughly, a sufficiently overlapping set of taxa between trees, see Ané et al. (2009) doi:10.1007/s00026-0090017x . In rare cases, a group of trees can have multiple groves. This argument indicates whether to get the grove with the most trees (<code>criterion = "trees"</code>) or the most taxa (<code>criterion = "taxa"</code>).

Details

If only one taxon name is given as input, `get_spp_from_taxon` is always set to TRUE.

Value

The output is determined by the argument `summary_format`:

- If** `summary_format = "citations"` The function returns a character vector of references.
- If** `summary_format = "mrca"` The function returns a named numeric vector of most recent common ancestor (mrca) ages.
- If** `summary_format = "newick_[all, sdm, or median]"` The function returns output chronograms as newick strings.
- If** `summary_format = "phylo_[all, sdm, median, or biggest]"` The function returns output chronograms as phylo or multiPhylo objects.
- If** `summary_format = "html" or "data_frame"` The function returns a 4 column table with data on mrca ages, number of taxa, references, and output chronograms as newick strings.

Examples

```
## Not run:

# For this example, we will set a temp working directory, but you can set
# your working directory as needed:
# we will use the tempdir() function to get a temporary directory:
tempwd <- tempdir()

# Obtain median ages from a set of source chronograms in newick format:
ages <- datelife_search(c(
  "Rhea americana", "Pterocnemis pennata", "Struthio camelus",
  "Mus musculus"
), summary_format = "newick_median")

# Save the tree in the temp working directory in newick format:
write(ages, file = file.path(tempwd, "some.bird.ages.txt"))
```

```

# Obtain median ages from a set of source chronograms in phylo format
# Will produce same tree as above but in "phylo" format:
ages.again <- datelife_search(c(
  "Rhea americana", "Pterocnemis pennata", "Struthio camelus",
  "Mus musculus"
), summary_format = "phylo_median")
plot(ages.again)
library(ape)
ape::axisPhylo()
mtext("Time (million years ago)", side = 1, line = 2, at = (max(get("last_plot.phylo",
  envir = .PlotPhyloEnv
)$xx) * 0.5))

# Save "phylo" object in newick format
write.tree(ages.again, file = file.path(tempwd, "some.bird.tree.again.txt"))

# Obtain MRCA ages and target chronograms from all source chronograms
# Generate an html output readable in any web browser:
ages.html <- datelife_search(c(
  "Rhea americana", "Pterocnemis pennata", "Struthio camelus",
  "Mus musculus"
), summary_format = "html")
write(ages.html, file = file.path(tempwd, "some.bird.trees.html"))
system(paste("open", file.path(tempwd, "some.bird.trees.html")))

## End(Not run) # end dontrun

```

datelife_use

Generate one or multiple chronograms for a set of given taxon names.

Description

datelife_use gets secondary calibrations available for any pair of given taxon names, mined from the [opentree_chronograms](#) object, congruifies them, and uses them to date a given tree topology with the algorithm defined in `dating_method`. If no tree topology is provided, it will attempt to get one for the given taxon names from Open Tree of Life synthetic tree, using [make_bold_otol_tree\(\)](#).

Usage

```
datelife_use(input = NULL, each = FALSE, dating_method = "bladj", ...)
```

Arguments

input One of the following:

- A character vector** With taxon names as a single comma separated starting or concatenated with `c()`.
- A phylogenetic tree with taxon names as tip labels** As a phylo or multiPhylo object, OR as a newick character string.

	A datelifeQuery object An output from <code>make_datelife_query()</code> .
<code>each</code>	Boolean, default to FALSE: all calibrations are returned in the same <code>data.frame</code> . If TRUE, calibrations from each chronogram are returned in separate data frames.
<code>dating_method</code>	Tree dating algorithm to use. Options are "bladj" or "pathd8" (Webb et al., 2008, doi:10.1093/bioinformatics/btn358 ; Britton et al., 2007, doi:10.1080/10635150701613783).
<code>...</code>	Arguments passed on to <code>make_datelife_query</code>
<code>use_tnrs</code>	Whether to use Open Tree of Life's Taxonomic Name Resolution Service (TNRS) to process input taxon names. Default to TRUE, it corrects misspellings and taxonomic name variations with <code>tnrs_match()</code> , a wrapper of <code>rotl::tnrs_match_names()</code> .
<code>get_spp_from_taxon</code>	Whether to search ages for all species belonging to a given taxon or not. Default to FALSE. If TRUE, it must have same length as input. If input is a newick string with some clades it will be converted to a phylo object, and the order of <code>get_spp_from_taxon</code> will match <code>phy\$tip.label</code> .
<code>taxonomic_source</code>	Used if <code>get_spp_from_taxon = TRUE</code> . A character vector with the desired taxonomic sources. Options are "ott", "ncbi", "gbif" or "irmng". The function defaults to "ott".

Details

If input is a vector of taxon names, the function will attempt to reconstruct a BOLD tree with `make_bold_otol_tree()` to get a tree with branch lengths. If it fails, it will get an Open Tree of Life synthetic tree topology. The function then calls `use_calibrations()`.

Value

A phylo or multiPhylo object with branch lengths proportional to time.

More

The output object stores the used calibrations and `dating_method` as `attributes(output)$datelife_calibrations` and `attributes(output)$dating_method`.

`datelife_use_datelifequery`

Generate one or multiple chronograms for a set of taxon names given as a datelifeQuery object.

Description

`datelife_use` gets secondary calibrations available for any pair of given taxon names, mined from the `opentree_chronograms` object, congruifies them, and uses them to date a given tree topology with the algorithm defined in `dating_method`. If no tree topology is provided, it will attempt to get one for the given taxon names from Open Tree of Life synthetic tree, using `make_bold_otol_tree()`.

Usage

```
datelife_use_datelifequery(
  datelife_query = NULL,
  dating_method = "bladj",
  each = FALSE
)
```

Arguments

`datelife_query` A `datelifeQuery` object, usually an output of `make_datelife_query()`.

`dating_method` Tree dating algorithm to use. Options are "bladj" or "pathd8" (Webb et al., 2008, [doi:10.1093/bioinformatics/btn358](https://doi.org/10.1093/bioinformatics/btn358); Britton et al., 2007, [doi:10.1080/10635150701613783](https://doi.org/10.1080/10635150701613783)).

`each` Boolean, default to FALSE: all calibrations are returned in the same `data.frame`. If TRUE, calibrations from each chronogram are returned in separate `data.frames`.

Details

If `phy` has no branch lengths, `dating_method` is ignored, and the function applies secondary calibrations to date the tree with the BLADJ algorithm. See `make_bladj_tree()` and `use_calibrations_bladj()`. If `phy` has branch lengths, the function can use the PATHd8 algorithm. See `use_calibrations_pathd8()`.

Value

A `phylo` or `multiPhylo` object with branch lengths proportional to time.

More

The output object stores the used calibrations and `dating_method` as `attributes(output)$datelife_calibrations` and `attributes(output)$dating_method`.

`date_with_pbdb` *Date with Paleobiology Database and paleotree.*

Description

This will take a topology, look up information about fossils for taxa on the tree, and use `paleotree::timePaleoPhy()` to compute branch lengths.

Usage

```
date_with_pbdb(phy, recent = FALSE, assume_recent_if_missing = TRUE)
```

Arguments

`phy` A `phylo` object.

`recent` If TRUE, forces the minimum age to be zero for any taxon

`assume_recent_if_missing` If TRUE, any taxon missing from PBDB is assumed to be recent.

Value

A dated tree.

Examples

```
## Not run: # This is a flag for package development. You are welcome to run the example.

taxa <- c(
  "Archaeopteryx", "Pinus", "Quetzalcoatlus", "Homo sapiens",
  "Tyrannosaurus rex", "Megatheriidae", "Metasequoia", "Aedes", "Panthera"
)
phy <- tree_from_taxonomy(taxa, sources = "The Paleobiology Database")$phy

## End(Not run) # end dontrun
```

extract_calibrations_dateliferesult

Use congruification to extract secondary calibrations from a datelifeResult object.

Description

This function extracts node ages for each taxon pair given in `input$tip.labels`. It applies the congruification method described in Eastman et al. (2013) doi:[10.1111/2041210X.12051](https://doi.org/10.1111/2041210X.12051), implemented with the function `geiger::congruify.phylo()`, to create a `data.frame` of taxon pair node ages that can be used as secondary calibrations.

Usage

```
extract_calibrations_dateliferesult(input = NULL, each = FALSE)
```

Arguments

<code>input</code>	A <code>datelifeResult</code> object.
<code>each</code>	Boolean, default to FALSE: all calibrations are returned in the same <code>data.frame</code> . If TRUE, calibrations from each chronogram are returned in separate <code>data.frames</code> .

Details

The function takes a `datelifeResult` object and calls `summarize_datelife_result()` with `summary_format = "phylo_aeResultobject"` to `aphyloormultiPhylo` object that is passed to `extract_calibrations_phylo()`.

Value

An object of class `calibrations`, which is a `data.frame` (if `each = FALSE`) or a list of `data.frames` (if `each = TRUE`) of node ages for each pair of taxon names. You can access the input data from which the calibrations were extracted with `attributes(output)$chronograms`.

extract_calibrations_phylo

Use congruification to extract secondary calibrations from a phylo or multiPhylo object with branch lengths proportional to time.

Description

This function extracts node ages for each taxon pair given in `input$tip.labels`. It applies the congruification method described in Eastman et al. (2013) [doi:10.1111/2041210X.12051](https://doi.org/10.1111/2041210X.12051), implemented with the function `geiger::congruify.phylo()`, to create a `data.frame` of taxon pair node ages that can be used as secondary calibrations.

Usage

```
extract_calibrations_phylo(input = NULL, each = FALSE)
```

Arguments

<code>input</code>	A phylo or multiPhylo object with branch lengths proportional to time.
<code>each</code>	Boolean, default to FALSE: all calibrations are returned in the same <code>data.frame</code> . If TRUE, calibrations from each chronogram are returned in separate data frames.

Value

An object of class `calibrations`, which is a `data.frame` (if `each = FALSE`) or a list of `data.frames` (if `each = TRUE`) of node ages for each pair of taxon names. You can access the input data from which the calibrations were extracted with `attributes(output)$chronograms`.

References

Eastman et al. (2013) "Congruification: support for time scaling large phylogenetic trees". *Methods in Ecology and Evolution*, 4(7), 688-691, [doi:10.1111/2041210X.12051](https://doi.org/10.1111/2041210X.12051).

extract_ott_ids

Get OTT ids from a character vector containing species names and OTT ids.

Description

Get OTT ids from a character vector containing species names and OTT ids.

Usage

```
extract_ott_ids(x, na.rm = TRUE)
```

```
## Default S3 method:
```

```
extract_ott_ids(x, na.rm = TRUE)
```


Arguments

<code>x</code>	A character vector of taxon names, or a phylo object with tip names containing OTT ids.
<code>na.rm</code>	A logical value indicating whether NA values should be stripped from the output.

Value

An object of class numeric containing OTT ids only.
 NULL

Examples

```
canis <- rotl::tnrs_match_names("canis")
canis_taxonomy <- rotl::taxonomy_subtree(canis$ott_id)
my_ott_ids <- extract_ott_ids(x = canis_taxonomy$tip_label)
# Get the problematic elements from input
canis_taxonomy$tip_label[attr(my_ott_ids, "na.action")]
```

`felid_gdr_phylo_all` *datelifeSummary of a datelifeResult object of all Felidae species.*

Description

`datelifeSummary` of a `datelifeResult` object of all Felidae species.

Usage

```
felid_gdr_phylo_all
```

Format

A list of three elements, containing the summary of a `datelifeResult` object

phylo_all List of subset chronograms in phylo format

taxon_distribution A data frame with taxon presence across subset chronograms

absent_taxa A dataframe with names of taxon not found in any chronogram

Details

```
Generated with: felid_spp <- make_datelife_query(input = "felidae", get_spp_from_taxon = TRUE)
felid_gdr <- get_datelife_result(input = felid_spp, get_spp_from_taxon = TRUE) felid_gdr_phylo_all
<- summarize_datelife_result(datelife_result = felid_gdr, taxon_summary = "summary", summary_format
= "phylo_all", datelife_query = felid_spp) usethis::use_data(felid_gdr_phylo_all)
```

Source

<http://opentreeoflife.org>

felid_sdm	<i>SDM tree of a datelifeResult object of all Felidae species.</i>
-----------	--

Description

SDM tree of a datelifeResult object of all Felidae species.

Usage

```
felid_sdm
```

Format

A list of two elements, containing the summary of a datelifeResult object

phy An ultrametric phylo object with the SDM tree.

data A datelifeResult object with data used to construct phy

Details

```
Generated with: felid_spp <- make_datelife_query(input = "felidae", get_spp_from_taxon = TRUE)
felid_gdr <- get_datelife_result(input = felid_spp, get_spp_from_taxon = TRUE)
felid_sdm <- datelife_result_sdm_phylo(felid_gdr)
usethis::use_data(felid_sdm)
```

Source

<http://opentreeoflife.org>

filter_for_grove	<i>Filter a datelifeResult object to find the largest grove.</i>
------------------	--

Description

Filter a datelifeResult object to find the largest grove.

Usage

```
filter_for_grove(datelife_result, criterion = "taxa", n = 2)
```

Arguments

datelife_result	A datelifeResult object. Only needed for criterion = "taxa".
criterion	Defaults to criterion = "taxa". Used for chronogram summarizing, i.e., obtaining a single summary chronogram from a group of input chronograms. For summarizing approaches that return a single summary tree from a group of phylogenetic trees, it is necessary that the latter form a grove, roughly, a sufficiently overlapping set of taxa between trees, see Ané et al. (2009) doi:10.1007/s00026-0090017x . In rare cases, a group of trees can have multiple groves. This argument indicates whether to get the grove with the most trees (criterion = "trees") or the most taxa (criterion = "taxa").
n	The degree of taxon name overlap among input chronograms. Defaults to n = 2, i.e., at least two overlapping taxon names.

Value

A datelifeResult object filtered to only include one grove of trees.

force_ultrametric	<i>Force a non-ultrametric phylo object to be ultrametric with <code>phytools::force.ultrametric()</code>.</i>
-------------------	--

Description

Force a non-ultrametric phylo object to be ultrametric with `phytools::force.ultrametric()`.

Usage

```
force_ultrametric(phy)
```

Arguments

phy	A phylo object.
-----	-----------------

Value

A phylo object.

get_all_calibrations *Get secondary calibrations from a chronogram database for a set of given taxon names*

Description

get_all_calibrations performs a `datelife_search()` and gets divergence times (i.e., secondary calibrations) from a chronogram database for each taxon name pair given as input.

get_all_calibrations performs a `datelife_search()` and gets divergence times (i.e., secondary calibrations) from a chronogram database for each taxon name pair given as input.

Usage

```
get_all_calibrations(input = NULL, each = FALSE)
```

```
get_all_calibrations(input = NULL, each = FALSE)
```

Arguments

input	One of the following: A character vector With taxon names as a single comma separated starting or concatenated with <code>c()</code> . A phylogenetic tree with taxon names as tip labels As a phylo or multiPhylo object, OR as a newick character string. A datelifeQuery object An output from <code>make_datelife_query()</code> .
each	Boolean, default to FALSE: all calibrations are returned in the same data.frame. If TRUE, calibrations from each chronogram are returned in separate data frames.

Value

An object of class `calibrations`, which is a `data.frame` (if `each = FALSE`) or a list of `data.frames` (if `each = TRUE`) of node ages for each pair of taxon names. You can access the input data from which the calibrations were extracted with `attributes(output)$chronograms`.

get_best_grove *Get grove from a datelifeResult object that can be converted to phylo from a median summary matrix*

Description

Get grove from a `datelifeResult` object that can be converted to phylo from a median summary matrix

Usage

```
get_best_grove(datelife_result, criterion = "taxa", n = 2)
```

Arguments

datelife_result A datelifeResult object. Only needed for criterion = "taxa".

criterion Defaults to criterion = "taxa". Used for chronogram summarizing, i.e., obtaining a single summary chronogram from a group of input chronograms. For summarizing approaches that return a single summary tree from a group of phylogenetic trees, it is necessary that the latter form a grove, roughly, a sufficiently overlapping set of taxa between trees, see Ané et al. (2009) [doi:10.1007/s00026-0090017x](https://doi.org/10.1007/s00026-0090017x). In rare cases, a group of trees can have multiple groves. This argument indicates whether to get the grove with the most trees (criterion = "trees") or the most taxa (criterion = "taxa").

n The degree of taxon name overlap among input chronograms. Defaults to n = 2, i.e., at least two overlapping taxon names.

Value

A list of two elements:

best_grove A datelifeResult object filtered to only include one grove of trees that can be summarized with median or sdm.

overlap The degree of taxon names overlap among trees in the best grove.

```
get_biggest_multiphylo
```

Get the tree with the most tips from a multiPhylo object: the biggest tree.

Description

Get the tree with the most tips from a multiPhylo object: the biggest tree.

Usage

```
get_biggest_multiphylo(trees)
```

Arguments

trees A list of trees as multiPhylo or as a generic list object.

Value

The largest tree from those given in trees, as a phylo object with an additional \$citation element containing the reference of the original publication.

```
get_calibrations_datelifequery
```

Search and extract available secondary calibrations for taxon names in a given datelifeQuery object

Description

The function searches DateLife's local database of phylogenetic trees with branch lengths proportional to time (chronograms) with `datelife_search()`, and extracts available node ages for each pair of given taxon names with `extract_calibrations_phylo()`.

Usage

```
get_calibrations_datelifequery(datelife_query = NULL, each = FALSE)
```

Arguments

`datelife_query` A `datelifeQuery` object.

`each` Boolean, default to FALSE: all calibrations are returned in the same `data.frame`. If TRUE, calibrations from each chronogram are returned in separate data frames.

Details

The function calls `datelife_search()` with `summary_format = "phylo_all"` to get all chronograms in the database containing at least two taxa in input, and generates a `phylo` or `multiPhylo` object object that will be passed to `extract_calibrations_phylo()`.

Value

An object of class `calibrations`, which is a `data.frame` (if `each = FALSE`) or a list of `data.frames` (if `each = TRUE`) of node ages for each pair of taxon names. You can access the input data from which the calibrations were extracted with `attributes(output)$chronograms`.

```
get_calibrations_vector
```

Search and extract secondary calibrations for a given character vector of taxon names

Description

The function searches DateLife's local database of phylogenetic trees with branch lengths proportional to time (chronograms) with `datelife_search()`, and extracts available node ages for each pair of given taxon names with `extract_calibrations_phylo()`.

Usage

```
get_calibrations_vector(input = NULL, each = FALSE)
```

Arguments

input	A character vector of taxon names.
each	Boolean, default to FALSE: all calibrations are returned in the same data.frame. If TRUE, calibrations from each chronogram are returned in separate data frames.

Details

The function calls `datelife_search()` with `summary_format = "phylo_all"` to get all chronograms in the database containing at least two taxa in `input`, and generates a `phylo` or `multiPhylo` object that will be passed to `extract_calibrations_phylo()`.

Value

An object of class `calibrations`, which is a `data.frame` (if `each = FALSE`) or a list of `data.frames` (if `each = TRUE`) of node ages for each pair of taxon names. You can access the input data from which the calibrations were extracted with `attributes(output)$chronograms`.

```
get_dated_otol_induced_subtree
```

Get a dated OpenTree induced synthetic subtree from a set of given taxon names, from blackrim's FePhyFoFum service.

Description

Get a dated OpenTree induced synthetic subtree from a set of given taxon names, from blackrim's FePhyFoFum service.

Usage

```
get_dated_otol_induced_subtree(input = NULL, ott_ids = NULL, ...)
```

Arguments

input	Optional. A character vector of names or a <code>datelifeQuery</code> object.
ott_ids	If not NULL, it takes this argument and ignores <code>input</code> . A numeric vector of ott ids obtained with <code>rotl::taxonomy_taxon_info()</code> or <code>rotl::tnrs_match_names()</code> or <code>tnrs_match()</code> .
...	Arguments passed on to <code>check_ott_input</code>

Details

OpenTree dated tree from Stephen Smith's OpenTree scaling service at <https://github.com/FePhyFoFum/gophy> if you want to make an LTT plot of a dated OpenTree tree you'll need to get rid of singleton nodes with `ape::collapse.singles()` and also probably do `phytools::force.ultrametric()`.

Value

A phylo object with edge length proportional to time in Myrs. It will return NA if any ott_id is invalid.

get_datelife_result *Get a patristic matrix of time of lineage divergence data for a given set of taxon names*

Description

get_datelife_result takes as input a vector of taxon names, a newick string, a phylo object, or adatelifeQuery object. It searches the chronogram database specified in cache for chronograms matching two or more given taxon names. For each matching chronogram, it extracts time of lineage divergence data and stores it as a patristic matrix. It then lists all resulting patristic matrices. Each list element is named with the study citation of the source chronogram.

Usage

```
get_datelife_result(
  input = NULL,
  partial = TRUE,
  cache = "opentree_chronograms",
  update_opentree_chronograms = FALSE,
  ...
)
```

Arguments

input	One of the following: A character vector With taxon names as a single comma separated starting or concatenated with <code>c()</code> . A phylogenetic tree with taxon names as tip labels As a phylo or multiPhylo object, OR as a newick character string. A datelifeQuery object An output from <code>make_datelife_query()</code> .
partial	Whether to return or exclude partially matching source chronograms, i.e. those that match some and not all of taxa given in datelife_query. Options are TRUE or FALSE. Defaults to TRUE: return all matching source chronograms.
cache	A character vector of length one, with the name of the data object to cache. Default to "opentree_chronograms", a data object storing Open Tree of Life's database chronograms and other associated information.

update_opentree_chronograms Whether to update the chronogram database or not. Defaults to FALSE.

... Arguments passed on to [make_datelife_query](#)

use_tnrs Whether to use Open Tree of Life's Taxonomic Name Resolution Service (TNRS) to process input taxon names. Default to TRUE, it corrects misspellings and taxonomic name variations with [tnrs_match\(\)](#), a wrapper of [rotl::tnrs_match_names\(\)](#).

get_spp_from_taxon Whether to search ages for all species belonging to a given taxon or not. Default to FALSE. If TRUE, it must have same length as input. If input is a newick string with some clades it will be converted to a phylo object, and the order of get_spp_from_taxon will match phy\$tip.label.

taxonomic_source Used if get_spp_from_taxon = TRUE. A character vector with the desired taxonomic sources. Options are "ott", "ncbi", "gbif" or "irmng". The function defaults to "ott".

Value

A datelifeResult object – a named list of patristic matrices.

```
get_datelife_result_datelifequery
```

Get a list of patristic matrices from a given datelifeQuery object

Description

Get a list of patristic matrices from a given datelifeQuery object

Usage

```
get_datelife_result_datelifequery(
  datelife_query = NULL,
  partial = TRUE,
  cache = "opentree_chronograms",
  update_opentree_chronograms = FALSE,
  ...
)
```

Arguments

datelife_query A datelifeQuery object, usually an output of [make_datelife_query\(\)](#).

partial Whether to return or exclude partially matching source chronograms, i.e. those that match some and not all of taxa given in datelife_query. Options are TRUE or FALSE. Defaults to TRUE: return all matching source chronograms.

cache A character vector of length one, with the name of the data object to cache. Default to "opentree_chronograms", a data object storing Open Tree of Life's database chronograms and other associated information.

update_opentree_chronograms Whether to update the chronogram database or not. Defaults to FALSE.

... Arguments passed on to [make_datelife_query](#)

input Taxon names as one of the following:

- A character vector of taxon names** With taxon names as a single comma separated starting or concatenated with [c\(\)](#).
- A phylogenetic tree with taxon names as tip labels** As a phylo or multiPhylo object, OR as a newick character string.

use_tnrs Whether to use Open Tree of Life's Taxonomic Name Resolution Service (TNRS) to process input taxon names. Default to TRUE, it corrects misspellings and taxonomic name variations with [tnrs_match\(\)](#), a wrapper of [rotl::tnrs_match_names\(\)](#).

get_spp_from_taxon Whether to search ages for all species belonging to a given taxon or not. Default to FALSE. If TRUE, it must have same length as input. If input is a newick string with some clades it will be converted to a phylo object, and the order of get_spp_from_taxon will match phy\$tip.label.

taxonomic_source Used if get_spp_from_taxon = TRUE. A character vector with the desired taxonomic sources. Options are "ott", "ncbi", "gbif" or "irmng". The function defaults to "ott".

Details

If there is just one taxon name in `input$cleaned_names`, the function will run [make_datelife_query\(\)](#) setting `get_spp_from_taxon = TRUE`. The `datelifeQuery` used as input can be accessed with `attributes(datelifeResult)$query`.

Value

A `datelifeResult` object – a named list of patristic matrices.

<code>get_fossil_range</code>	<i>Get the ages for a taxon from PBDB</i>
-------------------------------	---

Description

This uses the Paleobiology Database's API to gather information on the ages for all specimens of a taxon. It will also look for all descendants of the taxon. It fixes name misspellings if possible.

Usage

```
get_fossil_range(taxon, recent = FALSE, assume_recent_if_missing = TRUE)
```

Arguments

<code>taxon</code>	The scientific name of the taxon you want the range of occurrences of
<code>recent</code>	If TRUE, forces the minimum age to be zero
<code>assume_recent_if_missing</code>	If TRUE, any taxon missing from pbdb is assumed to be recent

Value

a data.frame of max_ma and min_ma for the specimens

get_goodmatrices	<i>Get indices of good matrices to apply Super Distance Matrix (SDM) method with make_sdm().</i>
------------------	--

Description

Get indices of good matrices to apply Super Distance Matrix (SDM) method with [make_sdm\(\)](#).

Usage

```
get_goodmatrices(unpadded.matrices)
```

Arguments

unpadded.matrices
A list of patristic matrices, a datelifeResult object.

Value

A numeric vector of good matrix indices in unpadded.matrices.

get_mrbayes_node_constraints	<i>Makes a block of node constraints and node calibrations for a MrBayes run file from a list of taxa and ages, or from a dated tree</i>
------------------------------	--

Description

Makes a block of node constraints and node calibrations for a MrBayes run file from a list of taxa and ages, or from a dated tree

Usage

```
get_mrbayes_node_constraints(  
  constraint = NULL,  
  taxa = NULL,  
  missing_taxa = NULL,  
  ncalibration = NULL,  
  age_distribution = "fixed",  
  root_calibration = FALSE,  
  mrbayes_constraints_file = NULL,  
  clockratepr = "prset clockratepr = fixed(1);"  
)
```

Arguments

constraint	The constraint tree: a phylo object or a newick character string, with or without branch lengths.
taxa	A character vector with taxon names to be maintained in tree
missing_taxa	A tree, a data frame or a vector enlisting all missing taxa you want to include. A tree Either as a phylo object or as a newick character string. It contains all taxa that you want at the end, both missing and non missing. This tree will be used as a hard constraint. A data.frame It contains two columns named "taxon" and "clade". The first one contains a character vector of missing taxon names. The second one contains a character or numeric vector of nodes from a constraint tree to which each taxon will be assigned. A character vector It contains the names of the missing taxa. They will be added at random to the constraint tree.
ncalibration	The node calibrations: a phylo object with branch lengths proportional to time; in this case all nodes from ncalibration will be used as calibration points. Alternatively, a list with two elements: the first is a character vector with node names from phy to calibrate; the second is a numeric vector with the corresponding ages to use as calibrations.
age_distribution	A character string specifying the type of calibration. Only "fixed" and "uniform" are implemented for now. fixed The age given in ncalibration will be used as fixed age. lognormal The age given in ncalibration will be used as mean age. The standard deviation can be provided. # still need to add this option. By default, a 95 CI sd is used. uniform The age given in ncalibration will be used as mean age. Where min_age = 0.9 * mean age, and max_age = 1.1 * mean age.
root_calibration	Used to set a calibration at the root or not. Default to FALSE. Only relevant if ncalibration is specified.
mrbayes_constraints_file	NULL or a character vector indicating the name of mrbayes constraint and/or calibration block file.
clockratepr	A character vector indicating the clockrateprior to be used.

Value

A set of MrBayes constraints and/or calibration commands printed in console as character strings or as a text file specified in mrbayes_constraints_file.

`get_opentree_chronograms`*Get all chronograms from Open Tree of Life database*

Description

Get all chronograms from Open Tree of Life database

Usage

```
get_opentree_chronograms(max_tree_count = "all")
```

```
get_otol_chronograms(max_tree_count = "all")
```

Arguments

`max_tree_count` Default to "all", it gets all available chronograms. For testing purposes, a numeric value indicating the max number of trees to be cached.

Value

A list of 4 elements:

authors A list of lists of author names of the original studies that published chronograms currently stored in the Open Tree of Life database.

curators A list of lists of curator names that uploaded chronograms to the Open Tree of Life database.

studies A list of study identifiers from original studies that published chronograms currently stored in the Open Tree of Life database.

trees A `multiPhylo` object storing the chronograms from Open Tree of Life database.

update A character vector indicating the time when the database object was last updated.

version A character vector indicating the `datelife` package version when the object was last updated.

`get_opentree_species` *Get all species belonging to a taxon from the Open Tree of Life Taxonomy*

Description

Get all species belonging to a taxon from the Open Tree of Life Taxonomy

Usage

```
get_opentree_species(taxon_name, ott_id, synth_tree_only = TRUE)
```

Arguments

taxon_name	A character vector providing an inclusive taxonomic name.
ott_id	A numeric vector providig an Open Tree Taxonomic id number for a taxonomic name. If provided, taxon_name is ignored. used by Open Tree of Life Taxonomy to detect invalid taxon names.
synth_tree_only	Whether to include species that are in synthetic Open Tee only or not. Default to TRUE.

Value

A list of unique OTT names and OTT ids of species withing the provided taxon.

get_otol_synthetic_tree

Get an Open Tree of Life synthetic subtree of a set of given taxon names.

Description

Get an Open Tree of Life synthetic subtree of a set of given taxon names.

Usage

```
get_otol_synthetic_tree(
  input = NULL,
  ott_ids = NULL,
  otol_version = "v3",
  resolve = FALSE,
  ...
)
```

Arguments

input	Optional. A character vector of names or a datelifeQuery object.
ott_ids	If not NULL, it takes this argument and ignores input. A numeric vector of ott ids obtained with <code>rotl::taxonomy_taxon_info()</code> or <code>rotl::tnrs_match_names()</code> or <code>tnrs_match()</code> .
otol_version	Version of Open Tree of Life to use
resolve	Defaults to TRUE. Whether to resolve the tree at random or not.
...	Arguments passed on to <code>check_ott_input</code>

Value

A phylo object

get_ott_children	<i>Use this instead of <code>rotl::tol_subtree()</code> when taxa are not in synthesis tree and you still need to get all species or an induced OpenTree subtree</i>
------------------	--

Description

Use this instead of `rotl::tol_subtree()` when taxa are not in synthesis tree and you still need to get all species or an induced OpenTree subtree

Usage

```
get_ott_children(input = NULL, ott_ids = NULL, ott_rank = "species", ...)
```

Arguments

input	Optional. A character vector of names or a datelifeQuery object.
ott_ids	If not NULL, it takes this argument and ignores input. A numeric vector of ott ids obtained with <code>rotl::taxonomy_taxon_info()</code> or <code>rotl::tnrs_match_names()</code> or <code>tnrs_match()</code> .
ott_rank	A character vector with the ranks you wanna get lineage children from.
...	Other arguments to pass to <code>get_valid_children()</code> .

Value

A data.frame object.

Examples

```
# An example with the dog genus:

# It is currently not possible to get an OpenTree subtree of a taxon that is
# missing from the OpenTree synthetic tree.
# The dog genus is not monophyletic in the OpenTree synthetic tree, so in
# practice, it has no node to extract a subtree from.
tnrs <- tnrs_match("Canis")

## Not run: # This is a flag for package development. You are welcome to run the example.
rotl::tol_subtree(tnrs$ott_id[1])
#> Error: HTTP failure: 400
#> [/v3/tree_of_life/subtree] Error: node_id was not found (broken taxon).

## End(Not run) # end dontrun

ids <- tnrs$ott_id[1]
names(ids) <- tnrs$unique_name
children <- get_ott_children(ott_ids = ids) # or
```

```

children <- get_ott_children(input = "Canis")
str(children)
ids <- children$Canis$ott_id
names(ids) <- rownames(children$Canis)
tree_children <- datelife::get_otol_synthetic_tree(ott_ids = ids)
plot(tree_children, cex = 0.3)

# An example with flowering plants:

## Not run: # This is a flag for package development. You are welcome to run the example.

oo <- get_ott_children(input = "magnoliophyta", ott_rank = "order")
# Get the number of orders of flowering plants that we have
sum(oo$Magnoliophyta$rank == "order")

## End(Not run) # end dontrun

```

get_ott_clade	<i>Get the Open Tree of Life Taxonomic identifiers (OTT ids) and name of one or several given taxonomic ranks from one or more input taxa.</i>
---------------	--

Description

Get the Open Tree of Life Taxonomic identifiers (OTT ids) and name of one or several given taxonomic ranks from one or more input taxa.

Usage

```
get_ott_clade(input = NULL, ott_ids = NULL, ott_rank = "family")
```

Arguments

input	Optional. A character vector of names or a datelifeQuery object.
ott_ids	If not NULL, it takes this argument and ignores input. A numeric vector of ott ids obtained with rotl::taxonomy_taxon_info() or rotl::tnrs_match_names() or tnrs_match() .
ott_rank	A character vector with the ranks you wanna get lineage children from.

Value

A list of named numeric vectors with OTT ids from input and all requested ranks.

get_ott_lineage	<i>Get the Open Tree of Life Taxonomic identifier (OTT id) and name of all lineages from one or more input taxa.</i>
-----------------	--

Description

Get the Open Tree of Life Taxonomic identifier (OTT id) and name of all lineages from one or more input taxa.

Usage

```
get_ott_lineage(input = NULL, ott_ids = NULL)
```

Arguments

input	Optional. A character vector of names or a datelifeQuery object.
ott_ids	If not NULL, it takes this argument and ignores input. A numeric vector of ott ids obtained with <code>rotl::taxonomy_taxon_info()</code> or <code>rotl::tnrs_match_names()</code> or <code>tnrs_match()</code> .

Value

A list of named numeric vectors of ott ids from input and all the clades it belongs to.

Examples

```
## Not run: # This is a flag for package development. You are welcome to run the example.

taxa <- c("Homo", "Bacillus anthracis", "Apis", "Salvia")
lin <- get_ott_lineage(taxa)
lin

# Look up an unknown OTT id:
get_ott_lineage(ott_id = 454749)

## End(Not run) # end dontrun
```

get_subset_array_dispatch

Figure out which subset function to use.

Description

get_subset_array_dispatch is used inside `get_datelife_result()`

Usage

```

get_subset_array_dispatch(
  study_element,
  taxa,
  phy = NULL,
  phy4 = NULL,
  dating_method = "PATHd8"
)

```

Arguments

study_element	The thing being passed in: an array or a phylo object to serve as reference for congruification.
taxa	Vector of taxon names to get a subset for.
phy	A user tree to congruify as phylo object (ape).
phy4	A user tree to congruify in phylo4 format (phylobase).
dating_method	The method used for tree dating.

Value

A patristic matrix with ages for the target taxa.

get_taxon_summary *Get a taxon summary of a datelifeResult object.*

Description

Get a taxon summary of a datelifeResult object.

Usage

```
get_taxon_summary(datelife_result = NULL, datelife_query = NULL)
```

Arguments

datelife_result	A datelifeResult object, usually an output of get_datelife_result() .
datelife_query	A datelifeQuery object, usually an output of make_datelife_query() .

Value

A datelifeTaxonSummary object, which is a list of 4 elements:

\$matrix Data as a presence/absence matrix of taxon names across chronograms.

\$summary A data.frame with taxon names as `row.names()` and two columns, one with the number of chronograms that contain a taxon name and the other one with the total number of chronograms that have at least 2 taxon names.

\$summary2 A data.frame with chronogram citations as `row.names()` and two columns, one with the number of taxon names found in each chronogram and the other one with the total number of taxon names.

\$absent_taxa A character vector of taxon names that are not found in the chronogram database.

get_valid_children	<i>Extract valid children from given taxonomic name(s) or Open Tree of Life Taxonomic identifiers (OTT ids) from a taxonomic source.</i>
--------------------	--

Description

Extract valid children from given taxonomic name(s) or Open Tree of Life Taxonomic identifiers (OTT ids) from a taxonomic source.

Usage

```
get_valid_children(input = NULL, ott_ids = NULL, taxonomic_source = "ncbi")
```

Arguments

input	Optional. A character vector of names or a datelifeQuery object.
ott_ids	If not NULL, it takes this argument and ignores input. A numeric vector of ott ids obtained with <code>rotl::taxonomy_taxon_info()</code> or <code>rotl::tnrs_match_names()</code> or <code>tnrs_match()</code> .
taxonomic_source	A character vector with the desired taxonomic sources. Options are "ncbi", "gbif" or "irmng". Any other value will retrieve data from all taxonomic sources. The function defaults to "ncbi".

Details

GBIF and other taxonomies contain deprecated taxa that are not marked as such in the Open Tree of Life Taxonomy. We are relying mainly in the NCBI taxonomy for now.

Value

A named list containing valid taxonomic children of given taxonomic name(s).

Examples

```
# genus Dictyophyllidites with ott id = 6003921 has only extinct children
# in cases like this the same name will be returned

tti <- rotl::taxonomy_taxon_info(6003921, include_children = TRUE)
gvc <- get_valid_children(ott_ids = 6003921)

# More examples:

get_valid_children(ott_ids = 769681) # Psilotopsida
get_valid_children(ott_ids = 56601) # Marchantiophyta
```

input_process	<i>Process a phylo object or a character string to determine if it's correct newick</i>
---------------	---

Description

Process a phylo object or a character string to determine if it's correct newick

Usage

```
input_process(input)
```

Arguments

input	Taxon names as one of the following: A character vector of taxon names With taxon names as a single comma separated starting or concatenated with <code>c()</code> . A phylogenetic tree with taxon names as tip labels As a phylo or multiPhylo object, OR as a newick character string.
-------	---

Value

A phylo object or NA if input is not a tree .

is_datelife_query	<i>Check if input is a datelifeQuery object</i>
-------------------	---

Description

is_datelife_query checks for two things to be TRUE or FALSE. First, that input is of class datelifeQuery. Second, that input is a list that contains at least two elements of a datelifeQuery object:

cleaned_names A character vector of taxon names.

phy Either NA or a phylo object.

Usage

```
is_datelife_query(input)
```

Arguments

input	An object to be checked as an object with essential properties of a 'datelife-Query' object.
-------	--

Details

If the object has the correct format but it has a class different than datelifeQuery, the class is not modified.

Value

Is determined by the second condition.

```
is_datelife_result_empty
```

Check if we obtained an empty search with the given taxon name(s).

Description

Check if we obtained an empty search with the given taxon name(s).

Usage

```
is_datelife_result_empty(datelife_result, use_tnrs = FALSE)
```

Arguments

datelife_result	A datelifeResult object, usually an output of get_datelife_result() .
use_tnrs	Whether to use Open Tree of Life's Taxonomic Name Resolution Service (TNRS) to process input taxon names. Default to TRUE, it corrects misspellings and taxonomic name variations with tnrs_match() , a wrapper of <code>rotl::tnrs_match_names()</code> .

Value

Boolean. If TRUE, no chronograms were found for the given taxon name(s). If FALSE, the chronogram search was successful.

is_good_chronogram *Check if a tree is a valid chronogram.*

Description

Check if a tree is a valid chronogram.

Usage

```
is_good_chronogram(phy)
```

Arguments

phy A phylo object.

Value

TRUE if it is a valid tree.

is_n_overlap *Function for computing n-overlap for two vectors of names (ie., phy1\$tip.label, phy2\$tip.label) and seeing if they have n overlap*

Description

This function implements definition 2.8 for n-overlap from Ané et al. (2009) [doi:10.1007/s00026-0090017x](https://doi.org/10.1007/s00026-0090017x).

Usage

```
is_n_overlap(names_1, names_2, n = 2)
```

Arguments

names_1 First vector of names
 names_2 Second vector of names
 n Degree of overlap required

Value

Boolean for whether the degree of overlap was met or not.

References

Ané, C., Eulenstein, O., Piaggio-Talice, R., & Sanderson, M. J. (2009). "Groves of phylogenetic trees". *Annals of Combinatorics*, 13(2), 139-167, [doi:10.1007/s000260090017x](https://doi.org/10.1007/s000260090017x).

make_all_associations *Find all authors and where they have deposited their trees*

Description

Find all authors and where they have deposited their trees

Usage

```
make_all_associations(outputfile = "depositorcache.RData")
```

Arguments

outputfile Path including file name. NULL to prevent saving.

Value

a data.frame of "person" and "urls".

make_bladj_tree *Use the BLADJ algorithm to get a chronogram from a tree topology for which you have age data for some of its nodes.*

Description

The function takes a tree topology and uses the BLADJ algorithm implemented with [phylocomr::ph_bladj\(\)](#) to assign node ages and branch lengths, given a set of fixed node ages and respective node names.

Usage

```
make_bladj_tree(tree = NULL, nodenames = NULL, nodeages = NULL)
```

Arguments

tree A tree either as a newick character string or as a phylo object.
 nodenames A character vector with names of nodes in tree with known ages
 nodeages A numeric vector with the actual ages of named nodes

Details

Input tree can be dated or not, \$edge.length is ignored. Ages given in nodeages are fixed on their corresponding nodes given in nodenames.

Value

A phylo object.

make_bold_otol_tree *Use genetic data from the Barcode of Life Database (BOLD) to reconstruct branch lengths on a tree.*

Description

make_bold_otol_tree takes taxon names from a tree topology or a vector of names to search for genetic markers in the Barcode of Life Database (BOLD), create an alignment, and reconstruct branch lengths on a tree topology with Maximum Likelihood.

Usage

```
make_bold_otol_tree(
  input = c("Rhea americana", "Struthio camelus", "Gallus gallus"),
  marker = "COI",
  otol_version = "v3",
  chronogram = TRUE,
  doML = FALSE,
  aligner = "muscle",
  ...
)
```

Arguments

input	One of the following: A character vector With taxon names as a single comma separated starting or concatenated with <code>c()</code> . A phylogenetic tree with taxon names as tip labels As a phylo or multiPhylo object, OR as a newick character string. A datelifeQuery object An output from <code>make_datelife_query()</code> .
marker	A character vector indicating the gene from BOLD system to be used for branch length estimation.
otol_version	Version of Open Tree of Life to use
chronogram	Default to TRUE, branch lengths returned are estimated with <code>ape::chronompl()</code> . If FALSE, branch lengths returned are estimated with <code>phangorn::acctran()</code> and represent relative substitution rates.
doML	Default to FALSE. If TRUE, it does ML branch length optimization with <code>phangorn::optim.pml()</code> . Only relevant if chronogram = TRUE.
aligner	A character vector indicating whether to use MAFFT or MUSCLE to align BOLD sequences. It is not case sensitive. Default to MUSCLE, supported using the <code>msa</code> package from Bioconductor, which needs to be installed using <code>BiocManager::install()</code> .
...	Arguments passed on to <code>get_otol_synthetic_tree</code>
resolve	Defaults to TRUE. Whether to resolve the tree at random or not.

`ott_ids` If not NULL, it takes this argument and ignores input. A numeric vector of ott ids obtained with `rotl::taxonomy_taxon_info()` or `rotl::tnrs_match_names()` or `tnrs_match()`.

Details

If input is a phylo object or a newick string, it is used as backbone topology. If input is a character vector of taxon names, an induced synthetic OpenTree subtree is used as backbone.

Value

A phylo object. If there are enough BOLD sequences available for the input taxon names, the function returns a tree with branch lengths proportional to relative substitution rate. If not enough BOLD sequences are available for the input taxon names, the function returns the topology given as input, or a synthetic Open Tree of Life for the taxon names given in input, obtained with `get_oto1_synthetic_tree()`.

make_contributor_cache

Create a cache from Open Tree of Life

Description

Create a cache from Open Tree of Life

Usage

```
make_contributor_cache(outputfile = "contributorcache.RData")
```

Arguments

`outputfile` Path including file name

Value

List containing author and curator results

make_datelife_query *Go from taxon names to a datelifeQuery object*

Description

Go from taxon names to a datelifeQuery object

Usage

```
make_datelife_query(
  input = c("Rhea americana", "Pterocnemia pennata", "Struthio camelus"),
  use_tnrs = TRUE,
  get_spp_from_taxon = FALSE,
  taxonomic_source = "ott"
)
```

Arguments

input	Taxon names as one of the following: A character vector of taxon names With taxon names as a single comma separated starting or concatenated with <code>c()</code> . A phylogenetic tree with taxon names as tip labels As a phylo or multiPhylo object, OR as a newick character string.
use_tnrs	Whether to use Open Tree of Life's Taxonomic Name Resolution Service (TNRS) to process input taxon names. Default to TRUE, it corrects misspellings and taxonomic name variations with <code>tnrs_match()</code> , a wrapper of <code>rotl::tnrs_match_names()</code> .
get_spp_from_taxon	Whether to search ages for all species belonging to a given taxon or not. Default to FALSE. If TRUE, it must have same length as input. If input is a newick string with some clades it will be converted to a phylo object, and the order of <code>get_spp_from_taxon</code> will match <code>phy\$tip.label</code> .
taxonomic_source	Used if <code>get_spp_from_taxon = TRUE</code> . A character vector with the desired taxonomic sources. Options are "ott", "ncbi", "gbif" or "irmng". The function defaults to "ott".

Details

It processes phylo objects and newick character string inputs with `input_process()`. If input is a multiPhylo object, only the first phylo element will be used. Similarly, if an input newick character string has multiple trees, only the first one will be used.

Value

A datelifeQuery object, which is a list of three elements:

\$phy A phylo object or NA, if input is not a tree.

\$cleaned_names A character vector of cleaned taxon names.

\$ott_ids A numeric vector of OTT ids if use_tnrs = TRUE, or NULL if use_tnrs = FALSE.

make_mrbayes_runfile *Make a mrBayes run block file with a constraint topology and a set of node calibrations and missing taxa*

Description

Make a mrBayes run block file with a constraint topology and a set of node calibrations and missing taxa

Usage

```
make_mrbayes_runfile(
  constraint = NULL,
  taxa = NULL,
  ncalibration = NULL,
  missing_taxa = NULL,
  age_distribution = "fixed",
  root_calibration = FALSE,
  mrbayes_output_file = "mrbayes_run.nexus"
)
```

Arguments

- | | |
|--------------|--|
| constraint | The constraint tree: a phylo object or a newick character string, with or without branch lengths. |
| taxa | A character vector with taxon names to be maintained in tree |
| ncalibration | The node calibrations: a phylo object with branch lengths proportional to time; in this case all nodes from ncalibration will be used as calibration points. Alternatively, a list with two elements: the first is a character vector with node names from phy to calibrate; the second is a numeric vector with the corresponding ages to use as calibrations. |
| missing_taxa | A tree, a data frame or a vector enlisting all missing taxa you want to include.
A tree Either as a phylo object or as a newick character string. It contains all taxa that you want at the end, both missing and non missing. This tree will be used as a hard constraint.
A data.frame It contains two columns named "taxon" and "clade". The first one contains a character vector of missing taxon names. The second one contains a character or numeric vector of nodes from a constraint tree to which each taxon will be assigned.
A character vector It contains the names of the missing taxa. They will be added at random to the constraint tree. |

age_distribution

A character string specifying the type of calibration. Only "fixed" and "uniform" are implemented for now.

fixed The age given in ncalibration will be used as fixed age.

lognormal The age given in ncalibration will be used as mean age. The standard deviation can be provided. # still need to add this option. By default, a 95 CI sd is used.

uniform The age given in ncalibration will be used as mean age. Where $\text{min_age} = 0.9 * \text{mean age}$, and $\text{max_age} = 1.1 * \text{mean age}$.

root_calibration

Used to set a calibration at the root or not. Default to FALSE. Only relevant if ncalibration is specified.

mrbayes_output_file

A character vector specifying the name of mrBayes run file and outputs (can specify directory too).

Value

A MrBayes block run file in nexus format.

make_mrbayes_tree	<i>Take a constraint tree and use mrBayes to get node ages and branch lengths given a set of node calibrations without any data.</i>
-------------------	--

Description

Take a constraint tree and use mrBayes to get node ages and branch lengths given a set of node calibrations without any data.

Usage

```
make_mrbayes_tree(
  constraint = NULL,
  taxa = NULL,
  ncalibration = NULL,
  missing_taxa = NULL,
  age_distribution = "fixed",
  root_calibration = FALSE,
  mrbayes_output_file = "mrbayes_run.nexus"
)
```

Arguments

constraint	The constraint tree: a phylo object or a newick character string, with or without branch lengths.
taxa	A character vector with taxon names to be maintained in tree

- ncalibration** The node calibrations: a phylo object with branch lengths proportional to time; in this case all nodes from ncalibration will be used as calibration points. Alternatively, a list with two elements: the first is a character vector with node names from phy to calibrate; the second is a numeric vector with the corresponding ages to use as calibrations.
- missing_taxa** A tree, a data frame or a vector enlisting all missing taxa you want to include.
A tree Either as a phylo object or as a newick character string. It contains all taxa that you want at the end, both missing and non missing. This tree will be used as a hard constraint.
A data.frame It contains two columns named "taxon" and "clade". The first one contains a character vector of missing taxon names. The second one contains a character or numeric vector of nodes from a constraint tree to which each taxon will be assigned.
A character vector It contains the names of the missing taxa. They will be added at random to the constraint tree.
- age_distribution** A character string specifying the type of calibration. Only "fixed" and "uniform" are implemented for now.
fixed The age given in ncalibration will be used as fixed age.
lognormal The age given in ncalibration will be used as mean age. The standard deviation can be provided. # still need to add this option. By default, a 95 CI sd is used.
uniform The age given in ncalibration will be used as mean age. Where $\text{min_age} = 0.9 * \text{mean age}$, and $\text{max_age} = 1.1 * \text{mean age}$.
- root_calibration** Used to set a calibration at the root or not. Default to FALSE. Only relevant if ncalibration is specified.
- mrBayes_output_file** A character vector specifying the name of mrBayes run file and outputs (can specify directory too).

Value

A phylo object with branch lengths proportional to time. It saves all mrBayes outputs in the working directory.

make_otol_associations

Associate Open Tree of Life authors with studies

Description

Associate Open Tree of Life authors with studies

Usage

```
make_otol_associations()
```

Value

data.frame with author last name, author first and other names, and comma delimited URLs for OToL studies

make_overlap_table	<i>Create an overlap table</i>
--------------------	--------------------------------

Description

Create an overlap table

Usage

```
make_overlap_table(results_table)
```

Arguments

results_table An "author.results" or "curator.results" data.frame

Value

A data.frame with information on curators and what clades they've worked on

make_sdm	<i>Make a Super Distance Matrix (SDM) from a list of good matrices obtained with get_goodmatrices()</i>
----------	---

Description

Make a Super Distance Matrix (SDM) from a list of good matrices obtained with [get_goodmatrices\(\)](#)

Usage

```
make_sdm(unpadded.matrices, weighting = "flat")
```

Arguments

- unpadded.matrices A list of patristic matrices, a `datelifeResult` object.
- weighting A character vector indicating how much weight to give to each tree in input during the SDM analysis. Options are:
weighting = "flat" All trees have equal weighting.
weighting = "taxa" Weight is proportional to number of taxa.
weighting = "inverse" Weight is proportional to 1 / number of taxa.
 Defaults to `weighting = "flat"`.

Value

A matrix.

make_treebase_associations *Associate TreeBase authors with studies*

Description

Associate TreeBase authors with studies

Usage

```
make_treebase_associations()
```

Value

`data.frame` with author last name, author first and other names, and comma delimited URLs for TreeBase studies

make_treebase_cache *Create a cache from TreeBase*

Description

Create a cache from TreeBase

Usage

```
make_treebase_cache(outputfile = "treebasecache.RData")
```

Arguments

- outputfile Path including file name

Value

List containing author and curator results

map_nodes_ott	<i>Add Open Tree of Life Taxonomy to tree nodes.</i>
---------------	--

Description

Add Open Tree of Life Taxonomy to tree nodes.

Usage

```
map_nodes_ott(tree)
```

Arguments

tree A tree either as a newick character string or as a phylo object.

Value

A phylo object with "nodelabels".

Examples

```
## Not run: # This is a flag for package development. You are welcome to run the example.

# Load the Open Tree chronograms database cached in datelife:
utils::data(opentree_chronograms)

# Get the small chronograms (i.e., chronograms with less than ten tips) to generate a pretty plot:
small <- opentree_chronograms$trees[unlist(sapply(opentree_chronograms$trees, ape::Ntip)) < 10]

# Now, map the Open Tree taxonomy to the nodes of the first tree
phy <- map_nodes_ott(tree = small[[1]])
# and plot it:
# plot_phylo_all(phy)
library(ape)
plot(phy)
nodelabels(phy$node.label)

## End(Not run) #end dontrun
```

 match_all_calibrations

Match calibrations to nodes of a given tree

Description

match_all_calibrations searches a given tree for the most recent common ancestor (mrca) of all taxon name pairs in a datelifeCalibration. It uses `phytools::findMRCA()`.

Usage

```
match_all_calibrations(phy, calibrations)
```

Arguments

`phy` A phylo object.
`calibrations` A calibrations object, an output of `extract_calibrations_phylo()`.

Details

The function takes pairs of taxon names in a secondary calibrations data frame, and looks for them in the vector of tip labels of the tree. If both are present, then it gets the node that represents the most recent common ancestor (mrca) for that pair of taxa in the tree. Nodes of input phy can be named or not.

Value

A list of two elements:

phy A phylo object with nodes renamed with `tree_add_nodelabels()`.

matched_calibrations A matchedCalibrations object, which is the input calibrations object with two additional columns storing results from the mrca search with `phytools::findMRCA()`: `$mrca_node_number` and `$mrca_node_name`.

 matrices_to_table

Go from a list of patristic distance matrix to a table of node ages

Description

Go from a list of patristic distance matrix to a table of node ages

Usage

```
matrices_to_table(matrices)
```

Arguments

matrices A names list of patristic distance matrices. Names correspond to the study reference.

Value

A single data.frame of "taxonA", "taxonB", and "age".

matrix_to_table *Go from a patristic distance matrix to a node ages table*

Description

Go from a patristic distance matrix to a node ages table

Usage

```
matrix_to_table(matrix, reference)
```

Arguments

matrix A patristic distance matrix.
reference A character vector with the study reference from where the ages come from.

Value

A data.frame of "taxonA", "taxonB", and "age".

message_multiplylo *Message for a multiPhylo input*

Description

Message for a multiPhylo input

Usage

```
message_multiplylo()
```

Value

A relevant message as a character string.

missing_taxa_check	<i>Checks that missing_taxa argument is ok to be used by make_mrbayes_runfile inside tree_add_dates functions.</i>
--------------------	--

Description

Checks that missing_taxa argument is ok to be used by make_mrbayes_runfile inside tree_add_dates functions.

Usage

```
missing_taxa_check(missing_taxa = NULL, dated_tree = NULL)
```

Arguments

missing_taxa	<p>A tree, a data frame or a vector enlisting all missing taxa you want to include.</p> <p>A tree Either as a phylo object or as a newick character string. It contains all taxa that you want at the end, both missing and non missing. This tree will be used as a hard constraint.</p> <p>A data.frame It contains two columns named "taxon" and "clade". The first one contains a character vector of missing taxon names. The second one contains a character or numeric vector of nodes from a constraint tree to which each taxon will be assigned.</p> <p>A character vector It contains the names of the missing taxa. They will be added at random to the constraint tree.</p>
dated_tree	a tree (newick or phylo) with branch lengths proportional to absolute time

Value

A phylo object, a newick character string or a dataframe with taxonomic assignments

mrca_calibrations	<i>Identify nodes of a tree topology that are most recent common ancestor (mrca) of taxon pairs from a calibrations object</i>
-------------------	--

Description

mrca_calibrations get nodes of a tree topology given in phy that correspond to the most recent common ancestor (mrca) of taxon pairs given in calibrations. It uses `phytools::findMRCA()` to get mrca nodes.

Usage

```
mrca_calibrations(phy, calibrations)
```

Arguments

- phy** A phylo object.
- calibrations** A calibrations object, an output of `extract_calibrations_phylo()`.

Details

The function takes pairs of taxon names in a calibrations data frame, and looks for them in the vector of tip labels of the tree. If both are present, then it gets the node that represents the most recent common ancestor (mrca) for that pair of taxa in the tree. Nodes of input phy can be named or not. They will be renamed.

Value

A list of two elements:

matched_phy A phylo object with nodes renamed to match results of the mrca search. Nodes are renamed using `tree_add_nodelabels()`.

matched_calibrations A matchedCalibrations object, which is the input calibrations object with two additional columns storing results from the mrca search with `phytools::findMRCA()`: `$mrca_node_number` and `$mrca_node_name`.

opentree_chronograms *Chronogram database*

Description

Now storing >200 chronograms from Open Tree of Life

Usage

```
opentree_chronograms
```

Format

A list of four elements, containing data from Open Tree of Life chronograms

authors A list of lists of author names of the original studies that published chronograms in the Open Tree of Life database.

curators A list of lists of curator names that uploaded chronograms to the Open Tree of Life database.

studies A list of study identifiers.

trees A multiPhylo object storing the chronograms from Open Tree of Life database.

update A character vector indicating the time when the database object was last updated.

version A character vector indicating the datelife `utils::packageVersion()` when the database was last updated.

Details

Generated with devtools::install_github("ropensci/rotl", ref = devtools::github_pull("137")) remotes::install_github("ROpenS opentree_chronograms <- get_opentree_chronograms() opentree_chronograms\$update <- Sys.time() opentree_chronograms\$version <- '2022.01.28' usethis::use_data(opentree_chronograms, overwrite = T, compress = "xz") and updated with update_datelife_cache()

Source

<http://opentreeoflife.org>

patristic_matrix_array_congruify
patristic_matrix_array_congruify is used for patristic_matrix_array_subset_both and patristic_matrix_array_congruify.

Description

patristic_matrix_array_congruify is used for patristic_matrix_array_subset_both and patristic_matrix_array_congruify.

Usage

```
patristic_matrix_array_congruify(
  patristic_matrix_array,
  taxa,
  phy = NULL,
  dating_method = "PATHd8"
)
```

Arguments

patristic_matrix_array A patristic matrix array, rownames and colnames must be taxa.
taxa Vector of taxon names to get a subset for.
phy A user tree to congruify as phylo object (ape).
dating_method The method used for tree dating.

Value

A patristic matrix with ages for the target taxa.

patristic_matrix_array_phylo_congruify

Congruify a patristic matrix array from a given phylo object.

Description

Congruify a patristic matrix array from a given phylo object.

Usage

```
patristic_matrix_array_phylo_congruify(
  patristic_matrix,
  target_tree,
  dating_method = "PATHd8",
  attempt_fix = TRUE
)
```

Arguments

patristic_matrix	A patristic matrix, rownames and colnames must be taxa.
target_tree	A phylo object. Use this in case you want a specific backbone for the output tree.
dating_method	The method used for tree dating.
attempt_fix	Default to TRUE. If congruification results in NA branch lengths, it will attempt to fix them.

Value

A matrix.

patristic_matrix_array_split

Split a patristic matrix array Used inside: patristic_matrix_array_congruify

Description

Split a patristic matrix array Used inside: patristic_matrix_array_congruify

Usage

```
patristic_matrix_array_split(patristic_matrix_array)
```

Arguments

`patristic_matrix_array`
A patristic matrix array, rownames and colnames must be taxa.

Value

A patristic matrix 3d array.

`patristic_matrix_array_subset`
Subset a patristic matrix array

Description

Subset a patristic matrix array

Usage

```
patristic_matrix_array_subset(patristic_matrix_array, taxa, phy4 = NULL)
```

Arguments

`patristic_matrix_array`
A patristic matrix array, rownames and colnames must be taxa.

`taxa`
Vector of taxon names to get a subset for.

`phy4`
A user tree to congruify in phylo4 format (phylobase).

Value

A list with a patristic matrix array and a \$problem if any.

`patristic_matrix_array_subset_both`
Are all desired taxa in the patristic matrix array?

Description

`patristic_matrix_array_subset_both` is used inside [get_subset_array_dispatch\(\)](#).

Usage

```
patristic_matrix_array_subset_both(  
  patristic_matrix_array,  
  taxa,  
  phy = NULL,  
  phy4 = NULL,  
  dating_method = "PATHd8"  
)
```

Arguments

<code>patristic_matrix_array</code>	A patristic matrix array, rownames and colnames must be taxa.
<code>taxa</code>	Vector of taxon names to get a subset for.
<code>phy</code>	A user tree to congruify as phylo object (ape).
<code>phy4</code>	A user tree to congruify in phylo4 format (phylobase).
<code>dating_method</code>	The method used for tree dating.

Value

A patristic matrix with ages for the target taxa.

`patristic_matrix_list_to_array`
Convert list of patristic matrices to a 3D array.

Description

`patristic_matrix_list_to_array` is used inside [summarize_datelife_result\(\)](#), [patristic_matrix_array_congruify](#)

Usage

```
patristic_matrix_list_to_array(patristic_matrix_list, pad = TRUE)
```

Arguments

<code>patristic_matrix_list</code>	List of patristic matrices
<code>pad</code>	If TRUE, pad missing entries

Value

A 3d array of patristic matrices

patristic_matrix_MRCA *Get time of MRCA from patristic matrix. Used in [datelife_result_MRCA\(\)](#).*

Description

Get time of MRCA from patristic matrix. Used in [datelife_result_MRCA\(\)](#).

Usage

```
patristic_matrix_MRCA(patristic_matrix, na_rm = TRUE)
```

Arguments

patristic_matrix
A patristic matrix (aka a datelifeResult object of length 1)

na_rm
If TRUE, it drops rows containing NAs from the datelifeResult patristic matrix; if FALSE, it returns NA where there are missing entries.

Value

The depth of the MRCA as a numeric vector.

patristic_matrix_name_order_test
Test the name order of a patristic matrix so that row and column labels are in alphabetical order.

Description

patristic_matrix_name_order_test is only used in [patristic_matrix_list_to_array\(\)](#).

Usage

```
patristic_matrix_name_order_test(  
  patristic_matrix,  
  standard.rownames,  
  standard.colnames  
)
```

Arguments

patristic_matrix
A patristic matrix, rownames and colnames must be taxa.

standard.rownames
A character vector of row names.

standard.colnames
A character vector of column names.

Value

Boolean.

patristic_matrix_name_reorder

Reorder a matrix so that row and column labels are in alphabetical order.

Description

patristic_matrix_name_reorder is only used in: [patristic_matrix_pad\(\)](#).

Usage

```
patristic_matrix_name_reorder(patristic_matrix)
```

Arguments

patristic_matrix

A patristic matrix, rownames and colnames must be taxa.

Value

A patristic matrix with row and column names for taxa in alphabetical order.

patristic_matrix_pad *Fill in empty cells in a patristic matrix for missing taxa.*

Description

Used in: [patristic_matrix_list_to_array\(\)](#).

Usage

```
patristic_matrix_pad(patristic_matrix, all_taxa)
```

Arguments

patristic_matrix

A patristic matrix, rownames and colnames must be taxa.

all_taxa

A vector of names of all taxa you want, including ones not in the patristic matrix.

Value

A patristic matrix, with NA for entries between taxa where at least one was not in the original patristic matrix.

`patristic_matrix_taxa_all_matching`*Are all desired taxa in the patristic matrix?*

Description

`patristic_matrix_taxa_all_matching` is used inside: [results_list_process\(\)](#).

Usage

```
patristic_matrix_taxa_all_matching(patristic_matrix, taxa)
```

Arguments

`patristic_matrix`

A patristic matrix, rownames and colnames must be taxa.

`taxa`

Vector of taxon names to get a subset for.

Value

A Boolean.

`patristic_matrix_to_newick`*Convert patristic matrix to a newick string. Used inside: summarize_datelife_result.*

Description

Convert patristic matrix to a newick string. Used inside: `summarize_datelife_result`.

Usage

```
patristic_matrix_to_newick(patristic_matrix)
```

Arguments

`patristic_matrix`

A patristic matrix

Value

A newick string

patristic_matrix_to_phylo

Convert a patristic matrix to a phylo object.

Description

Function `patristic_matrix_to_phylo` is used inside `summarize_datelife_result()`.

Usage

```
patristic_matrix_to_phylo(
  patristic_matrix,
  clustering_method = "nj",
  fix_negative_brlen = TRUE,
  fixing_method = 0,
  ultrametric = TRUE,
  variance_matrix = NULL
)
```

Arguments

<code>patristic_matrix</code>	A patristic matrix
<code>clustering_method</code>	A character vector indicating the method to construct the tree. Options are: nj Neighbor-Joining method applied with <code>ape::nj()</code> . upgma Unweighted Pair Group Method with Arithmetic Mean method applied with <code>phangorn::upgma()</code> . bionj An improved version of the Neighbor-Joining method applied with <code>ape::bionj()</code> . triangle Triangles method applied with <code>ape::triangMtd()</code> mvr Minimum Variance Reduction method applied with <code>ape::mvr()</code> .
<code>fix_negative_brlen</code>	Boolean indicating whether to fix negative branch lengths in resulting tree or not. Default to TRUE.
<code>fixing_method</code>	A character vector specifying the method to fix branch lengths: "bladj", "mr-bayes" or a number to be assigned to all branches meeting <code>fixing_criterion</code>
<code>ultrametric</code>	Boolean indicating whether to force ultrametric or not.
<code>variance_matrix</code>	A variance matrix from a <code>datelifeResult</code> object, usually an output from <code>datelife_result_variance_</code> . Only used if <code>clustering_method = "mvr"</code> .

Details

We might add the option to insert a function as `clustering_method` in the future. Before, we had hard-coded the function to try Neighbor-Joining (NJ) first; if it errors, it will try UPGMA. Now, it uses NJ for a "phylo_all" summary, and we are using our own algorithm to get a tree from a summary matrix.

Value

A rooted phylo object.

patristic_matrix_unpad

Function to remove missing taxa from a datelifeResult object.

Description

Used in [datelife_result_sdm_phylo\(\)](#).

Usage

```
patristic_matrix_unpad(patristic_matrix)
```

Arguments

patristic_matrix

A patristic matrix with row and column names for taxa

Value

patristic_matrix for all_taxa

phylo_check

Checks if phy is a phylo object and/or a chronogram.

Description

Checks if phy is a phylo object and/or a chronogram.

Usage

```
phylo_check(phy = NULL, brlen = FALSE, dated = FALSE)
```

Arguments

phy A phylo object.

brlen Boolean. If TRUE it checks if phylo object has branch lengths.

dated Boolean. If TRUE it checks if phylo object is ultrametric.

Value

Nothing

phylo_congruify	<i>Congruify a reference tree and a target tree given as phylo objects.</i>
-----------------	---

Description

Congruify a reference tree and a target tree given as phylo objects.

Usage

```
phylo_congruify(  
  reference_tree,  
  target_tree,  
  dating_method = "PATHd8",  
  attempt_fix = TRUE  
)
```

Arguments

reference_tree	A phylo object.
target_tree	A phylo object. Use this in case you want a specific backbone for the output tree.
dating_method	The method used for tree dating.
attempt_fix	Default to TRUE. If congruification results in NA branch lengths, it will attempt to fix them.

Value

A matrix.

phylo_generate_uncertainty	<i>Generate uncertainty in branch lengths using a lognormal.</i>
----------------------------	--

Description

Generate uncertainty in branch lengths using a lognormal.

Usage

```

phylo_generate_uncertainty(
  phy,
  size = 100,
  uncertainty_method = "other",
  age_distribution = "uniform",
  age_sd = NULL,
  age_var = 0.1,
  age_scale = 0,
  alpha = 0.025,
  rescale = TRUE
)

```

Arguments

phy	A phylo object.
size	A numeric vector indicating the number of samples to be generated.
uncertainty_method	A character vector specifying the method to generate uncertainty. <code>mrBayes</code> is default.
age_distribution	A character string specifying the type of calibration. Only "fixed" and "uniform" are implemented for now. fixed The age given in <code>ncalibration</code> will be used as fixed age. lognormal The age given in <code>ncalibration</code> will be used as mean age. The standard deviation can be provided. # still need to add this option. By default, a 95 CI sd is used. uniform The age given in <code>ncalibration</code> will be used as mean age. Where <code>min_age</code> = 0.9 * mean age, and <code>max_age</code> = 1.1 * mean age.
age_sd	The standard deviation around the age to use for generating the uncertainty. If not a numeric value, <code>var</code> will be used to calculate it.
age_var	The variance to calculate <code>age_sd</code> and generate uncertainty.
age_scale	How to scale <code>sd</code> by the depth of the node. If 0, same <code>sd</code> for all. If not, older nodes have more uncertainty
alpha	The significance level on uncertainty to generate. By default 0.025
rescale	Boolean. If true, observed age will be rescaled each round.

Details

If you want to change the size of sampled trees you do not need to run `mrBayes` again. Just use `sample_trees("mrBayes_trees_file_directory", size = new_size)` and you will get a `multiPhylo` object with a new tree sample.

Value

A phylo or `multiPhylo` object with the same topology as `phy` but different branch lengths

Examples

```
## Not run:
# Generate uncertainty over feline species SDM chronogram.
# Load the data:

data(felid_sdm)

# By default, generates a sample of 100 trees with var = 0.1:

unc <- phylo_generate_uncertainty(felid_sdm$phy)
length(unc)

# Make an LTT plot:

max_age <- max(sapply(unc, ape::branching.times))
ape::ltt.plot(phy = unc[[1]], xlim = c(-max_age, 0), col = "#cce5ff50")
for (i in 2:100) {
  ape::ltt.lines(phy = unc[[i]], col = "#cce5ff50")
}
ape::ltt.lines(felid_sdm$phy, col = "red")
title(c("fake uncertainty", "in Felidae SDM chronogram"))

## End(Not run) # end dontrun
```

phylo_get_node_numbers

Gets node numbers from any phylogeny

Description

Gets node numbers from any phylogeny

Usage

```
phylo_get_node_numbers(phy)
```

Arguments

phy A phylo object.

Value

A numeric vector with node numbers

`phylo_get_subset_array`*Get a subset array from a phylo object*

Description

Get a subset array from a phylo object

Usage

```
phylo_get_subset_array(  
  reference_tree,  
  taxa,  
  phy4 = NULL,  
  dating_method = "PATHd8"  
)
```

Arguments

`reference_tree` A phylo object.
`taxa` Vector of taxon names to get a subset for.
`phy4` A user tree to congruify in phylo4 format (phylobase).
`dating_method` The method used for tree dating.

Value

A list with a patristic matrix array and a \$problem if any.

`phylo_get_subset_array_congruify`*Get a congruified subset array from a phylo object*

Description

Get a congruified subset array from a phylo object

Usage

```
phylo_get_subset_array_congruify(  
  reference_tree,  
  taxa,  
  phy = NULL,  
  dating_method = "PATHd8"  
)
```

Arguments

reference_tree A phylo object.
 taxa Vector of taxon names to get a subset for.
 phy A user tree to congruify as phylo object (ape).
 dating_method The method used for tree dating.

Value

A list with a patristic matrix array and a \$problem if any.

phylo_has_brlen *Check if a tree has branch lengths*

Description

Check if a tree has branch lengths

Usage

phylo_has_brlen(phy)

Arguments

phy A phylo object.

Value

A TRUE or FALSE

phylo_prune_missing_taxa
*Prune missing taxa from a phylo object Used inside
 phylo_get_subset_array and phylo_get_subset_array_congruify.*

Description

Prune missing taxa from a phylo object Used inside phylo_get_subset_array and phylo_get_subset_array_congruify.

Usage

phylo_prune_missing_taxa(phy, taxa)

Arguments

phy A user tree to congruify as phylo object (ape).
 taxa Vector of taxon names to get a subset for.

Value

A phylo object.

phylo_subset_both *Subset a reference and a target tree given as phylo objects.*

Description

Subset a reference and a target tree given as phylo objects.

Usage

```
phylo_subset_both(
  reference_tree,
  taxa,
  phy = NULL,
  phy4 = NULL,
  dating_method = "PATHd8"
)
```

Arguments

reference_tree A phylo object.
 taxa Vector of taxon names to get a subset for.
 phy A user tree to congruify as phylo object (ape).
 phy4 A user tree to congruify in phylo4 format (phylobase).
 dating_method The method used for tree dating.

Value

A list with a patristic matrix array and a \$problem if any.

phylo_tiplabel_space_to_underscore

Convert spaces to underscores in trees.

Description

phylo_tiplabel_space_to_underscore is used in: [make_mrbayes_runfile\(\)](#), [tree_get_singleton_outgroup\(\)](#), [congruify_and_check\(\)](#), [patristic_matrix_array_phylo_congruify\(\)](#).

Usage

```
phylo_tiplabel_space_to_underscore(phy)
```

Arguments

phy A phylo object.

Value

A phylo object.

phylo_tiplabel_underscore_to_space

Convert underscores to spaces in trees.

Description

phylo_tiplabel_underscore_to_space is used inside [patristic_matrix_array_phylo_congruify\(\)](#), [congruify_and_check\(\)](#).

Usage

```
phylo_tiplabel_underscore_to_space(phy)
```

Arguments

phy A phylo object.

Value

A phylo object.

 phylo_to_patristic_matrix

Get a patristic matrix from a phylo object.

Description

Get a patristic matrix from a phylo object.

Usage

```
phylo_to_patristic_matrix(phy, test = TRUE, tol = 0.01, option = 2)
```

Arguments

phy	A phylo object.
test	Default to TRUE. Whether to test if phy has branch lengths and is ultrametric or not.
tol	branching time in reference above which secondary constraints will be applied to target
option	an integer (1 or 2; see details).

Value

A patristic matrix.

 pick_grove

Pick a grove in the case of multiple groves in a set of trees.

Description

Pick a grove in the case of multiple groves in a set of trees.

Usage

```
pick_grove(grove_list, criterion = "taxa", datelife_result)
```

Arguments

grove_list	A list of vectors of tree indices. Each element is a grove.
criterion	Defaults to criterion = "taxa". Used for chronogram summarizing, i.e., obtaining a single summary chronogram from a group of input chronograms. For summarizing approaches that return a single summary tree from a group of phylogenetic trees, it is necessary that the latter form a grove, roughly, a sufficiently overlapping set of taxa between trees, see Ané et al. (2009) doi:10.1007/s00026-0090017x . In rare cases, a group of trees can have multiple groves. This argument indicates whether to get the grove with the most trees (criterion = "trees") or the most taxa (criterion = "taxa").

datelife_result

A datelifeResult object. Only needed for criterion = "taxa".

Value

A numeric vector of the elements of the picked grove.

plant_bold_otol_tree *Some plants chronogram*

Description

Some plants chronogram

Usage

```
plant_bold_otol_tree
```

Format

A phylo object with 6 tips and 5 internal nodes

edge Integer vector with edge (branch) numbers

tip.label Character vector with species names of plants

Nnode Integer vector with the number of nodes

node.label Character vector with node names

edge.length Numeric vector with edge (branch) lengths

Details

Generated with `make_bold_otol_tree(input = "(Zea mays,Oryza sativa),((Arabidopsis thaliana,(Glycine max,Medicago sativa)),Solanum lycopersicum)Pentapetalae;") usethis::use_data(plant_bold_otol_tree)`

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Source

<http://opentreeoflife.org>

<http://www.boldsystems.org>

problems	<i>Problematic chronograms from Open Tree of Life.</i>
----------	--

Description

Problematic chronograms from Open Tree of Life.

Usage

```
problems
```

Format

A list of trees with unmapped taxa

Details

Before we developed tools to clean and map tip labels for our cached trees we found some trees that were stored with unmapped tip labels we extracted them and saved them to be used for testing functions. Generated with `problems <- opentree_chronograms$trees[sapply(sapply(opentree_chronograms$trees, "[", "tip.label"), function(x) any(grepl("not.mapped", x)))]` `usethis::use_data(problems)` opentree_chronograms object from commit <https://github.com/phyloTastic/datelife/tree/be894448f6fc437241cd0916fab45e84ac3e09c6> `[", "tip.label"), function(x) any(grepl("not.mapped", x)))]`: R:%22,%20%22tip.label%22),%20function(x)%20any(grepl(%22

Source

<http://opentreeoflife.org>

recover_mrcaott	<i>Get an mrcaott tag from an OpenTree induced synthetic tree and get its name and ott id</i>
-----------------	---

Description

Get an mrcaott tag from an OpenTree induced synthetic tree and get its name and ott id

Usage

```
recover_mrcaott(tag)
```

Arguments

tag A character vector with the mrca tag

Value

A numeric vector with ott id from original taxon named with the corresponding ott name

relevant_curators_tabulate

Return the relevant curators for a set of studies.

Description

Return the relevant curators for a set of studies.

Usage

```
relevant_curators_tabulate(results.index, cache = "opentree_chronograms")
```

Arguments

`results.index` A vector from [datelife_result_study_index\(\)](#) with the indices of the relevant studies.

`cache` The cached chronogram database.

Value

A vector with counts of each curator, with names equal to curator names.

results_list_process *Take results_list and process it.*

Description

results_list_process is used inside: [get_datelife_result\(\)](#)

Usage

```
results_list_process(results_list, taxa = NULL, partial = FALSE)
```

Arguments

`results_list` A list returned from using [get_subset_array_dispatch\(\)](#) on `opentree_chronograms$trees`

`taxa` Vector of taxon names to get a subset for.

`partial` If TRUE, return matrices that have only partial matches.

Value

A list with the patristic.matrices that are not NA.

run	<i>Core function to generate results</i>
-----	--

Description

Core function to generate results

Usage

```
run(
  input = c("Rhea americana", "Pterocnemia pennata", "Struthio camelus"),
  format = "citations",
  partial = "yes",
  plot.width = 600,
  plot.height = 600,
  use_tnrs = "no",
  opentree_chronograms = NULL
)
```

Arguments

input	A newick string or vector of taxa
format	The output format
partial	How to deal with trees that have a subset of taxa in the query
plot.width	Width in pixels for output plot
plot.height	Height in pixels for output plot
use_tnrs	Whether to use OpenTree's TNRS for the input
opentree_chronograms	The list of lists containing the input trees and other info

Value

results in the desired format

run_mrbayes	<i>Runs MrBayes from R</i>
-------------	----------------------------

Description

Runs MrBayes from R

Usage

```
run_mrbayes(mrbayes_output_file = NULL)
```

Arguments

mrBayes_output_file

A character vector specifying the name of mrBayes run file and outputs (can specify directory too).

Value

A phylo object with the consensus tree. MrBayes output files are stored in the working directory.

sample_trees	<i>Sample trees from a file containing multiple trees. Usually from a bayesian analysis output trees file.</i>
--------------	--

Description

Sample trees from a file containing multiple trees. Usually from a bayesian analysis output trees file.

Usage

```
sample_trees(trees_file, trees_object = NULL, burnin = 0.25, size = 100)
```

Arguments

trees_file A character vector indicating the name and directory of file with trees to sample.

trees_object An R object containing a list of trees already read into R from a tree file from a bayesian analysis output.

burnin A numeric vector indicating the burnin fraction. It should be a number between 0 and 1. Default to 0.25

size A numeric vector indicating the number of samples to be generated.

Value

A multiPhylo object with a random sample of trees.

some_ants_datelife_result
datelifeResult object of some ants

Description

datelifeResult object of some ants

Usage

```
some_ants_datelife_result
```

Format

A list of one element, containing a named patristic matrix

Details

Generated with:

```
some_ants_input <- "(Aulacopone_relicta,(((Myrmecia_gulosa,(Aneuretus_simoni,Dolichoderus_mariae))),
some_ants_datelife_query <- make_datelife_query(input = some_ants_input) some_ants_datelife_result
<- get_datelife_result(input = some_ants_datelife_query) usethis::use_data(some_ants_datelife_result)
```

Source

<http://opentreeoflife.org>

subset2_search *A list with datelifeQuery and datelifeResult objects from a search of taxon names from subset2_taxa*

Description

A list with datelifeQuery and datelifeResult objects from a search of taxon names from subset2_taxa

Usage

```
subset2_search
```

Format

A list with two named elements. datelifeResult object with 24 patristic matrices

datelife_query A datelifeQuery object using names_subset 2 as input.

datelife_result A datelifeResult object resulting from a search of names in datelifeQuery

Details

Generated with: `datelife_query <- make_datelife_query(subset2_taxa) datelife_result <- get_datelife_result(datelife_query)`
`subset2_search <- list(query = datelife_query, result = datelife_result) usethis::use_data(subset2_search,`
`overwrite = TRUE)`

subset2_taxa	<i>Long list of >2.7k virus, bacteria, plant and animal taxon names</i>
--------------	--

Description

Long list of >2.7k virus, bacteria, plant and animal taxon names

Usage

```
subset2_taxa
```

Format

A character vector of length 2778

Details

Generated with: `subset2_taxa <- rphylostatic::url_get_scientific_names("https://github.com/phylostatic/rphylostatic/blob/main/phylostatic/tests/testthat/testthat.R")`
`usethis::use_data(subset2_taxa)`

Source

<https://github.com/phylostatic/rphylostatic/tree/master/tests/testthat>

summarize_congruifiedCalibrations	<i>Get summary statistics of ages in a congruifiedCalibrations object.</i>
-----------------------------------	--

Description

Function `summarize_congruifiedCalibrations` returns a table of summary statistic for each node in `congruified_calibrations` argument.

Usage

```
summarize_congruifiedCalibrations(congruified_calibrations, age_column)
```

Arguments

- `congruified_calibrations` A `congruifiedCalibrations` object, output of `congruify_and_mrca_multiPhylo()`.
- `age_column` A character string indicating the name of the column to be summarized.

Value

A `data.frame` of summarized ages.

`summarize_datelife_result`

Summarize a `datelifeResult` object.

Description

Get different types of summaries from a `datelifeResult` object, an output from `get_datelife_result()`. This allows rapid processing of data. If you need a list of chronograms from your `datelifeResult` object, this is the function you are looking for.

Usage

```
summarize_datelife_result(
  datelife_result = NULL,
  datelife_query = NULL,
  summary_format = "phylo_all",
  na_rm = TRUE,
  summary_print = c("citations", "taxa"),
  taxon_summary = c("none", "summary", "matrix"),
  criterion = "taxa"
)
```

Arguments

- `datelife_result` A `datelifeResult` object, usually an output of `get_datelife_result()`.
- `datelife_query` A `datelifeQuery` object, usually an output of `make_datelife_query()`.
- `summary_format` A character vector of length one, indicating the output format for results of the `DateLife` search. Available output formats are:
- "citations"** A character vector of references where chronograms with some or all of the target taxa are published (source chronograms).
 - "mrca"** A named numeric vector of most recent common ancestor (mrca) ages of target taxa defined in input, obtained from the source chronograms. Names of mrca vector are equal to citations.
 - "newick_all"** A named character vector of newick strings corresponding to target chronograms derived from source chronograms. Names of newick_all vector are equal to citations.

	<p>"newick_sdm" Only if multiple source chronograms are available. A character vector with a single newick string corresponding to a target chronogram obtained with SDM supertree method (Criscuolo et al. 2006).</p> <p>"newick_median" Only if multiple source chronograms are available. A character vector with a single newick string corresponding to a target chronogram from the median of all source chronograms.</p> <p>"phylo_sdm" Only if multiple source chronograms are available. A phylo object with a single target chronogram obtained with SDM supertree method (Criscuolo et al. 2006).</p> <p>"phylo_median" Only if multiple source chronograms are available. A phylo object with a single target chronogram obtained from source chronograms with median method.</p> <p>"phylo_all" A named list of phylo objects corresponding to each target chronogram obtained from available source chronograms. Names of phylo_all list correspond to citations.</p> <p>"phylo_biggest" The chronogram with the most taxa. In the case of a tie, the chronogram with clade age closest to the median age of the equally large trees is returned.</p> <p>"html" A character vector with an html string that can be saved and then opened in any web browser. It contains a 4 column table with data on target taxa: mrca, number of taxa, citations of source chronogram and newick target chronogram.</p> <p>"data_frame" A 4 column data.frame with data on target taxa: mrca, number of taxa, citations of source chronograms and newick string.</p>
na_rm	If TRUE, it drops rows containing NAs from the datelifeResult patristic matrix; if FALSE, it returns NA where there are missing entries.
summary_print	<p>A character vector specifying the type of summary information to be printed to screen. Options are:</p> <p>"citations" Prints references of chronograms where target taxa are found.</p> <p>"taxa" Prints a summary of the number of chronograms where each target taxon is found.</p> <p>"none" Nothing is printed to screen.</p> <p>Defaults to c("citations", "taxa"), which displays both.</p>
taxon_summary	A character vector specifying if data on target taxa missing in source chronograms should be added to the output as a "summary" or as a presence/absence "matrix". Default to "none", no information on taxon_summary added to the output.
criterion	Defaults to criterion = "taxa". Used for chronogram summarizing, i.e., obtaining a single summary chronogram from a group of input chronograms. For summarizing approaches that return a single summary tree from a group of phylogenetic trees, it is necessary that the latter form a grove, roughly, a sufficiently overlapping set of taxa between trees, see Ané et al. (2009) doi:10.1007/s00026-0090017x . In rare cases, a group of trees can have multiple groves. This argument indicates whether to get the grove with the most trees (criterion = "trees") or the most taxa (criterion = "taxa").

Value

The output is determined by the argument `summary_format`:

- If** `summary_format = "citations"` The function returns a character vector of references.
- If** `summary_format = "mrca"` The function returns a named numeric vector of most recent common ancestor (mrca) ages.
- If** `summary_format = "newick_[all, sdm, or median]"` The function returns output chronograms as newick strings.
- If** `summary_format = "phylo_[all, sdm, median, or biggest]"` The function returns output chronograms as phylo or multiPhylo objects.
- If** `summary_format = "html" or "data_frame"` The function returns a 4 column table with data on mrca ages, number of taxa, references, and output chronograms as newick strings.

References

Ané, C., Eulenstein, O., Piaggio-Talice, R., & Sanderson, M. J. (2009). "Groves of phylogenetic trees". *Annals of Combinatorics*, 13(2), 139-167, [doi:10.1007/s000260090017x](https://doi.org/10.1007/s000260090017x).

`summarize_fossil_range`

Summarize taxon age from PBDB to just a single min and max age

Description

This uses the Paleobiology Database's API to gather information on the ages for all specimens of a taxon. It will also look for all descendants of the taxon. It fixes name misspellings if possible. It is basically a wrapper for `get_fossil_range`.

Usage

```
summarize_fossil_range(taxon, recent = FALSE, assume_recent_if_missing = TRUE)
```

Arguments

<code>taxon</code>	The scientific name of the taxon you want the range of occurrences of
<code>recent</code>	If TRUE, forces the minimum age to be zero
<code>assume_recent_if_missing</code>	If TRUE, any taxon missing from pbdb is assumed to be recent

Value

a single row `data.frame` of `max_ma` and `min_ma` for the specimens, with `rowname` equal to `taxon` input

```
summarize_summary_matrix
```

Gets all ages per taxon pair from a distance matrix Internal function used in `summary_matrix_to_phylo_all()`.

Description

Gets all ages per taxon pair from a distance matrix Internal function used in `summary_matrix_to_phylo_all()`.

Usage

```
summarize_summary_matrix(summ_matrix)
```

Arguments

`summ_matrix` Any summary patristic distance matrix, such as the ones obtained with `datelife_result_sdm_matrix()` or `datelife_result_median_matrix()`.

Value

A data.frame of pairwise ages, with row number equal to the combinatory of column names (or row names), estimated as $\text{ncol}(\text{summ_matrix})^2 - \text{sum}(1:(\text{ncol}(\text{summ_matrix})-1))$.

```
summary.datelifeResult
```

Summarize a datelifeResult object.

Description

Summarize a datelifeResult object.

Usage

```
## S3 method for class 'datelifeResult'
summary(object, datelife_query, na_rm = TRUE, ...)
```

Arguments

`object` An object of class `datelifeResult`, usually an output of `get_datelife_result()`.
`datelife_query` A `datelifeQuery` object, usually an output of `make_datelife_query()`.
`na_rm` Default to TRUE, whether to include partial matches or not.
`...` Further arguments passed to or from other methods.

Value

A named list of 11 elements:

- "citations"** A character vector of references where chronograms with some or all of the target taxa are published (source chronograms).
- "mrca"** A named numeric vector of most recent common ancestor (mrca) ages of target taxa defined in input, obtained from the source chronograms. Names of mrca vector are equal to citations.
- "newick_all"** A named character vector of newick strings corresponding to target chronograms derived from source chronograms. Names of newick_all vector are equal to citations.
- "newick_sdm"** Only if multiple source chronograms are available. A character vector with a single newick string corresponding to a target chronogram obtained with SDM supertree method (Criscuolo et al. 2006).
- "newick_median"** Only if multiple source chronograms are available. A character vector with a single newick string corresponding to a target chronogram from the median of all source chronograms.
- "phylo_sdm"** Only if multiple source chronograms are available. A phylo object with a single target chronogram obtained with SDM supertree method (Criscuolo et al. 2006).
- "phylo_median"** Only if multiple source chronograms are available. A phylo object with a single target chronogram obtained from source chronograms with median method.
- "phylo_all"** A named list of phylo objects corresponding to each target chronogram obtained from available source chronograms. Names of phylo_all list correspond to citations.
- "phylo_biggest"** The chronogram with the most taxa. In the case of a tie, the chronogram with clade age closest to the median age of the equally large trees is returned.
- "html"** A character vector with an html string that can be saved and then opened in any web browser. It contains a 4 column table with data on target taxa: mrca, number of taxa, citations of source chronogram and newick target chronogram.
- "data_frame"** A 4 column data.frame with data on target taxa: mrca, number of taxa, citations of source chronograms and newick string.

summary.matchedCalibrations

*Summarize a matchedCalibrations object
summary.matchedCalibrations gets the node age distribution
from a matchedCalibrations object.*

Description

Summarize a matchedCalibrations object summary.matchedCalibrations gets the node age distribution from a matchedCalibrations object.

Usage

```
## S3 method for class 'matchedCalibrations'  
summary(object, ...)
```

Arguments

object A matchedCalibrations object, usually an element of the output of `match_all_calibrations()`.
 ... Further arguments passed to or from other methods.

Details

Columns `in_phy$mrca_node_name` and `in_phy$reference` are factors.

Value

A `summaryMatchedCalibrations` object, which is a list of two `matchedCalibrations` objects:

not_in_phy A `data.frame` subset of input `matchedCalibrations` object containing taxon name pairs that were not present in the given tree. NULL if all input taxon names are found in the given tree.

in_phy A `data.frame` subset of input `matchedCalibrations` object containing all taxon name pairs that were present in the given tree.

summary_matrix_to_phylo

Go from a summary matrix to an ultrametric phylo object.

Description

Go from a summary matrix to an ultrametric phylo object.

Usage

```
summary_matrix_to_phylo(
  summ_matrix,
  datelife_query = NULL,
  target_tree = NULL,
  total_distance = TRUE,
  use = "mean",
  ...
)
```

Arguments

`summ_matrix` Any summary patristic distance matrix, such as the ones obtained with `datelife_result_sdm_matrix()` or `datelife_result_median_matrix()`.

`datelife_query` A `datelifeQuery` object, usually an output of `make_datelife_query()`.

`target_tree` A phylo object. Use this in case you want a specific backbone for the output tree.

total_distance	Whether the input <code>summ_matrix</code> stores total age distance (from tip to tip) or distance from node to tip. Default to <code>TRUE</code> , divides the matrix in half, if <code>FALSE</code> it will take it as is.
use	A character vector indicating what type of age to use for summary tree. One of the following: "mean" It will use the <code>mean()</code> of the node ages in <code>summ_matrix</code> . "median" It uses the <code>stats::median()</code> age of node ages in <code>summ_matrix</code> . "min" It will use the <code>min()</code> age from node ages in <code>summ_matrix</code> . "max" Choose this if you wanna be conservative; it will use the <code>max()</code> age from node ages in <code>summ_matrix</code> . "midpoint" It will use the mean of minimum age and maximum age.
...	Arguments passed on to <code>summary_matrix_to_phylo_all</code>

Details

It can take a regular patristic distance matrix, but there are simpler methods for that implemented in `patristic_matrix_to_phylo()`.

Value

An ultrametric phylo object.

`summary_matrix_to_phylo_all`

Get minimum, median, mean, midpoint, and maximum summary chronograms from a summary matrix of a `datelifeResult` object.

Description

Get minimum, median, mean, midpoint, and maximum summary chronograms from a summary matrix of a `datelifeResult` object.

Usage

```
summary_matrix_to_phylo_all(
  summ_matrix,
  datelife_query = NULL,
  target_tree = NULL,
  total_distance = TRUE,
  ...
)
```

Arguments

summ_matrix	Any summary patristic distance matrix, such as the ones obtained with <code>datelife_result_sdm_matrix()</code> or <code>datelife_result_median_matrix()</code> .
datelife_query	A <code>datelifeQuery</code> object, usually an output of <code>make_datelife_query()</code> .
target_tree	A phylo object. Use this in case you want a specific backbone for the output tree.
total_distance	Whether the input <code>summ_matrix</code> stores total age distance (from tip to tip) or distance from node to tip. Default to TRUE, divides the matrix in half, if FALSE it will take it as is.
...	Arguments passed on to <code>get_otol_synthetic_tree</code>
otol_version	Version of Open Tree of Life to use
resolve	Defaults to TRUE. Whether to resolve the tree at random or not.
input	Optional. A character vector of names or a <code>datelifeQuery</code> object.
ott_ids	If not NULL, it takes this argument and ignores <code>input</code> . A numeric vector of ott ids obtained with <code>rotl::taxonomy_taxon_info()</code> or <code>rotl::tnrs_match_names()</code> or <code>tnrs_match()</code> .

Details

With this function users can choose the minimum, mean or maximum ages from the summary matrix as calibration points to get a single summary chronogram. Users get all three summary chronograms in a `multiPhylo` object.

Value

A `multiPhylo` object of length 5. It contains min, mean, median, midpoint, and max summary chronograms.

summary_patristic_matrix_array

Summarize patristic matrix array (by default, median). Used inside: summarize_datelife_result.

Description

Summarize patristic matrix array (by default, median). Used inside: `summarize_datelife_result`.

Usage

```
summary_patristic_matrix_array(patristic_matrix_array, fn = stats::median)
```

Arguments

patristic_matrix_array	3D array of patristic matrices
fn	The function to use to summarize

Value

A 2d array with the median (or max, or mean, etc) of the input array

threebirds_dr	<i>datelifeResult object of three birds "Rhea americana", "Pterocnemia pennata", and "Struthio camelus"</i>
---------------	---

Description

datelifeResult object of three birds "Rhea americana", "Pterocnemia pennata", and "Struthio camelus"

Usage

```
threebirds_dr
```

Format

A list of 9 named patristic matrix

Details

Generated with: `threebirds_dr <- get_datelife_result(input=c("Rhea americana", "Pterocnemia pennata", "Struthio camelus"), partial = TRUE, use_tnrs = FALSE, approximate_match = TRUE, cache = "opentree_chronograms") use_data(threebirds_dr)`

Source

<http://opentreeoflife.org>

tnrs_match	<i>Taxon name resolution service (tnrs) applied to a vector of names by batches</i>
------------	---

Description

Taxon name resolution service (tnrs) applied to a vector of names by batches

Usage

```
tnrs_match(input, reference_taxonomy, tip, ...)
```

```
## Default S3 method:
```

```
tnrs_match(input, reference_taxonomy = "otl", ...)
```

```
## S3 method for class 'phylo'
```

```
tnrs_match(input, reference_taxonomy = "otl", tip = NULL, ...)
```

Arguments

input	A character vector of taxon names, or a phylo object with tip names, to be matched to taxonomy.
reference_taxonomy	A character vector specifying the reference taxonomy to use for tnrs.
tip	A vector of mode numeric or character specifying the tips to match. If left empty all tips will be matched.
...	Arguments passed on to <code>rotl::tnrs_match_names</code>
context_name	name of the taxonomic context to be searched (length-one character vector or NULL). Must match (case sensitive) one of the values returned by <code>tnrs_contexts</code> . Default to "All life".
do_approximate_matching	A logical indicating whether or not to perform approximate string (a.k.a. "fuzzy") matching. Using FALSE will greatly improve speed. Default, however, is TRUE.
ids	A vector of ids to use for identifying names. These will be assigned to each name in the names array. If ids is provided, then ids and names must be identical in length.
include_suppressed	Ordinarily, some quasi-taxa, such as incertae sedis buckets and other non-OTUs, are suppressed from TNRS results. If this parameter is true, these quasi-taxa are allowed as possible TNRS results.

Details

There is no limit to the number of names that can be queried and matched.

The output will preserve all elements from original input phylo object and will add

phy\$mapped A character vector indicating the state of mapping of `phy$tip.labels`:

original Tnrs matching was not attempted. Original labeling is preserved.

ott Matching was manually made by a curator in Open Tree of Life.

tnrs Tnrs matching was attempted and successful with no approximate matching. Original label is replaced by the matched name.

approximated Tnrs matching was attempted and successful but with approximate matching. Original labeling is preserved.

unmatched Tnrs matching was attempted and unsuccessful. Original labeling is preserved.

phy\$original.tip.label A character vector preserving all original labels.

phy\$ott_ids A numeric vector with ott id numbers of matched tips. Unmatched and original tips will be NaN.

if tips are duplicated, tnrs will only be run once (avoiding increases in function running time) but the result will be applied to all duplicated tip labels

Value

An object of class data frame or phylo, with the added class `match_names`.

NULL

NULL

Examples

```
tnrs_match(input = c("Mus"))
tnrs_match(input = c("Mus", "Mus musculus"))
tnrs_match(input = c("Mus", "Echinus", "Homo", "Mus"))
```

treebase_cache	<i>Information on contributors, authors, study ids and clades from studies with chronograms in Open tree of Life</i>
----------------	--

Description

Information on contributors, authors, study ids and clades from studies with chronograms in Open tree of Life

Usage

```
treebase_cache
```

Format

A list of five data sets

tb.author.pretty A dataframe with two elements: author names and number of studies in TreeBase authored by each

tb.author.results A dataframe with two elements: author names and study identifiers

Details

Generated with `make_treebase_cache()`

Source

TreeBASE database, no longer available online <https://en.wikipedia.org/wiki/TreeBASE>

tree_add_dates	<i>Add missing taxa to a dated tree and fabricate node ages for these missing taxa.</i>
----------------	---

Description

This function adds missing taxa to a chronogram given in `dated_tree`. It is still work in progress.

Usage

```
tree_add_dates(
  dated_tree = NULL,
  missing_taxa = NULL,
  dating_method = "mrbayes",
  adding_criterion = "random",
  mrbayes_output_file = "mrbayes_tree_add_dates.nexus"
)
```

Arguments

dated_tree a tree (newick or phylo) with branch lengths proportional to absolute time

missing_taxa A tree, a data frame or a vector enlisting all missing taxa you want to include.

A tree Either as a phylo object or as a newick character string. It contains all taxa that you want at the end, both missing and non missing. This tree will be used as a hard constraint.

A data.frame It contains two columns named "taxon" and "clade". The first one contains a character vector of missing taxon names. The second one contains a character or numeric vector of nodes from a constraint tree to which each taxon will be assigned.

A character vector It contains the names of the missing taxa. They will be added at random to the constraint tree.

dating_method The method used for tree dating, options are "mrbayes" and "bladj".

adding_criterion Only used when `dating_method = "mrbayes"`. A character vector to specify how `missing_taxa` should be added to `dated_tree`. Choose one of:

adding_method = "random" `missing_taxa` will be added at random to `dated_tree`.

adding_method = "taxonomy" taxa will be added to `dated_tree` following a dataframe with taxonomic assignments given in `missing_taxa` argument. If no dataframe is given, OpenTree's reference taxonomy will be used.

adding_method = "tree" taxa will be added to `dated_tree` following a tree given in `missing_taxa` argument. If no tree is given, OpenTree's synthetic tree will be used.

mrbayes_output_file A character vector specifying the name of mrBayes run file and outputs (can specify directory too).

Value

A phylo object.

tree_add_nodelabels *Adds labels to nodes with no assigned label*

Description

Adds labels to nodes with no assigned label

Usage

```
tree_add_nodelabels(tree = NULL, node_prefix = "n", node_index = "node_number")
```

Arguments

tree	A tree either as a newick character string or as a phylo object.
node_prefix	Character vector. If length 1, it will be used to name all nodes with no labels, followed by a number which can be the node_number or consecutive, as specified in node_index.
node_index	Character vector. Choose between "from_1" and "node_number" as numeric index for node labels. It will use consecutive numbers from 1 to total node number in the first case and phylo node numbers in the second case (i.e, from Ntip + 1).

Value

A phylo object

tree_add_outgroup *Function to add an outgroup to any phylogeny, in phylo or newick format*

Description

Function to add an outgroup to any phylogeny, in phylo or newick format

Usage

```
tree_add_outgroup(tree = NULL, outgroup = "outgroup")
```

Arguments

tree	A tree either as a newick character string or as a phylo object.
outgroup	A character vector with the name of the outgroup. If it has length>1, only first element will be used.

Value

A phylo object with no root edge.

tree_check	<i>Checks if a tree is a phylo class object otherwise it uses input_process. Additionally it can check if tree is a chronogram with phylo_check</i>
------------	---

Description

Checks if a tree is a phylo class object otherwise it uses input_process. Additionally it can check if tree is a chronogram with phylo_check

Usage

```
tree_check(tree = NULL, ...)
```

Arguments

tree	A tree either as a newick character string or as a phylo object.
...	Arguments passed on to phylo_check
brlen	Boolean. If TRUE it checks if phylo object has branch lengths.
dated	Boolean. If TRUE it checks if phylo object is ultrametric.

Value

If tree is correctly formatted, it returns a phylo object.

tree_fix_brlen	<i>Take a tree with branch lengths and fix negative or zero length branches.</i>
----------------	--

Description

Take a tree with branch lengths and fix negative or zero length branches.

Usage

```
tree_fix_brlen(
  tree = NULL,
  fixing_criterion = "negative",
  fixing_method = 0,
  ultrametric = TRUE
)
```

Arguments

tree	A tree either as a newick character string or as a phylo object.
fixing_criterion	A character vector specifying the type of branch length to be fixed: "negative" or "zero" (the number 0 is also allowed).
fixing_method	A character vector specifying the method to fix branch lengths: "bladj", "mr-bayes" or a number to be assigned to all branches meeting fixing_criterion
ultrametric	Boolean indicating whether to force ultrametric or not.

Value

A phylo object with no negative or zero branch lengths.

tree_from_taxonomy	<i>Gets a taxonomic tree from a vector of taxa</i>
--------------------	--

Description

This uses the taxize package's wrapper of the Global Names Resolver to get taxonomic paths for the vector of taxa you pass in. Sources is a vector of source labels in order (though it works best if everything uses the same taxonomy, so we recommend doing just one source). You can see options by doing taxize::gnr_datasources(). Our default is Catalogue of Life. The output is a phylo object (typically with many singleton nodes if collapse_singles is FALSE: nodes with only one descendant (like "Homo" having "Homo sapiens" as its only descendant) but these singletons typically have node.labels

Usage

```
tree_from_taxonomy(
  taxa,
  sources = "Catalogue of Life",
  collapse_singles = TRUE
)
```

Arguments

taxa	Vector of taxon names
sources	Vector of names of preferred sources; see taxize::gnr_datasources(). Currently supports 100 taxonomic resources, see details.
collapse_singles	If true, collapses singleton nodes

Value

A list containing a phylo object with resolved names and a vector with unresolved names

Examples

```
## Not run: # This is a flag for package development. You are welcome to run the example.

taxa <- c(
  "Homo sapiens", "Ursus arctos", "Pan paniscus", "Tyrannosaurus rex",
  "Ginkgo biloba", "Vulcan", "Klingon"
)
results <- tree_from_taxonomy(taxa)
print(results$unresolved) # The taxa that do not match
ape::plot.phylo(results$phy) # may generate warnings due to problems with singletons
ape::plot.phylo(ape::collapse.singles(results$phy), show.node.label = TRUE)
# got rid of singles, but this also removes a lot of the node.labels

## End(Not run) # end dontrun
```

tree_get_node_data	<i>Get node numbers, node names, descendant tip numbers and labels of nodes from any tree, and node ages from dated trees.</i>
--------------------	--

Description

Get node numbers, node names, descendant tip numbers and labels of nodes from any tree, and node ages from dated trees.

Usage

```
tree_get_node_data(
  tree = NULL,
  nodes = NULL,
  node_data = c("node_number", "node_label", "node_age", "descendant_tips_number",
    "descendant_tips_label")
)
```

Arguments

tree	A tree either as a newick character string or as a phylo object.
nodes	Numeric vector with node numbers from which you want to obtain data. Default to NULL: obtain data for all nodes in the tree.
node_data	A character vector containing one or all from: "node_number", "node_label", "node_age", "descendant_tips_number", "descendant_tips_label"

Value

A list

`tree_get_singleton_outgroup`*Identify the presence of a single lineage outgroup in a phylogeny*

Description

Identify the presence of a single lineage outgroup in a phylogeny

Usage

```
tree_get_singleton_outgroup(tree = NULL)
```

Arguments

`tree` A tree either as a newick character string or as a phylo object.

Value

A character vector with the name of the single lineage outgroup. Returns NA if there is none.

`tree_node_tips`*To get tip numbers descending from any given node of a tree*

Description

To get tip numbers descending from any given node of a tree

Usage

```
tree_node_tips(tree = NULL, node = NULL, curr = NULL)
```

Arguments

`tree` a phylogenetic tree as an object of class "phylo".
`node` an integer specifying a node number in the tree.
`curr` the set of previously stored node numbers - used in recursive function calls.

Value

A numeric vector with tip numbers descending from a node

update_all_cached	<i>Update all data files as data objects for the package</i>
-------------------	--

Description

This includes opentree chronograms, contributors, treebase and curators For speed, datelife caches chronograms and other information. Running this (within the checked out version of datelife) will refresh these. Then git commit and git push them back

Usage

```
update_all_cached()
```

Value

None

update_datelife_cache	<i>Create an updated OpenTree chronograms database object</i>
-----------------------	---

Description

The function calls `get_opentree_chronograms()` to update the OpenTree chronograms database cached in datelife. It has the option to write the updated object as an .Rdata file, that will be independent of the opentree_chronograms data object that you can load with `data("opentree_chronograms", package = "datelife")`.

Usage

```
update_datelife_cache(
  write = TRUE,
  updated_name = "opentree_chronograms_updated",
  file_path = file.path(tempdir()),
  ...
)
```

Arguments

write	Defaults to TRUE, it saves an .Rdata file named indicated by argument name, containing available chronograms from Open Tree of Life. Saves to path indicated by argument path.
updated_name	Used if write = TRUE. Defaults to "opentree_chronograms_updated". A character vector of length one indicating the name to assign to both the updated OpenTree chronogram database object and the ".Rdata" file. For example, if name = "my_database", the function will assign the updated chronogram database to an object named my_database and will write it to a file named "my_database.Rdata" in the path indicated by argument file_path.

`file_path` Used if `write = TRUE`. A character vector of length 1 indicating the path to write the updated database ".Rdata" file to, excluding file name. Defaults to temporary directory obtained with `base::tempdir()` and formatted with `base::file.path()`.

...

`max_tree_count` Default to "all", it gets all available chronograms. For testing purposes, a numeric value indicating the max number of trees to be cached.

Value

A list of 4 elements:

authors A list of lists of author names of the original studies that published chronograms currently stored in the Open Tree of Life database.

curators A list of lists of curator names that uploaded chronograms to the Open Tree of Life database.

studies A list of study identifiers from original studies that published chronograms currently stored in the Open Tree of Life database.

trees A multiPhylo object storing the chronograms from Open Tree of Life database.

update A character vector indicating the time when the database object was last updated.

version A character vector indicating the datelife package version when the object was last updated.

use_all_calibrations *Date a given tree topology using a given set of congruified calibrations or ages*

Description

`use_all_calibrations` generates one or multiple chronograms (i.e., phylogenetic trees with branch lengths proportional to time) by dating a tree topology given in `phy`, and secondary calibrations given in `calibrations`, using the algorithm specified in the argument `dating_method`.

Usage

```
use_all_calibrations(
  phy = NULL,
  calibrations = NULL,
  each = FALSE,
  dating_method = "bladj",
  ...
)
```

Arguments

phy	A phylo object to use as tree topology.
calibrations	A calibrations object, an output of <code>get_all_calibrations()</code> .
each	Boolean, default to FALSE: all calibrations are returned in the same data.frame. If TRUE, calibrations from each chronogram are returned in separate data frames.
dating_method	Tree dating algorithm to use. Options are "bladj" or "pathd8" (Webb et al., 2008, doi:10.1093/bioinformatics/btn358 ; Britton et al., 2007, doi:10.1080/10635150701613783).
...	Arguments passed on to <code>use_calibrations</code>
type	The type of age to use as calibration. Options are "median", "mean", "min", or "max".

Details

If phy has no branch lengths, dating_method is ignored, and the function applies secondary calibrations to date the tree with the BLADJ algorithm. See `make_bladj_tree()` and `use_calibrations_bladj()`. If phy has branch lengths, the function can use the PATHd8 algorithm. See `use_calibrations_pathd8()`.

Value

A phylo or multiPhylo object with branch lengths proportional to time.

More

The output object stores the used calibrations and dating_method as `attributes(output)$datelife_calibrations` and `attributes(output)$dating_method`.

References

- Webb, C. O., Ackerly, D. D., & Kembel, S. W. (2008). "Phylocom: software for the analysis of phylogenetic community structure and trait evolution". *Bioinformatics*, 24(18), [doi:10.1093/bioinformatics/btn358](https://doi.org/10.1093/bioinformatics/btn358).
- Britton, T., Anderson, C. L., Jacquet, D., Lundqvist, S., & Bremer, K. (2007). "Estimating divergence times in large phylogenetic trees". *Systematic biology*, 56(5), 741-752. [doi:10.1080/10635150701613783](https://doi.org/10.1080/10635150701613783).

use_calibrations *Date a given tree topology using a combined set of given calibrations*

Description

`use_calibrations` combines all given calibrations and uses them as constraints to perform a dating analysis on a given tree topology, using BLADJ if it has no branch lengths, or PATHd8 if the given tree topology has initial branch lengths.

Usage

```

use_calibrations(
  phy = NULL,
  calibrations = NULL,
  dating_method = "bladj",
  type = "median",
  ...
)

```

Arguments

phy	A phylo object to use as tree topology.
calibrations	A calibrations object, an output of get_all_calibrations() .
dating_method	Tree dating algorithm to use. Options are "bladj" or "pathd8" (Webb et al., 2008, doi:10.1093/bioinformatics/btn358 ; Britton et al., 2007, doi:10.1080/10635150701613783).
type	The type of age to use as calibration. Options are "median", "mean", "min", or "max".
...	Arguments passed on to use_calibrations_pathd8
expand	How much to expand by each step to get consistent calibrations. Should be between 0 and 1.
giveup	How many expansions to try before giving up

Details

If phy has no branch lengths, dating_method is ignored, and the function applies secondary calibrations to date the tree with the BLADJ algorithm. See [make_bladj_tree\(\)](#) and [use_calibrations_bladj\(\)](#). If phy has branch lengths, the function can use the PATHd8 algorithm. See [use_calibrations_pathd8\(\)](#).

Value

A phylo object with branch lengths proportional to time.

More

The output object stores the used calibrations and dating_method as `attributes(output)$datelife_calibrations` and `attributes(output)$dating_method`.

use_calibrations_bladj

Use calibrations to date a topology with the BLADJ algorithm.

Description

The function `use_calibrations_bladj` prepares the input for BLADJ and calls [make_bladj_tree\(\)](#).

Usage

```
use_calibrations_bladj(phy = NULL, calibrations, type = "median", root_age)
```

Arguments

phy	A phylo object with or without branch lengths.
calibrations	A data.frame of secondary calibrations for any pair of taxon names in phy, usually obtained with get_all_calibrations() .
type	The type of age to use as calibration. Options are "median", "mean", "min", or "max".
root_age	Numeric specifying the age of the root. Only used if there are no ages for the root node in calibrations argument. If missing, NULL, or not numeric, the value of the oldest calibration plus one unit of the mean differences across calibrations, will be used as root calibration. If there is one single age point provided as calibrations, the root age will be set to 10% more than the age of the single calibration.

Details

The BLADJ algorithm is part of the Phylocom software, presented in Webb et al. (2008) [doi:10.1093/bioinformatics/btn358](https://doi.org/10.1093/bioinformatics/btn358).

Value

A chronogram: a phylo object with branch lengths proportional to time.

References

Webb, C. O., Ackerly, D. D., & Kembel, S. W. (2008). "Phylocom: software for the analysis of phylogenetic community structure and trait evolution". *Bioinformatics*, 24(18), [doi:10.1093/bioinformatics/btn358](https://doi.org/10.1093/bioinformatics/btn358).

```
use_calibrations_bladj.matchedCalibrations
```

Use calibrations to date a topology with the BLADJ algorithm.

Description

The function prepares the input for BLADJ and calls [make_bladj_tree\(\)](#)

Usage

```
use_calibrations_bladj.matchedCalibrations(
  calibrations,
  type = "mean",
  root_age = NULL
)
```

Arguments

calibrations	A data.frame of secondary calibrations for any pair of taxon names in phy, usually obtained with <code>get_all_calibrations()</code> .
type	The type of age to use as calibration. Options are "median", "mean", "min", or "max".
root_age	Not implemented yet. Numeric specifying the age of the root. If there are no calibrations for it. If NULL or not numeric, the maximum calibration plus a unit of the mean differences will be used as root calibration. If there is only one internal calibration, the root age will be set to 10% more than the age of the calibration.

Details

The BLADJ algorithm is part of the Phylocom software, presented in Webb et al. (2008) [doi:10.1093/bioinformatics/btn358](https://doi.org/10.1093/bioinformatics/btn358).

Value

A phylo object with branch lengths proportional to time.

References

Webb, C. O., Ackerly, D. D., & Kembel, S. W. (2008). "Phylocom: software for the analysis of phylogenetic community structure and trait evolution". *Bioinformatics*, 24(18), [doi:10.1093/bioinformatics/btn358](https://doi.org/10.1093/bioinformatics/btn358).

use_calibrations_each *Date a given tree topology by using a given list of calibrations independently, to generate multiple hypothesis of time of divergence*

Description

use_calibrations_each wraps use_calibrations to take each set of given calibrations and use it independently as constraints for BLADJ or PATHd8 to date a given tree topology.

Usage

```
use_calibrations_each(phy = NULL, calibrations = NULL, ...)
```

Arguments

phy	A phylo object to use as tree topology.
calibrations	A calibrations object, an output of <code>get_all_calibrations()</code> .
...	Arguments passed on to <code>use_calibrations</code>

`dating_method` Tree dating algorithm to use. Options are "bladj" or "pathd8" (Webb et al., 2008, [doi:10.1093/bioinformatics/btn358](https://doi.org/10.1093/bioinformatics/btn358); Britton et al., 2007, [doi:10.1080/10635150701613783](https://doi.org/10.1080/10635150701613783)).

`type` The type of age to use as calibration. Options are "median", "mean", "min", or "max".

Details

If `phy` has no branch lengths, `dating_method` is ignored, and the function applies secondary calibrations to date the tree with the BLADJ algorithm. See [make_bladj_tree\(\)](#) and [use_calibrations_bladj\(\)](#). If `phy` has branch lengths, the function can use the PATHd8 algorithm. See [use_calibrations_pathd8\(\)](#).

Value

A `multiPhylo` object of trees with branch lengths proportional to time.

More

The output object stores the used calibrations and `dating_method` as `attributes(output)$datelife_calibrations` and `attributes(output)$dating_method`.

use_calibrations_pathd8

Date a tree with secondary calibrations using PATHd8

Description

`use_calibrations_pathd8` uses secondary calibrations to date a tree with initial branch lengths using PATHd8.

Usage

```
use_calibrations_pathd8(
  phy = NULL,
  calibrations = NULL,
  expand = 0.1,
  giveup = 100
)
```

Arguments

<code>phy</code>	A phylo object with branch lengths.
<code>calibrations</code>	A <code>data.frame</code> of secondary calibrations for any pair of taxon names in <code>phy</code> , usually obtained with get_all_calibrations() .
<code>expand</code>	How much to expand by each step to get consistent calibrations. Should be between 0 and 1.
<code>giveup</code>	How many expansions to try before giving up

Details

This function implements the **PATHd8** algorithm described in Britton et al. (2007) [doi:10.1080/10635150701613783](https://doi.org/10.1080/10635150701613783), with `geiger::PATHd8.phylo()`. The function first attempts to use the given calibrations as fixed ages. If that fails (often due to conflict between calibrations), it will expand the range of the minimum age and maximum age and try again. And repeat. If `expand = 0`, it uses the summarized calibrations. In some cases, it returns edge lengths in relative time (with maximum tree depth = 1) instead of absolute time, as given by calibrations. In this case, the function returns NA. This is an issue from PATHd8.

Value

A phylo object with branch lengths proportional to time.

References

Britton, T., Anderson, C. L., Jacquet, D., Lundqvist, S., & Bremer, K. (2007). "Estimating divergence times in large phylogenetic trees". *Systematic biology*, 56(5), 741-752. [doi:10.1080/10635150701613783](https://doi.org/10.1080/10635150701613783).

use_calibrations_treePL

Date a tree with initial branch lengths with treePL.

Description

Date a tree with initial branch lengths with treePL.

Usage

```
use_calibrations_treePL(phy, calibrations)
```

Arguments

phy	A phylo object with or without branch lengths.
calibrations	A data.frame of secondary calibrations for any pair of taxon names in phy, usually obtained with <code>get_all_calibrations()</code> .

Details

This function uses treePL as described in Smith, S. A., & O'Meara, B. C. (2012). [doi:10.1093/bioinformatics/bts492](https://doi.org/10.1093/bioinformatics/bts492), with the function `treePL.phylo`. It attempts to use the calibrations as fixed ages. If that fails (often due to conflict between calibrations), it will expand the range of the minimum age and maximum age and try again. And repeat. If `expand = 0`, it uses the summarized calibrations. In some cases, it returns edge lengths in relative time (with maximum tree depth = 1) instead of absolute time, as given by calibrations. In this case, the function returns NA. This is an issue from PATHd8.

Value

A phylo object

References

Smith, S. A., & O'Meara, B. C. (2012). "treePL: divergence time estimation using penalized likelihood for large phylogenies". *Bioinformatics*, 28(20), 2689-2690, doi:[10.1093/bioinformatics/bts492](https://doi.org/10.1093/bioinformatics/bts492).

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