

Package ‘delimtools’

September 30, 2025

Type Package

Title Helper Functions for Species Delimitation Analysis

Version 0.2.1

Date 2025-09-29

Description Helpers functions to process, analyse, and visualize the output of single locus species delimitation methods.
For full functionality, please install suggested software at
<<https://legallab.github.io/delimtools/articles/install.html>>.

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Depends R (>= 4.2.0)

Imports cli, dplyr, glue, ggtree, methods, purrr, rlang, stringr, tidyr, tidyselect

Suggests ape, bGMYC (>= 1.0.2), forcats, furrr, future, ggfun, ggplot2, gtools, here, knitr, patchwork, randomcoloR, readr, RColorBrewer, scales, splits (>= 1.0.20), spider, tibble, tidytree, vctrs, withr, rmarkdown

Additional_repositories <https://r-forge.r-project.org/>,
<https://pedrosenna.github.io/drat/>

Config/Needs/website bGMYC=github::https://github.com/pedrosenna/bGMYC,
splits=url::https://download.r-forge.r-project.org/src/contrib/splits_1.0-20.tar.gz

Encoding UTF-8

LazyData true

RoxygenNote 7.3.2

NeedsCompilation no

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URL <https://github.com/legalLab/delimtools>,
<https://legallab.github.io/delimtools/>

BugReports <https://github.com/legalLab/delimtools/issues>

VignetteBuilder knitr

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Repository CRAN

Date/Publication 2025-09-29 22:10:02 UTC

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delimtools-package	<i>Helper Functions for Species Delimitation Analysis</i>
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Description

Helpers functions to process, analyse, and visualize the output of single locus species delimitation methods. For full functionality, please install suggested software at <https://legallab.github.io/delimtools/articles/install.html>.

Author(s)

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See Also

Useful links:

- <https://github.com/legallab/delimtools>
- <https://legallab.github.io/delimtools/>
- Report bugs at <https://github.com/legallab/delimtools/issues>

abgd_tbl	<i>A Command-Line Interface for ABGD - Automatic Barcode Gap Discovery</i>
----------	--

Description

`abgd_tbl()` returns species partition hypothesis estimated by ABGD software (<https://bioinfo.mnhn.fr/abi/public/abgd/>).

Usage

```
abgd_tbl(  
  infile,  
  exe = NULL,  
  haps = NULL,  
  slope = 1.5,  
  model = 3,  
  outfolder = NULL,  
  webserver = NULL,  
  delimname = "abgd"  
)
```

Arguments

<code>infile</code>	Path to fasta file.
<code>exe</code>	Path to an ABGD executable.
<code>haps</code>	Optional. A vector of haplotypes to keep into the <code>tbl_df</code> .
<code>slope</code>	Numeric. Relative gap width (slope). Default to 1.5.
<code>model</code>	An integer specifying evolutionary model to be used. Available options are: • 0: Kimura-2P • 1: Jukes-Cantor (default) • 2: Tamura-Nei • 3: simple distance (p-distance)
<code>outfolder</code>	Path to output folder. Default to NULL. If not specified, a temporary location is used.
<code>webserver</code>	A .txt file containing ABGD results obtained from a webserver. Default to NULL.
<code>delimname</code>	Character. String to rename the delimitation method in the table. Default to 'abgd'.

Details

`abgd_tbl()` relies on `system` to invoke ABGD software through a command-line interface. Hence, you must have the software available as an executable file on your system in order to use this function properly. `abgd_tbl()` saves all output files in `outfolder` and imports the first recursive partition file generated to Environment. Alternatively, `abgd_tbl()` can parse a .txt file obtained from a webserver such as (<https://bioinfo.mnhn.fr/abi/public/abgd/abgdweb.html>).

Value

an object of class `tbl_df`

Author(s)

N. Puillandre, A. Lambert, S. Brouillet, G. Achaz

Source

Puillandre N., Lambert A., Brouillet S., Achaz G. 2012. ABGD, Automatic Barcode Gap Discovery for primary species delimitation. *Molecular Ecology* 21(8):1864-77.

Examples

```
#' # get path to fasta file
path_to_file <- system.file("extdata/geophagus.fasta", package = "delimtools")

# run ABGD
abgd_df <- abgd_tbl(
  infile = path_to_file,
```

```

    exe = "/usr/local/bin/abgd",
    model = 3,
    slope = 0.5,
    outfolder = NULL
  )

# check
abgd_df

```

asap_tbl

A Command-Line Interface for ASAP - Assemble Species by Automatic Partitioning

Description

asap_tbl() returns species partition hypothesis estimated by ASAP software (<https://bioinfo.mnhn.fr/abi/public/asap/>).

Usage

```

asap_tbl(
  infile,
  exe = NULL,
  haps = NULL,
  model = 3,
  outfolder = NULL,
  webserver = NULL,
  delimname = "asap"
)

```

Arguments

infile	Path to fasta file.
exe	Path to an ASAP executable.
haps	Optional. A vector of haplotypes to keep into the tbl_df .
model	An integer specifying evolutionary model to be used. Available options are: • 0: Kimura-2P • 1: Jukes-Cantor (default) • 2: Tamura-Nei • 3: simple distance (p-distance)
outfolder	Path to output folder. Default to NULL. If not specified, a temporary location is used.
webserver	A .csv file containing ASAP results obtained from a webserver. Default to NULL.
delimname	Character. String to rename the delimitation method in the table. Default to 'asap'.

Details

`asap_tbl()` relies on [system](#) to invoke ASAP software through a command-line interface. Hence, you must have the software available as an executable file on your system in order to use this function properly. `asap_tbl()` saves all output files in `outfolder` and imports the first partition file generated to `Environment`. Alternatively, `asap_tbl()` can parse a .csv file obtained from webserver such as (<https://bioinfo.mnhn.fr/abi/public/asap/asapweb.html>).

Value

an object of class `tbl_df`

Author(s)

Nicolas Puillandre, Sophie Brouillet, Guillaume Achaz.

Source

Puillandre N., Brouillet S., Achaz G. 2021. ASAP: assemble species by automatic partitioning. *Molecular Ecology Resources* 21:609–620.

Examples

```
#' # get path to fasta file
path_to_file <- system.file("extdata/geophagus.fasta", package = "delimtools")

# run ASAP
asap_df <- asap_tbl(infile = path_to_file, exe= "/usr/local/bin/asap", model= 3)

# check
asap_df
```

as_dwc

Rename Columns using Darwin Core Standard Terms

Description

`as_dwc()` rename columns in a `tbl_df` using a vector of terms defined by Darwin Core Standard.

Usage

```
as_dwc(dwc, data, terms)
```

Arguments

dwc	a list of standard terms and definitions created using <code>get_dwc()</code> .
data	a <code>tbl_df</code> .
terms	a vector or list of terms to be used as replacement.

Details

`as_dwc()` will replace current column names by the ones defined in terms. For each column in data, Darwin Core equivalent terms must be informed in the same order by the user. If terms and column names do not match in length or if terms used are not found in Darwin Core standard, an error will be printed on Console.

Value

an object of class `tbl_df`.

Author(s)

Pedro S. Bittencourt, Rupert A. Collins.

Examples

```
# get dwc terms and definitions
dwc <- get_dwc(type = "simple")

# create a data frame with sample metadata
my_df <- tibble::tibble(
  species = c("sp1", "sp2", "sp3"),
  location = c("loc1", "loc2", "loc3"),
  voucher = c("M01", "M02", "M03"),
  collector = c("John", "Robert", "David")
)

# rename columns
as_dwc(dwc, my_df, terms = c("scientificName", "locality", "catalogNumber", "recordedBy"))
```

`bgmyc_tbl`*Turns bGMYC Results Into a Tibble*

Description

`bgmyc_tbl()` processes output from `bgmyc.singlephy` into an object of class `tbl_df`.

Usage

```
bgmyc_tbl(bgmyc_res, ppcutoff = 0.05, delimname = "bgmyc")
```

Arguments

bgmyc_res	Output from bgmyc.singlephy .
ppcutoff	Posterior probability threshold for clustering samples into species partitions. See bgmyc.point for details. Default to 0.05.
delimname	Character. String to rename the delimitation method in the table. Default to 'bgmyc'.

Details

bGMYC package uses [spec.probmat](#) to create a matrix of probability of conspecificity and [bgmyc.point](#) to split samples into a list which individuals meets the threshold specified by ppcutoff. `bgmyc_tbl()` wraps up these two functions into a single one and turns these inputs into a tibble which matches the output from [gmyc_tbl](#) and [locmin_tbl](#).

Value

an object of class `tbl_df`.

Author(s)

Noah M. Reid.

Source

Reid N.M., Carstens B.C. 2012. Phylogenetic estimation error can decrease the accuracy of species delimitation: a Bayesian implementation of the general mixed Yule-coalescent model. *BMC Evolutionary Biology* 12 (196).

Examples

```
# run bGMYC
bgmyc_res <- bGMYC::bgmyc.singlephy(ape::as.phylo(geophagus_beast),
  mcmc = 11000,
  burnin = 1000,
  thinning = 100,
  t1 = 2,
  t2 = ape::Ntip(geophagus_beast),
  start = c(1, 0.5, 50)
)

# create a tibble
bgmyc_df <- bgmyc_tbl(bgmyc_res, ppcutoff = 0.05)

# check
bgmyc_df
```

check_delim	<i>Checks If Two or More Species Delimitation Outputs are (Nearly) Equal</i>
-------------	--

Description

check_delim() checks if two or more species delimitation outputs have differences in its dimensions, labels, and values.

Usage

```
check_delim(list)
```

Arguments

list a [list](#) containing two or more species delimitation outputs to check.

Details

check_delim() will check if two or more species delimitation outputs have different dimensions (rows, columns), if labels are the same or if there are any duplicated or absent labels, and if there are any NA values or if partitions were set using non numeric values. If TRUE for any of the cases listed above, check_delim() will return an error.

Value

A single logical value, TRUE or FALSE.

Author(s)

Pedro S. Bittencourt, Rupert A. Collins.

Examples

```
# create dummy delimitation outputs
delim_1 <- tibble::tibble(
  labels = paste0("seq", 1:10),
  method_A = c(rep(1, 5), rep(2, 5))
)

delim_2 <- tibble::tibble(
  labels = paste0("seq", 1:10),
  method_B = c(rep(1, 3), rep(2, 2), rep(3, 5))
)

delim_3 <- tibble::tibble(
  labels = paste0("seq", 1:10),
  method_C = c(rep(1, 3), rep(2, 2), rep(3, 3), rep(4, 2))
)
```

```
# check outputs
check_delim(list(delim_1, delim_2, delim_3))
```

check_identifiers	<i>Checks for Differences Between Identifiers in Metadata and DNA Sequence Files</i>
-------------------	--

Description

check_identifiers() checks for differences between identifiers in metadata and DNA sequence files.

Usage

```
check_identifiers(data, identifier, dna)
```

Arguments

data	an object of class tbl_df containing sequence metadata.
identifier	column in data which contains sequence identifiers.
dna	a DNABin object.

Details

check_identifiers() is a helper function to check for inconsistencies between identifiers in metadata and DNA sequences files, such as absence, mistyping, duplicated entries, or differences in size lengths. If any of these problems are found, warnings will appear in Console and corrections should be made to prevent unintended consequences later. A list containing erroneous identifiers is returned invisibly.

Value

A list containing erroneous identifiers between metadata and sequence file.

Author(s)

Pedro S. Bittencourt, Rupert A. Collins.

Examples

```
check_identifiers(geophagus_info, "gbAccession", geophagus)
```

clean_dna	<i>Removes Gaps, Ambiguities and Missing Data from DNA Sequences</i>
-----------	--

Description

clean_dna() removes all character not a valid ACTG base from a [DNABin](#) object.

Usage

```
clean_dna(dna, verbose = TRUE)
```

Arguments

dna	an object of class DNABin .
verbose	logical. Returns a warning if any sequence contains non ACTG bases.

Details

clean_dna() detects and removes any non ACTG bases from alignment. This includes: "N", "-", "?", "R", "Y", etc. If verbose = TRUE, returns a warning if these characters are inside the sequences, i.e, are not alignment padding chars at the ends.

Value

an object of class [DNABin](#).

Author(s)

Rupert A. Collins

Examples

```
geo_clean <- clean_dna(geophagus)
```

collapse_others	<i>Summarise Haplotype Metadata Down to One Row</i>
-----------------	---

Description

collapse_others() returns a [tbl_df](#) summarising all unique haplotype frequencies, duplicates and selected metadata into a single row.

Usage

```
collapse_others(data, hap_tbl, labels, cols)
```

Arguments

data	An object of class <code>tbl_df</code> containing sequence metadata.
hap_tbl	Output from <code>haplotype_tbl</code> .
labels	Column name which contains sequence names.
cols	A character vector of variables to collapse.

Details

`collapse_others()` is a helper function to summarise metadata along with `haplotype_tbl`. For any given cols, `collapse_others()` flattens its content by unique haplotypes and its duplicates in `hap_tbl`.

Value

an object of class `tbl_df`.

Author(s)

Pedro S. Bittencourt, Rupert A. Collins.

Examples

```
# summarise haplotypes
hap_tbl <- haplotype_tbl(geophagus)

# summarise country
others_df <- collapse_others(geophagus_info, hap_tbl, "gbAccession", "country")
```

confidence_intervals *Confidence Intervals for Species Delimitations Methods*

Description

These functions compute confidence intervals for various species delimitation methods, including GMYC, bGMYC, Local Minima, and mPTP.

Usage

```
gmyc_ci(tr, posterior, method = "single", interval = c(0, 5))

bgmyc_ci(
  tr,
  posterior,
  ppcutoff = 0.05,
  mcmc,
  burnin,
```

```

    thinning,
    py1 = 0,
    py2 = 2,
    pc1 = 0,
    pc2 = 2,
    t1 = 2,
    t2 = 51,
    scale = c(20, 10, 5),
    start = c(1, 0.5, 50)
)

locmin_ci(dna, block = 1, reps = 100, threshold = 0.01, haps = NULL, ...)

mptp_ci(
  infile,
  bootstraps,
  exe = NULL,
  outfolder = NULL,
  method = c("multi", "single"),
  minbrlen = 1e-04,
  webserver = NULL
)

```

Arguments

<code>tr</code>	An ultrametric, dichotomous tree object in ape format.
<code>posterior</code>	Trees from posterior. An object of class multiphylo .
<code>method</code>	Method of analysis, either "single" for single-threshold version or "multiple" for multiple-threshold version.
<code>interval</code>	Upper and lower limit of estimation of scaling parameters, e.g. <code>c(0,10)</code>
<code>ppcutoff</code>	Posterior probability threshold for clustering samples into species partitions. See bgmyc.point for details. Default to 0.05.
<code>mcmc</code>	number of samples to take from the Markov Chain
<code>burnin</code>	the number of samples to discard as burn-in
<code>thinning</code>	the interval at which samples are retained from the Markov Chain
<code>py1</code>	governs the prior on the Yule (speciation) rate change parameter. using the default prior distribution, this is the lower bound of a uniform distribution. this can be the most influential prior of the three. rate change is parameterized as n^{py} where n is the number of lineages in a waiting interval (see Pons et al. 2006). if there are 50 sequences in an analysis and the Yule rate change parameter is 2, this allows for a potential 50-fold increase in speciation rate. this unrealistic parameter value can cause the threshold between Yule and Coalescent process to be difficult to distinguish. are more reasonable upper bound for the prior would probably be less than 1.5 (a potential 7-fold increase). Or you could modify the prior function to use a different distribution entirely.
<code>py2</code>	governs the prior on the Yule rate change parameter. using the default prior distribution, this is the upper bound of a uniform distribution.

pc1	governs the prior on the coalescent rate change parameter. using the default prior distribution, this is the lower bound of a uniform distribution. rate change is parameterized as $(n(n-1))^{pc}$ where n is the number of lineages in a waiting interval (see Pons et al. 2006). In principle pc can be interpreted as change in effective population size ($pc < 1$ decline, $pc > 1$ growth) but because identical haplotypes must be excluded from this analysis an accurate biological interpretation is not possible.
pc2	governs the prior on the coalescent rate change parameter. using the default prior distribution, this is the upper bound of a uniform distribution.
t1	governs the prior on the threshold parameter. the lower bound of a uniform distribution. the bounds of this uniform distribution should not be below 1 or greater than the number of unique haplotypes in the analysis.
t2	governs the prior on the threshold parameter. the upper bound of a uniform distribution
scale	a vector of scale parameters governing the proposal distributions for the markov chain. the first to are the Yule and coalescent rate change parameters. increasing them makes the proposals more conservative. the third is the threshold parameter. increasing it makes the proposals more liberal.
start	a vector of starting parameters in the same order as the scale parameters, py , pc , t . t may need to be set so that it is not impossible given the dataset.
dna	an object of class DNABin .
block	integer. Number of columns to be resampled together. Default to 1.
reps	Number of bootstrap replicates. Default to 100.
threshold	Distance cutoff for clustering. Default of 0.01. See localMinima for details.
haps	Optional. A vector of haplotypes to keep into the tbl_df .
...	Further arguments to be passed to dist.dna .
infile	Path to tree file in Newick format. Should be dichotomous and rooted.
bootstraps	Bootstrap trees. An object of class multiphylo .
exe	Path to an mPTP executable.
outfolder	Path to output folder. Default to NULL. If not specified, a temporary location is used.
minbrlen	Numeric. Branch lengths smaller or equal to the value provided are ignored from computations. Default to 0.0001. Use min_brlen for fine tuning.
webserver	A .txt file containing mPTP results obtained from a webserver. Default to NULL.

Details

Both `gmyc_ci` and `bgmyc_ci` can take a very long time to process, depending on how many posterior trees are provided. As an alternative, these analyses can be sped up significantly by running in parallel using [plan](#).

Value

A vector containing the number of species partitions in tr, dna or infile followed by the number of partitions in posterior, reps or bootstraps.

Author(s)

Pedro S. Bittencourt, Rupert A. Collins.

Examples

```
# gmyc confidence intervals

# compute values using multisession mode
{
  future::plan("multisession")

  gmyc_res <- gmyc_ci(ape::as.phylo(geophagus_beast), geophagus_posterior)

  # reset future parameters
  future::plan("sequential")
}

# plot distribution
plot(density(gmyc_res))

# tabulate
tibble::tibble(
  method = "gmyc",
  point_estimate = gmyc_res[1],
  CI_95 = as.integer(quantile(gmyc_res[-1], probs = c(0.025, 0.975))) |>
    stringr::str_flatten(collapse = "-"),
  CI_mean = as.integer(mean(gmyc_res[-1])),
  CI_median = as.integer(stats::median(gmyc_res[-1]))
)
```

Description

delim_autoplot() returns a phylogenetic tree plotted using ggtree alongside with a customized tile plot using [geom_tile](#) combined by [wrap_plots](#).

Usage

```
delim_autoplot(
  delim,
  tr,
  consensus = TRUE,
  n_match = NULL,
  delim_order = NULL,
  tbl_labs = NULL,
  col_vec = NULL,
  hexexpand = 0.1,
  widths = c(0.5, 0.2)
)
```

Arguments

delim	Output from delim_join .
tr	A treedata object. Both phylogram and ultrametric trees are supported.
consensus	Logical. Should the majority-vote consensus to be estimated?
n_match	An Integer. If consensus = TRUE, threshold for majority-vote calculations. See delim_consensus for details.
delim_order	A character vector of species delimitation names ordered by user. Default to NULL.
tbl_labs	A tbl_df of customized labels for tree plotting. The first column must match tip labels of the tr object, while the second column should have customized labels.
col_vec	A color vector for species delimitation partitions. See delim_brewer for customized color palette options.
hexexpand	Numeric. Expand xlim of tree by a ratio of x axis range. Useful if tiplabels become truncated when plotting. Default to 0.1.
widths	A numeric vector containing the relative widths of the tree and species delimitation bars. See wrap_plots for details. Defaults to c(0.5, 0.2).

Details

delim_autoplot() is a wrapper for tree plotting with associated data implemented using ggtree, ggplot2, and patchwork. If consensus = TRUE, a consensus bar will be plotted next to the species delimitation plot, summarizing partitions across samples. If no consensus is reached, an "X" will be plotted instead.

Value

A patchwork object.

Author(s)

Pedro S. Bittencourt, Rupert A. Collins.

Examples

```
# view partitions using an ultrametric tree
p <- delim_autoplot(geophagus_delims, geophagus_beast)
p

# view partitions using a phylogram
p1 <- delim_autoplot(geophagus_delims, geophagus_raxml)
```

delim_autoplot2

Plot Phylogenetic Trees With Species Delimitation Partitions

Description

delim_autoplot2() returns a phylogenetic tree plotted using ggtree alongside with a customized tile plot using [geom_tile](#) combined by [wrap_plots](#).

Usage

```
delim_autoplot2(
  delim,
  tr,
  consensus = TRUE,
  n_match = NULL,
  delim_order = NULL,
  tbl_labs,
  species,
  hexpand = 0.1,
  widths = c(0.5, 0.2)
)
```

Arguments

delim	Output from delim_join .
tr	A treedata object. Both phylogram and ultrametric trees are supported.
consensus	Logical. Should the majority-vote consensus to be estimated?
n_match	An Integer. If consensus = TRUE, threshold for majority-vote calculations. See delim_consensus for details.
delim_order	A character vector of species delimitation names ordered by user. Default to NULL.
tbl_labs	A tbl_df of customized labels for tree plotting. The first column must match tip labels of the tr object, while the second column should have customized labels.
species	column name in tbl_labs which contains species names for each tip of the tree.
hexpand	Numeric. Expand xlim of tree by a ratio of x axis range. Useful if tiplabels become truncated when plotting. Default to 0.1.
widths	A numeric vector containing the relative widths of the tree and species delimitation bars. See wrap_plots for details. Defaults to c(0.5, 0.2).

Details

`delim_autoplot2()` is a wrapper for tree plotting with associated data implemented using `ggtree`, `ggplot2`, and `patchwork`. If `consensus = TRUE`, a consensus bar will be plotted next to the species delimitation plot, summarizing partitions across samples. If no consensus is reached, an "X" will be plotted instead. This function is a modified version of [delim_autoplot](#) which plots species partitions using a black and grey color scheme.

Value

A patchwork object.

Author(s)

Pedro S. Bittencourt, Rupert A. Collins.

Examples

```
# create labels
labs <- geophagus_info |> dplyr::select(gbAccession, scientificName)

# view partitions using an ultrametric tree
p <- delim_autoplot2(geophagus_delims,
  geophagus_beast,
  tbl_labs = labs,
  species = "scientificName"
)
p

# view partitions using a phylogram
p1 <- delim_autoplot2(geophagus_delims,
  geophagus_raxml,
  tbl_labs = labs,
  species = "scientificName"
)
```

`delim_brewer`*Customize Delimitation Colors*

Description

`delim_brewer()` returns a set of colors created by interpolating or using color palettes from [RColorBrewer](#), [viridisLite](#) or [randomcoloR](#).

Usage

```
delim_brewer(delim, package = NULL, palette = NULL, seed = NULL)
```

Arguments

delim	Output from delim_join .
package	Package which contains color palettes. Available options are "RColorBrewer", "viridisLite" or "randomcoloR".
palette	A palette name. brewer.pal for RColorBrewer or viridis for viridisLite options.
seed	Integer. Number to initialize random number generator.

Details

`delim_brewer()` interpolates over a color palette and returns a vector of random colors whose length is equal to the sum of unique species delimitation partitions in `delim`. For reproducibility, make sure to provide a seed. If not provided, [Sys.time](#) will be used as seed instead. One should also try different seeds to get best color combinations for plotting.

Value

A character vector of hexadecimal color codes.

Author(s)

Rupert A. Collins, Pedro S. Bittencourt

Examples

```
# create a vector of colors
cols <- delim_brewer(geophagus_delims, package = "randomcoloR")
```

delim_consensus	<i>Estimate a Majority-Vote Consensus</i>
-----------------	---

Description

`delim_consensus()` estimates a majority-vote consensus over the output of [delim_join](#) in a row-wise manner.

Usage

```
delim_consensus(delim, n_match = NULL)
```

Arguments

delim	Output from delim_join .
n_match	An integer. Threshold for Majority-Vote calculations. If not specified, returns a warning and the threshold will be defined as <code>ceiling(ncol(delim[, -1])/2)</code> .

Details

delim_consensus() iterates row-by-row, counting the number of matching species partition names across all species delimitations methods in [delim_join](#) output. If the sum of identical partition names is greater or equal n_match, the consensus column will be filled with its partition name. Otherwise, consensus column will be filled with [NA](#).

Value

an object of class [tbl_df](#).

Author(s)

Pedro S. Bittencourt

Examples

```
# estimate a majority vote consensus
delim_consensus <- delim_consensus(geophagus_delims, n_match= 5)

# check
delim_consensus
```

delim_join

Join Multiple Species Delimitation Methods Outputs

Description

delim_join() returns a [tbl_df](#) of species delimitation outputs whose partitions are consistent across different methods.

Usage

```
delim_join(delim)
```

Arguments

delim A [list](#) or [data.frame](#) of multiple species delimitation methods outputs.

Details

delim_join() is a helper function to join multiple lists or columns of species delimitation outputs into a single [tbl_df](#) while keeping consistent identifications across multiple methods. Species delimitation outputs are in general a list or data frame of sample labels and its species partitions (Species 1, Species 2, etc.). These partition names may be or not the same across two or more methods. delim_join() standardizes partition names across two or more species delimitation outputs while keeping its underlying structure intact.

Value

an object of class `tbl_df`.

Author(s)

Pedro S. Bittencourt, Rupert A. Collins.

Examples

```
## run GMYC
gmyc_res <- splits::gmyc(ape::as.phylo(geophagus_beast), method = "single")

# create a tibble
gmyc_df <- gmyc_tbl(gmyc_res)

## run bGMYC
bgmyc_res <- bGMYC::bgmyc.singlephy(ape::as.phylo(geophagus_beast),
  mcmc = 11000,
  burnin = 1000,
  thinning = 100,
  t1 = 2,
  t2 = ape::Ntip(ape::as.phylo(geophagus_beast)),
  start = c(1, 0.5, 50)
)

# create a tibble
bgmyc_df <- bgmyc_tbl(bgmyc_res, ppcutoff = 0.05)

## LocMin

# create a distance matrix
mat <- ape::dist.dna(geophagus, model = "raw", pairwise.deletion = TRUE)

# estimate local minima from `mat`
locmin_res <- spider::localMinima(mat)

# create a tibble
locmin_df <- locmin_tbl(mat,
  threshold = locmin_res$localMinima[1],
  haps = ape::as.phylo(geophagus_beast)$tip.label
)

# join delimitations
all_delims <- delim_join(list(gmyc_df, bgmyc_df, locmin_df))

# check
all_delims
```

drop_sequences	<i>Remove Sequences of a DNABin list object</i>
----------------	---

Description

drop_sequences() removes sequences of a FASTA file by its names.

Usage

```
drop_sequences(dna, identifier, drop = TRUE)
```

Arguments

dna	a DNABin list object.
identifier	a character vector containing sequence names.
drop	Logical. If TRUE, sequence names in identifier will be dropped from dna. If FALSE, sequence names absent in identifier will be dropped instead.

Details

drop_sequences() relies on exact match between sequence names within a fasta file and identifier argument.

Value

an object of class [DNABin](#).

Author(s)

Pedro S. Bittencourt

Examples

```
# Create a vector of sequence names to drop or keep.
identifier <- names(geophagus)[1:3]

# Remove sequences listed in identifier
drop_sequences(geophagus, identifier, drop = TRUE)

# Remove sequences not listed in identifier
drop_sequences(geophagus, identifier, drop = FALSE)
```

dwc_terms

*Print Darwin Core Terms, Definitions and Examples as Bullet Lists***Description**

dwc_terms() checks a vector or list of terms and return definitions and examples for each one of them.

Usage

```
dwc_terms(dwc, terms)
```

Arguments

dwc	a list of standard terms and definitions created using get_dwc .
terms	a vector or list of terms to check.

Details

For each term in a vector or list, dwc_terms will return a bullet list containing the term, followed by its definition and examples.

Value

a bullet list.

Author(s)

Pedro S. Bittencourt, Rupert A. Collins.

Examples

```
dwc <- get_dwc(type= "simple")
dwc_terms(dwc, c("genus", "scientificName"))
```

geophagus

*Cytochrome C Oxidase Sequences of Geophagus Eartheaters***Description**

This is a set of 354 sequences of the mitochondrial gene cytochrome c oxidase subunit I (COI-5P) of the eartheaters of the *Geophagus sensu stricto* species group downloaded from GenBank. Most of these sequences are from the data analysed by Ximenes et al. (2021).

Usage

geophagus

Format

An object of class [DNABin](#)

Source

Ximenes AM, Bittencourt PS, Machado VN, Hrbek T, Farias IP. 2021. Mapping the hidden diversity of the *Geophagus* sensu stricto species group (Cichlidae: Geophagini) from the Amazon basin. PeerJ 9:e12443.

geophagus_beast	<i>Geophagus Eartheaters Ultrametric Tree</i>
-----------------	---

Description

This is a Maximum Clade Credibility (MCC) tree containing unique haplotypes from [geophagus](#) estimated using BEAST2 v2.6.7. Unique haplotypes were select using [hap_collapse](#).

Usage

geophagus_beast

Format

An object of class [treedata](#).

geophagus_bootstraps	<i>Geophagus Eartheaters Bootstrap Trees</i>
----------------------	--

Description

This is a set of 100 Maximum Likelihood trees sampled from bootstrap trees used to estimate [geophagus_raxml](#) using RAxML-NG v. 1.1.0-master. Meant to be used for [confidence_intervals](#) estimation.

Usage

geophagus_bootstraps

Format

An object of class [multiphylo](#)

geophagus_delims	<i>Geophagus Eartheaters Species Partitions</i>
------------------	---

Description

This is a data frame containing species delimitation partitions for all the 137 unique haplotypes of [geophagus](#) generated using functions contained in this package. Use [report_delim](#) to check number of lineages per method.

Usage

```
geophagus_delims
```

Format

A dataframe with 137 rows and 9 columns:

labels Unique haplotype labels
abgd species partitions for ABGD method
asap species partitions for ASAP method
bgmyc species partitions for bGMYC method
gmyc species partitions for GMYC method
locmin species partitions for locmin method
morph species partitions following NCBI taxonomy
mptp species partitions for mPTP method
ptp species partitions for PTP method

geophagus_info	<i>Geophagus Earthearts Associated Metadata</i>
----------------	---

Description

This is the associated metadata for the 354 sequences of the mitochondrial gene cytochrome c oxidase subunit I (COI-5P) of the *Geophagus sensu stricto* species group downloaded from GenBank and stored in [geophagus](#).

Usage

```
geophagus_info
```

Format

A data frame with 354 rows and 19 columns:

scientificName scientific name

scientificNameGenBank scientific name following NCBI taxonomy

class class

order order

family family

genus genus

dbid NCBI Nucleotide Database internal ID

gbAccession NCBI Nucleotide Database accession number

gene Gene acronym

length Sequence length in base pairs (bp)

organelle Organelle from which gene was sequenced

catalogNumber An identifier for the record within a data set or collection

country Name of the Country followed by sampling locality (when available)

publishedAs Title of the article which generated the sequences

publishedIn Journal which published the article

publishedBy A person, group, or organization responsible for depositing the sequence

date Date published

decimalLatitude Latitude in decimal degrees

decimalLongitude Longitude in decimal degrees

geophagus_posterior	<i>Geophagus Eartheaters Posterior Trees</i>
---------------------	--

Description

This is a set of 100 ultrametric trees sampled from the posterior trees used to estimate [geophagus_beast](#) using BEAST2 v2.6.7. Meant to be used for [confidence_intervals](#) estimation.

Usage

```
geophagus_posterior
```

Format

An object of class [multiphylo](#)

geophagus_raxml	<i>Geophagus Eartheaters Phylogram</i>
-----------------	--

Description

This is a Maximum Likelihood Estimation Tree containing unique haplotypes from [geophagus](#) estimated using RAxML-NG v. 1.1.0-master. Unique haplotypes were select using [hap_collapse](#).

Usage

```
geophagus_raxml
```

Format

An object of class [treedata](#).

get_delim_cols	<i>Extract Labels and Colors from Species Delimitation Partitions</i>
----------------	---

Description

`get_delim_cols()` returns a [tbl_df](#) format containing extracted and processed data from [delim_autoplot](#).

Usage

```
get_delim_cols(p, delimname = NULL, hap_tbl = NULL)
```

Arguments

<code>p</code>	Output from delim_autoplot .
<code>delimname</code>	A character vector of species delimitation names (optional). If provided, the function filters the data to only include rows matching such terms. Default to NULL.
<code>hap_tbl</code>	output from haplotype_tbl (optional). If provided, the function will annotate color and fill data for collapsed haplotypes. Default to NULL.

Details

`get_delim_cols()` is a convenience function to extract labels, species partitions, color and fill data from the output of [delim_autoplot](#) in a [tbl_df](#) format. It is best used when combined with haplotype information from [haplotype_tbl](#) or when combined with other metadata, such as GPS coordinates for map plotting.

Value

an object of class [tbl_df](#).

Author(s)

Pedro S. Bittencourt.

Examples

```
# plot using autoplot
p <- delim_autoplot(geophagus_delims, geophagus_beast)

# view
p

# get haplotypes
hap_tbl <- haplotype_tbl(geophagus)

# extract colors for consensus
get_delim_cols(p, delimname= "consensus", hap_tbl= hap_tbl)
```

get_dwc

Get Darwin Core Terms and Definitions

Description

get_dwc() returns a list of standardized terms and definitions used by the Darwin Core Maintenance Interest Group <https://dwc.tdwg.org/>.

Usage

```
get_dwc(type)
```

Arguments

type	Which type of distribution files to download. Available options are: • simple Simple Darwin Core Terms. • all All Darwin Core Terms.
------	--

Details

get_dwc() reads Darwin Core distribution documents and terms from Github repository <https://github.com/tdwg/dwc> directly into Environment. This function will return a list containing the most recent accepted terms as a vector and a [tbl_df](#) containing terms, definitions, examples and details about each one of them.

Value

a list.

Author(s)

Pedro S. Bittencourt, Rupert A. Collins

Examples

```
dwc <- get_dwc(type= "simple")
```

gmyc_tbl

Turns GMYC Results Into a Tibble

Description

gmyc_tbl() processes output from [gmyc](#) into an object of class [tbl_df](#).

Usage

```
gmyc_tbl(gmyc_res, delimname = "gmyc")
```

Arguments

gmyc_res	Output from gmyc .
delimname	Character. String to rename the delimitation method in the table. Default to 'gmyc'.

Details

splits package uses [gmyc](#) to optimize genetic clusters and [spec.list](#) to cluster samples into species partitions. gmyc_tbl() turns these results into a tibble which matches the output from [bgmyc_tbl](#) and [locmin_tbl](#).

Value

An object of class [tbl_df](#).

Author(s)

Thomas Ezard, Tomochika Fujisawa, Tim Barraclough.

Source

Pons J., Barraclough T. G., Gomez-Zurita J., Cardoso A., Duran D. P., Hazell S., Kamoun S., Sumlin W. D., Vogler A. P. 2006. Sequence-based species delimitation for the DNA taxonomy of undescribed insects. *Systematic Biology*. 55:595-609.

Monaghan M. T., Wild R., Elliot M., Fujisawa T., Balke M., Inward D. J. G., Lees D. C., Ranaivosolo R., Eggleton P., Barraclough T. G., Vogler A. P. 2009. Accelerated species inventory on Madagascar using coalescent-based models of species delineation. *Systematic Biology*. 58:298-311.

Fujisawa T., Barraclough T. G. 2013. Delimiting Species Using Single-Locus Data and the Generalized Mixed Yule Coalescent Approach: A Revised Method and Evaluation on Simulated Data Sets. *Systematic Biology*. 62(5):707–724.

Examples

```
# run GMYC
gmyc_res <- splits::gmyc(ape::as.phylo(geophagus_beast))

# create a tibble
gmyc_df <- gmyc_tbl(gmyc_res)

# check
gmyc_df
```

haplotype_tbl	<i>Summarise Haplotypes Down to One Row</i>
---------------	---

Description

haplotype_tbl() returns a [tbl_df](#) summarising all unique haplotype frequencies and duplicates into a single row.

Usage

```
haplotype_tbl(dna, clean = TRUE, collapseSubstrings = TRUE, verbose = TRUE)
```

Arguments

dna	an object of class DNABin .
clean	logical. Whether to remove or not remove non ACTG bases from alignment.
collapseSubstrings	logical. Whether to collapse or not collapse shorter but identical sequences.
verbose	logical. Returns a warning if any sequence contains non ACTG bases. See clean_dna for details.

Details

haplotype_tbl() uses a combination of [clean_dna](#) and [hap_collapse](#) to summarise haplotypes into a tibble. Each row of the tibble has an unique haplotype, its frequency and all its collapsed duplicates in a flattened string.

Value

an object of class [tbl_df](#).

Author(s)

Rupert A. Collins, Pedro S. Bittencourt.

Examples

```
# get haplotype table
haplotype_tbl(geophagus)
```

hap_collapse	<i>Removes Duplicated Sequences from Alignment</i>
--------------	--

Description

hap_collapse() collapses haplotypes from a [DNABin](#) object, keeping unique haplotypes only.

Usage

```
hap_collapse(dna, clean = TRUE, collapseSubstrings = TRUE, verbose = TRUE)
```

Arguments

dna	A DNABin object.
clean	logical. Whether to remove or not remove non ACTG bases from alignment.
collapseSubstrings	logical. Whether to collapse or not collapse shorter but identical sequences.
verbose	logical. Returns a warning if any sequence contains non ACTG bases. See clean_dna for details.

Details

hap_collapse() collapses a [DNABin](#) object, keeping unique haplotypes only. If clean = TRUE, the function will call [clean_dna](#) to remove any non ACTG bases from alignment prior to collapsing haplotypes. If clean = FALSE, the function will treat data as it is, and will not remove any bases. If collapseSubstrings = TRUE, the function will consider shorter but identical sequences as the same haplotype and collapse them, returning the longest sequence. If collapseSubstrings = FALSE, the function will consider shorter but identical sequences as different haplotypes and will keep them.

Value

A [DNABin](#) object.

Author(s)

Rupert A. Collins

Examples

```
# collapse into unique haplotypes, including shorter sequences
hap_collapse(geophagus, clean = TRUE, collapseSubstrings = TRUE)

# collapse into unique haplotypes keeping shorter sequences
hap_collapse(geophagus, clean = TRUE, collapseSubstrings = FALSE)
```

hap_unite

Unite Haplotype Summaries with Species Delimitation Outputs

Description

hap_unite() returns a single [tbl_df](#) combining all results from [haplotype_tbl](#) or [collapse_others](#) with results from [delim_join](#) or [delim_consensus](#).

Usage

```
hap_unite(hap_tbl, delim)
```

Arguments

hap_tbl output from [haplotype_tbl](#) or [collapse_others](#).
delim output from [delim_join](#) or [delim_consensus](#).

Details

Many functions in this package relies on the usage of unique haplotypes due to known issues when using identical or duplicated sequences for species delimitation analysis. Thus, these outputs will very often refer only to unique haplotypes within a given dataset, which can be determined by using functions like [hap_collapse](#). Assuming that a duplicated or identical sequence should share the same properties as the first sequence of the group has, hap_unite() combines the output of [haplotype_tbl](#) with the output of [delim_join](#). Alternatively, one may use [collapse_others](#) and [delim_consensus](#) as well. This output may be used for downstream analysis or to determine in which cluster a given sequence belongs.

Value

an object of class [tbl_df](#).

Author(s)

Pedro S. Bittencourt

Examples

```
# get haplotype table
hap_tbl <- haplotype_tbl(geophagus)

# unite
hap_unite(hap_tbl, geophagus_delims)
```

locmin_tbl*Turns Local Minima Results into a Tibble*

Description

locmin_tbl() processes output from [tclust](#) into an object of class [tbl_df](#).

Usage

```
locmin_tbl(distobj, threshold = 0.01, haps = NULL, delimname = "locmin")
```

Arguments

distobj	A distance object (usually from dist.dna).
threshold	Distance cutoff for clustering. Default of 0.01. See localMinima for details.
haps	Optional. A vector of haplotypes to keep into the tbl_df .
delimname	Character. String to rename the delimitation method in the table. Default to 'locmin'.

Details

spider package uses [localMinima](#) to determine possible thresholds for any distance matrix and [tclust](#) to cluster samples within a given threshold into species partitions. locmin_tbl() turns these inputs into a tibble which matches the output from [gmyc_tbl](#) and [bgmyc_tbl](#).

Value

An object of class [tbl_df](#).

Author(s)

Samuel Brown.

Source

Brown S.D.J., Collins R.A., Boyer S., Lefort M.-C., Malumbres-Olarte J., Vink C.J., Cruickshank, R.H. 2012. Spider: An R package for the analysis of species identity and evolution, with particular reference to DNA barcoding. Molecular Ecology Resources, 12: 562-565.

Examples

```
# create a distance matrix
mat <- ape::dist.dna(geophagus, model = "raw", pairwise.deletion = TRUE)

# run Local Minima
locmin_res <- spider::localMinima(mat)

# create a tibble
locmin_df <- locmin_tbl(mat,
                        threshold = locmin_res$localMinima[1],
                        haps = ape::as.phylo(geophagus_beast)$tip.label)

# check
locmin_df
```

match_ratio	<i>Compute Agreement Between Alternative Species Delimitation Partitions</i>
-------------	--

Description

match_ratio() uses the Match Ratio statistic of Ahrens et al. (2014) to compute agreement between all pairs of species delimitation partitions in [delim_join](#) output.

Usage

```
match_ratio(delim)
```

Arguments

delim Output from [delim_join](#).

Details

match_ratio() iterates between all species delimitation partitions in [delim_join](#) output and returns a [tbl_df](#) containing the following columns:

- pairs pairs of species delimitation methods analyzed.
- delim_1 number of species partitions in method 1.
- delim_2 number of species partitions in method 2.
- n_match number of identical species partitions in methods 1 and 2.
- match_ratio match ratio statistic, where 0 indicates no agreement between pairs of species delimitation partitions and 1 indicates complete agreement between them.

Value

an object of class [tbl_df](#).

Author(s)

Pedro S. Bittencourt

Source

Ahrens D., Fujisawa T., Krammer H. J., Eberle J., Fabrizi S., Vogler A. P. 2016. Rarity and Incomplete Sampling in DNA-Based Species Delimitation. *Systematic Biology* 65 (3): 478-494.

Examples

```
# estimate match ratio statistics
match_ratio(geophagus_delims)
```

min_brlen	<i>A function to report the smallest tip-to-tip distances in a phylogenetic tree</i>
-----------	--

Description

min_brlen() returns a table of smallest tip-to-tip distances in a phylogenetic tree.

Usage

```
min_brlen(tree, n = 5, verbose = TRUE)
```

Arguments

tree	A path to tree file in Newick format, or a phylogenetic tree object of class phylo .
n	Number of distances to report (default = 5).
verbose	Logical of whether to print the result to screen (default = TRUE).

Details

min_brlen() tabulates the smallest tip-to-tip distances in a phylogenetic tree using [cophenetic.phylo](#) and prints a table to screen. This is useful when excluding identical or near-identical haplotypes using the '-minbr' parameter in mPTP.

Value

an object of class [tbl_df](#)

Author(s)

Rupert A. Collins

Examples

```
# estimate minimum branch length from raxml tree
min_brlen(ape::as.phylo(geophagus_raxml), n = 5)
```

morph_tbl

*Generating a Morphological Delimitation Table***Description**

morph_tbl() returns species partition hypothesis estimated from a prior taxonomic identifications supplied by the user.

Usage

```
morph_tbl(labels, sppVector, delimname = "morph")
```

Arguments

labels	Vector of unique sequence ID labels.
sppVector	Vector of corresponding morphological species delimitation groups.
delimname	Character. String to rename the delimitation method in the table. Default to 'morph'.

Details

morph_tbl() uses information in a species name vector to label each unique sample with a number corresponding to this name.

Value

an object of class [tbl_df](#).

Author(s)

Rupert A. Collins

Examples

```
# create a tibble
morph_df <- morph_tbl(
  labels = geophagus_info$gbAccession,
  sppVector = geophagus_info$scientificName
)

# check
morph_df
```

mptp_tbl

*A Command-Line Interface for mPTP - multi-rate Poisson Tree Processes***Description**

mptp_tbl() returns species partition hypothesis estimated by mPTP software <https://github.com/Pas-Kapli/mptp>.

Usage

```
mptp_tbl(
  infile,
  exe = NULL,
  outfolder = NULL,
  method = c("multi", "single"),
  minbrlen = 1e-04,
  webserver = NULL,
  delimname = "mptp"
)
```

Arguments

infile	Path to tree file in Newick format. Should be dichotomous and rooted.
exe	Path to an mPTP executable.
outfolder	Path to output folder. Default to NULL. If not specified, a temporary location is used.
method	Which algorithm for Maximum Likelihood point-estimate to be used. Available options are: • single Single-rate PTP model. It assumes that every species evolved with the same rate. • multi Multi-rate mPTP model. It assumes that all species have different evolutionary rates.
minbrlen	Numeric. Branch lengths smaller or equal to the value provided are ignored from computations. Default to 0.0001. Use min_brlen for fine tuning.
webserver	A .txt file containing mPTP results obtained from a webserver. Default to NULL.
delimname	Character. String to rename the delimitation method in the table. Default to 'mptp'.

Details

mptp_tbl() relies on [system](#) to invoke mPTP software through a command-line interface. Hence, you must have the software available as an executable file on your system in order to use this function properly. mptp_tbl() saves all output files in outfolder and imports the results generated

to Environment. If an outfolder is not provided by the user, then a temporary location is used. Alternatively, `mptp_tbl()` can parse a file obtained from webserver such as <https://mptp.h-its.org/>.

Value

an object of class `tbl_df`

Author(s)

Paschalia Kapli, Sarah Lutteropp, Jiajie Zhang, Kassian Kobert, Pavlos Pavlides, Alexandros Stamatakis, Tomáš Flouri.

Source

Kapli T., Lutteropp S., Zhang J., Kobert K., Pavlidis P., Stamatakis A., Flouri T. 2016. Multi-rate Poisson tree processes for single-locus species delimitation under maximum likelihood and Markov chain Monte Carlo. *Bioinformatics* 33(11):1630-1638.

Examples

```
# get path to phylogram
path_to_file <- system.file("extdata/geophagus_raxml.nwk", package = "delimtools")

# run mPTP in single threshold mode (PTP)
ptp_df <- mptp_tbl(
  infile = path_to_file,
  exe = "/usr/local/bin/mptp",
  method = "single",
  minbrlen = 0.0001,
  delimname = "ptp",
  outfolder = NULL
)

# check
ptp_df

# run mPTP in multi threshold mode (mPTP)

mptp_df <- mptp_tbl(
  infile = path_to_file,
  exe = "/usr/local/bin/mptp",
  method = "single",
  minbrlen = 0.0001,
  delimname = "mptp",
  outfolder = NULL
)

# check
mptp_df
```

report_delim	<i>Report Unique Species Partitions</i>
--------------	---

Description

report_delim() reports the number of unique species partitions in delim.

Usage

```
report_delim(delim, verbose = TRUE)
```

Arguments

delim	Output from any *_tbl() (e.g. gmyc_tbl), delim_join or delim_consensus .
verbose	Logical. If TRUE, returns a message and a tabulated summary of delim.

Details

For each column in delim, report_delim() will calculate the number of unique partitions and print them to Console. If delim is an output from *_tbl(), report_delim() will get unique species partitions using [vec_unique_count](#). If delim is an output from [delim_join](#) or [delim_consensus](#), values are summarized by using [n_distinct](#) with na.rm = TRUE. This is to prevent any columns with NA values to be interpreted as species partitions.

Value

an object of class [tbl_df](#).

Author(s)

Rupert A. Collins, Pedro S. Bittencourt

Examples

```
# report geophagus delimitations
report_delim(geophagus_delims)
```

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