

# Package ‘delimtools’

May 8, 2026

**Type** Package

**Title** Helper Functions for Species Delimitation Analysis

**Version** 0.2.2

**Date** 2026-03-20

**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>>.

**License** MIT + file LICENSE

**Depends** R (>= 4.2.0)

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

**Suggests** ape, bGMYC (>= 1.0.2), forcats, furr, 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](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** 2026-03-23 08:30:02 UTC

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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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- Tomas Hrbek <hrbek@evoamazon.net> ([ORCID](#)) [contributor]

**See Also**

Useful links:

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

**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: <ul style="list-style-type: none"><li>• 0: Kimura-2P</li><li>• 1: Jukes-Cantor (default)</li><li>• 2: Tamura-Nei</li><li>• 3: simple distance (p-distance)</li></ul>
<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 = "delimitools")

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

```

exe = "/usr/local/bin/abgd",
model = 3,
slope = 0.5,
outfolder = NULL
)
)
# check
try(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 <a href="#">tbl_df</a> .
model	An integer specifying evolutionary model to be used. Available options are: <ul style="list-style-type: none"> <li>• 0: Kimura-2P</li> <li>• 1: Jukes-Cantor (default)</li> <li>• 2: Tamura-Nei</li> <li>• 3: simple distance (p-distance)</li> </ul>
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 = "delimitools")

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

# check
try(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 <a href="#">bgmyc.singlephy</a> .
ppcutoff	Posterior probability threshold for clustering samples into species partitions. See <a href="#">bgmyc.point</a> 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 <- try( 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 <- try( bgmyc_tbl(bgmyc_res, ppcutoff = 0.05) )

# check
try(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 <a href="#">tbl_df</a> containing sequence metadata.
identifier	column in data which contains sequence identifiers.
dna	a <a href="#">DNABin</a> 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, ...)

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

```

### Arguments

tr	An ultrametric, dichotomous tree object in ape format.
posterior	Trees from posterior. An object of class <a href="#">multiphylo</a> .
method	Method of analysis, either "single" for single-threshold version or "multiple" for multiple-threshold version.
interval	Upper and lower limit of estimation of scaling parameters, e.g. c(0,10)
ppcutoff	Posterior probability threshold for clustering samples into species partitions. See <a href="#">bgmyc.point</a> for details. Default to 0.05.
mcmc	number of samples to take from the Markov Chain
burnin	the number of samples to discard as burn-in
thinning	the interval at which samples are retained from the Markov Chain
py1	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 $n^{\text{py}}$ 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.
py2	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 <a href="#">DNABin</a> .
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 <a href="#">localMinima</a> for details.
haps	Optional. A vector of haplotypes to keep into the <a href="#">tbl_df</a> .
...	Further arguments to be passed to <a href="#">dist.dna</a> .
infile	Path to tree file in Newick format. Should be dichotomous and rooted.
bootstraps	Bootstrap trees. An object of class <a href="#">multiphylo</a> .
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 <a href="#">min_brlen</a> 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
{
  try( future::plan("multisession") )

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

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

# plot distribution
try(plot(density(gmyc_res)))

# tabulate
try( 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,
  hexpand = 0.1,
  widths = c(0.5, 0.2)
)
```

**Arguments**

delim	Output from <a href="#">delim_join</a> .
tr	A <a href="#">treedata</a> 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 <a href="#">delim_consensus</a> for details.
delim_order	A character vector of species delimitation names ordered by user. Default to NULL.
tbl_labs	A <a href="#">tbl_df</a> 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 <a href="#">delim_brewer</a> for customized color palette options.
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 <a href="#">wrap_plots</a> 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 <a href="#">delim_join</a> .
tr	A <a href="#">treedata</a> 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 <a href="#">delim_consensus</a> for details.
delim_order	A character vector of species delimitation names ordered by user. Default to NULL.
tbl_labs	A <a href="#">tbl_df</a> 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 <code>tbl_labs</code> 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 <a href="#">wrap_plots</a> for details. Defaults to <code>c(0.5, 0.2)</code> .

## Details

`delimautoplot2()` 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 `delimautoplot` 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 <- delimautoplot2(geophagus_delims,
  geophagus_beast,
  tbl_labs = labs,
  species = "scientificName"
)
p

# view partitions using a phylogram
p1 <- delimautoplot2(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 <a href="#">delim_join</a> .
package	Package which contains color palettes. Available options are "RColorBrewer", "viridisLite" or "randomcoloR".
palette	A palette name. <a href="#">brewer.pal</a> for RColorBrewer or <a href="#">viridis</a> 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 <a href="#">delim_join</a> .
n_match	An integer. Threshold for Majority-Vote calculations. If not specified, returns a warning and the threshold will be defined as $\text{ceiling}(\text{ncol}(\text{delim}[, -1])/2)$ .

### 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 <- try( splits::gmyc(ape::as.phylo(geophagus_beast), method = "single") )

# create a tibble
gmyc_df <- try( gmyc_tbl(gmyc_res) )

## run bGMYC
bgmyc_res <- try( bGMYC::bgmyc.singlelephy(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 <- try( bgmyc_tbl(bgmyc_res, ppcutoff = 0.05) )

## LocMin

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

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

# create a tibble
locmin_df <- try( locmin_tbl(mat,
  threshold = locmin_res$localMinima[1],
  haps = ape::as.phylo(geophagus_beast)$tip.label
)
)
# join delimitations
all_delims <- try( delim_join(list(gmyc_df, bgmyc_df, locmin_df)) )

# check
try(all_delims)
```

---

drop\_sequences      *Remove Sequences of a DNABin list object*

---

### 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**

<code>dwc</code>	a list of standard terms and definitions created using <a href="#">get_dwc</a> .
<code>terms</code>	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      *Geophagus Eartheaters Ultrametric Tree*

---

**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      *Geophagus Eartheaters Bootstrap Trees*

---

**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     *Geophagus Eartheaters Posterior Trees*

---

**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 <a href="#">delim_autoplot</a> .
<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 <a href="#">haplotype_tbl</a> (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 <a href="#">gmyc</a> .
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 <- try( splits::gmyc(ape::as.phylo(geophagus_beast)) )

# create a tibble
gmyc_df <- try( gmyc_tbl(gmyc_res) )

# check
try(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 <a href="#">DNABin</a> .
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 <a href="#">clean_dna</a> 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 <a href="#">DNABin</a> 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 <a href="#">clean_dna</a> 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 <a href="#">dist.dna</a> ).
threshold	Distance cutoff for clustering. Default of 0.01. See <a href="#">localMinima</a> for details.
haps	Optional. A vector of haplotypes to keep into the <a href="#">tbl_df</a> .
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 <a href="#">phylo</a> .
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: <ul style="list-style-type: none"> <li>• single Single-rate PTP model. It assumes that every species evolved with the same rate.</li> <li>• multi Multi-rate mPTP model. It assumes that all species have different evolutionary rates.</li> </ul>
minbrlen	Numeric. Branch lengths smaller or equal to the value provided are ignored from computations. Default to 0.0001. Use <a href="#">min_brlen</a> 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., Pavlides 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 = "delimitools")

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

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

**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)**

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**Examples**

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

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