

Package ‘avotrex’

April 12, 2024

Version 1.0.0

Type Package

Title A Global Dataset of Anthropogenic Extinct Birds and their Traits: Phylogeny Builder

Description Grafts the extinct bird species from the 'Avotrex' database (Sayol et al., in review) on to the 'BirdTree' phylogenies <<https://birdtree.org>>, using a set of different commands.

Encoding UTF-8

RoxygenNote 7.2.3

Depends R (>= 4.0.0)

biocViews

LazyData true

Imports ape, doParallel, doSNOW, dplyr, foreach, parallel, phytools, snow, stringr, tidytree (>= 0.4.6), utils

License GPL-3

Suggests testthat, markdown, knitr, rmarkdown, covr

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

Date/Publication 2024-04-12 15:30:05 UTC

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AvoBind	<i>AvoBind - Bind extinct species to the tree</i>
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Description

Binds an extinct species at a randomly selected point along a branch, after truncating either end.

Usage

```
AvoBind(tree, node, per, per_fixed = FALSE, sp_name)
```

Arguments

tree	Tree object (i.e., phylogeny)
node	Target node
per	The fraction (0-1) of total branch length to truncate at either end of the branch for grafting (e.g. 0.2 cuts of 20% of the total branch length from either end) if <code>per_fixed == FALSE</code> . If <code>per_fixed == TRUE</code> , then the point along the branch where the grafting occurs: value between 0-1, with a larger number meaning the grafting occurs closer to the rootward end of the branch
per_fixed	Logical argument: whether to graft a species on at an exact point along a branch (TRUE), which is chosen using the <code>per</code> argument, rather than random (FALSE; default)
sp_name	Name of the grafted species

Value

Returns a tree of class "phylo", with the extinct species grafted on.

AvoPhylo	<i>AvoPhylo: Building phylogenies based on the AvoTrex extinct bird trait database and BirdTree backbone</i>
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Description

Grafting extinct species onto BirdTree phylogenies using the AvoTrex database

Usage

```
AvoPhylo(ctrees, avotrex, tax, PER = 0.2, PER_FIXED = 0.75, Ntree,
         n.cores = 1, cluster.ips = NULL)
```

Arguments

ctrees	Either (i) object (of class multiPhylo) containing multiple BirdTree phylogenies. Individual trees within the multiPhylo object must be of class 'phylo', see the ape package. Or (ii) an individual tree object of class 'phylo'.
avotrex	The AvoTrex extinct species phylogeny database. This database contains the information and commands required to graft the extinct species on to the BirdTree trees.
tax	The Jetz et al. (2012) BirdTree taxonomy .csv. Supplied as data within the package.
PER	Percentage/fraction for branch truncation based on random grafting (see AvoBind for more details). Can be left at the default value.
PER_FIXED	Point along a branch (expressed as a fraction of the branch length, rootward) to graft the species in the phylogeny database (avotrex argument) which are set to TRUE in the per_fixed column (to reduce very short branch lengths) (see AvoBind for more details). Can be left at the default value.
Ntree	The number of trees to sample from the supplied number of BirdTree trees (i.e., ctrees). Value must be greater than the number of supplied trees (length(ctrees)).
n.cores	Number of cores used to build the phylogeny. Default is one (will run with parallel processing)
cluster.ips	Cluster location. Keep as default.

Details

Function to build phylogenies incorporating the extinct species from the AvoTrex extinct birds database (Sayol et al.). AvoTrex provides data on geographical location, island endemism, volancy, body size and standard external and skeleton morphological measurements for 602 extinct bird species. The AvoPhylo function provides a pipeline to incorporate the extinct species from AvoTrex into the "BirdTree" phylogenies of extant birds (Jetz et al. 2012). Utilising codes assigned to each species based on their known taxonomic affinities, the function binds each species in turn to a provided BirdTree phylogeny. Input phylogenies (i.e., BirdTree trees) must be of class 'phylo', see [phylo](#).

BirdTree phylogenies can be sourced from: <https://birdtree.org/>

The species are grafted onto the tree in a set order provided in the column "Id_sps", as certain species need to be grafted onto the tree before other species. Some species are assigned to groups within the data. These species are assigned a code "xS" within the column "phylo_id2". These species groups consist of close relatives, whose exact taxonomic relationships are unknown. Therefore, the order in which they are joined is randomised. See Sayol et al. and Matthews et al. for further details.

As some of the codes (see table below) randomly place the given species within a group of species, a genus, or a family, and some species groups are randomised before grafting (see above), it is useful to run the grafting procedure over a number of trees to average out the randomisation. Therefore, the function can be run in parallel using the argument `n.cores`. Note that the function will run on one core as default and if only one tree is supplied. Trees can also be randomly selected from a number of trees by giving the function a group of trees using the argument `ctrees` and then defining a smaller number using `Ntree`. If the maximum number of trees is to be used, `Ntree` should equal `length(ctrees)`.

If `Ntree > 1`, a progress bar will be displayed.

A variety of different plotting options are available, see the [plot.avophylo](#) documentation.

Codes	Full name	Definition
S	Sister	Grafted as a sister to a known extant or extinct species already in the tree
SSG	Sister species group	Grafted as a sister to a group of extant and/or extinct species already in the tree
SGG	Sister genus group	Grafted as a sister to an entire extant or extinct genus (i.e., for the first grafted representative)
SGG2	Sister genus group 2	Grafted as sister to multiple genera. This was for when a species was sister to a subgenus
SFG	Sister family group	Grafted as a sister to an entire extant or extinct family already present in the tree (i.e., for the first grafted representative)
SOG	Sister order group	Grafted as a sister to an entire order already present in the tree (i.e., for the first grafted representative)
RSG	Random species group	Grafted to a randomly selected species from a pre-defined group of species (i.e., from a list)
RGG	Random genus group	Grafted to a randomly selected species from a given genus. For example, if an extinct species was sister to a genus, it would be grafted to a randomly selected species from that genus
RGG2	Random genus group 2	Grafted to a randomly selected species from a group of genera (e.g. when all that is known is that a species was sister to a group of genera)
RFG	Random family group	Grafted to a randomly selected species from a given family
RSGG	Random sister genus group	Grafted as sister to a randomly selected genus from a pre-defined group of genera
RSGG2	Random sister genus group 2	Grafted as sister to a randomly selected genus from a pre-defined family

Value

The function returns an object of class 'multiAvophylo', which is a list consisting of N trees (each of class 'avophylo' and 'phylo') that were randomly selected from the supplied number. These trees have all had the extinct species from AvoTrex grafted on. For more details on the grafting, see: Sayol et al. (IN PREP).

References

Matthews et al. (IN REVIEW) The global loss of avian functional and phylogenetic diversity from extinctions in the Holocene and Late Pleistocene

Sayol et al. (IN PREP) The global loss of avian functional and phylogenetic diversity from extinctions in the Holocene and Late Pleistocene

Examples

```
# data(BirdTree_trees)
# data(BirdTree_tax)
# data(AvotrexPhylo)
# trees <- AvoPhylo(ctrees = BirdTree_trees,
# avotrex = AvotrexPhylo, PER = 0.2, PER_FIXED = 0.75,
# tax = BirdTree_tax, Ntree = 1, n.cores = 1, cluster.ips = NULL)
# class(trees)
# trees[[1]]
# class(trees[[1]])

#See the plot.avophylo documentation for the different available
#plotting options.
```

 AvotrexPhylo

Avotrex phylo dataset

Description

The dataset provides instructions to graft extinct bird species from Sayol et al. (IN PREP) on to existing BirdTree phylogenies using the AvoPhylo function from the Avotrex package. Instructions are provided in various columns (see format).

Usage

```
data("AvotrexPhylo")
```

Format

A data frame with 604 observations on the following * variables.

Id_sps a character vector detailing the order in which species are joined

phylo_id2 a character vector detailing the order in which species are joined and whether a species is part of a group (see details)

per_fixed a character vector

Group a numeric vector detailing a group code or NA (see details)

species a character vector detailing species name with an underscore

Order a character vector detailing species order

Family a character vector detailing species family

Genus a character vector detailing species genus

Jetz_Order a character vector detailing species order within the Jetz phylogeny

Jetz_Family a character vector detailing species family within the Jetz phylogeny

Jetz_Genus a character vector detailing species genus within the Jetz phylogeny

Type a character vector of codes. The codes determine how and where the species is grafted to the tree. See details and function "AvoPhylo"

`Sister_order` a character vector. Provides the order within the BirdTree backbone tree to join the extinct species to, or randomly within, depending on the code within the column "Type"

`Sister_clade` a character vector. Provides the clade within the BirdTree backbone tree to join the extinct species to, or randomly within, depending on the code within the column "Type"

`Sister_family` a character vector. Provides the family within the BirdTree backbone tree to join the extinct species to, or randomly within, depending on the code within the column "Type"

`Sister_genus` a character vector. Provides the genus within the BirdTree backbone tree to join the extinct species to, or randomly within, depending on the code within the column "Type"

`Sister_species` a character vector. Provides the species within the BirdTree backbone tree to join the extinct species to depending on the code within the column "Type"

`Sister_species_group` a character vector. Provides the group of species within the BirdTree backbone tree to join the extinct species to, or randomly within, depending on the code within the column "Type"

Details

The species are grafted onto the tree in a set order provided in the column " phylo_id", as certain species need to be grafted onto the tree before other species. Some species are assigned to groups within the data (column "Group"). These species are assigned a code "xS" within the column "phylo_id2". These species groups consist of close relatives, whose exact taxonomic relationships are unknown. Therefore, the order in which they are joined is randomised before they are grafted on to the tree.

As some of the codes within the column "Type" (see table below) randomly place the given species within a group of species, a genus, or a family, and some species groups are randomised before grafting (see above), it is useful to run the grafting procedure over a a number of trees to average out the randomisation (see function "AvoPhylo").

Codes	Full name	Definition
S	Sister	Grafted as a sister to a known extant or extinct species already in the tree
SSG	Sister species group	Grafted as a sister to a group of extant and/or extinct species already in the tree
SGG	Sister genus group	Grafted as a sister to an entire extant or extinct genus (i.e., for the first grafted representative of an extinct genus)
SGG2	Sister genus group 2	Grafted as sister to multiple genera. This was for when a species was sister to a subfamily or some other large specific clade
SFG	Sister family group	Grafted as a sister to an entire extant or extinct family already present in the tree (i.e., for the first grafted representative of an extinct family)
SOG	Sister order group	Grafted as a sister to an entire order already present in the tree (i.e., for the first grafted representative of an extinct order)
RSG	Random species group	Grafted to a randomly selected species from a pre-defined group of species (i.e., from which is believed to have close affinities)
RGG	Random genus group	Grafted to a randomly selected species from a given genus. For example, if an extinct species was believed to be a finch derived from a European finch species, but the exact sister species

is unknown. |
RGG2	Random genus group 2	Grafted to a randomly selected species from a group of genera (e.g. when all that is known is that the species is from a specific subfamily). Currently not used in the database, but the relevant functionality has been kept in the R script, as it could be useful for future studies
RFG	Random family group	Grafted to a randomly selected species from a given family
RSGG	Random sister genus group	Grafted as sister to a randomly selected genus from a pre-defined group of genera
RSGG2	Random sister genus group 2	Grafted as sister to a randomly selected genus from a pre-defined family

Source

Matthews et al. (IN REVIEW) The global loss of avian functional and phylogenetic diversity from extinctions in the Holocene and Late Pleistocene
 Sayol et al. (IN PREP) The global loss of avian functional and phylogenetic diversity from extinctions in the Holocene and Late Pleistocene

References

Matthews et al. (IN REVIEW) The global loss of avian functional and phylogenetic diversity from extinctions in the Holocene and Late Pleistocene
 Sayol et al. (IN PREP) The global loss of avian functional and phylogenetic diversity from extinctions in the Holocene and Late Pleistocene

Examples

```
data(AvotrexPhylo)
```

BirdTree_tax	<i>Bird Tree taxonomic data</i>
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Description

Dataset from Jetz et al. (2012) detailing the BirdTree taxonomy used in the BirdTree backbone phylogenetic trees.

Usage

```
data("BirdTree_tax")
```

Format

A data frame with 9993 observations on the following 11 variables.

Genus a character vector detailing the Bird Tree genus

Species a character vector detailing the Bird Tree species name

TipLabel a character vector detailing the tip label (genus and species name separated by an underscore)

English a character vector detailing the common name for the species

Taxonomy a character vector detailing the Bird Tree taxonomy

Clade a character vector detailing the Bird Tree clade

BLFamilyLatin a character vector detailing the Bird Tree family name (latin)

BLFamilyEnglish a character vector detailing the Bird Tree family name (common)

FamSequID a numeric vector

Order a character vector detailing the Bird Tree order

OscSubOsc a character vector

Details

If necessary, more details than the `__description__` above ~~

Source

Jetz, W., Thomas, G., Joy, J. et al. The global diversity of birds in space and time. *Nature* 491, 444–448 (2012). <https://doi.org/10.1038/nature11631>

References

Jetz, W., Thomas, G., Joy, J. et al. The global diversity of birds in space and time. *Nature* 491, 444–448 (2012). <https://doi.org/10.1038/nature11631>

Examples

```
data(BirdTree_tax)
```

BirdTree_trees

Bird Tree trees

Description

Two Bird Tree backbone trees obtained from Jetz et al. (2012).

Usage

```
data("BirdTree_trees")
```

Format

A multiPhylo object consisting of two elements.

Details

If necessary, more details than the `__description__` above

Source

Jetz, W., Thomas, G., Joy, J. et al. The global diversity of birds in space and time. *Nature* 491, 444–448 (2012). <https://doi.org/10.1038/nature11631>

References

Jetz, W., Thomas, G., Joy, J. et al. The global diversity of birds in space and time. *Nature* 491, 444–448 (2012). <https://doi.org/10.1038/nature11631>

Examples

```
data(BirdTree_trees)
```

```
plot.avophylo
```

Plot Model Fits for an 'avophylo' Object

Description

S3 method for class 'avophylo'. `plot.avophylo` creates plots for objects of class 'avophylo'. The exact plot(s) constructed depends on the argument values provided (see examples below and also the package vignette). The function uses the ape package's [plot.phylo](#) and can take any argument from that function (e.g. the type argument).

If [AvoPhylo](#) is used to produce a list of trees of class 'multiAvophylo', then `plot.multiAvophylo` is first called. This plots individual trees in turn (with the user required to press 'enter' to move to the next plot).

The user will need to play around with plotting window size, and/or export the image, particularly if many tips are included.

Note - if using the `lvls` argument, a warning is provided. This comes from the `tidytree::tree_subset` function and appears to be a bug (but the plot should be checked for sense).

Usage

```
## S3 method for class 'avophylo'
plot(
  x,
  tips = "extinct",
  tips_col = NULL,
  order = NULL,
  family = NULL,
  genus = NULL,
  species = NULL,
  avotrex,
  tax,
  lvls = NULL,
  ...
)
```

Arguments

x	An object of class 'avophylo'.
tips	What tip labels to present. Can be one of "extinct" (just tip labels of extinct species), "none" (no tip labels) or "all_same" (show all labels, with same colour labels for all species), or "all_dif" (show all labels, with different colour labels for extant and extinct species). The latter needs to be used in combination with the tips_col argument.
tips_col	Colour of tip labels. If tips = "all_dif" this needs to be a vector of length two, with the first value being the colour for extinct species, and the second for extant species.
order	Prune the tree to only show a specific order (should be a character vector of length = 1). Taxonomy follows BirdTree, see the data(BirdTree_taxa) file. For extinct order names, see the data(AvotrexPhylo) file.
family	As for order, but for families.
genus	As for order, but for genera.
species	Prune the tree to only show a specific set of species. Should be a vector of at least length = 1. If only a single species name is provided, the lvls argument also needs to be provided.
avotrex	The Avotrex phylo dataset used to generate the trees. For most use cases, this will have been loaded using data(AvotrexPhylo).
tax	The Jetz et al. (2012) BirdTree taxonomy .csv. Supplied as data within the package.
lvls	If species is just a single species, how many levels back (rootward) should be plotted. Uses the tidytree::tree_subset function (see help documentation of that function for further info).
...	Other plotting arguments from the ape package's plot.phylo can be provided.

Value

Generates a phylogeny plot of x.

Examples

```
# Generate a set of trees
# data(BirdTree_trees)
# data(BirdTree_tax)
# data(AvotrexPhylo)
# trees <- AvoPhylo(ctrees = BirdTree_trees,
# avotrex = AvotrexPhylo, PER = 0.2, PER_FIXED = 0.75,
# tax = BirdTree_tax, Ntree = 3, n.cores = 3,
# cluster.ips = NULL)

#For here, we can load in an example set of two trees
#generated using the above code

data(treesEx)
```

```

#order (owls) - just show extinct tip names (in red) and using
#a fan plot
plot(treesEx[[1]], avotrex = AvotrexPhylo, tax = BirdTree_tax,
     order = "Strigiformes", tips = "extinct",
     type = "fan", tip.color = "red", cex = 0.4)

#family (plot all three trees this time)
plot(treesEx, avotrex = AvotrexPhylo, tax = BirdTree_tax,
     family = "Threskiornithidae", tips = "extinct",
     tip.color = "red", cex = 0.5)

#genus - cladogram plot
plot(treesEx[[1]], avotrex = AvotrexPhylo, tax = BirdTree_tax,
     genus = "Aplonis", tips = "extinct",
     type = "cladogram",
     tip.color = "red", cex = 0.5)

#species (& show all tip names in same colour)
species2 <- c("Anas_itchtucknee", "Anas_sp_VitiLevu",
             "Anas_platyrhynchos", "Ara_tricolor")

plot(treesEx[[2]], avotrex = AvotrexPhylo, tax = BirdTree_tax,
     species = species2, tips = "all_same",
     type = "cladogram",
     tip.color = "blue", cex = 0.5)

#same as previous, but extinct and extant diff colours
plot(treesEx[[2]], avotrex = AvotrexPhylo, tax = BirdTree_tax,
     species = species2,
     cex = 0.5, tips = "all_dif",
     tips_col = c("red", "darkgreen"),
     type = "cladogram")

##single species 2 levels back
plot(treesEx[[2]], avotrex = AvotrexPhylo, tax = BirdTree_tax,
     species = "Ara_tricolor",
     tips = "all_dif",
     tips_col = c("red", "darkgreen"),
     lvls = 2,
     type = "phylogram",
     cex = 0.6)

```

plot.multiAvophylo *Plot Model Fits for an 'multiAvophylo' Object*

Description

S3 method for class 'multiAvophylo'. See the [plot.avophylo](#) documentation for more information.

Plots individual trees in turn (with the user required to press 'enter' to move to the next plot).

Usage

```
## S3 method for class 'multiAvophylo'
plot(
  x,
  tips = "extinct",
  tips_col = NULL,
  order = NULL,
  family = NULL,
  genus = NULL,
  species = NULL,
  avotrex,
  tax,
  lvls = NULL,
  ...
)
```

Arguments

x	An object of class 'multiAvophylo'.
tips	What tip labels to present. Can be one of "extinct" (just tip labels of extinct species), "none" (no tip labels) or "all_same" (show all labels, with same colour labels for all species), or "all_dif" (show all labels, with different colour labels for extant and extinct species). The latter needs to be used in combination with the tips_col argument.
tips_col	Colour of tip labels. If tips = "all_dif" this needs to be a vector of length two, with the first value being the colour for extinct species, and the second for extant species.
order	Prune the tree to only show a specific order (should be a character vector of length = 1). Taxonomy follows BirdTree, see the data(BirdTree_taxa) file. For extinct order names, see the data(AvotrexPhylo) file.
family	As for order, but for families.
genus	As for order, but for genera.
species	Prune the tree to only show a specific set of species. Should be a vector of at least length = 1. If only a single species name is provided, the lvls argument also needs to be provided.
avotrex	The Avotrex phylo dataset used to generate the trees. For most use cases, this will have been loaded using data(AvotrexPhylo).
tax	The Jetz et al. (2012) BirdTree taxonomy .csv. Supplied as data within the package.
lvls	If species is just a single species, how many levels back (rootward) should be plotted. Uses the tidytree::tree_subset function (see help documentation of that function for further info).
...	Other plotting arguments from the ape package's plot.phylo can be provided.

Value

Generates a phylogeny plot for each tree in x.

Examples

```
#See the plot.avophylo documentation for further examples
data(treesEx)
#family (plot both trees in turn)
plot(treesEx, avotrex = AvotrexPhylo, tax = BirdTree_tax,
     family = "Threskiornithidae", tips = "extinct",
     tip.color = "red", cex = 0.5)
```

treesEx

A set of three AvoPhylo trees

Description

A "multiAvophylo" object containing two AvoPhylo trees, generated using the AvoPhylo function. Includes 605 extinct species.

Usage

```
data(treesEx)
```

Format

An object of class 'multiAvophylo'

Examples

```
data(treesEx)
```

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