Package 'rase'

September 22, 2017

Title Range Ancestral State Estimation for Phylogeography and
Comparative Analyses

Version 0.3-3

Date 2017-03-21

Depends R (>= 2.14.0), ape (>= 3.1-0), polyCub (>= 0.5-0), spatstat
(>= 1.36-0)

Imports mvtnorm (>= 1.0-0), rgl, sm, methods, grDevices, stats,

Suggests sp, coda, rpanel

Description Implements the Range Ancestral State Estimation for phylogeography described in Quintero, I., Keil, P., Jetz, W., & Crawford, F. W. (2015) <DOI:10.1093/sysbio/syv057>. It also includes Bayesian inference of ancestral states under a Brownian Motion model of character evolution and Maximum Likelihood estimation of rase for n-dimensional data. Visualizing functions in 3D are implemented using the rgl package.

License GPL (>= 2)

NeedsCompilation no

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Repository CRAN

Date/Publication 2017-09-22 21:36:43 UTC

R topics documented:

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  rase-package   *Range Ancestral State Estimation*

Description

The rase package primarily implements the Range Ancestral State Estimation for phylogeography
described in Quintero, I., Keil, P., Jetz, W., Crawford, F. W. 2015 Historical Biogeography Using
Species Geographical Ranges. Systematic Biology. doi: 10.1093/sysbio/syv057. It also includes
Bayesian inference of ancestral states under a Brownian Motion model of character evolution and
Maximum Likelihood estimation of rase for n-dimensional data. Visualizing functions in 3D are
implemented using the rgl package.

Details

Package:	rase
Type:	Package
Version:	0.3-2
Date:	2017-03-21
License:	GLP (>=2)

Author(s)

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References

Quintero, I., Keil, P., Jetz, W., Crawford, F. W. 2015 Historical Biogeography Using Species Geo-
graphical Ranges. *Systematic Biology*.doi: 10.1093/sysbio/syv057

Examples

```
# Here the application in the paper of Quintero et al.,
# on the Psophia trumpeters
# is shown using rase package.
```

```
    #load data
    data(rase_data, package = 'rase')

    ## Not run:
      # check the data we are going to use
      # the phylogenetic tree
      psophia_tree

      # the GPC polygons of Psophia distribution.
      psophia_poly

      # Species names of polygons (in order)
      pnames <- c('dextralis', 'viridis', 'leucoptera', 'interjecta',
        'obscura', 'crepitans', 'ochroptera', 'napensis')

      # name the polygons
      psophia_poly <- name.poly(psophia_poly, psophia_tree,
        poly.names = pnames)

      # Run rase for 10 iterations
      rase_results <- rase(psophia_tree, psophia_poly, niter = 100)
      # Run with higher number of iterations
      # rase_results <- rase(psophia_tree, polygons)
       # Use the amazing 'coda' package to explore the MCMC
      require(coda)

      # post-MCMC handling
      rasemcmc <- coda::mcmc(rase_results)

      #plot the traces for all the parameters
      plot(rasemcmc)

  ## End(Not run)
```

---

add.dens   *Plot the Posterior Density for each Ancestor in 3D Space*

Description

Plots a user-specified credible interval from the posterior density for each ancestor according to rase results. It is mapped in 3D space, where the x/y axes are longitude/latitude, and the z axis is time. Although it works by itself, the posterior densities are intended to overlay an existing phylo.3d plot (see example).

Usage

```
add.dens(df3, res, nlevels = 20, z.scale = 1, col = c(1:nnode), ...)
```

Arguments

df3	an object from `data.for.3d`.
res	the output from a rase run.
nlevels	the credible interval to be plotted for every posterior probabilities. The nlevels is the inverse of the credible interval (CI) to be plotted (e.g., `nlevels = 10` will plot the 90% CI, `nlevels = 20` (the default) will plot the 95% CI).
z.scale	the scale of the time axis (vertical axis). Effectively, the time variable is multiplied by this number. It is very useful for visualization purposes. It should correspond with the z.scale argument in `phylo.3d`
col	vector of colors for the polygons.
...	further arguments to be passed to `polygon3d`.

Author(s)

Ignacio Quintero

References

Quintero, I., Keil, P., Jetz, W., Crawford, F. W. 2015 Historical Biogeography Using Species Geographical Ranges. *Systematic Biology*. doi: 10.1093/sysbio/syv057

See Also

`data.for.3d`, `phylo.3d`, `add.polygons`

Examples

```
# load the mcmc results from rase run, polygons and tree
data(rase_data, package = 'rase')

pnames <- c('dextralis', 'viridis', 'leucoptera', 'interjecta',
'obscura', 'crepitans', 'ochroptera', 'napensis')
psophia_poly <- name.poly(psophia_poly, psophia_tree, poly.names = pnames)

# transform the data for 3d plotting
df3 <- data.for.3d(mcmc, psophia_tree, psophia_poly)

## Not run:
  # plot the tree in 3D
  phylo.3d(df3, z.scale = 10, pts = TRUE)

  # add the polygons representing the tip distributions
  add.polygons(df3)

  # add the posterior density at each node of the 3d tree
  add.dens(df3, mcmc, z.scale = 10, col = c(2:8))

## End(Not run)
```

---

add.polygons	*Plot the Distributions for the Phylogenetic Tips in 3D*

Description

Plots the polygon surfaces of the tips of the phylogeny. It is mapped in 3D space, where the x/y axes are longitude/latitude, and the z axis is time. Although it works by itself, the polygons are intended to overlay an existing `phylo.3d` plot (see example).

Usage

```
add.polygons(df3, axes = 2, ...)
```

Arguments

df3	an object from `data.for.3d`.
axes	number of axes to be plotted (1 = 'x', 2 = 'x' & 'y', 3 = 'x', 'y' & 'z').
...	further arguments to be passed to `polygon3d`.

Details

The polygons do not have to be non-overlapping, however, when they do, they "flicker".

Author(s)

Petr Keil

References

Quintero, I., Keil, P., Jetz, W., Crawford, F. W. 2015 Historical Biogeography Using Species Geographical Ranges. *Systematic Biology*. doi: 10.1093/sysbio/syv057

See Also

`data.for.3d`, `phylo.3d`, `add.dens`

Examples

```
# load the mcmc results from rase run, polygons and tree
data(rase_data, package = 'rase')

pnames <- c('dextralis', 'viridis', 'leucoptera', 'interjecta',
'obscura', 'crepitans', 'ochroptera', 'napensis')
psophia_poly <- name.poly(psophia_poly, psophia_tree, poly.names = pnames)

# transform the data for 3d plotting
df3 <- data.for.3d(mcmc, psophia_tree, psophia_poly)
```

```
## Not run:
  # plot the tree in 3D
  phylo.3d(df3, z.scale = 10, pts = TRUE)

  # add the polygons representing the tip distributions
  add.polygons(df3)

  # add the posterior density at each node of the 3d tree
  add.dens(df3, mcmc, z.scale = 10, col = c(2:8))

## End(Not run)
```

---

bm_ase   *Bayesian Ancestral State Estimation with Points*

Description

Performs a bayesian two-dimensional ancestral state estimation with single values as input (contrast with [rase](#)) according to a Brownian Motion model of trait evolution (or dispersal for phylogeography). It uses Gibbs sampling to approximate the posterior distribution.

Usage

```
bm_ase(tree, values, niter = 1e3, logevery = 10,
sigma2_scale = 0.05, screenlog = TRUE, params0 = NA)
```

Arguments

tree	phylogenetic tree of class "phylo".
values	2-dimensional trait values (e.g., coordinates for phylogeography). Should be a data.frame with two columns named x & y, or a list with two elements named x & y.
niter	number of MCMC iterations. By default niter = 1000.
logevery	iteration cycle to print current iteration. By default logevery = 10.
sigma2_scale	optional. Window proposal for sigma2x & sigma2y.
screenlog	if TRUE (default), prints current iteration every logevery to the screen.
params0	optional. A vector of initial parameter values in the following order: x ancestors, y ancestors, sigma2x and sigma2y. If params0 = NA (default), an initial Maximum Likelihood optimization using [ace](#) provides the starting parameter values.

Value

returns a matrix where every column represents one parameter. The first columns (i.e., nX_x) give the ancestral locations for trait x in the order of nodes in the tree (see the phylo class for details), followed by the ancestral locations of trait y (i.e., nX_y), and the rate parameter in x (sigma2x) and y (sigma2y).

Author(s)

Forrest Crawford, Ignacio Quintero

References

Quintero, I., Keil, P., Jetz, W., Crawford, F. W. 2015 Historical Biogeography Using Species Geographical Ranges. *Systematic Biology*. doi: 10.1093/sysbio/syv057

See Also

For the maximum likelihood version see `point.like.bm`; for the incorporation of polygon uncertainty see `rase`.

Examples

```
### Create some data to be analyzed
# Number of taxa
ntaxa <- 10

# Known parameters
mean_x <- 0
mean_y <- 0
sigma_x <- 1
sigma_y <- 1

# Create a random tree
tree <- ape::rtree(n = ntaxa)

# Create random data according to tree structure
x_locs <- as.numeric(mvtnorm::rmvnorm(1, rep(mean_x,ntaxa), sigma=sigma_x*vcv(tree)))
y_locs <- as.numeric(mvtnorm::rmvnorm(1, rep(mean_y,ntaxa), sigma=sigma_y*vcv(tree)))
values = list(x = x_locs, y = y_locs)
## Not run:
  # run bm_ase for 10 iterations
  bm_results = bm_ase(tree, values, niter = 10)

## End(Not run)
```

---

data.for.3d	*Transform Output for 3D Plotting*

Description

Takes the output from a `rase` run, the corresponding phylogenetic tree and tip polygonal distributions to create and object used for the different 3D plotting functions.

Usage

```
data.for.3d(res, tree, polygons)
```

Arguments

`res`	the output file from a [rase](#) run.
`tree`	phylogenetic tree of class ″phylo″ used as input for [rase](#).
`polygons`	list of polygons in [owin.object](#) format used as input for [rase](#).

Value

Returns an object required by the plotting functions [phylo.3d](#), [add.dens](#) and [add.polygons](#). It is efectively a list with the following elements: `$xyz` containing the 3D coordinates, `$edge` containing the `tree$edge` and `$pol` containing the polygons.

Author(s)

Petr Keil, Ignacio Quintero

References

Quintero, I., Keil, P., Jetz, W., Crawford, F. W. 2015 Historical Biogeography Using Species Geographical Ranges. *Systematic Biology*. doi: 10.1093/sysbio/syv057

See Also

[phylo.3d](#), [add.dens](#), [add.polygons](#), [rase](#)

Examples

```
# load the mcmc results from rase run, polygons and tree
data(rase_data, package = 'rase')

pnames <- c('dextralis', 'viridis', 'leucoptera', 'interjecta',
'obscura', 'crepitans', 'ochroptera', 'napensis')
psophia_poly <- name.poly(psophia_poly, psophia_tree, poly.names = pnames)

# transform the data for 3d plotting
df3 <- data.for.3d(mcmc, psophia_tree, psophia_poly)

## Not run:
  # plot the tree in 3D
  phylo.3d(df3, z.scale = 10, pts = TRUE)

  # add the polygons representing the tip distributions
  add.polygons(df3)

  # add the posterior density at each node of the 3d tree
  add.dens(df3, mcmc, z.scale = 10, col = c(2:8))

## End(Not run)
```

name.poly

Name & Order Polygons According to the Phylogeny

Description

Names polygons and orders them according to the phylogenetic tree. If they match the tree perfectly, the following message should appear: `"tip labels and polygon names match and are in the same order"`.

Usage

```
name.poly(polygons, tree, poly.names = NA)
```

Arguments

polygons	list of polygons in [owin.object](#) format.
tree	phylogenetic tree of class ″phylo″.
poly.names	optional. Vector of names for the polygons. They should be in the same order as the polygons. If poly.names = NA, the function assumes the polygons are already named and only checks if they match the tip labels of the phylogenetic tree.

Value

Returns the polygon list with the names of the tip values in order.

Author(s)

Ignacio Quintero

See Also

[shape.to.rase](#)

Examples

```
# attach polygon data
data(rase_data, package = 'rase')

## Not run:
  # polygons already in format used by rase.
  psophia_poly

  # check the phylogenetic tree
  psophia_tree

  # Species names of polygons (in order)
  pnames <- c('dextralis', 'viridis', 'leucoptera', 'interjecta',
```

```
        'obscura', 'crepitans', 'ochroptera', 'napensis')

    # check tree's' tip labels
    psophia_tree$tip.label

    # name the polygons
    polygons <- name.poly(psophia_poly, psophia_tree, poly.names = pnames)

## End(Not run)
```

---

phylo.3d   *Plots a Phylogenic Tree in 3D*

Description

Plots a phylogenetic tree in 3D using rgl. It is mapped in 3D space, where the x/y axes are longitude/latitude, and the z axis is time. It is used as the first plot function to visualize the results of rase with [add.dens](#) and [add.polygons](#) (see example).

Usage

```
phylo.3d(df3, z.scale = 1, pts = TRUE, ...)
```

Arguments

df3	an object from [data.for.3d](#).
z.scale	the scale of the time axis (vertical axis). Effectively, the time variable is multiplied by this number. It is very useful for visualization purposes. It should correspond with the z.scale argument in [add.dens](#).
pts	if TRUE, points in the verices are plotted.
...	further arguments to be passed to [lines3d](#).

Author(s)

Petr Keil

References

Quintero, I., Keil, P., Jetz, W., Crawford, F. W. 2015 Historical Biogeography Using Species Geographical Ranges. *Systematic Biology*. doi: 10.1093/sysbio/syv057

See Also

[data.for.3d](#), [add.dens](#), [add.polygons](#)

Examples

```
# load the mcmc results from rase run, polygons and tree
data(rase_data, package = 'rase')

pnames <- c('dextralis', 'viridis', 'leucoptera', 'interjecta',
'obscura', 'crepitans', 'ochroptera', 'napensis')
psophia_poly <- name.poly(psophia_poly, psophia_tree, poly.names = pnames)

# transform the data for 3d plotting
df3 <- data.for.3d(mcmc, psophia_tree, psophia_poly)

## Not run:
  # plot the tree in 3D
  phylo.3d(df3, z.scale = 10, pts = TRUE)

  # add the polygons representing the tip distributions
  add.polygons(df3)

  # add the posterior density at each node of the 3d tree
  add.dens(df3, mcmc, z.scale = 10, col = c(2:8))

## End(Not run)
```

| point.like.bm | *n-dimensional Maximum Likelihood of Point Brownian Motion* |

Description

Estimates Most Recent Common Ancestor (MRCA) states and the Brownian rate according to a Brownian Motion model of trait evolution using Maximum Likelihood. It can be used for several dimensions simultaneously. For 1-dimensional traits, we recommend the more stable ace function.

Usage

```
point.like.bm(tree, values, start_values = NA, dimen = NA)
```

Arguments

tree	phylogenetic tree of class ″phylo″.
values	a list, with each element being one-dimensional values for one trait.
start_values	Optional. A vector of starting values for the Maximum Likelihood optimization. The funtion only estimates the MRCA and the rates for each trait, and that should be the order of the input starting values.
dimen	Optional. Number of dimensions (number of traits being analyzed). If dimen = NA, dimensions are obtained from values.

Value

Returns a list with the following components:

mrcas	Most recent common ancestor estimates for each trait (in the same order of the input `values`).
rates	Brownian motion rate parameters for each trait(in the same order of the input values).
nlm.details	A list with the results from nlm optimization. For details see [nlm](#).

Author(s)

Ignacio Quintero

References

Schluter, D., et al. 1997 Likelihood of ancestor states in adaptive radiation. *Evolution*: 1699-1711.

See Also

[ace](#), ML taking into account ranges [ranges.like.bm](#).

Examples

```
# Number of taxa to simulate tree
# Number of taxa
ntaxa <- 10

# Known parameters
mean_x <- 0
mean_y <- 0
sigma_x <- 1
sigma_y <- 1

# Create a random tree
tree <- ape::rtree(n = ntaxa)

# Create random data according to tree structure
x_locs <- as.numeric(mvtnorm::rmvnorm(1, rep(mean_x,ntaxa), sigma=sigma_x*vcv(tree)))
y_locs <- as.numeric(mvtnorm::rmvnorm(1, rep(mean_y,ntaxa), sigma=sigma_y*vcv(tree)))
values <- list(x_locs,y_locs)

## Not run:
# run point.like.bm
bm_results = point.like.bm(tree, values)

## End(Not run)
```

| ranges.like.bm | *n-dimensional Maximumn Likelihood of Range Brownian Motion* |

Description

Estimates Most Recent Common Ancestor (MRCA) states and the Brownian rate according to a Brownian Motion model of trait evolution using Maximum Likelihood. The input for each trait is a one-dimensional range for every tip of the phylogenetic tree (e.g., if your trait is weight, instead of a 1 value input for each tip, usually the average, you can input the whole range of weights for that tip). It can be used for several dimensions simultaneously.

Usage

```
ranges.like.bm(tree, lower_bounds, upper_bounds, start_values = NA, dimen = NA)
```

Arguments

tree	phylogenetic tree of class ″phylo″.
lower_bounds	a list, with each element being one-dimensional lower bounds for a trait.
upper_bounds	a list, with each element being one-dimensional upper bounds for a trait.
start_values	Optional. A vector of starting values for the Maximum Likelihood optimization. The funtion only estimates the MRCA and the rates for each trait, and that should be the order of the input starting values.
dimen	Optional. Number of dimensions (number of traits being analyzed). If dimen = NA, dimensions are obtained from values.

Value

Returns a list with the following components:

mrcas	Most recent common ancestor estimates for each trait
rates	Brownian motion rate parameters for each trait.
nlm.details	A list with the results from nlm optimization. For details see nlm.

Author(s)

Ignacio Quintero

References

Quintero, I., Keil, P., Jetz, W., Crawford, F. W. 2015 Historical Biogeography Using Species Geographical Ranges. *Systematic Biology*. doi: 10.1093/sysbio/syv057

See Also

Contrast with point.like.bm

Examples

```
# Number of taxa to simulate tree
ntaxa <- 10

# Known parameters
# for three dimension
mean_x <- 0
mean_y <- 0
mean_z <- 0

sigma2x <- 1
sigma2y <- 2
sigma2z <- 3

# Create a random tree
tree <- ape::rtree(n = ntaxa)

# Create random data according to tree structure
x_locs <- as.numeric(mvtnorm::rmvnorm(1, rep(mean_x,ntaxa), sigma=sigma2x*vcv(tree)))
y_locs <- as.numeric(mvtnorm::rmvnorm(1, rep(mean_y,ntaxa), sigma=sigma2y*vcv(tree)))
z_locs <- as.numeric(mvtnorm::rmvnorm(1, rep(mean_z,ntaxa), sigma=sigma2z*vcv(tree)))

# random shifts to the mean to create ranges
xshift <- rexp(ntaxa)
yshift <- rexp(ntaxa)
zshift <- rexp(ntaxa)
x_lower <- x_locs - xshift
x_upper <- x_locs + xshift
y_lower <- y_locs - yshift
y_upper <- y_locs + yshift
z_lower <- z_locs - zshift
z_upper <- z_locs + zshift

# store rectangles: this is the trait data:
lower_bounds <- list(xl=x_lower, yl=y_lower, zl=z_lower )
upper_bounds <- list(xu=x_upper, yu=y_upper, zu=z_upper)

## Not run:
#run range.like.bm
range_results <- ranges.like.bm(tree, lower_bounds, upper_bounds)

## End(Not run)
```

---

rase   *Bayesian Range Ancestral State Estimation of Polygons*

Description

Performs a bayesian two-dimensional ancestral state estimation with polygonal distributions as in-
put (contrast with [bm_ase](#)) according to a Brownian Motion model of trait evolution (or dispersal for

phylogeography). It uses Gibbs sampling to approximate the posterior distribution. See reference at the end for more detailed information.

Usage

```
rase(tree, polygons, niter = 1000, logevery = 10,
sigma2_scale = 0.05, screenlog = TRUE, params0 = NA, nGQ = 20)
```

Arguments

tree	phylogenetic tree of class ″phylo″.
polygons	list of polygons in `owin.object` format.
niter	number of MCMC iterations. By default `niter = 1000`.
logevery	iteration cycle to print current iteration. By default `logevery = 10`.
sigma2_scale	optional. window proposal for sigma2x & sigma2y.
screenlog	if TRUE (default), prints current iteration every `logevery` to the screen.
params0	optional. A vector of initial parameter values in the following order: x ancestors, y ancestors, sigma2x and sigma2y. If `params0 = NA` (default), an initial Maximum Likelihood optimization with polygon centroids using `ace` provides the starting parameter values.
nGQ	degree of the one-dimensional Gauss-Legendre quadrature rule (default = 20) as given by `polyCub.SV` in package polyCub. Bigger numbers make the integration more precise, but takes longer.

Value

returns a matrix where every column represents one parameter. The first columns (i.e., nX_x; where X = node 1, ..., node i) give the ancestral locations for trait x in the order of nodes in the tree (see the phylo class for details), followed by the ancestral locations of trait y (i.e., nX_y), and the rate parameter in x (sigma2x) and y (sigma2y). We recommend the using the coda package for plotting and summarizing the resulting mcmc, as in the example below.

Author(s)

Forrest Crawford, Ignacio Quintero

References

Quintero, I., Keil, P., Jetz, W., Crawford, F. W. 2015 Historical Biogeography Using Species Geographical Ranges. *Systematic Biology*. doi: 10.1093/sysbio/syv057

See Also

Contrast with the point ancestral state estimation `bm_ase`. For the maximum likelihood version of ranges see `ranges.like.bm`.

Examples

```
# Here the application in the paper of Quintero et al.,
# on the Psophia trumpeters
# is shown using rase package.

#load data
data(rase_data, package = 'rase')

## Not run:
  # check the data we are going to use
  # the phylogenetic tree
  psophia_tree

  # the GPC polygons of Psophia distribution.
  psophia_poly

  # Species names of polygons (in order)
  pnames <- c('dextralis', 'viridis', 'leucoptera', 'interjecta',
    'obscura', 'crepitans', 'ochroptera', 'napensis')

  # name the polygons
  psophia_poly <- name.poly(psophia_poly, psophia_tree,
    poly.names = pnames)

  # Run rase for 10 iterations
  rase_results <- rase(psophia_tree, psophia_poly, niter = 100)
  # Run with higher number of iterations
  # rase_results <- rase(psophia_tree, polygons)

  # Use the amazing 'coda' package to explore the MCMC
  require(coda)

  # post-MCMC handling
  rasemcmc <- coda::mcmc(rase_results)

  #plot the traces for all the parameters
  plot(rasemcmc)

## End(Not run)
```

---

rase.slice   *Ancestral State Estimation At Any Given Time Slice*

Description

Estimates the geographical location of ancestors (at branches or, much less likely, at nodes) at any given point in time integrating over a rase. It first uses tree.slice to identify the branches that the slice intersects with and then uses MCMC sampling to approximate the posterior distribution of the ancestor locations.

Usage

```
rase.slice(tree, slice, res, polygons,
params0 = NA, niter = 1000, logevery = 10, nGQ = 20)
```

Arguments

tree   phylogenetic tree of class "phylo". The same used in the coderase run.

slice   the time at which to slice. It should be in the same units of the phylogenetic tree.

res   output from rase. Ideally, it should be the post-handled mcmc (i.e., already
              applied burnin and thinning, if applicable).

polygons   list of polygons in owin.object format used as input for rase.

params0   optional. A vector of initial parameter values in the following order: x ancestors
              for each branch in the order given by tree.slice, followed by y ancestors in
              the same order.

niter   number of MCMC iterations. By default niter = 1000.

logevery   iteration cycle to print current iteration. By default logevery = 10.

nGQ   degree of the one-dimensional Gauss-Legendre quadrature rule (default = 20) as
              given by polyCub.SV in package polyCub. Bigger numbers make the integration
              more precise, but takes longer.

Value

returns a matrix where every column represents one parameter. The first columns (i.e., bX_x; where
X = branch 1, ..., branch i) give the ancestral locations for trait x in the order given by tree.slice,
followed by the ancestral locations of trait y (i.e., bX_y).

Author(s)

Ignacio Quintero Forrest Crawford

References

Quintero, I., Keil, P., Jetz, W., Crawford, F. W. 2015 Historical Biogeography Using Species Geo-
graphical Ranges. *Systematic Biology*.doi: 10.1093/sysbio/syv057

See Also

tree.slice, rase

Examples

```
#load data
data(rase_data, package = 'rase')

## Not run:
  # check the data we are going to use

  # examine the mcmc result from rase
```

```
    # after it has been applied a burnin
    # phase and a thinning
    str(mcmc)

    # the phylogenetic tree used in the rase run
    psophia_tree

    # the polygons used in the rase run
    str(psophia_poly)

    # define the slice of time;
    # for now, let's say 1 Million
    # years ago (Ma)
    slice <- 1

    # Species names of polygons (in order)
    pnames <- c('dextralis', 'viridis', 'leucoptera', 'interjecta',
      'obscura', 'crepitans', 'ochroptera', 'napensis')

    # name the polygons
    psophia_poly <- name.poly(psophia_poly, psophia_tree, poly.names = pnames)

    # run rase slice for 100 iterations
    slice_results <- rase.slice(psophia_tree, slice = slice, res = mcmc,
          psophia_poly, niter = 100)

    #check results
    str(slice_results)

## End(Not run)
```

---

rase_data   *Psophia Data Used for rase Package*

Description

Data used for Quintero et al, (2015) extracted from Ribas et al (2012). It contains the phylogenetic tree and current geographic distributions for the genus *Psophia*.

Usage

```
rase_data
```

Format

psophia_shp contains the distributions of Psophia species as shapefiles in the format `SpatialPolygonsDataFrame`. psophia_poly contains the distributions of Psophia species as a list of polygons in `owin.object` format used as input for `rase`. psophia_tree contains Psophia's phylogenetic tree in `phylo` format. mcmc contains the MCMC chain of rase run over the Psophia data after a 2000 burnin period and sampling every 10 iterations.

Source

Ribas, C. C., Aleixo, A., Nogueira, A. C. R., Miyaki, C. Y., and Cracraft, J. 2011 A palaeobiogeographic model for biotic diversification within Amazonia over the past three million years. *Proc. R. Soc. B*.

Quintero, I., Keil, P., Jetz, W., Crawford, F. W. 2015 Historical Biogeography Using Species Geographical Ranges. *Systematic Biology*. doi: 10.1093/sysbio/syv057

---

shape.to.rase   *Transform a Shapefile into* owin.object *Format*

Description

Transforms a Shapefile in format `SpatialPolygonsDataFrame` to the format `owin.object` used by `rase`.

Usage

```
shape.to.rase(shape_poly)
```

Arguments

shape_poly   an object of class `SpatialPolygonsDataFrame`.

Value

Returns a list of polygons in `owin.object` format.

Author(s)

Ignacio Quintero

See Also

`readShapePoly`

Examples

```
## Not run:
# the Shapefiles for the distributions of the tips of the tree
data(rase_data, package = 'rase')

psophia_shp

# Transform the shapefile into the format used by rase
polygons = shape.to.rase(psophia_shp)

# check the structure of the polygons
polygons
```

```
## End(Not run)
```

---

tree.slice   *Identify Tree Branches That Intersect With a Given Time Slice.*

Description

Identifies the branches in a phylogenetic tree that the slice intersects with. It is used by rase.slice.

Usage

```
tree.slice(tree, slice)
```

Arguments

tree   phylogenetic tree of class "phylo".

slice   the time at which to slice. It should be in the same units of the phylogenetic tree.

Details

The tree must be fully dichotomous and all the tips should be extant lineages (time = 0).

Value

returns a matrix where each row is an intersecting branch with the following columns: two integers associating the branch (i.e., ancestor, descendant), the age of the ancestral node, and the age of the descendant node.

Author(s)

Ignacio Quintero

References

Quintero, I., Keil, P., Jetz, W., Crawford, F. W. 2015 Historical Biogeography Using Species Geographical Ranges. *Systematic Biology*. doi: 10.1093/sysbio/syv057

See Also

rase.slice

Examples

```
#load data
data(rase_data, package = 'rase')

## Not run:

# a phylogenetic tree used in the rase run
psophia_tree

# define the slice of time;
# say, 1 Million years ago (Ma)
slice <- 1

# slice the tree
slice_results <- tree.slice(psophia_tree, slice = slice)

#check results
slice_results

## End(Not run)
```

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