

Package ‘phyloraster’

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Title Evolutionary Diversity Metrics for Raster Data

Version 2.2.0

Description Phylogenetic Diversity (PD, Faith 1992), Evolutionary Distinctiveness (ED, Isaac et al. 2007), Phylogenetic Endemism (PE, Rosauer et al. 2009; Laffan et al. 2016), and Weighted Endemism (WE, Laffan et al. 2016) for presence-absence raster. Faith, D. P. (1992) [<doi:10.1016/0006-3207\(92\)91201-3 >](https://doi.org/10.1016/0006-3207(92)91201-3) Isaac, N. J. et al. (2007) [<doi:10.1371/journal.pone.0000296 >](https://doi.org/10.1371/journal.pone.0000296) Laffan, S. W. et al. (2016) [<doi:10.1111/2041-210X.12513 >](https://doi.org/10.1111/2041-210X.12513) Rosauer, D. et al. (2009) [<doi:10.1111/j.1365-294X.2009.04311.x >](https://doi.org/10.1111/j.1365-294X.2009.04311.x).

License GPL (>= 3)

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<https://github.com/gabferreira/phyloraster>,
<https://gabferreira.github.io/phyloraster/>,
<https://doi.org/10.1111/ecog.06902>

BugReports <https://github.com/gabferreira/phyloraster/issues>

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arg.check	<i>Check for missing arguments in function call</i>
-----------	---

Description

Check for missing arguments using function call and a provided vector with argument names to check

Usage

```
arg.check(
  call,
  arguments = c("LR", "inv.R", "branch.length", "n.descen", "tree")
)
```

Arguments

call	match.call(). To get function call with all of the specified arguments and their full names.
arguments	character. Arguments to be checked

Value

logical

Author(s)

Neander Marcel Heming

Examples

```
geop <- function(x, tree, ...){
  f4 <- arg.check(match.call(),
                 c("LR", "inv.R",
                   "branch.length", "n.descen"))
  f1 <- arg.check(match.call(),
                 c("tree"))
  c(f1, f4)
}

geop(1, 1)
geop(1)
geop(1, LR=1)
```

canape.rast

Classify Phylogenetic Endemism using rasters

Description

Use the results of `rast.pe.ses()` to identify centers of paleo-, neo-, super-, and mixed- endemism following the CANAPE scheme of Mishler et al., 2014.

Usage

```
canape.rast(
  pe.obs.p.upper,
  pe.alt.obs.p.upper,
  rpe.obs.p.upper,
  rpe.obs.p.lower,
  filename = NULL,
  overwrite = FALSE
)
```

Arguments

pe.obs.p.upper	SpatRaster. Upper p-value comparing the observed phylogenetic endemism and the randomized phylogenetic endemism values
pe.alt.obs.p.upper	SpatRaster. Upper p-value comparing the alternate phylogenetic endemism and the randomized alternate phylogenetic endemism
rpe.obs.p.upper	SpatRaster. Upper p-value comparing the relative phylogenetic endemism and the randomized relative phylogenetic endemism
rpe.obs.p.lower	SpatRaster. Lower p-value comparing the relative phylogenetic endemism and the randomized relative phylogenetic endemism
filename	character. Output filename
overwrite	logical. If TRUE, filename is overwritten

Value

SpatRaster

See Also

[rast.pe.ses](#), [SESraster](#)

Examples

```
library(SESraster)
library(terra)
library(phylo raster)
x <- rast(system.file("extdata", "rast.presab.tif", package="phylo raster"))
tree <- ape::read.tree(system.file("extdata", "tree.nex",
package="phylo raster"))
data <- phylo.pres(x, tree)
ses <- rast.pe.ses(x = data$x, data$tree,
                 aleats = 5, metric = "all")
# CANAPE
canape <- canape.rast(ses$p.upper.PE, ses$p.upper.PE.alt,
                    ses$p.upper.RPE, ses$p.lower.RPE)
unique(canape)
plot(canape)
```

dataR	<i>Presence-absence of 33 Australian tree frogs (Rosauer 2017)</i>
-------	--

Description

A dataset containing presence-absence of 33 Australian tree frogs. This dataset also provide coordinates x and y for each site.

Usage

```
dataR
```

Format

A matrix with 2891 rows and 35 columns.

Source

Rosauer, 2017. Available on: https://github.com/DanRosauer/phylospatial/tree/master/PhyloEndemism_in_R/Tree%20Frog%20Data

delta.grid	<i>Delta of Diversity Metrics</i>
------------	-----------------------------------

Description

Calculates the difference of rasterized diversity metrics (richness, phylogenetic endemism, phylogenetic diversity, weighted endemism, evolutionary distinctiveness) between time periods.

Usage

```
delta.grid(r1, r2, filename = NULL, cores = 1, ...)
```

Arguments

r1	SpatRaster. Rasterized diversity metrics for time 1 (e.g phylogenetic diversity in present). To calculate some diversity metrics for rasters see <code>phyloraster::geo.phylo</code> function.
r2	SpatRaster. Rasterized diversity metrics for time 2 (e.g phylogenetic diversity in future).
filename	character. Output filename.
cores	positive integer. If <code>cores > 1</code> , a 'parallel' package cluster with that many cores is created and used.
...	additional arguments to be passed passed down from a calling function.

Details

The two input rasters (r1 and r2) must have the same extent and resolution.

Value

SpatRaster

Examples

```
# data
x <- terra::rast(system.file("extdata", "rast.presab.tif",
package="phyloraster"))
tree <- ape::read.tree(system.file("extdata", "tree.nex",
package="phyloraster"))

# metric SR richness
riq.pres <- rast.sr(x)
# imagine we lost some species in the future
riq.fut <- rast.sr(x[[c(1:15)]])
dg <- delta.grid(riq.pres, riq.fut)
terra::plot(dg)
```

df2rast

Transform a data.frame to raster

Description

The function transforms a data.frame or a matrix of presence- absence in a raster of distribution.

Usage

```
df2rast(x, CRS = "+proj=longlat +datum=WGS84", ...)
```

Arguments

x	data.frame. A data.frame or matrix with species names in columns and sites in rows. The first two columns must provide longitude and latitude, respectively.
CRS	character. Description of the Coordinate Reference System (map projection) in PROJ.4.
...	additional arguments to be passed passed down from a calling function.

Value

SpatRaster

Examples

```
dat <- phyloraster::load.data.rosauer()
df2rast(dat$presab, crs = "+proj=longlat +datum=WGS84 +ellps=WGS84
+towgs84=0,0,0")
```

geo.phylo

*Calculate phylogenetic community metrics for raster data***Description**

Calculate species richness, phylogenetic diversity, evolutionary distinctiveness, phylogenetic endemism and weighted endemism using rasters as input.

Usage

```
geo.phylo(
  x,
  tree,
  inv.R,
  edge.path,
  branch.length,
  n.descen,
  full_tree_metr = TRUE,
  filename = "",
  ...
)
```

Arguments

x	SpatRaster. A SpatRaster containing presence-absence data (0 or 1) for a set of species. The layers (species) will be sorted according to the tree order. See the <code>phylo.pres</code> function.
tree	phylo. A dated tree.
inv.R	SpatRaster. Inverse of range size. See inv.range
edge.path	matrix. Matrix representing the paths through the tree from root to each tip. See phylo.pres
branch.length	numeric. A Named numeric vector of branch length for each species. See phylo.pres
n.descen	numeric. A Named numeric vector of number of descendants for each branch. See phylo.pres
full_tree_metr	logical. Whether edge.path, branch length and number of descendants should be calculated with the full (TRUE) or the pruned tree (FALSE). The default is TRUE.
filename	character. Output filename
...	additional arguments passed for <code>terra::app</code>

Details

Community metrics calculated:

- Phylogenetic diversity (Faith 1992)
- Species Richness
- Evolutionary distinctiveness by fair-proportion (Isaac et al. 2007)
- Phylogenetic endemism (Rosauer et al. 2009)
- Weighted endemism (Crisp et al. 2001, Williams et al. 1994)

Value

SpatRaster with one layer for each metric

Author(s)

Neander Marcel Heming

References

Rosauer, D. A. N., Laffan, S. W., Crisp, M. D., Donnellan, S. C. and Cook, L. G. (2009). Phylogenetic endemism: a new approach for identifying geographical concentrations of evolutionary history. *Molecular ecology*, 18(19), 4061-4072.

Faith, D. P. (1992). Conservation evaluation and phylogenetic diversity. *Biological conservation*, 61(1), 1-10.

Williams, P.H., Humphries, C.J., Forey, P.L., Humphries, C.J. and VaneWright, R.I. (1994). Biodiversity, taxonomic relatedness, and endemism in conservation. In: *Systematics and Conservation Evaluation* (eds Forey PL, Humphries C.J., Vane-Wright RI), p. 438. Oxford University Press, Oxford.

Crisp, M., Laffan, S., Linder, H. and Monro, A. (2001). Endemism in the Australian flora. *Journal of Biogeography*, 28, 183–198.

Isaac, N. J., Turvey, S. T., Collen, B., Waterman, C. and Baillie, J. E. (2007). Mammals on the EDGE: conservation priorities based on threat and phylogeny. *PLoS ONE* 2, e296.

Laffan, S. W., Rosauer, D. F., Di Virgilio, G., Miller, J. T., González-Orozco, C. E., Knerr, N., ... & Mishler, B. D. (2016). Range-weighted metrics of species and phylogenetic turnover can better resolve biogeographic transition zones. *Methods in Ecology and Evolution*, 7(5), 580-588.

See Also

[phylo.pres](#), [inv.range](#), [rast.ed](#), [rast.pd](#), [rast.we](#), [rast.pe](#), [rast.sr](#), [geo.phylo.ses](#),

Examples

```
library(terra)
library(phylo raster)
x <- terra::rast(system.file("extdata", "rast.presab.tif",
package="phylo raster"))[[1:10]]
tree <- ape::read.tree(system.file("extdata", "tree.nex",
```

```

package="phyloraster"))
data <- phylo.pres(x, tree)
inv.R <- inv.range(data$x)
t <- geo.phylo(data$x, inv.R = inv.R, edge.path = data$edge.path,
branch.length = data$branch.length, n.descen = data$n.descendants)
terra::plot(t)

```

geo.phylo.ses	<i>Calculate phylogenetic community metrics and their standardized effect sizes for raster data</i>
---------------	---

Description

Calculates the standardized effect size for phylogenetic community metrics. See Details for more information.

Usage

```

geo.phylo.ses(
  x,
  tree,
  inv.R,
  edge.path,
  branch.length,
  n.descen,
  full_tree_metr = TRUE,
  spat_alg = "bootspat_str",
  spat_alg_args = list(rprob = NULL, rich = NULL, fr_prob = NULL),
  aleats = 10,
  cores = 1,
  filename = "",
  ...
)

```

Arguments

x	SpatRaster. A SpatRaster containing presence-absence data (0 or 1) for a set of species. The layers (species) will be sorted according to the tree order. See the phylo.pres function.
tree	phylo. A dated tree.
inv.R	SpatRaster. Inverse of range size. See inv.range
edge.path	matrix. Matrix representing the paths through the tree from root to each tip. See phylo.pres
branch.length	numeric. A Named numeric vector of branch length for each species. See phylo.pres

n.descen	numeric. A Named numeric vector of number of descendants for each branch. See phylo.pres
full_tree_metr	logical. Whether edge.path, branch length and number of descendants should be calculated with the full (TRUE) or the pruned tree (FALSE). The default is TRUE.
spat_alg	A function with the algorithm implementing the desired randomization method. It must work with SpatRaster objects. See examples. Example of functions that work are: bootspat_naive , bootspat_str , bootspat_ff .
spat_alg_args	List of arguments passed to the randomization method chosen in 'spat_alg'. See bootspat_naive , bootspat_str , bootspat_ff
aleats	positive integer. A positive integer indicating how many times the calculation should be repeated.
cores	positive integer. If cores > 1, a 'parallel' package cluster with that many cores is created and used. You can also supply a cluster object. Ignored for functions that are implemented by terra in C++ (see under fun)
filename	character. Output filename
...	additional arguments passed for terra::app

Details

The dependency 'SESRaster' is used to calculate the null models. This package currently implements six algorithms to randomize binary species distribution with several levels of constraints: SIM1, SIM2, SIM3, SIM5, SIM6 and SIM9 (sensu Gotelli 2000). The methods implemented in 'SESRaster' are based on how species (originally rows) and sites (originally columns) are treated (i.e. fixed, equiprobable, or proportional sums) (Gotelli 2000). By default, the 'phyloraster' uses the function `bootspat_str()` from the 'SESRaster' package to conduct the randomizations, but the user is free to choose any of the other methods mentioned above through the `spat_alg` argument in the `*.ses()` functions of the 'phyloraster' package. The `bootspat_str()` is equivalent to the SIM5 (proportional-fixed) method of Gotelli (2000), which partially relaxes the spatial structure of species distributions, but keeps the spatial structure of the observed richness pattern across cells.

The dependency 'SESRaster' is used to calculate the null models. This package currently implements six algorithms to randomize binary species distribution with several levels of constraints: SIM1, SIM2, SIM3, SIM5, SIM6 and SIM9 (sensu Gotelli 2000). The methods implemented in 'SESRaster' are based on how species (originally rows) and sites (originally columns) are treated (i.e. fixed, equiprobable, or proportional sums) (Gotelli 2000). By default, the 'phyloraster' uses the function `bootspat_str()` from the 'SESRaster' package to conduct the randomizations, but the user is free to choose any of the other methods mentioned above through the `spat_alg` argument in the `*.ses()` functions of the 'phyloraster' package. The `bootspat_str()` is equivalent to the SIM5 (proportional-fixed) method of Gotelli (2000), which partially relaxes the spatial structure of species distributions, but keeps the spatial structure of the observed richness pattern across cells.

Value

SpatRaster. The function returns the observed value of the metric, the mean of the simulations calculated over n times, the standard deviation of the simulations, the standardized effect size (SES) for the metric, and the p-values.

Author(s)

Neander Marcel Heming

References

Gotelli, N. J. 2000. Null model analysis of species co-occurrence patterns. – Ecology 81: 2606–2621.
Heming, N. M., Mota, F. M. M. and Alves-Ferreira, G. 2023. SESraster: raster randomization for null hypothesis testing. <https://CRAN.R-project.org/package=SESraster>.

See Also

[phylo.pres](#), [inv.range](#), [geo.phylo](#), [rast.ed.ses](#), [rast.pd.ses](#), [rast.we.ses](#), [rast.pe.ses](#), [bootspat_str](#), [bootspat_naive](#), [bootspat_ff](#), [SESraster](#)

Examples

```
library(terra)
library(phyloraster)
require("SESraster")
x <- terra::rast(system.file("extdata", "rast.presab.tif",
package="phyloraster"))
tree <- ape::read.tree(system.file("extdata", "tree.nex",
package="phyloraster"))
tses <- geo.phylo.ses(x = x,
                    tree = tree,
                    spat_alg = "bootspat_str",
                    spat_alg_args = list(rprob = NULL,
                                         rich = NULL,
                                         fr_prob = NULL),
                    aleats = 2)
terra::plot(tses)
```

inv.range

Calculate the inverse of range size

Description

Get range size in square kilometers for all cells that are not NA, the inverse of range size and the inverse of range size multiplied by branch length for multiple species using a raster of presence-absence.

Usage

```
inv.range(x, filename = "", overwrite = FALSE, ...)
```

Arguments

x	SpatRaster. A SpatRaster containing presence-absence data (0 or 1) for a set of species. The layers (species) will be sorted according to the tree order. See the phylo.pres function.
filename	character. Output filename
overwrite	logical. If TRUE, filename is overwritten
...	additional arguments to be passed passed down from a calling function.

Value

SpatRaster and numeric

Author(s)

Neander Marcel Heming and Gabriela Alves-Ferreira

Examples

```
# calculating the inverse of range size
x <- terra::rast(system.file("extdata", "rast.presab.tif",
package="phyloraster"))
inv.range(x[[5]])
```

load.data.rosauer	<i>Load an example dataset with presence-absence data of 33 tree frogs and a phylogenetic tree for this species</i>
-------------------	---

Description

This function load a phylogenetic tree, a raster and a data.frame with presence-absence of 33 Australian tree frogs from Rosauer (2017). We also provide distribution shapefiles for ten species according to the IUCN.

Usage

```
load.data.rosauer()
```

Value

data.frame, SpatRaster, SpatVector and phylo

Source

Rosauer, 2017. Available on: [Github](#)

IUCN. 2022. The IUCN Red List of Threatened Species (spatial data). Version 2022-1. [IUCN](#)

 phylo.pres

Prepare rasters and phylogenetic tree to run community metrics

Description

Reorder a stack of rasters of species distribution to match the order of the tips of the tree, and get branch length and number of descendants for each species to calculate diversity metrics using `phyloraster::geo.phylo()`. The branch length and the number of descendants can be calculated based on the full tree or the raster based tree subset. The names must be the same in the phylogenetic tree and in the raster for the same species. For example, if you have the name "Leptodactylus_latrans" in the raster and "Leptodactylus latrans" in the tree, the function will not work. The same goes for uppercase and lowercase letters.

Usage

```
phylo.pres(x, tree, full_tree_metr = TRUE, ...)
```

Arguments

<code>x</code>	SpatRaster. A SpatRaster containing presence-absence data (0 or 1) for a set of species.
<code>tree</code>	phylo. A dated tree.
<code>full_tree_metr</code>	logical. Whether edge.path, branch length and number of descendants should be calculated with the full (TRUE) or the pruned tree (FALSE). The default is TRUE.
<code>...</code>	additional arguments to be passed passed down from a calling function.

Value

Returns a list containing a SpatRaster reordered according to the order that the species appear in the phylogenetic tree, a subtree containing only the species that are in the stack of rasters and finally two named numerical vectors containing the branch length and the number of descendants of each species.

Author(s)

Neander Marcel Heming and Gabriela Alves Ferreira

Examples

```
library(phyloraster)
x <- terra::rast(system.file("extdata", "rast.presab.tif",
  package="phyloraster"))
tree <- ape::read.tree(system.file("extdata", "tree.nex",
  package="phyloraster"))
phylo.pres(x[[1:3]], tree, full_tree_metr = TRUE)
```

```
# using the pruned tree
phylo.pres(x[[1:3]], tree, full_tree_metr = FALSE)
```

range_size

Calculate range size for a set of species using a raster as input

Description

This function calculate range size in square meters (by default) for all cells that are not NA. The size of the cells is constant in degrees but not in square meters, which was considered in the method applied to calculate the area.

Usage

```
range_size(x, cellSz, unit = "m", ...)
```

Arguments

x	SpatRaster. A SpatRaster containing presence-absence data (0 or 1) for a set of species. The layers (species) will be sorted according to the tree order. See the phylo.pres function.
cellSz	SpatRaster. A SpatRaster containing cellSize values. See cellSize
unit	character. One of "m", "km", or "ha"
...	additional arguments to be passed passed down from a calling function.

Value

vector

Author(s)

Gabriela Alves Ferreira and Neander Marcel Heming

Examples

```
x <- terra::rast(system.file("extdata", "rast.presab.tif",
package="phyloraster"))
range_size(x[[1:2]], cellSz <- terra::cellSize(x))
```

rast.ed

*Calculate Evolutionary distinctiveness for raster data***Description**

This function calculates evolutionary distinctiveness according to the fair-proportion index. The values represents the mean ED for species presents in each raster cell.

Usage

```

rast.ed(
  x,
  tree,
  edge.path,
  branch.length,
  n.descen,
  full_tree_metr = TRUE,
  filename = "",
  ...
)

```

Arguments

x	SpatRaster. A SpatRaster containing presence-absence data (0 or 1) for a set of species. The layers (species) will be sorted according to the tree order. See the phylo.pres function.
tree	phylo. A dated tree.
edge.path	matrix. Matrix representing the paths through the tree from root to each tip. See phylo.pres
branch.length	numeric. A Named numeric vector of branch length for each species. See phylo.pres
n.descen	numeric. A Named numeric vector of number of descendants for each branch. See phylo.pres
full_tree_metr	logical. Whether edge.path, branch length and number of descendants should be calculated with the full (TRUE) or the pruned tree (FALSE). The default is TRUE.
filename	character. Output filename
...	additional arguments passed for terra::app

Value

SpatRaster

Author(s)

Neander Marcel Heming and Gabriela Alves-Ferreira

References

Isaac, N. J., Turvey, S. T., Collen, B., Waterman, C. and Baillie, J. E. (2007). Mammals on the EDGE: conservation priorities based on threat and phylogeny. PLoS ONE 2, e296.

Examples

```
library(terra)
library(phylo raster)
x <- rast(system.file("extdata", "rast.presab.tif",
  package="phylo raster"))
# phylogenetic tree
tree <- ape::read.tree(system.file("extdata", "tree.nex",
  package="phylo raster"))
data <- phylo.pres(x[[1:3]], tree)
ed <- rast.ed(data$x, edge.path = data$edge.path,
  branch.length = data$branch.length,
  n.descen = data$n.descen)

plot(ed)
```

rast.ed.ses

Standardized effect size for Evolutionary distinctiveness

Description

Calculates the standardized effect size for evolutionary distinctiveness. See Details for more information.

Usage

```
rast.ed.ses(
  x,
  tree,
  edge.path,
  branch.length,
  n.descen,
  full_tree_metr = TRUE,
  spat_alg = "bootspat_str",
  spat_alg_args = list(rprob = NULL, rich = NULL, fr_prob = NULL),
  aleats = 10,
  filename = "",
  ...
)
```

Arguments

<code>x</code>	SpatRaster. A SpatRaster containing presence-absence data (0 or 1) for a set of species. The layers (species) will be sorted according to the tree order. See the <code>phylo.pres</code> function.
<code>tree</code>	phylo. A dated tree.
<code>edge.path</code>	matrix. Matrix representing the paths through the tree from root to each tip. See phylo.pres
<code>branch.length</code>	numeric. A Named numeric vector of branch length for each species. See phylo.pres
<code>n.descen</code>	numeric. A Named numeric vector of number of descendants for each branch. See phylo.pres
<code>full_tree_metr</code>	logical. Whether <code>edge.path</code> , <code>branch.length</code> and <code>n.descen</code> should be calculated with the full (TRUE) or the pruned tree (FALSE). The default is TRUE.
<code>spat_alg</code>	A function with the algorithm implementing the desired randomization method. It must work with SpatRaster objects. See examples. Example of functions that work are: bootspat_naive , bootspat_str , bootspat_ff .
<code>spat_alg_args</code>	List of arguments passed to the randomization method chosen in <code>'spat_alg'</code> . See bootspat_naive , bootspat_str , bootspat_ff
<code>aleats</code>	positive integer. A positive integer indicating how many times the calculation should be repeated.
<code>filename</code>	character. Output filename
<code>...</code>	additional arguments passed for <code>terra::app</code>

Details

The dependency ‘SESraster’ is used to calculate the null models. This package currently implements six algorithms to randomize binary species distribution with several levels of constraints: SIM1, SIM2, SIM3, SIM5, SIM6 and SIM9 (sensu Gotelli 2000). The methods implemented in ‘SESraster’ are based on how species (originally rows) and sites (originally columns) are treated (i.e. fixed, equiprobable, or proportional sums) (Gotelli 2000). By default, the ‘phyloraster’ uses the function `bootspat_str()` from the ‘SESraster’ package to conduct the randomizations, but the user is free to choose any of the other methods mentioned above through the `spat_alg` argument in the `*.ses()` functions of the ‘phyloraster’ package. The `bootspat_str()` is equivalent to the SIM5 (proportional-fixed) method of Gotelli (2000), which partially relaxes the spatial structure of species distributions, but keeps the spatial structure of the observed richness pattern across cells.

Value

SpatRaster. The function returns the observed value of the metric, the mean of the simulations calculated over `n` times, the standard deviation of the simulations, the standardized effect size (SES) for the metric, and the p-values.

Author(s)

Neander M. Heming and Gabriela Alves-Ferreira

References

- Gotelli, N. J. 2000. Null model analysis of species co-occurrence patterns. – Ecology 81: 2606–2621.
- Heming, N. M., Mota, F. M. M. and Alves-Ferreira, G. 2023. SESraster: raster randomization for null hypothesis testing. <https://CRAN.R-project.org/package=SESraster>.

See Also

[phylo.pres](#), [inv.range](#), [geo.phylo.ses](#), [rast.ed.ses](#), [rast.pd.ses](#), [rast.we.ses](#), [rast.pe.ses](#), [bootspat_str](#), [bootspat_naive](#), [bootspat_ff](#), [SESraster](#)

Examples

```
library(phylo raster)
library(SESraster)
x <- terra::rast(system.file("extdata", "rast.presab.tif",
package="phylo raster"))
tree <- ape::read.tree(system.file("extdata", "tree.nex",
package="phylo raster"))
t <- rast.ed.ses(x[[1:10]], tree, aleats = 3)
terra::plot(t)
```

rast.pd

Calculate phylogenetic diversity for raster data

Description

Calculate the sum of the branch length for species present in each cell of the raster.

Usage

```
rast.pd(
  x,
  tree,
  edge.path,
  branch.length,
  full_tree_metr = TRUE,
  filename = "",
  ...
)
```

Arguments

- x** SpatRaster. A SpatRaster containing presence-absence data (0 or 1) for a set of species. The layers (species) will be sorted according to the tree order. See the [phylo.pres](#) function.
- tree** phylo. A dated tree.

edge.path	matrix. Matrix representing the paths through the tree from root to each tip. See phylo.pres
branch.length	numeric. A Named numeric vector of branch length for each species. See phylo.pres
full_tree_metr	logical. Whether edge.path, branch length and number of descendants should be calculated with the full (TRUE) or the pruned tree (FALSE). The default is TRUE.
filename	character. Output filename
...	additional arguments passed for terra::app

Value

SpatRaster

Author(s)

Neander Marcel Heming and Gabriela Alves-Ferreira

References

Faith, D. P. (1992). Conservation evaluation and phylogenetic diversity. *Biological conservation*, 61(1), 1-10.

Examples

```
library(terra)
library(phylo raster)
x <- rast(system.file("extdata", "rast.presab.tif",
package="phylo raster"))
tree <- ape::read.tree(system.file("extdata", "tree.nex",
package="phylo raster"))
data <- phylo.pres(x[[1:3]], tree)
pd <- rast.pd(data$x, data$tree)
plot(pd)
```

rast.pd.ses

*Standardized effect size for Phylogenetic diversity***Description**

Calculates the standardized effect size for phylogenetic diversity. See Details for more information.

Usage

```

rast.pd.ses(
  x,
  tree,
  edge.path,
  branch.length,
  full_tree_metr = TRUE,
  spat_alg = "bootspat_str",
  spat_alg_args = list(rprob = NULL, rich = NULL, fr_prob = NULL),
  aleats = 10,
  filename = "",
  ...
)

```

Arguments

x	SpatRaster. A SpatRaster containing presence-absence data (0 or 1) for a set of species. The layers (species) will be sorted according to the tree order. See the <code>phylo.pres</code> function.
tree	phylo. A dated tree.
edge.path	matrix. Matrix representing the paths through the tree from root to each tip. See phylo.pres
branch.length	numeric. A Named numeric vector of branch length for each species. See phylo.pres
full_tree_metr	logical. Whether edge.path, branch length and number of descendants should be calculated with the full (TRUE) or the pruned tree (FALSE). The default is TRUE.
spat_alg	A function with the algorithm implementing the desired randomization method. It must work with SpatRaster objects. See examples. Example of functions that work are: bootspat_naive , bootspat_str , bootspat_ff .
spat_alg_args	List of arguments passed to the randomization method chosen in 'spat_alg'. See bootspat_naive , bootspat_str , bootspat_ff
aleats	positive integer. A positive integer indicating how many times the calculation should be repeated.
filename	character. Output filename
...	additional arguments passed for terra::app

Details

The dependency 'SESRaster' is used to calculate the null models. This package currently implements six algorithms to randomize binary species distribution with several levels of constraints: SIM1, SIM2, SIM3, SIM5, SIM6 and SIM9 (sensu Gotelli 2000). The methods implemented in 'SESRaster' are based on how species (originally rows) and sites (originally columns) are treated (i.e. fixed, equiprobable, or proportional sums) (Gotelli 2000). By default, the 'phyloraster' uses the function `bootspat_str()` from the 'SESRaster' package to conduct the randomizations, but the user is free to choose any of the other methods mentioned above through the `spat_alg` argument

in the `*.ses()` functions of the ‘phyloraster’ package. The `bootspat_str()` is equivalent to the SIM5 (proportional-fixed) method of Gotelli (2000), which partially relaxes the spatial structure of species distributions, but keeps the spatial structure of the observed richness pattern across cells.

Value

`SpatRaster`. The function returns the observed value of the metric, the mean of the simulations calculated over `n` times, the standard deviation of the simulations, the standardized effect size (SES) for the metric, and the p-values.

Author(s)

Gabriela Alves-Ferreira and Neander Heming

References

Gotelli, N. J. 2000. Null model analysis of species co-occurrence patterns. – *Ecology* 81: 2606–2621.
 Heming, N. M., Mota, F. M. M. and Alves-Ferreira, G. 2023. `SESRaster`: raster randomization for null hypothesis testing. <https://CRAN.R-project.org/package=SESRaster>.

See Also

[phylo.pres](#), [inv.range](#), [geo.phylo.ses](#), [rast.ed.ses](#), [rast.pd.ses](#), [rast.we.ses](#), [rast.pe.ses](#), [bootspat_str](#), [bootspat_naive](#), [bootspat_ff](#), [SESRaster](#)

Examples

```
library(terra)
library(phyloraster)
library(SESRaster)
x <- rast(system.file("extdata", "rast.presab.tif",
  package="phyloraster"))
tree <- ape::read.tree(system.file("extdata", "tree.nex",
  package="phyloraster"))
data <- phylo.pres(x[[1:10]], tree)
t <- rast.pd.ses(data$x, edge.path = data$edge.path,
  branch.length = data$branch.length, aleats = 3)
plot(t)
```

rast.pe

Calculate phylogenetic endemism for raster data

Description

Calculate the sum of the inverse of the range size multiplied by the branch length for the species present in raster data.

Usage

```

rast.pe(
  x,
  tree,
  inv.R,
  branch.length,
  full_tree_metr = TRUE,
  filename = "",
  ...
)

```

Arguments

x	SpatRaster. A SpatRaster containing presence-absence data (0 or 1) for a set of species. The layers (species) will be sorted according to the tree order. See the <code>phylo.pres</code> function.
tree	phylo. A dated tree.
inv.R	SpatRaster. Inverse of range size. See inv.range
branch.length	numeric. A Named numeric vector of branch length for each species. See phylo.pres
full_tree_metr	logical. Whether edge.path, branch length and number of descendants should be calculated with the full (TRUE) or the pruned tree (FALSE). The default is TRUE.
filename	character. Output filename
...	additional arguments passed for <code>terra::app</code>

Value

SpatRaster

Author(s)

Gabriela Alves-Ferreira and Neander Marcel Heming

References

Laffan, S. W., Rosauer, D. F., Di Virgilio, G., Miller, J. T., González-Orozco, C. E., Knerr, N., ... & Mishler, B. D. (2016). Range-weighted metrics of species and phylogenetic turnover can better resolve biogeographic transition zones. *Methods in Ecology and Evolution*, 7(5), 580-588.

Rosauer, D. A. N., Laffan, S. W., Crisp, M. D., Donnellan, S. C. and Cook, L. G. (2009). Phylogenetic endemism: a new approach for identifying geographical concentrations of evolutionary history. *Molecular ecology*, 18(19), 4061-4072.

Examples

```
library(terra)
library(phylo raster)
x <- rast(system.file("extdata", "rast.presab.tif",
  package = "phylo raster"))
tree <- ape::read.tree(system.file("extdata", "tree.nex",
  package = "phylo raster"))
pe <- rast.pe(x = x[[1:3]], tree)
plot(pe)
```

 rast.pe.ses

Standardized effect size for Phylogenetic endemism

Description

Calculates the standardized effect size for phylogenetic endemism. See Details for more information.

Usage

```
rast.pe.ses(
  x,
  tree,
  branch.length,
  branch.length.alt,
  inv.R,
  full_tree_metr = TRUE,
  spat_alg = "bootspat_str",
  spat_alg_args = list(rprob = NULL, rich = NULL, fr_prob = NULL),
  metric = c("pe", "pe.alt", "rpe", "all")[4],
  aleats = 10,
  cores = 1,
  filename = "",
  overwrite = TRUE,
  ...
)
```

Arguments

x	SpatRaster. A SpatRaster containing presence-absence data (0 or 1) for a set of species. The layers (species) will be sorted according to the tree order. See the <code>phylo.pres</code> function.
tree	phylo. A dated tree.
branch.length	numeric. A Named numeric vector of branch length for each species. See phylo.pres

<code>branch.length.alt</code>	numeric. Branch length calculated by using an alternative phylogeny with non-zero branch lengths converted to a constant value (1) and rescaled so the sum of all branch lengths is 1.
<code>inv.R</code>	SpatRaster. Inverse of range size. See inv.range
<code>full_tree_metr</code>	logical. Whether edge.path, branch length and number of descendants should be calculated with the full (TRUE) or the pruned tree (FALSE). The default is TRUE.
<code>spat_alg</code>	A function with the algorithm implementing the desired randomization method. It must work with SpatRaster objects. See examples. Example of functions that work are: bootspat_naive , bootspat_str , bootspat_ff .
<code>spat_alg_args</code>	List of arguments passed to the randomization method chosen in 'spat_alg'. See bootspat_naive , bootspat_str , bootspat_ff
<code>metric</code>	character. Names of biodiversity metrics to calculate (pe, pe_alt, rpe, all). See details.
<code>aleats</code>	positive integer. A positive integer indicating how many times the calculation should be repeated.
<code>cores</code>	positive integer. If <code>cores > 1</code> , a 'parallel' package cluster with that many cores is created and used. You can also supply a cluster object. Ignored for functions that are implemented by terra in C++ (see under fun)
<code>filename</code>	character. Output filename
<code>overwrite</code>	logical. If TRUE, filename is overwritten
<code>...</code>	additional arguments passed for terra::app

Details

The dependency 'SESRaster' is used to calculate the null models. This package currently implements six algorithms to randomize binary species distribution with several levels of constraints: SIM1, SIM2, SIM3, SIM5, SIM6 and SIM9 (sensu Gotelli 2000). The methods implemented in 'SESRaster' are based on how species (originally rows) and sites (originally columns) are treated (i.e. fixed, equiprobable, or proportional sums) (Gotelli 2000). By default, the 'phyloraster' uses the function `bootspat_str()` from the 'SESRaster' package to conduct the randomizations, but the user is free to choose any of the other methods mentioned above through the `spat_alg` argument in the `*.ses()` functions of the 'phyloraster' package. The `bootspat_str()` is equivalent to the SIM5 (proportional-fixed) method of Gotelli (2000), which partially relaxes the spatial structure of species distributions, but keeps the spatial structure of the observed richness pattern across cells. Biodiversity metrics available are:

- `pe`: Phylogenetic endemism (Rosauer et al., 2009)
- `pe.alt`: Alternate Phylogenetic endemism (Mishler et al., 2014)
- `rpe`: Relative Phylogenetic endemism (Mishler et al., 2014)
- `all`: Calculate all available metrics Alternate phylogenetic endemism (PE.alt, Mishler et al., 2014) is calculated using an alternate phylogeny with non-zero branch lengths converted to a constant value (here we use 1) and rescaled so the sum of all branch lengths is 1. Relative phylogenetic endemism (RPE, Mishler et al., 2014) is the ratio of phylogenetic endemism (PE, Rosauer et al., 2009) measured on the original tree versus PE measured on a alternate tree (PE.alt).

Value

SpatRaster. The function returns the observed value of the metric, the mean of the simulations calculated over n times, the standard deviation of the simulations, the standardized effect size (SES) for the metric, and the p-values.

Author(s)

Gabriela Alves-Ferreira and Neander Heming

References

- Gotelli, N. J. 2000. Null model analysis of species co-occurrence patterns. *Ecology* 81: 2606–2621.
- Heming, N. M., Mota, F. M. M. and Alves-Ferreira, G. 2023. SESraster: raster randomization for null hypothesis testing. <https://CRAN.R-project.org/package=SESraster>.
- Mishler, B. D., Knerr, N., González-Orozco, C. E., Thornhill, A. H., Laffan, S. W. and Miller, J. T. 2014. Phylogenetic measures of biodiversity and neo- and paleo-endemism in Australian Acacia. – *Nat. Commun.* 5: 4473.
- Rosauer, D. A. N., Laffan, S. W., Crisp, M. D., Donnellan, S. C., & Cook, L. G. (2009). Phylogenetic endemism: a new approach for identifying geographical concentrations of evolutionary history. *Molecular ecology*, 18(19), 4061-4072.

See Also

[phylo.pres](#), [inv.range](#), [geo.phylo.ses](#), [rast.ed.ses](#), [rast.pd.ses](#), [rast.we.ses](#), [rast.pe.ses](#), [bootspat_str](#), [bootspat_naive](#), [bootspat_ff](#), [SESraster](#)

Examples

```
library(terra)
library(phyloraster)
library(SESraster)
x <- terra::rast(system.file("extdata", "rast.presab.tif",
package="phyloraster"))
tree <- ape::read.tree(system.file("extdata", "tree.nex",
package="phyloraster"))
data <- phylo.pres(x[[1:3]], tree)
t <- rast.pe.ses(x = data$x, data$tree, aleats = 99, metric = "all")
plot(t)
```

rast.sr

Calculate species richness for raster data

Description

Calculate the species richness for raster data.

Usage

```
rast.sr(x, filename = "", ...)
```

Arguments

x	SpatRaster. A SpatRaster containing presence-absence data (0 or 1) for a set of species.
filename	character. Output filename.
...	additional arguments to be passed passed down from a calling function.

Value

SpatRaster

Author(s)

Gabriela Alves Ferreira and Neander Marcel Heming

Examples

```
x <- terra::rast(system.file("extdata", "rast.presab.tif",
  package="phyloraster"))
rse <- phyloraster::rast.sr(x)
terra::plot(rse)
```

rast.we

Calculate weighted endemism for raster data

Description

Calculate the weighted endemism for species present in raster data.

Usage

```
rast.we(x, inv.R, filename = "", ...)
```

Arguments

x	SpatRaster. A SpatRaster containing presence-absence data (0 or 1) for a set of species. The layers (species) will be sorted according to the tree order. See the <code>phylo.pres</code> function.
inv.R	SpatRaster. Inverse of range size. See inv.range
filename	character. Output filename
...	additional arguments passed for <code>terra::app</code>

Value

SpatRaster

Author(s)

Neander Marcel Heming and Gabriela Alves Ferreira

References

Laffan, S. W., Rosauer, D. F., Di Virgilio, G., Miller, J. T., González-Orozco, C. E., Knerr, N., ... & Mishler, B. D. (2016). Range-weighted metrics of species and phylogenetic turnover can better resolve biogeographic transition zones. *Methods in Ecology and Evolution*, 7(5), 580-588.

Williams, P.H., Humphries, C.J., Forey, P.L., Humphries, C.J., VaneWright, R.I. (1994). Biodiversity, taxonomic relatedness, and endemism in conservation. In: *Systematics and Conservation Evaluation* (eds Forey PL, Humphries CJ, Vane-Wright RI), p. 438. Oxford University Press, Oxford.

Crisp, M., Laffan, S., Linder, H., Monro, A. (2001). Endemism in the Australian flora. *Journal of Biogeography*, 28, 183–198.

Examples

```
library(terra)
library(phyloraster)
x <- rast(system.file("extdata", "rast.presab.tif",
package="phyloraster"))
inv.R <- inv.range(x)
we <- rast.we(x, inv.R)
plot(we)
```

rast.we.ses

Calculate weighted endemism standardized for species richness

Description

Calculates the standardized effect size for weighted endemism. See Details for more information.

Usage

```
rast.we.ses(
  x,
  inv.R,
  spat_alg = "bootspat_str",
  spat_alg_args = list(rprob = NULL, rich = NULL, fr_prob = NULL),
  aleats = 10,
  filename = "",
  ...
)
```

Arguments

x	SpatRaster. A SpatRaster containing presence-absence data (0 or 1) for a set of species. The layers (species) will be sorted according to the tree order. See the <code>phylo.pres</code> function.
inv.R	SpatRaster. Inverse of range size. See <code>inv.range</code>
spat_alg	A function with the algorithm implementing the desired randomization method. It must work with SpatRaster objects. See examples. Example of functions that work are: <code>bootspat_naive</code> , <code>bootspat_str</code> , <code>bootspat_ff</code> .
spat_alg_args	List of arguments passed to the randomization method chosen in 'spat_alg'. See <code>bootspat_naive</code> , <code>bootspat_str</code> , <code>bootspat_ff</code>
aleats	positive integer. A positive integer indicating how many times the calculation should be repeated.
filename	character. Output filename
...	additional arguments passed for <code>terra::app</code>

Details

The dependency 'SESRaster' is used to calculate the null models. This package currently implements six algorithms to randomize binary species distribution with several levels of constraints: SIM1, SIM2, SIM3, SIM5, SIM6 and SIM9 (sensu Gotelli 2000). The methods implemented in 'SESRaster' are based on how species (originally rows) and sites (originally columns) are treated (i.e. fixed, equiprobable, or proportional sums) (Gotelli 2000). By default, the 'phyloraster' uses the function `bootspat_str()` from the 'SESRaster' package to conduct the randomizations, but the user is free to choose any of the other methods mentioned above through the `spat_alg` argument in the `*.ses()` functions of the 'phyloraster' package. The `bootspat_str()` is equivalent to the SIM5 (proportional-fixed) method of Gotelli (2000), which partially relaxes the spatial structure of species distributions, but keeps the spatial structure of the observed richness pattern across cells.

Value

SpatRaster. The function returns the observed value of the metric, the mean of the simulations calculated over n times, the standard deviation of the simulations, the standardized effect size (SES) for the metric, and the p-values.

Author(s)

Gabriela Alves-Ferreira and Neander Heming

References

Gotelli, N. J. 2000. Null model analysis of species co-occurrence patterns. – *Ecology* 81: 2606–2621.
 Heming, N. M., Mota, F. M. M. and Alves-Ferreira, G. 2023. SESRaster: raster randomization for null hypothesis testing. <https://CRAN.R-project.org/package=SESRaster>.

See Also

`phylo.pres`, `inv.range`, `geo.phylo.ses`, `rast.ed.ses`, `rast.pd.ses`, `rast.we.ses`, `rast.pe.ses`, `bootspat_str`, `bootspat_naive`, `bootspat_ff`, `SESRaster`

values	typically a numeric vector of length 1 or nrow(x). If the length is below nrow(x) the values will be recycled to nrow(x). Only used when x is a matrix. Can also be a matrix or data.frame
filename	character. Output filename
...	additional arguments passed to fun

Value

SpatRaster

Examples

```
library(terra)

shp <- terra::vect(system.file("extdata", "shps_iucn_spps_rosauer.shp",
                             package="phyloraster"))

# create a polygon to use as mask with an extent
e <- terra::ext(113, 123, -43.64, -33.90)
p <- terra::as.polygons(e, crs="")
coun.crop <- terra::crop(p, terra::ext(shp))
coun.rast <- terra::rasterize(coun.crop,
                             terra::rast(terra::ext(shp), resolution = 0.5))

plot(coun.rast, col = "green")

# rasterizing with the mask of the polygon
shp.t <- shp2rast(shp, y = coun.rast, sps.col = "BINOMIAL",
                 ymask = TRUE, background = 0)
plot(shp.t, col = c("grey", "green"))

# rasterizing without using mask
shp.t2 <- shp2rast(shp, sps.col = "BINOMIAL", ymask = FALSE,
                  background = NA, resolution = 0.1)
plot(shp.t2[[9]], col = c("grey", "green"))
```

species.ed

*Calculate Evolutionary distinctiveness for each species***Description**

This function calculates evolutionary distinctiveness according to the fair-proportion index for each species.

Usage

```
species.ed(tree)
```

Arguments

tree phylo. A dated tree.

Value

data.frame

Author(s)

Neander Marcel Heming and Gabriela Alves-Ferreira

References

Isaac, N. J., Turvey, S. T., Collen, B., Waterman, C. and Baillie, J. E. (2007). Mammals on the EDGE: conservation priorities based on threat and phylogeny. PLoS ONE 2, e296.

Examples

```
library(phyloRaster)
tree <- ape::read.tree(system.file("extdata", "tree.nex",
package="phyloRaster"))
plot(tree)
ed <- species.ed(tree)
ed
```

species.tip.length *Compute species tip length*

Description

Computation of species tip length using a phylogeny.

Usage

```
species.tip.length(tree = NULL, edge.info = NULL, ...)
```

Arguments

tree phylo. A dated tree.

edge.info Object returned by [tip.root.path](#) consisting of a list containing the edge matrix (H1) with the path from tip to root and a numeric vector (edge.length) giving the length of each branch of the tree.

... additional arguments to be passed passed down from a calling function.

Details

Calculates tip lengths for all species in a phylogeny

Value

returns a numeric vector giving the length of species branch.

Author(s)

Neander M. Heming

Examples

```
library(phyloaster)
tree <- ape::read.tree(system.file("extdata", "tree.nex",
package="phyloaster"))

species.tip.length(tree)

library(ape)
set.seed(1)
tree <- rtree(n=40)

plot(tree)

species.tip.length(tree)

edge.info <- tip.root.path(tree)

species.tip.length(edge.info = edge.info)
```

tip.root.path

Compute tree edge lengths and node paths from root to each tip

Description

Computation of tree edge lengths and node paths from root to each tip to calculate PD for a entire phylogeny (= sum of all edge or branch lengths)

Usage

```
tip.root.path(tree)
```

Arguments

tree phylo. A dated tree.

Details

Based on the algorithm FastXtreePhylo of Peter D. Wilson

Value

returns a list with two components: matrix H1 representing the paths through the tree from root to each tip, and edge.length a numeric vector giving the length of each branch in the tree. Some matrix algebra and a summation of the resulting vector gives the whole-tree PD value.

Author(s)

Peter Wilson

Examples

```
library(phylo raster)
tree <- ape::read.tree(system.file("extdata", "tree.nex",
package="phylo raster"))

fxtp <- tip.root.path(tree)
H1 <- fxtp$H1
edge.length <- fxtp$edge.length
# PD for the whole community
pres <- rep(1, nrow(H1))
sum((crossprod(H1, pres)>0) * edge.length)

# PD for a random subset of the community
pres <- sample(c(1, 0), nrow(H1), TRUE)
sum((crossprod(H1, pres)>0) * edge.length)
```

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