Package 'phyloraster'

Title Evolutionary Diversity Metrics for Raster Data

Version 2.1.0

Description Phylogenetic Diversity (PD, Faith 1992), Evolutionary Distinctive-
ness (ED, Isaac et al. 2007), Phylogenetic Endemism (PE, Rosauer et al. 2009; Laf-
fan 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>
Isaac, N. J. et al. (2007) <doi:10.1371/journal.pone.0000296>
Laffan, S. W. et al. (2016) <doi:10.1111/2041-210X.12513>
Rosauer, D. et al. (2009) <doi:10.1111/j.1365-294X.2009.04311.x>.

License GPL (>= 3)

URL https://CRAN.R-project.org/package=phyloraster,

https://github.com/gabferreira/phyloraster,
https:https://gabferreira.github.io/phyloraster/

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

Depends R (>= 2.10)

Imports ape, methods, SESraster, stats, terra

Suggests knitr, maps, phylobase, rmarkdown, testthat (>= 2.0.0)

VignetteBuilder knitr

Config/testthat/edition 2

Encoding UTF-8

LazyData true

RoxygenNote 7.3.1

NeedsCompilation no

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Repository CRAN

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R topics documented:

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arg.check   *Check for missing arguments in function call*

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)
```

---

dataR   *Presence-absence of 33 Australian tree frogs (Rosauer 2017)*

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   *Delta of Diversity Metrics*

Description

Calculates the difference of rasterized diversity metrics (richness, phylogenetic endemism, phylo-
genetic 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 phyloraster::geo.phylo function.
r2	SpatRaster Rasterized diversity metrics for time 2 (e.g phylogenetic diversity in future).
filename	character. Output filename.
cores	positive integer. If cores > 1, 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.

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,
  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 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
filename	character. Output filename
...	additional arguments passed for terra::app

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(phyloraster)
x <- terra::rast(system.file("extdata", "rast.presab.tif",
package="phyloraster"))[[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	*Calculate phylogenetic community metrics and their standardized effect sizes for raster data*

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,
  spat_alg = "bootspat_str",
  spat_alg_args = list(rprob = NULL, rich = NULL, fr_prob = NULL),
  random = c("tip", "spat")[2],
  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 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
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
random	character. A character indicating the type of randomization. The currently available randomization methods are "tip", "site", "species" or "both" (site and species).
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 spatial randomization (spat) keeps the richness exact and samples species presences proportionally to their observed frequency (i.e. number of occupied pixels). The randomization will not assign values to cells with nodata.

Value

SpatRaster

Author(s)

Neander Marcel Heming

References

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 C.J., 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.

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,
                       # FUN_args = list(range.BL=area.branch$range.BL,
                       # inv.R=area.branch$inv.R,
                       # branch.length=data$branch.length,
                       # n.descen = data$n.descendants),
                       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	*Load an example dataset with presence-absence data of 33 tree frogs and a phylogenetic tree for this species*

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 = FALSE, ...)
```

Arguments

x	SpatRaster. A SpatRaster containing presence-absence data (0 or 1) for a set of species.
tree	phylo. A dated tree.
full_tree_metr	logical. Whether edge.path, branch length and number of descendants should be calculated with the full (TRUE) or the prunned tree (FALSE).
...	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 prunned 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, 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 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`
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(phyloraster)
x <- rast(system.file("extdata", "rast.presab.tif",
package="phyloraster"))
# phylogenetic tree
tree <- ape::read.tree(system.file("extdata", "tree.nex",
package="phyloraster"))
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   *Evolutionary distinctiveness standardized for specie richness*

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,
  spat_alg = "bootspat_str",
  spat_alg_args = list(rprob = NULL, rich = NULL, fr_prob = NULL),
  random = c("tip", "spat")[2],
  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 phylo.pres function.
tree	phylo. A dated tree.
edge.path	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
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
random	character. A character indicating the type of randomization. The currently available randomization methods are "tip", "site", "species" or "both" (site and species).
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 spatial randomization (spat) keeps the richness exact and samples species presences proportionally to their observed frequency (i.e. number of occupied pixels). The randomization will not assign values to cells with nodata. The phylogenetic randomization shuffles taxa names across all taxa included in phylogeny.

Value

SpatRaster

Author(s)

Neander M. 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.

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, geo.phylo.ses, rast.ed.ses, rast.pd.ses, rast.we.ses, rast.pe.ses, bootspat_str, bootspat_naive, bootspat_ff, SESraster

Examples

```
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"))
t <- rast.ed.ses(x[[1:10]], tree, aleats = 3, random = "spat")
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, 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 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
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(phyloraster)
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[[1:3]], tree)
pd <- rast.pd(data$x, edge.path = data$edge.path,
branch.length = data$branch.length)
plot(pd)
```

---

rast.pd.ses	*Phylogenetic diversity standardized for species richness*

Description

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

Usage

```
rast.pd.ses(
  x,
  tree,
  edge.path,
  branch.length,
  spat_alg = ”bootspat_str”,
  spat_alg_args = list(rprob = NULL, rich = NULL, fr_prob = NULL),
  random = c(”tip”, ”spat”)[2],
  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 phylo.pres function.
tree	phylo. A dated tree.
edge.path	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`
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`
random	character. A character indicating the type of randomization. The currently available randomization methods are "tip", "site", "species" or "both" (site and species).
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 spatial randomization (spat) keeps the richness exact and samples species presences proportionally to their observed frequency (i.e. number of occupied pixels). The randomization will not assign values to cells with nodata. The phylogenetic randomization shuffles taxa names across all taxa included in phylogeny.

The spatial randomization (spat) keeps the richness exact and samples species presences proportionally to their observed frequency (i.e. number of occupied pixels). The randomization will not assign values to cells with nodata. The phylogenetic randomization shuffles taxa names across all taxa included in phylogeny.

Value

SpatRaster

SpatRaster. The function returns the observed phylogenetic diversity, the mean of the simulations calculated over n times, the standard deviation of the simulations, and the standardized effect size (SES) for the phylogenetic diversity.

Author(s)

Gabriela Alves-Ferreira and Neander Heming

References

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

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,
                random = "spat")
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 = FALSE,
  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`
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 prunned tree (FALSE).
filename	character. Output filename
...	additional arguments passed for terra::app

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(phyloraster)
```

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

rast.pe.ses	*Phylogenetic endemism standardized for specie richness*

Description

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

Usage

```
rast.pe.ses(
  x,
  tree,
  branch.length,
  inv.R,
  spat_alg = "bootspat_str",
  spat_alg_args = list(rprob = NULL, rich = NULL, fr_prob = NULL),
  random = c("tip", "spat")[2],
  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.
branch.length	numeric. A Named numeric vector of branch length for each species. See phylo.pres
inv.R	SpatRaster. Inverse of range size. See inv.range
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

random	character. A character indicating the type of randomization. The currently available randomization methods are "tip", "site", "species" or "both" (site and species).
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 spatial randomization (spat) keeps the richness exact and samples species presences proportionally to their observed frequency (i.e. number of occupied pixels). The randomization will not assign values to cells with nodata. The phylogenetic randomization shuffles taxa names across all taxa included in phylogeny.

Value

SpatRaster

Author(s)

Gabriela Alves-Ferreira and Neander Heming

References

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)
range.BL <- inv.range(data$x)
```

```
t <- rast.pe.ses(x = data$x,  tree, aleats = 3,
random = "spat")
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 phylo.pres function.
inv.R	SpatRaster. Inverse of range size. See inv.range
filename	character. Output filename
...	additional arguments passed for terra::app

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 phylo.pres function.
inv.R	SpatRaster. Inverse of range size. See inv.range
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 spatial randomization (spat) keeps the richness exact and samples species presences proportionally to their observed frequency (i.e. number of occupied pixels). The randomization will not assign values to cells with nodata. The phylogenetic randomization shuffles taxa names across all taxa included in phylogeny.

Value

SpatRaster

Author(s)

Neander Marcel Heming and Gabriela Alves-Ferreira

References

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.

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(SESraster)
x <- terra::rast(system.file("extdata", "rast.presab.tif",
package="phyloraster"))
t <- rast.we.ses(x[[1:10]], aleats = 3)
plot(t)
```

---

shp2rast   *Rasterize shapefile*

Description

The function will rasterize the shapefile using the parameters of y, a SpatRaster. When the argument y is provided, the resolution parameter is ignored. When the argument ymask is TRUE, y is used as a mask for x.

Usage

```
shp2rast(
  x,
  y = NULL,
  sps.col,
  ymask = FALSE,
  background = NA,
  touches = TRUE,
  resolution,
  values = 1,
  filename = NULL,
  ...
)
```

Arguments

x	SpatVector or a two-column matrix (point coordinates)
y	SpatRaster
sps.col	character. It should be a variable name in x.
ymask	logical. If TRUE, y will be used as a mask for x.
background	numeric. Value to put in the cells that are not covered by any of the features of x. Default is NA
touches	logical. If TRUE, all cells touched by lines or polygons are affected, not just those on the line render path, or whose center point is within the polygon. If touches=TRUE, add cannot be TRUE
resolution	numeric vector of length 1 or 2 to set the spatial resolution (see [res](#)). If this argument is used, arguments ncols and nrows are ignored
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 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(phyloraster)
tree <- ape::read.tree(system.file("extdata", "tree.nex",
package="phyloraster"))

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

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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