Package 'divraster'

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Title Diversity Metrics Calculations for Rasterized Data

Version 1.0.4

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Description Alpha and beta diversity for taxonomic (TD), functional (FD), and phylogenetic (PD) dimensions based on rasters. Spatial and temporal beta diversity can be partitioned into replacement and richness difference components. It also calculates standardized effect size for FD and PD alpha diversity and the average individual traits across multilayer rasters. The layers of the raster represent species, while the cells represent communities. Methods details can be found at Cardoso et al. 2022 <https://CRAN.R-project.org/package=BAT> and Heming et al. 2023 <https://CRAN.R-project.org/package=SESraster>.

License GPL (>= 3)

URL https://github.com/flaviomoc/divraster,

https://flaviomoc.github.io/divraster/

BugReports https://github.com/flaviomoc/divraster/issues

Imports BAT, SESraster, stats, terra, utils

Suggests ape, knitr, rmarkdown, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

Encoding UTF-8

RoxygenNote 7.2.3

NeedsCompilation no

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R **topics documented:**

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inputs_chk   *Check if objects are valid*

Description

Check if objects are valid

Usage

```
inputs_chk(bin1, bin2, tree)
```

Arguments

bin1	A SpatRaster with presence-absence data (0 or 1) for a set of species.
bin2	A SpatRaster with presence-absence data (0 or 1) for a set of species. Species names in 'bin2' and 'bin1' must match!
tree	It can be a 'data.frame' with species traits or a 'phylo' with a rooted phylogenetic tree. Species names in 'tree', 'bin1', and 'bin2' must match!

Value

Either a success message or an error.

Examples

```
library(terra)
bin1 <- terra::rast(system.file("extdata", "ref.tif",
package = "divraster"))
bin2 <- terra::rast(system.file("extdata", "fut.tif",
package = "divraster"))
traits <- read.csv(system.file("extdata", "traits.csv",
package = "divraster"), row.names = 1)
```

```
tree <- ape::read.tree(system.file("extdata", "tree.tre",
package = "divraster"))
inputs_chk(bin1, bin2, tree)
```

| load.data | *Load data adapted from Mota et al. (2022), Tobias et al. (2022), and Jetz et al. (2014)* |

Description

Load data adapted from Mota et al. (2022), Tobias et al. (2022), and Jetz et al. (2014)

Usage

```
load.data()
```

Value

A list with binary maps of species for the reference and future climate scenarios, species traits, and a rooted phylogenetic tree for the species. The species names across these objects must match!

References

Mota, F. M. M. et al. 2022. Climate change is expected to restructure forest frugivorous bird communities in a biodiversity hot-point within the Atlantic Forest. - Diversity and Distributions 28: 2886–2897.

Tobias, J. A. et al. 2022. AVONET: morphological, ecological and geographical data for all birds. - Ecology Letters 25: 581–597.

Jetz, W. et al. 2014. Global Distribution and Conservation of Evolutionary Distinctness in Birds. - Current Biology 24: 919–930.

Examples

```
data <- load.data()
data
```

---

spat.alpha   *Alpha calculation for raster*

Description

Calculates alpha diversity for taxonomic (TD), functional (FD), and phylogenetic (PD) dimensions. Adapted from `alpha`

Usage

```
spat.alpha(bin, tree, cores = 1, filename = "", ...)
```

Arguments

`bin`	A SpatRaster with presence-absence data (0 or 1) for a set of species.
`tree`	It can be a 'data.frame' with species traits or a 'phylo' with a rooted phylogenetic tree. Species names in 'tree' and 'bin' must match!
`cores`	A positive integer. If cores > 1, a 'parallel' package cluster with that many cores is created and used.
`filename`	Character. Save results if a name is provided.
`...`	Additional arguments to be passed passed down from a calling function.

Details

Alpha calculations use a tree-based approach for TD, FD, and PD (Cardoso et al. 2014). In the FD calculation, a species traits matrix is transformed into a distance matrix and clustered to create a regional dendrogram (i.e. a dendrogram with all species in the raster stack), from which the total branch length is calculated. When computing FD for each community (i.e. raster cell), the regional dendrogram is subsetted to create a local dendrogram that includes only the species present in the local community. The branch lengths connecting these species are then summed to represent the functional relationships of the locally present species (Petchey and Gaston, 2002, 2006). Similarly, in PD, the cumulative branch lengths connecting species within a community indicate their shared phylogenetic relationships (Faith, 1992). Alpha TD can also be visualized using a tree diagram, where each species is directly connected to the root by an edge of unit length, reflecting the number of different taxa in the community (i.e. species richness) since all taxa are at the same level (Cardoso et al. 2014).

Value

A SpatRaster with alpha result.

References

Cardoso, P. et al. 2014. Partitioning taxon, phylogenetic and functional beta diversity into replacement and richness difference components. - Journal of Biogeography 41: 749–761.

Faith, D. P. 1992. Conservation evaluation and phylogenetic diversity. - Biological Conservation 61: 1–10.

Petchey, O. L. and Gaston, K. J. 2002. Functional diversity (FD), species richness and community composition. - Ecology Letters 5: 402–411.

Rodrigues, A. S. L. and Gaston, K. J. 2002. Maximising phylogenetic diversity in the selection of networks of conservation areas. - Biological Conservation 105: 103–111.

Examples

```
library(terra)
bin1 <- terra::rast(system.file("extdata", "ref.tif",
package = "divraster"))
traits <- read.csv(system.file("extdata", "traits.csv",
package = "divraster"), row.names = 1)
tree <- ape::read.tree(system.file("extdata", "tree.tre",
package = "divraster"))
spat.alpha(bin1)
spat.alpha(bin1, traits)
spat.alpha(bin1, tree)
```

---

spat.alpha.vec	*Alpha calculation for vector*

Description

Alpha calculation for vector

Usage

```
spat.alpha.vec(x, tree, resu, ...)
```

Arguments

x	A numeric vector with presence-absence data (0 or 1) for a set of species.
tree	It can be a data frame with species traits or a phylogenetic tree.
resu	Numeric. A vector to store results.
...	Additional arguments to be passed passed down from a calling function.

Value

A vector with alpha result.

---

spat.beta	*Spatial beta diversity for raster*

Description

Calculates spatial beta diversity for taxonomic (TD), functional (FD), and phylogenetic (PD) dimensions. Adapted from `beta`.

Usage

```
spat.beta(
  x,
  tree,
  filename = "",
  global = FALSE,
  fm = NULL,
  d = mean(terra::res(terra::rast(x))) * 2,
  type = "circle",
  na.policy = "omit",
  ...
)
```

Arguments

x	A SpatRaster with presence-absence data (0 or 1) for a set of species.
tree	It can be a 'data.frame' with species traits or a 'phylo' with a rooted phylogenetic tree. Species names in 'tree' and 'x' must match!
filename	Character. Save results if a name is provided.
global	Logical. Mean of pairwise comparisons between focal cell and its neighbors (default) or mean of all pairwise comparisons.
fm	Numeric. Focal matrix ("moving window").
d	Window radius to compute beta diversity.
type	Character. Window format. Default = "circle".
na.policy	Character. Default = "omit". See ?terra::focal3D for details.
...	Additional arguments to be passed passed down from a calling function.

Details

The TD beta diversity partitioning framework we used was developed by Podani and Schmera (2011) and Carvalho et al. (2012) and expanded to PD and FD by Cardoso et al. (2014).

Value

A SpatRaster with beta results (total, replacement, richness difference, and ratio).

References

Cardoso, P. et al. 2014. Partitioning taxon, phylogenetic and functional beta diversity into replacement and richness difference components. - Journal of Biogeography 41: 749–761.

Carvalho, J. C. et al. 2012. Determining the relative roles of species replacement and species richness differences in generating beta-diversity patterns. - Global Ecology and Biogeography 21: 760–771.

Podani, J. and Schmera, D. 2011. A new conceptual and methodological framework for exploring and explaining pattern in presence - absence data. - Oikos 120: 1625–1638.

Hidasi-Neto, J. et al. 2019. Climate change will drive mammal species loss and biotic homogenization in the Cerrado Biodiversity Hotspot. - Perspectives in Ecology and Conservation 17: 57–63.

Examples

```
library(terra)
bin1 <- terra::rast(system.file("extdata", "ref.tif",
package = "divraster"))
traits <- read.csv(system.file("extdata", "traits.csv",
package = "divraster"), row.names = 1)
rownames(traits) <- names(bin1)
tree <- ape::read.tree(system.file("extdata", "tree.tre",
package = "divraster"))
spat.beta(bin1)
spat.beta(bin1, traits)
spat.beta(bin1, tree)
```

---

spat.beta.vec *Spatial beta diversity for vector*

Description

Spatial beta diversity for vector

Usage

```
spat.beta.vec(x, tree, global = FALSE, spp, nspp, ...)
```

Arguments

x	A numeric vector with presence-absence data (0 or 1) for a set of species.
tree	It can be a data frame with species traits or a phylogenetic tree.
global	Logical. Mean of pairwise comparisons between focal cell and its neighbors (default) or mean of all pairwise comparisons.
spp	Character. Species names.
nspp	Numeric. Number of species.
...	Additional arguments to be passed passed down from a calling function.

Value

A vector with beta results (total, replacement, richness difference, and ratio).

---

spat.rand   *Standardized Effect Size (SES) for raster*

Description

Calculates the standardized effect size for functional and phylogenetic alpha diversity. See bootspat_str and bootspat_naive

Usage

```
spat.rand(
  x,
  tree,
  aleats,
  random = c("site", "species", "both", "spat"),
  cores = 1,
  filename = "",
  ...
)
```

Arguments

x	SpatRaster. A SpatRaster containing presence-absence data (0 or 1) for a set of species.
tree	It can be a 'data.frame' with species traits or a 'phylo' with a rooted phylogenetic tree. Species names in 'tree' and 'x' must match!
aleats	positive integer. A positive integer indicating how many times the calculation should be repeated.
random	character. A character indicating the type of randomization. The currently available randomization methods are "spat", "site", "species" or "both" (site and species).
cores	positive integer. If cores > 1, a 'parallel' package cluster with that many cores is created and used.
filename	character. Output filename.
...	additional arguments to be passed passed down from a calling function.

Value

SpatRaster with Mean, SD, Observed, and SES.

Examples

```
x <- terra::rast(system.file("extdata", "ref.tif",
package = "divraster"))
traits <- read.csv(system.file("extdata", "traits.csv",
package = "divraster"), row.names = 1)
tree <- ape::read.tree(system.file("extdata", "tree.tre",
package = "divraster"))
spat.rand(x, tree, 3, "site")
spat.rand(x, traits, 3, "site")
```

---

spat.trait   *Average trait calculation for raster*

Description

Compute average for each trait.

Usage

```
spat.trait(x, trait, cores = 1, filename = "", ...)
```

Arguments

x	A SpatRaster with presence-absence data (0 or 1) for a set of species.
trait	A 'data.frame' with species traits. Rownames must have species names that match with 'x'!
cores	A positive integer. If cores > 1, a 'parallel' package cluster with that many cores is created and used.
filename	Character. Save results if a name is provided.
...	Additional arguments to be passed passed down from a calling function.

Value

SpatRaster with average traits.

Examples

```
library(terra)
bin1 <- terra::rast(system.file("extdata", "ref.tif",
package = "divraster"))
traits <- read.csv(system.file("extdata", "traits.csv",
package = "divraster"), row.names = 1)
spat.trait(bin1, traits)
```

---

spat.trait.vec   *Average trait calculation for vector*

Description

Average trait calculation for vector

Usage

```
spat.trait.vec(x, col_trait, ...)
```

Arguments

x	A numeric vector with presence-absence data (0 or 1) for a set of species.
col_trait	A numeric vector with trait numbers.
...	Additional arguments to be passed passed down from a calling function.

Value

Vector of average trait.

---

temp.beta   *Temporal beta diversity calculation for raster*

Description

Calculates temporal beta diversity for taxonomic (TD), functional (FD), and phylogenetic (PD) dimensions. Adapted from [beta](#)

Usage

```
temp.beta(bin1, bin2, tree, filename = "", cores = 1, ...)
```

Arguments

bin1	A SpatRaster with presence-absence data (0 or 1) for a set of species.
bin2	A SpatRaster with presence-absence data (0 or 1) for a set of species. Species names in 'bin2' and 'bin1' must match!
tree	It can be a 'data.frame' with species traits or a 'phylo' with a rooted phylogenetic tree. Species names in 'tree', 'bin1', and 'bin2' must match!
filename	Character. Save results if a name is provided.
cores	A 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 TD beta diversity partitioning framework we used was developed by Podani and Schmera (2011) and Carvalho et al. (2012) and expanded to PD and FD by Cardoso et al. (2014).

Value

A SpatRaster with beta results (total, replacement, richness difference, and ratio).

References

Cardoso, P. et al. 2014. Partitioning taxon, phylogenetic and functional beta diversity into replacement and richness difference components. - Journal of Biogeography 41: 749–761.

Carvalho, J. C. et al. 2012. Determining the relative roles of species replacement and species richness differences in generating beta-diversity patterns. - Global Ecology and Biogeography 21: 760–771.

Podani, J. and Schmera, D. 2011. A new conceptual and methodological framework for exploring and explaining pattern in presence - absence data. - Oikos 120: 1625–1638.

Hidasi-Neto, J. et al. 2019. Climate change will drive mammal species loss and biotic homogenization in the Cerrado Biodiversity Hotspot. - Perspectives in Ecology and Conservation 17: 57–63.

Examples

```
library(terra)
bin1 <- terra::rast(system.file("extdata", "ref.tif",
package = "divraster"))
bin2 <- terra::rast(system.file("extdata", "fut.tif",
package = "divraster"))
traits <- read.csv(system.file("extdata", "traits.csv",
package = "divraster"), row.names = 1)
tree <- ape::read.tree(system.file("extdata", "tree.tre",
package = "divraster"))
temp.beta(bin1, bin2)
temp.beta(bin1, bin2, traits)
temp.beta(bin1, bin2, tree)
```

---

temp.beta.vec *Temporal beta diversity calculation for vector*

Description

Temporal beta diversity calculation for vector

Usage

```
temp.beta.vec(x, nspp, spp, tree, resu, ...)
```

Arguments

x	A numeric vector with presence-absence data (0 or 1) for a set of species.
nspp	Numeric. Number of species.
spp	Character. Species name.
tree	It can be a data frame with species traits or a phylogenetic tree.
resu	Numeric. A vector to store results.
...	Additional arguments to be passed passed down from a calling function.

Value

A vector with beta results (total, replacement, richness difference, and ratio).

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