Package ‘fundiversity’

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Author Matthias Grenié [aut, cre] (<https://orcid.org/0000-0002-4659-7522>), Hugo Gruson [aut] (<https://orcid.org/0000-0002-4094-1476>)

Maintainer Matthias Grenié <matthias.grenie@gmail.com>

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fd_fdis  

Compute Functional Dispersion (FDi)

Description

This function computes Functional Dispersion (FDi) following Laliberté & Legendre (2010). NB: when a site contains no species FDi is equal to 0.

Usage

`fd_fdis(traits, sp_com)`

Arguments

- `traits` Trait matrix with species as rows and traits as columns. It has to contain exclusively numerical values. This can be either a matrix, a data.frame, or a Matrix::Matrix() object.
- `sp_com` Site-species matrix with sites as rows and species as columns if not provided, the function considers all species with equal abundance in a single site. This can be either a matrix, a data.frame, or a Matrix::Matrix() object.

Value

A data.frame with two columns:

- `site` the names of the sites as the row names of the input `sp_com`,
- `FDi` the values of functional dispersion at each site.

NB: when a site contains no species FDi is equal to 0.

Parallelization

The computation of this function can be parallelized thanks to future::plan(). To get more information on how to parallelize your computation please refer to the parallelization vignette with: vignette("fundiversity_1-parallel", package = "fundiversity")
References


Examples

data(traits_birds)
data(site_sp_birds)
fd_fdis(traits_birds, site_sp_birds)

fd_fdiv

Compute Functional Divergence (FDiv)

Description

This function computes Functional Divergence (FDiv) following Villéger et al. (2008). NB: when a site contains no species FDiv is equal to 0. If for a site there are less traits than species, then FDiv is equal to NaN.

Usage

fd_fdiv(traits, sp_com)

Arguments

traits Trait matrix with species as rows and traits as columns. It has to contain exclusively numerical values. This can be either a matrix, a data.frame, or a Matrix::Matrix() object.

sp_com Site-species matrix with sites as rows and species as columns if not provided, the function considers all species with equal abundance in a single site. This can be either a matrix, a data.frame, or a Matrix::Matrix() object.

Details

By default, when loading fundiversity, the functions to compute convex hulls are memoised through the memoise package if it is installed. To deactivate this behavior you can set the option fundiversity.memoise to FALSE by running the following line: options(fundiversity.memoise = FALSE). If you use it interactively it will only affect your current session. Add it to your script(s) or .Rprofile file to avoid toggling it each time.

Value

a data.frame with two columns:

- site the names of the sites as the row names of the input sp_com,
- FDiv the values of functional divergence at each site.

NB: when a site contains no species FDiv is equal to 0. If for a site there are less traits than species, then FDiv is equal to NaN.
Parallelization

The computation of this function can be parallelized thanks to `future::plan()`. To get more information on how to parallelize your computation please refer to the parallelization vignette with:

```r
to run example
vignette("fundiversity_1-parallel", package = "fundiversity")
```

References


Examples

data(traits_birds)
fd_fdiv(traits_birds)

---

**fd_feve**

*Compute Functional Evenness (FEve)*

**Description**

This function computes Functional Evenness (FEve) following Villéger et al. (2008). NB: By definition FEve is equal to NA when the number of species per site is strictly lower than 3.

**Usage**

```r
fd_feve(traits = NULL, sp_com, dist_matrix = NULL)
```

**Arguments**

- `traits` Trait matrix with species as rows and traits as columns. It has to contain exclusively numerical values. This can be either a matrix, a data.frame, or a `Matrix::Matrix()` object.
- `sp_com` Site-species matrix with sites as rows and species as columns if not provided, the function considers all species with equal abundance in a single site. This can be either a matrix, a data.frame, or a `Matrix::Matrix()` object.
- `dist_matrix` A dissimilarity matrix that can be provided instead of a trait data.frame (default: NULL). This can be either a matrix, a data.frame, or a `Matrix::Matrix()` object.

**Value**

A data.frame with two columns:

- `site` character column that contains site names based on input `sp_com` row names,
- `FEve` numeric column that contains FEve values corresponding to each site.

NB: By definition FEve is equal to NA when the number of species per site is strictly lower than 3.
Parallelization

The computation of this function can be parallelized thanks to `future::plan()`. To get more information on how to parallelize your computation please refer to the parallelization vignette with:

```
vignette("fundiversity_1-parallel", package = "fundiversity")
```

References


Examples

```
data(traits_birds)
fd_feve(traits_birds)
```

### `fd_fric`

**Compute Functional Richness (FRic)**

#### Description

Functional Richness is computed as the volume of the convex hull from all included traits following Villéger et al. (2008). NB: FRic is equal to `NA` when there are strictly less species in a site than the number of provided traits.

#### Usage

```
fd_fric(traits, sp_com, stand = FALSE)
```

#### Arguments

- **traits**
  - Trait matrix with species as rows and traits as columns. It has to contain exclusively numerical values. This can be either a matrix, a `data.frame`, or a `Matrix::Matrix()` object.

- **sp_com**
  - Site-species matrix with sites as rows and species as columns if not provided, the function considers all species with equal abundance in a single site. This can be either a matrix, a `data.frame`, or a `Matrix::Matrix()` object.

- **stand**
  - a boolean indicating whether to standardize FRic values over the observed maximum over all species (default: `FALSE`). This scales FRic between 0 and 1. NB: The maximum FRic values only considers species that are present in both site-species and trait matrices. If you want to consider species that are absent in the site-species matrix, add corresponding columns of 0s.
Details

By default, when loading fundiversity, the functions to compute convex hulls are memoised through the memoise package if it is installed. To deactivate this behavior you can set the option fundiversity.memoise to FALSE by running the following line: options(fundiversity.memoise = FALSE). If you use it interactively it will only affect your current session. Add it to your script(s) or .Rprofile file to avoid toggling it each time.

Value

a data.frame with two columns:

- site the names of the sites as the row names of the input sp_com,
- FRic the values of functional richness at each site.

NB: FRic is equal to NA when there are strictly less species in a site than the number of provided traits. Note that only species with strictly different trait combinations are considered unique, species that share the exact same trait values across all traits are considered as one species.

Parallelization

The computation of this function can be parallelized thanks to future::plan(). To get more information on how to parallelize your computation please refer to the parallelization vignette with:

vignette("fundiversity_1-parallel", package = "fundiversity")

References


Examples

data(traits_birds)
fd_fric(traits_birds)

---

fd_fric_intersect  Intersection between convex hulls of pairs of sites

Description

Compute volume of the intersection of the convex hulls of all pairs of sites (including self-intersection, which corresponds to their convex hull). Note that when standardizing convex hulls of intersections, this function uses the convex hull of all provided traits, thus standardized volume of self-intersection hulls can be lower than one. NB: FRic_intersect is equal to NA when there are strictly less species in one of the sites than the number of provided traits.

Usage

fd_fric_intersect(traits, sp_com, stand = FALSE)
Arguments

- **traits**
  Trait matrix with species as rows and traits as columns. It has to contain exclusively numerical values. This can be either a matrix, a data.frame, or a Matrix::Matrix() object.

- **sp_com**
  Site-species matrix with sites as rows and species as columns if not provided, the function considers all species with equal abundance in a single site. This can be either a matrix, a data.frame, or a Matrix::Matrix() object.

- **stand**
  a boolean indicating whether to standardize FRic values over the observed maximum over all species (default: FALSE). This scales FRic between 0 and 1. NB: The maximum FRic values only considers species that are present in both site-species and trait matrices. If you want to consider species that are absent in the site-species matrix, add corresponding columns of 0s.

Details

By default, when loading fundiversity, the functions to compute convex hulls are memoised through the memoise package if it is installed. To deactivate this behavior you can set the option fundiversity.memoise to FALSE by running the following line: options(fundiversity.memoise = FALSE). If you use it interactively it will only affect your current session. Add it to your script(s) or .Rprofile file to avoid toggling it each time.

Value

a data.frame with three columns:

- **first_site** the names of the first site used in the pair sp_com,
- **second_site** the names of the first site used in the pair,
- **FRic_intersect** the volume of the convex hulls intersection of each pair of site.

NB: FRic_intersect is equal to NA when there are strictly less species in one of the sites than the number of provided traits. Note that only species with strictly different trait combinations are considered unique, species that share the exact same trait values across all traits are considered as one species.

Parallelization

The computation of this function can be parallelized thanks to future::plan(). To get more information on how to parallelize your computation please refer to the parallelization vignette with: vignette("fundiversity_1-parallel", package = "fundiversity")

See Also

fd_fric(), geometry::intersectn(), geometry::convhulln()

Examples

data(traits_birds)
fd_fric_intersect(traits_birds)
Compute Rao’s entropy index (Rao’s Q)

Description
This function computes Rao’s Quadratic Entropy following Rao (1982). NB: Rao’s quadratic entropy is 0 when there are no species in the site.

Usage
fd_raoq(traits = NULL, sp_com, dist_matrix = NULL)

Arguments
- traits Trait matrix with species as rows and traits as columns. It has to contain exclusively numerical values. This can be either a matrix, a data.frame, or a Matrix::Matrix() object.
- sp_com Site-species matrix with sites as rows and species as columns if not provided, the function considers all species with equal abundance in a single site. This can be either a matrix, a data.frame, or a Matrix::Matrix() object.
- dist_matrix A dissimilarity matrix that can be provided instead of a trait data.frame (default: NULL). This can be either a matrix, a data.frame, or a Matrix::Matrix() object.

Value
a data.frame with two columns:
- site the names of the sites as the row names of the input sp_com,
- Q the values of Rao’s quadratic entropy at each site.

NB: Rao’s quadratic entropy is 0 when there are no species in the site.

References

Examples
data(traits_birds)
fd_raoq(traits_birds)
**site_sp_birds**  
*Site-species matrix of birds along a Tropical Gradient*

**Description**  
Presences and absences of birds at different elevations along a tropical gradient. Species names are indicated as column names.

**Usage**  
`site_sp_birds`

**Format**  
A matrix with 217 columns (1 per species) and 8 rows:

- **elev_250** is species present at 250 m elevation? 0=No, 1=Yes
- **elev_500** is species present at 500 m elevation? 0=No, 1=Yes
- **elev_1000** is species present at 1000 m elevation? 0=No, 1=Yes
- **elev_1500** is species present at 1500 m elevation? 0=No, 1=Yes
- **elev_2000** is species present at 2000 m elevation? 0=No, 1=Yes
- **elev_2500** is species present at 2500 m elevation? 0=No, 1=Yes
- **elev_3000** is species present at 3000 m elevation? 0=No, 1=Yes
- **elev_3500** is species present at 3500 m elevation? 0=No, 1=Yes

**Source**  
Nowak, Larissa et al. (2019), Data from: Projecting consequences of global warming for the functional diversity of fleshy-fruited plants and frugivorous birds along a tropical elevational gradient, Dryad, Dataset, doi:10.5061/dryad.c0n737b

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**site_sp_plants**  
*Site-species matrix of plants along a Tropical Gradient*

**Description**  
Presences and absences of plants at different elevations along a tropical gradient. Species names are indicated as column names.

**Usage**  
`site_sp_plants`
**Format**

A matrix with 392 columns (1 per species) and 10 rows:

- **elev_250** is species present at 250 m elevation? 0=No, 1=Yes
- **elev_500** is species present at 500 m elevation? 0=No, 1=Yes
- **elev_1000** is species present at 1000 m elevation? 0=No, 1=Yes
- **elev_1500** is species present at 1500 m elevation? 0=No, 1=Yes
- **elev_2000** is species present at 2000 m elevation? 0=No, 1=Yes
- **elev_2500** is species present at 2500 m elevation? 0=No, 1=Yes
- **elev_3000** is species present at 3000 m elevation? 0=No, 1=Yes
- **elev_3500** is species present at 3500 m elevation? 0=No, 1=Yes
- **elev_3750** is species present at 3750 m elevation? 0=No, 1=Yes
- **elev_4000** is species present at 4000 m elevation? 0=No, 1=Yes

**Source**

Nowak, Larissa et al. (2019), Data from: Projecting consequences of global warming for the functional diversity of fleshy-fruited plants and frugivorous birds along a tropical elevational gradient, Dryad, Dataset, doi:10.5061/dryad.c0n737b

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**traits_birds**

*Functional Traits of Frugivorous Birds along a Tropical Gradient*

**Description**

A dataset containing some functional traits of frugivorous birds in the Manú biosphere reserve, southeast Peru. Given are species mean trait values. The row names of the dataset give species names. Morphological traits have been measured on museum specimen following Eck et al. (2011). Traits have been measured only for adult and, if possible, for a minimum of two female and two male specimens. Body mass was taken from Dunning et al. (2007).

**Usage**

traits_birds

**Format**

A data frame with 217 rows and 4 variables:

- **Bill.width.mm.** bill width, in mm
- **Bill.length.mm.** bill length, in mm
- **Kipp.s.index** Kipp’s index indicating wing Pointedness
- **Bodymass..g.** adult’s bodymass, in g
Source
Nowak, Larissa et al. (2019), Data from: Projecting consequences of global warming for the functional diversity of fleshy-fruited plants and frugivorous birds along a tropical elevational gradient, Dryad, Dataset, doi:10.5061/dryad.c0n737b

Description
Taxonomy and functional traits of 392 fleshy-fruit plant species from the Manu National Park in south-east Peru. Given are fruit length and width (mm), plant height (m) and crop mass (g). Fruit traits have been measured on fresh fruit samples. Number of fruits per plant (used to determine the crop mass) and plant height have been estimated in the field. Species names are indicated as row names.

Usage
traits_plants

Format
A data frame with 392 rows and 4 variables:

- **Fruit.length.mm.** fruit length, in mm
- **Fruit.width.mm.** fruit width, in mm
- **Plant.height.m.** plant height, in m
- **Crop.mass..g.** seed mass, in g

Source
Nowak, Larissa et al. (2019), Data from: Projecting consequences of global warming for the functional diversity of fleshy-fruited plants and frugivorous birds along a tropical elevational gradient, Dryad, Dataset, doi:10.5061/dryad.c0n737b
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