Package: isoniche (via r-universe)

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Title Calculating Density-Independent Niche Breadth Indices from Abundance Data

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Description Deriving isodar-based niche breadth indices from abundance data of two or more habitats, including several methods based on pairwise isodars, multidimensional isodars, and isodar-adjusted inequality.

License GPL-3

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Author Shahar Dubiner [aut, cre] (ORCID: <`https://orcid.org/0000-0003-1771-0087`>), Itai Granot [aut], Jonathan Belmaker [aut]

Maintainer Shahar Dubiner <`dubiner@mail.tau.ac.il`>

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Contents

`fit_isodar` *Fit pairwise isodars between two or more habitats*

Description

Fits pairwise isodar relationships between all habitat pairs using `lmodel2::lmodel2()` (Model II regression). Each output row represents the relationship:

$$habitat\_y = intercept + slope \times habitat\_x$$

Usage

```
fit_isodar(
  data,
  hab_cols = NULL,
  n_habitats = ncol(data),
  flip_intercept = TRUE
)
```

Arguments

`data`	A data frame of abundance data with one column per habitat.
`hab_cols`	A character vector of length `n\_habitats`, detailing the abundance columns. Currently defaults to first columns.
`n_habitats`	Integer (>= 2). Number of habitat columns to use, starting at column 1.
`flip_intercept`	Logical. If TRUE (default), flip axes when intercept < 0.

Details

It is crucial to either place the columns with abundance for each habitat as the FIRST columns, or to explicitly state the habitat columns in `hab\_cols`.

If the fitted intercept is negative, the relationship is flipped (axes swapped) to provide a biologically interpretable representation (negative intercepts are meaningless in this context) and model refitted.

The `sd` column is the residual SD from vertical residuals in the reported equation.

Value

A tibble with one row per habitat pair containing:

- `habitat_x`, `habitat_y`
- slope, intercept
- sd: residual SD in the reported equation
- `p_slope`, `p_intercept`
- flipped: TRUE if axes were flipped (due to int<0), FALSE otherwise

Examples

```
set.seed(1)
isod <- simulate_isodars(1, 2, 5, 1, noise = 2, n = 10)
fit_isodar(isod, n_habitats = 3)
```

`isodar_adj_niche` *Compute the isodar-adjusted inequality index for one or more total abundances*

Description

Reconstructs habitat abundances for each requested total abundance by solving a weighted least-squares system defined by the pairwise isodars:

$$habitat\_y = intercept + slope \times habitat\_x$$

Usage

```
isodar_adj_niche(
  isodars,
  abundances = NULL,
  weights = NULL,
  alpha = 0.1,
  sig_weights = c(sig = 1, nonsig = 0),
  method = c("gini"),
  plot = FALSE,
  max_search = 10000
)
```

Arguments

`isodars`	A data frame returned by `fit_isodar()`
`abundances`	Numeric vector of total abundances. If NULL, the minimal total abundance yielding occupancy in all habitats ("baseline") is chosen when possible; otherwise a default exploratory sequence is used
`weights`	Weighting scheme. One of: • `NULL`: equal weights • numeric vector of length `nrow(isodars)` • `"1/var"`: weights proportional to `1/sd^2` • `"sig"`: weights based on significance of intercepts, using `sig_weights`
`alpha`	Numeric in (0, 1). Significance threshold used when `weights = "sig"`
`sig_weights`	Numeric vector of length 2 giving weights for significant and non-significant isodars when `weights = "sig"`. Can be named `c(sig = , nonsig = )` or unnamed `c(sig, nonsig)`. Default is `c(sig = 1, nonsig = 0)`.

`method`	Character. Currently only `method = "gini"` available
`plot`	Logical. If TRUE, plots adjusted niche breadth versus total abundance
`max_search`	Integer. Maximum total abundance to search when `abundances = NULL`, in order to find baseline n

Details

The reconstruction is constrained to be nonnegative and to sum to the requested total abundance (active-set heuristic). Niche breadth is then computed from the reconstructed habitat vector; currently defined as:

$$nichebreadth = 1 - Gini(x)$$

of isodar-reconstructed abundances at a given N.

To emphasize the intercept component, use baseline abundances provided by `abundances = NULL`. To emphasize the slope component, we recommend to set `abundances` to the highest n in your dataset. To see how niche breadth changes as a function of n, enter a vector of increasing abundances.

Value

A tibble with one row per total abundance containing:

- `total_abundance`
- niche_breadth
- one column per habitat with reconstructed abundance

Examples

```
set.seed(1)
isod <- simulate_isodars(1, 2, 5, 1, noise = 2, n = 10)
INB <- fit_isodar(isod, n_habitats = 3)
isodar_adj_niche(INB, max_search = 100) # automatically checks only baseline abundance
isodar_adj_niche(INB, abundances = c(15, 30, 45), max_search = 100) # set specific values
```

`ndim_isoniche` *Multidimensional isodar-based niche breadth indices*

Description

Computes vector- and orthogonal isodar-based niche breadth components from abundance data across all habitats simultaneously, generalizing the slope (density-dependent) and intercept/baseline (density-independent) components of isodars to n dimensions.

Usage

```
ndim_isoniche(data, n_habitats = ncol(data), scale = TRUE, weights = TRUE)
```

Arguments

`data`	A data frame of abundance data (one column per habitat).
`n_habitats`	Integer (>=2). Number of habitat columns to use, starting at column 1.
`scale`	Logical. If `TRUE`, results are raised to the power of $n\_habitats - 1$ to compensate for reduced sensitivity due to added dimensions.
`weights`	Logical. If `TRUE`, habitats are weighted by inverse residual variance. If `FALSE`, uniform weights are used.

Details

Both indices return values between 0 and 1, where 1 indicates a perfect generalist and 0 a specialist. Habitat axes can optionally be weighted by inverse residual variance.

Value

A tibble with `vector`, `orthogonal`, and `n_habitats`.

Examples

```
set.seed(1)
isod <- simulate_isodars(1, 2, 5, 1, noise = 2, n = 10)
```

`pairwise_isoniche` *Pairwise isodar-based niche breadth indices*

Description

Computes niche breadth indices from a set of pairwise isodars (slopes and intercepts) in the format of the output table of `fit_isodar()`. Two methods are available: a weighted mean of isodar components and a weighted inverse variance of the isodars' divergence from neutrality.

Usage

```
pairwise_isoniche(
  data,
  method = c("inverse_variance", "mean"),
  weights = NULL,
  alpha = 0.1,
  sig_weights = c(sig = 1, nonsig = 0)
)
```

Arguments

`data`	A data frame returned by `fit_isodar()`.
`method`	Character. One of `"mean"` or `"inverse_variance"`.
`weights`	Weighting scheme for pairwise isodars. One of: • `NULL`: uniform weights • numeric vector of length `nrow(data)` • `"1/var"`: weights proportional to 1/sd^2 (sd from `fit_isodar`) • `"sig"`: weights based on significance of intercepts, using `sig_weights`
`alpha`	Numeric in (0, 1). Significance threshold used when `weights = "sig"`.
`sig_weights`	Numeric vector of length 2 giving weights for significant and non-significant isodars when `weights = "sig"`. Can be named `c(sig = ..., nonsig = ...)` or unnamed `c(sig, nonsig)`. Default is `c(sig = 1, nonsig = 0)`.

Value

A one-row tibble with columns `intercept`, `slope`, and `method`.

Examples

```
set.seed(1)
isod <- simulate_isodars(1, 2, 5, 1, noise = 2, n = 10)
INB <- fit_isodar(isod, n_habitats = 3)
pairwise_isoniche(INB, method = "inverse_variance", weights = "1/var")
pairwise_isoniche(INB, method = "inverse_variance", weights = "sig",
             sig_weights = c(sig = 1, nonsig = 0.25), alpha = 0.1)
```

`simulate_isodars` *Simulate abundances across three habitats*

Description

Simulates abundance data for three habitats across `n` sites using sequential linear relationships (isodars) with Gaussian noise:

- hab2 is generated from hab1 using `slope1` and `int1`
- hab3 is generated from hab2 using `slope2` and `int2`

Usage

```
simulate_isodars(
  slope1,
  slope2,
  int1,
  int2,
  noise = 1,
```

```
  n = 30,
  hab1_max = 100/(slope1^1.2) - int1
)
```

Arguments

`slope1`	Numeric. Isodar slope for `hab2 ~ hab1`.
`slope2`	Numeric. Isodar slope for `hab3 ~ hab2`.
`int1`	Numeric. Isodar intercept for `hab2 ~ hab1`.
`int2`	Numeric. Isodar intercept for `hab3 ~ hab2`.
`noise`	Numeric (>= 0). Standard deviation of Gaussian noise.
`n`	Integer (> 0). Number of simulated sites.
`hab1_max`	Integer. maximum abundance value in habitat 1 (other maxima calculated from hab1_max). Default is derived to generally suit the isodar parameters, but is arbitrary.

Details

The output includes simple per-site niche metrics (CV and Gini) computed from the three habitat abundances.

Value

A tibble with one row per simulated site containing:

- hab1, hab2, hab3: simulated abundances (nonnegative integers)
- total_abundance: hab1 + hab2 + hab3
- mean_abundance: total_abundance divided by 3
- sd: scaled standard deviation of habitat abundances
- cv: coefficient of variation (NA if mean_abundance == 0)
- gini: Gini coefficient of habitat abundances

Examples

```
set.seed(1)
simulate_isodars(1, 2, 5, 1, noise = 2, n = 10)
```

Index