

Package ‘ascent’

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Title Multi-Layer Decomposition of Functional Community Restructuring

Version 0.1.1

Description Implements the 'ASC-CFD' (Assemblage Shift Characterization - Community Functional Dynamics) framework for decomposing functional community restructuring into positional (centroid displacement), dispersive (functional dispersion), and boundary (convex hull volume) components. Provides hierarchical null models (structural, quantitative, identity) to evaluate statistical significance and species-level leverage analysis to identify taxa driving functional shifts. Supports both temporal (paired) and spatial (pairwise) comparisons.

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Imports cluster, ggplot2, stats, utils, vegan, geometry

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

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URL <https://github.com/V3ndetta96/ascent>

BugReports <https://github.com/V3ndetta96/ascent/issues>

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asc_baseline	<i>Baseline Functional Topology of Entities</i>
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Description

Calculates the absolute functional centroid (CWM), functional dispersion (FDis), and convex hull volume (FRic) for each community or site independently.

Usage

```
asc_baseline(
  traits,
  abund,
  dist_method = "gower",
  dim_retention = c("variance", "broken_stick"),
  var_tol = 0.8,
  na.rm = TRUE
)
```

Arguments

traits	A data frame or matrix of functional traits.
abund	A data frame or matrix of species abundances.
dist_method	Distance metric for the trait matrix. Default is "gower".
dim_retention	Character. Method for dimensionality reduction. Options are "variance" or "broken_stick".
var_tol	Numeric. Proportion of cumulative variance to retain. Default is 0.80.
na.rm	Logical. Remove missing values? Default is TRUE.

Value

An S3 object of class `ascfcd_base`.

Examples

```
traits <- data.frame(
  Mass = c(15, 30, 60, 150, 400),
  Beak = c(10, 15, 28, 45, 85)
)
rownames(traits) <- paste0("Sp", 1:5)

abund <- rbind(
  Forest = c(0, 5, 25, 20, 10),
  Field = c(30, 20, 10, 0, 0)
)

base <- asc_baseline(traits, abund, dist_method = "euclidean")
summary(base)
```

asc_entities

*Identify Functional Entities (Species Clustering)***Description**

Clusters species into discrete functional entities based on shared morphological, physiological, or ecological traits.

Usage

```
asc_entities(
  traits,
  dist_method = "gower",
  hclust_method = "ward.D2",
  k = NULL,
  h = NULL
)
```

Arguments

<code>traits</code>	A data frame or matrix of functional traits.
<code>dist_method</code>	Character. Distance metric. Default is "gower" to handle mixed data types.
<code>hclust_method</code>	Character. Agglomeration method for hierarchical clustering. Default is "ward.D2".
<code>k</code>	Integer. Desired number of functional entities (clusters). If NULL, h must be provided.
<code>h</code>	Numeric. Height at which to cut the dendrogram. If both k and h are NULL, defaults to k = 3.

Value

An S3 object of class `ascfcd_entities`.

Examples

```
traits <- data.frame(
  Mass = c(15, 30, 60, 150, 400),
  Beak = c(10, 15, 28, 45, 85),
  Diet = factor(c(0, 1, 1, 1, 0))
)
rownames(traits) <- paste0("Sp", 1:5)

ent <- asc_entities(traits, k = 2)
summary(ent)
```

asc_null

Multi-Level Null Models for Multidimensional Functional Shifts

Description

Evaluates the statistical significance of functional shifts using three null models: Structural (Curveball), Quantitative (SAD Reshuffle), and Identity (Trait Shuffle).

Usage

```
asc_null(x, n_perm = 999, seed = NULL)
```

Arguments

<code>x</code>	An object of class <code>ascfcd</code> or <code>ascfcd_pw</code> .
<code>n_perm</code>	Integer. Number of permutations. Default is 999.
<code>seed</code>	Integer. Random seed for reproducibility.

Value

The original object with an appended `null_models` data frame.

Note

Model A (Structural): After curveball permutation, all species present receive uniform relative abundance ($1/S_{\text{local}}$). This means the null distribution for FDis conflates the effect of taxonomic identity with the assumption of equitability. The SES tests whether the observed shift is extreme given random species composition, *not* given random composition with the observed SAD.

Model B (Quantitative): Because incidence is held fixed, the convex hull is invariant across permutations. Delta FRic under Model B is reported as NA (not applicable), not zero.

Model C (Identity): Statistical power is limited when the regional species pool is small (< 15 species). With few species, the number of unique trait permutations is small, reducing the resolution of the null distribution. Consider increasing `n_perm` and interpreting marginal p-values ($0.05 < p < 0.10$) with caution.

Scope: When multiple contrasts are evaluated simultaneously, the curveball operates on the full stacked matrix, assuming a shared regional species pool. For biogeographically independent sites, run `asc_null()` on each contrast separately.

Examples

```
traits <- data.frame(
  Mass = c(15, 30, 60, 150, 400),
  Beak = c(10, 15, 28, 45, 85),
  Diet = factor(c(0, 1, 1, 1, 0))
)
rownames(traits) <- paste0("Sp", 1:5)

abund <- rbind(
  Reference = c(0, 10, 25, 20, 5),
  Impacted = c(30, 15, 5, 0, 0)
)

res <- asc_paired(
  traits, abund,
  sites = c("S1", "S1"),
  time = c("Reference", "Impacted"),
  ref_time = "Reference"
)
res <- asc_null(res, n_perm = 99, seed = 42)
res$null_models
```

asc_paired

Paired Functional Multidimensional Restructuring

Description

Calculates centroid displacement (Layer 1), dispersion shift (Layer 2 - FDis), and volume shift (Layer 3 - FRic) between paired states.

Usage

```
asc_paired(
  traits,
  abund,
  sites,
  time,
  ref_time,
```

```

    dist_method = "gower",
    dim_retention = c("variance", "broken_stick"),
    var_tol = 0.8,
    na.rm = TRUE
  )

```

Arguments

<code>traits</code>	A data frame or matrix of functional traits.
<code>abund</code>	A data frame or matrix of species abundances.
<code>sites</code>	A vector indicating the site identifier.
<code>time</code>	A vector indicating the temporal state.
<code>ref_time</code>	A character string specifying the reference state.
<code>dist_method</code>	Distance metric for the trait matrix. Default is "gower".
<code>dim_retention</code>	Character. Method for dimensionality reduction.
<code>var_tol</code>	Numeric. Proportion of cumulative variance to retain. Default is 0.80.
<code>na.rm</code>	Logical. Remove missing values? Default is TRUE.

Value

An S3 object of class `ascfcd`.

Note

Normalization: Delta FDis and Delta FRic are absolute differences, not normalized by the regional pool. Values are not directly comparable across studies with different species pools or trait scales. Only `rDelta_C` (position) is normalized by `Dmax_regional`.

FRic = NA: When a community has fewer species than retained PCoA axes, the convex hull is geometrically undefined and FRic is set to NA, which propagates to Delta_FRic.

Temporal replicates: When multiple rows share the same site and temporal state (e.g., three reference plots), their relative abundances are averaged (column means) before computing the centroid. This is equivalent to treating replicates as a single pooled community. Intra-state variability is not propagated to downstream metrics.

Examples

```

# Simulate deforestation impact on a bird community
traits <- data.frame(
  Mass = c(15, 30, 60, 150, 400),
  Beak = c(10, 15, 28, 45, 85),
  Diet = factor(c(0, 1, 1, 1, 0))
)
rownames(traits) <- paste0("Sp", 1:5)

abund <- rbind(
  Reference = c(0, 10, 25, 20, 5),
  Impacted = c(30, 15, 5, 0, 0)
)

```

```

)

res <- asc_paired(
  traits, abund,
  sites = c("Site1", "Site1"),
  time = c("Reference", "Impacted"),
  ref_time = "Reference"
)
summary(res)

```

asc_pairwise

*Pairwise Functional Spatial Divergence***Description**

Calculates spatial functional divergence across three layers: position (Delta C), dispersion (FDis), and volume (FRic).

Usage

```

asc_pairwise(
  traits,
  abund,
  dist_method = "gower",
  dim_retention = c("variance", "broken_stick"),
  var_tol = 0.8,
  na.rm = TRUE
)

```

Arguments

traits	A data frame or matrix of functional traits.
abund	A data frame or matrix of species abundances.
dist_method	Distance metric for the trait matrix. Default is "gower".
dim_retention	Character. Method for dimensionality reduction.
var_tol	Numeric. Proportion of cumulative variance to retain. Default is 0.80.
na.rm	Logical. Remove missing values? Default is TRUE.

Value

An S3 object of class `ascfcd_pw`.

Note

Leverage direction: In pairwise mode, leverage is computed from Community_A toward Community_B. Reversing the pair order reverses the leverage signs. The direction is determined by alphabetical ordering of community names.

Normalization: Delta FDis and Delta FRic are absolute differences (see [asc_paired](#) for details).

Examples

```

traits <- data.frame(
  Mass = c(15, 30, 60, 150, 400),
  Beak = c(10, 15, 28, 45, 85)
)
rownames(traits) <- paste0("Sp", 1:5)

abund <- rbind(
  Forest = c(0, 5, 25, 20, 10),
  Field  = c(30, 20, 10, 0, 0),
  Wetland = c(5, 10, 15, 15, 5)
)

res_pw <- asc_pairwise(traits, abund, dist_method = "euclidean")
summary(res_pw)

```

asc_transitions

*Extract Functional Transitions and Species Leverage***Description**

Calculates the multidimensional Functional Leverage of each species, quantifying their direct contribution to the positional shift (Layer 1 - Delta C) of the ecosystem.

Usage

```
asc_transitions(x, ...)
```

Arguments

x An object of class `ascfcd` or `ascfcd_pw`.

... Further arguments passed to or from other methods.

Value

An S3 object of class `ascfcd_transitions`.

Examples

```

traits <- data.frame(
  Mass = c(15, 30, 60, 150, 400),
  Beak = c(10, 15, 28, 45, 85)
)
rownames(traits) <- paste0("Sp", 1:5)

abund <- rbind(
  Ref = c(0, 10, 25, 20, 5),
  Imp = c(30, 15, 5, 0, 0)
)

```

```
)

res <- asc_paired(
  traits, abund,
  sites = c("S1", "S1"),
  time = c("R", "I"), ref_time = "R",
  dist_method = "euclidean"
)
drivers <- asc_transitions(res)
drivers$S1$species_leverage
```

assess_functional_space

Assess Functional Space Quality

Description

Diagnostic tool to evaluate the quality of the PCoA-based functional space constructed from a trait matrix. Intended for use before running core analyses (asc_paired, asc_pairwise, etc.) to identify potential distortion from negative eigenvalues or excessive dimensionality reduction.

Usage

```
assess_functional_space(
  traits,
  dist_method = "gower",
  dim_retention = c("variance", "broken_stick"),
  var_tol = 0.8
)
```

Arguments

traits	A data frame or matrix of functional traits.
dist_method	Distance metric for the trait matrix. Default is "gower".
dim_retention	Character. Method for dimensionality reduction. Options are "variance" or "broken_stick". Default is "variance".
var_tol	Numeric. Proportion of cumulative variance to retain (used when dim_retention = "variance"). Default is 0.80.

Details

The Gower distance is not strictly Euclidean, which means PCoA may produce negative eigenvalues. This function reports the full eigenvalue spectrum and computes a quality index so users can decide whether the functional space is an adequate representation of the original distance matrix.

A quality below 0.80 indicates that negative eigenvalues represent more than 20%

- Reviewing the trait data for problematic variables.
- Applying a Cailliez or Lingoes correction to the distance matrix before ordination.
- Using a different distance metric (e.g., "euclidean" for purely continuous traits).

Value

A list of class `ascfcd_space` with:

quality Numeric. PCoA quality index ($\text{sum}(\text{positive_eig}) / \text{sum}(\text{abs}(\text{all_eig}))$). Values above 0.80 are generally acceptable.

n_species Integer. Number of species in the trait matrix.

n_traits Integer. Number of traits.

k_retained Integer. Number of PCoA axes retained.

var_retained Numeric. Cumulative variance explained by retained axes.

axis_var Numeric vector. Relative variance per retained axis.

n_neg_eigenvalues Integer. Count of negative eigenvalues.

neg_eigenvalue_pct Numeric. Percentage of total absolute eigenvalue represented by negative eigenvalues.

eigenvalues Numeric vector. All raw eigenvalues from PCoA.

Examples

```
traits <- data.frame(
  Mass = c(15, 30, 60, 150, 400),
  Beak = c(10, 15, 28, 45, 85),
  Diet = factor(c(0, 1, 1, 1, 0))
)
rownames(traits) <- paste0("Sp", 1:5)

diag <- assess_functional_space(traits)
diag
```

plot.ascfcd

Plot Multidimensional Functional Restructuring

Description

Visualizes the functional trajectory (Centroid shift) and volume shift (Convex Hull) of a specific site/contrast in the PCoA space, alongside the species leverage.

Usage

```
## S3 method for class 'ascfcd'
plot(x, contrast, type = c("both", "pcoa", "leverage"), n_sp = 10, ...)
```

Arguments

x	An object of class ascfcd.
contrast	Character. The exact name of the site/contrast to plot.
type	Character. What to plot? "pcoa" (Trajectory & Hull), "leverage" (Drivers), or "both". Default is "both".
n_sp	Integer. Number of top species to display in the leverage plot. Default is 10.
...	Additional graphical arguments.

Value

A ggplot object (or patchwork object if type = "both").

plot.ascfcd_entities *Plot Functional Entities Dendrogram*

Description

Plots the hierarchical clustering dendrogram of the functional entities.

Usage

```
## S3 method for class 'ascfcd_entities'  
plot(x, ...)
```

Arguments

x	An object of class ascfcd_entities.
...	Additional graphical arguments passed to plot.hclust.

Value

No return value, called for side effects (plots a dendrogram).

plot.ascfcd_pw	<i>Plot Pairwise Functional Spatial Divergence</i>
----------------	--

Description

Visualizes spatial functional restructuring (Centroid & Hull) between two communities.

Usage

```
## S3 method for class 'ascfcd_pw'
plot(x, contrast, type = c("both", "pcoa", "leverage"), n_sp = 10, ...)
```

Arguments

x	An object of class ascfcd_pw.
contrast	Character. The contrast to plot (e.g., "SiteA_vs_SiteB").
type	Character. What to plot? "pcoa", "leverage", or "both".
n_sp	Integer. Number of top species to display. Default is 10.
...	Additional graphical arguments.

Value

A ggplot object.

plot.ascfcd_transitions	<i>Plot Functional Leverage</i>
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Description

Visualizes the top species driving functional centroid displacement.

Usage

```
## S3 method for class 'ascfcd_transitions'
plot(x, contrast, n_sp = 10, ...)
```

Arguments

x	An object of class ascfcd_transitions.
contrast	Character. The contrast to plot.
n_sp	Integer. Number of top species to display. Default is 10.
...	Additional graphical arguments.

Value

A ggplot object.

summary.ascfcd

Summary for Paired Functional Centroid Displacement

Description

Provides a concise, multi-layer overview of the paired ASC-CFD analysis, including null models and top functional drivers.

Usage

```
## S3 method for class 'ascfcd'
summary(object, ...)
```

Arguments

object	An object of class ascfcd.
...	Further arguments passed to or from other methods.

Value

Invisibly returns a data frame with the displacement metrics.

summary.ascfcd_base

Summary for Baseline Functional Entities

Description

Provides an overview of the baseline functional topology of the evaluated entities.

Usage

```
## S3 method for class 'ascfcd_base'
summary(object, ...)
```

Arguments

object	An object of class ascfcd_base.
...	Further arguments passed to or from other methods.

Value

Invisibly returns the entities results data frame.

summary.ascfcd_entities

Summary for Functional Entities Classification

Description

Provides an overview of the species clustering into functional entities.

Usage

```
## S3 method for class 'ascfcd_entities'
summary(object, ...)
```

Arguments

object	An object of class ascfcd_entities.
...	Further arguments passed to or from other methods.

Value

Invisibly returns the classification data frame.

summary.ascfcd_pw

Summary for Pairwise Functional Spatial Divergence

Description

Provides a comprehensive overview of the spatial network ASC-CFD analysis.

Usage

```
## S3 method for class 'ascfcd_pw'
summary(object, ...)
```

Arguments

object	An object of class ascfcd_pw.
...	Further arguments passed to or from other methods.

Value

Invisibly returns the pairwise results data frame.

`summary.ascfcd_transitions`*Summary for Functional Leverage Analysis*

Description

Provides an overview of the species leverage for each contrast.

Usage

```
## S3 method for class 'ascfcd_transitions'  
summary(object, n_sp = 5, ...)
```

Arguments

<code>object</code>	An object of class <code>ascfcd_transitions</code> .
<code>n_sp</code>	Integer. Number of top species to display per contrast. Default is 5.
<code>...</code>	Further arguments passed to or from other methods.

Value

Invisibly returns the object.

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