Package ‘ordiBreadth’

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Type Package
Title Ordinated Diet Breadth
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Author James Fordyce
Maintainer James A. Fordyce <jfordyce@utk.edu>
Description Calculates ordinated diet breadth with some plotting functions.
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R topics documented:

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**Description**

Calculates ordinated diet breadth and provides plotting functions.

**Details**

```
Package: ordiBreadth
Type: Package
Version: 1.0
Date: 2015-08-07
License: GPL 3.0
```

Users provide a matrix of host associations, where rows are consumers (e.g., herbivores) and columns are resources (e.g., plants). The function `ordi.breadth` calculates the ordinated breadth for all consumers in the matrix and `summary.hbreadth` summarizes the output and `dist.group.plot` can be used for visualization.

**Author(s)**

James Fordyce

Maintainer: James Fordyce <jfordyce@utk.edu>

**References**


```
**dist.group.plot**

**Description**

This function plots the ordination and shows the centroid for a focal herbivore

**Usage**

dist.group.plot(specialization, id, cex = 1, PCoA = c(1, 2), seg.col = "pink", seg.wd = 2, seg.lty = 1, pt.col = "red", pt.pch = 19, pt.cex = 1.5, x.lim = NULL, y.lim = NULL, plant.plot = "all.names", rel.pch = 19, rel.cex = 1.5, rel.col = "red", nrel.pch = 19, nrel.cex = 1.5, nrel.col = "red", verbose = TRUE, scaled = TRUE)
```
Arguments

specialization  The object created by the function `ordi.breadth`.
id  A numeric indicating which species of herbivore to plot from list `specialization`.
cex  A numeric indicating the font size for diet item names.
PCoA  A vector length two indicated which two PCo axes to plot.
seg.col  The color of segments joining diet items to centroid.
seg.wd  A value indicating the line width of segments joining diet items to centroid.
seg.lty  A value indicating the line type of segments joining diet items to centroid.
pt.col  The color of centroid plotting character.
pt.pch  A value indicating the plotting character for centroid.
pt.cex  A value indicating the character expansion for centroid plotting character.
x.lim  A vector length two indicating the min and max of x axis.
y.lim  A vector length two indicating the min and max of y axis.
plant.plot  A value taking on "all.names", "relevent", or "points". 'all.names' plots the names of host plants, 'relevent' plots only the names of host plants used by focale herbivore (indicated by argument id), 'points' points all host plants as points.
rel.pch  A value indicating the plotting character for host plants used by herbivore.
rel.cex  A value indicating the character expansion for host plants used by herbivore.
rel.col  A value indicating the color for host plants used by herbivore.
nrel.pch  A value indicating the plotting character for host plants not used by herbivore.
nrel.cex  A value indicating the character expansion for host plants not used by herbivore.
nrel.col  A value indicating the color for host plants not used by herbivore.
verbose  A logical indicating whether information on taxonomic and ordinated host breadth is included in plot.
scaled  A logical indicating whether to return scaled ordinated host breadth.

Author(s)

James Fordyce

References


Examples

testdata<-
c( 0,0,0,0,1,0,0,0,0,#1 0,0,0,0,0,1,1,0,0,#2 1,1,1,0,0,0,0,0,0,#3
focal.profPlot

Description

Plots the profile plot of distance from herbivore centroid to host plants calculated by excluding the focal herbivore. Useful for exploratory data analysis.

Usage

focal.profPlot(dat, focal.bug, dist.method = "jaccard", col = c("black", "red"))

Arguments

dat A matrix of diet associations. Rows are herbivores and columns are diet items.
focal.bug A value indicating which herbivore is the focal herbivore.
dist.method Dissimilarity index passed on to vegdist in the vegan package.
col A vector length 2 indicating colors for plotting. First color is for non-diet items, second color is for diet items.

Value

A profile plot

Author(s)

James Fordyce
References

Examples

testdata<-c(
0,0,0,0,1,0,0,0,0,0,#1
0,0,0,0,0,1,1,0,0,#2
1,1,0,0,0,0,0,0,#3
0,0,0,0,0,0,1,0,1,#4
1,1,0,0,0,1,0,0,#4
1,1,0,0,1,0,0,0,#4
0,0,1,0,0,0,1,1,#4
1,0,1,0,1,0,0,1, #5
1,1,0,0,1,0,0,1,1,#6
1,1,1,0,1,0,1,1,1) #8

dat<-array(dim=c(10,10),data=testdata)
dat<-t(dat)
colnames(dat)<-paste(letters[1:10],sep="")
rownames(dat)<-paste("bug",1:10,sep="")
focal.profplot(dat,4)

description
Calculates the diet breadth of a hypothetical herbivore placed in ordination space.

Usage
hyp.ordi.breadth(dat, grouping, dist.method = "jaccard", distance = FALSE)

Arguments
dat A matrix of diet associations. Rows are herbivores and columns are diet items.
grouping a vector of ones and zeros or TRUE and FALSE indicting diet items of hypothetical herbivore
dist.method Dissimilarity index passed on to vegdist in the vegan package
distance a logical indicating whether to return distance of hypothetical herbivore centroid to plants used in PCoA space and the coordinates of the centroid in PCoA space
Value

tot.breadth  Ordinated host breadth of hypothetical herbivore

distances  Distance from centroid to diet items in PCoA space

centroid  Coordinates of the centroid of hypothetical herbivore

Author(s)

James Fordyce

References


Examples

testdata<-
c(
0,0,0,1,0,0,0,0,#1
0,0,0,0,0,1,0,0,#2
1,1,0,0,0,0,0,0,#3
0,0,0,1,1,0,1,0,#4
1,1,0,0,1,0,0,0,#4
1,1,0,1,0,1,0,0,#4
0,0,1,0,0,1,0,1,#4
1,0,1,0,1,0,0,1, #5
1,1,0,1,0,0,1,1,#6
1,1,1,0,1,0,1,1) #8

dat<array(dim=c(10,10),data=testdata)
dat<-t(dat)
colnames(dat)<-paste("",LETTERS[1:10],sep="")
rownames(dat)<-paste("bug",1:10,sep="")

group<-c(TRUE,TRUE,TRUE,FALSE,FALSE,FALSE,FALSE,FALSE,FALSE,FALSE)
hyp.ordi.breadth(dat,group)
hyp.ordi.breadth(dat,group,distance=TRUE)

group<-c(1,1,1,1,1,1,1,1)
hyp.ordi.breadth(dat,group)#extreme generalist
hyp.ordi.breadth(dat,group,distance=TRUE)
**null.breadth**

---

**null.breadth**

---

**Description**

This function calculates the null expectation of host breadth if herbivores sample diet items randomly.

**Usage**

```r
null.breadth(dat, dist.method = "jaccard", rep = 100, quantiles = c(0.025, 0.975), scaled = FALSE)
```

**Arguments**

- **dat**: A matrix of diet associations. Rows are herbivores and columns are diet items.
- **dist.method**: Dissimilarity index passed on to vegdist in the ‘vegan’ package.
- **rep**: The number of permutations to generate a null distribution.
- **quantiles**: A vector length of two indicating the lower and upper quantiles to report for the null distribution.
- **scaled**: A logical indicating whether to report the scaled ordinated host breadth.

**Value**

An array show the lower and upper quantiles of the null distribution for each taxonomic richness.

**Author(s)**

James Fordyce

**References**


**Examples**

```r
testdata<-
c(
0,0,0,0,1,0,0,0,0,0,
0,0,0,0,0,1,1,0,0,0,
1,1,1,0,0,0,0,0,0,0,
0,0,0,0,1,1,0,1,0,1,
1,1,1,0,0,1,0,0,0,0,
1,1,0,0,1,0,1,0,0,0,
0,0,0,1,0,0,1,0,1,1,
1,0,1,0,1,0,0,0,0,1,
1,1,0,0,1,0,0,1,1,1,
1,0,0,1,0,0,1,1,1,1,
)
```
null.breadth.focal

1,1,1,0,1,1,0,1,1,1)

dat<-array(dim=c(10,10),data=testdata)
dat<-t(dat)
colnames(dat)<-paste("",LETTERS[1:10],sep="")
rownames(dat)<-paste("bug",1:10,sep="")

null.breadth(dat)

Description

This function calculates the null expectation of ordinated host breadth for each herbivore individually. The ordination for each herbivore is based on PCoA where the focal herbivore is not included.

Usage

null.breadth.focal(dat, dis.method = "jaccard", reps = 100)

Arguments

dat A matrix of diet associations. Rows are herbivores and columns are diet items.
dis.method Dissimilarity index passed on to vegdist in the vegan package.
reps The number of permutations to generate a null distribution.

Details

In situations where the focal herbivore is the only species using a particular diet item, that diet item is not included in the ordination. This is the modified plant richness.

Value

A list containing the following:

species Name of herbivore species (row name of dat)

observed.breadth Ordinated diet breadth
scale.factor Ordinated diet breadth of most extreme generalist herbivore based on ordination
observed.breadth.scaled Scaled ordinated diet breadth
totalplantrichness Taxonomic diet richness of focal species
modplantrichness Modified taxonomic diet richness of focal species (see details)
null A vector of null ordinated diet values
null.breadth.focal.summary

Author(s)

James Fordyce

References


Examples

testdata<-
c( 0,0,0,0,1,0,0,0,0,0,#1 0,0,0,0,0,1,1,0,0,#2 1,1,1,0,0,0,0,0,0,#3 0,0,0,1,1,0,1,0,1,#4 1,1,1,0,0,1,0,0,0,#4 1,1,0,0,1,0,1,0,0,#4 0,0,0,1,0,0,1,0,1,#4 1,0,1,0,1,0,0,0,1,#5 1,1,0,0,1,0,1,1,1,#6 1,1,1,0,1,0,1,1,1) #8

dat<-array(dim=c(10,10),data=testdata) dat<-t(dat) colnames(dat)<-paste(LETTERS[1:10],sep='') rownames(dat)<-paste("bug",1:10,sep='')

null.breadth.focal(dat)

null.breadth.focal.summary

null.breadth.focal.summary

Description

Summarizes results contained in object created by null.breadth.focal

Usage

null.breadth.focal.summary(null.breadth.focal.out, quantiles = c(0.025, 0.975), round = 5, scaled = FALSE)
null.breadth.focal.summary

Arguments

null.breadth.focal.out
Object created by null.breadth.focal

quantiles
A vector length of two indicating the lower and upper quantiles to report for the null distribution.

round
A value indicating the number of digits to round results

scaled
Logical indicating whether to return scaled ordinated host breadth.

Value

Returns a dataframe of summarized results.

Author(s)

James Fordyce

References


Examples

testdata<-
c(
  0,0,0,1,0,0,0,0,#1
  0,0,0,0,0,1,1,0,#2
  1,1,0,0,0,1,0,0,#3
  0,0,0,1,1,0,1,0,#4
  1,1,0,0,1,0,0,0,#4
  1,1,0,1,0,0,0,0,#4
  0,0,0,1,1,0,0,0,#4
  1,0,1,0,0,0,0,1,#5
  1,0,0,1,0,0,1,1,#6
  1,1,0,1,1,0,1,1) #8

dat<array(dim=c(10,10),data=testdata)
dat<-t(dat)
colnames(dat)<-paste("",LETTERS[1:10],sep="")
rownames(dat)<-paste("bug",1:10,sep="")

x<-null.breadth.focal(dat)
null.breadth.focal.summary(x)
**ordi.breadth**

**Description**

This function calculates ordinated diet breadth

**Usage**

```r
ordi.breadth(dat, dist.method = "jaccard")
```

**Arguments**

- `dat` A matrix of diet associations. Rows are herbivores and columns are diet items.
- `dist.method` Dissimilarity index passed on to vegdist in the vegan package.

**Value**

A list containing the following

- `species` A vector of the herbivore species names (row names of `dat`)
- `eig` The eigen values for each of the PCo axes
- `tot.breadth` A vector of the raw ordinated host breadth for each species
- `scaled.breadth` A vector of the scaled ordinated host breadth for each species
- `distances` A list of vectors giving the distance of each diet item from the centroid of each herbivore
- `group.vectors` A matrix of logicals indicating diet items (columns) for each herbivore (rows)
- `centroids.group` A matrix giving the centroid on PCo (columns) for each herbivore (rows)
- `plants.ord` A matrix of the coordinates for each plant in PCoA space
- `dist.method` Dissimilarity index used for PCoA

**Author(s)**

James Fordyce

**References**


**See Also**

`summaryhbreadth`
Examples

testdata<-c(0,0,0,1,0,0,0,0,#1 0,0,0,0,1,1,0,0,#2 1,1,0,0,0,0,0,0,#3 0,0,0,1,1,0,1,1,#4 1,1,0,0,0,1,0,0,#4 1,1,0,0,1,0,1,0,#4 0,0,1,1,0,0,0,1, #5 1,0,1,0,1,0,0,0,1, #5 1,1,0,0,1,0,0,1,1,1,#6 1,1,1,1,0,1,1,1,1) #8

dat<-array(dim=c(10,10),data=testdata) dat<-t(dat) colnames(dat)<-paste(“,LETTERS[1:10],sep=”) rownames(dat)<-paste(“bug”,1:10,sep=”)

ordi.breadth(dat)

Description
This function computes the ordinated host breadth based on ordination where each herbivore is excluded from the ordination.

Usage
ordi.focal.drop(dat, dist.method = "jaccard")

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>dat</td>
<td>A matrix of diet associations. Rows are herbivores and columns are diet items.</td>
</tr>
<tr>
<td>dist.method</td>
<td>Dissimilarity index passed on to vegdist in the vegan package.</td>
</tr>
</tbody>
</table>

Value
A list containing the following:

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>species</td>
<td>Name of herbivore species (row name of dat)</td>
</tr>
<tr>
<td>odb</td>
<td>Ordinated diet breadth</td>
</tr>
<tr>
<td>odb.scaled</td>
<td>Scaled ordinated diet breadth</td>
</tr>
</tbody>
</table>
focal.distances

Distance to each diet item from herbivore centroid based on ordination excluding focal herbivore

focal.breadth

Ordinated diet breadth of herbivore based on ordination where focal herbivore is excluded

focal.scale.factor

The ordinated diet breadth of an extreme generalist in the ordinated space when focal herbivore is excluded from the ordination

focal.scale.breadth

Scaled ordinated diet breadth of herbivore based on ordination where focal herbivore is excluded

Author(s)

James Fordyce

References


Examples

testdata<-c(0,0,0,1,0,0,0,0,0,
0,0,0,0,0,1,1,0,0,
1,1,1,0,0,0,0,0,0,
0,0,0,1,1,0,1,0,1,
1,1,1,0,0,0,1,0,0,
1,1,0,0,1,0,1,0,0,
0,0,0,1,0,0,1,0,1,1,
1,0,1,0,1,1,0,0,0,1,
1,1,0,0,1,0,0,1,1,1,
1,1,1,0,1,1,0,1,1,1)

dat<-array(dim=c(10,10),data=testdata)
dat<-t(dat)
colnames(dat)<-paste("",LETTERS[1:10],sep="")
rownames(dat)<-paste("bug",1:10,sep="")

ordi.focal.drop(dat)
profPlot

Description

Plots the profile plot of distance from herbivore centroid to host plants. Useful for exploratory data analysis.

Usage

profPlot(specialization, id, col = c("black", "red"))

Arguments

specialization  The object created by the function ordi.breadth.

id  A numeric identifying which species of herbivore to plot from list specialization.

col  A vector length 2 indicating colors for plotting. First color is for non-diet items, second color is for diet items.

Value

A profile plot

Author(s)

James Fordyce

References


Examples

testdata<-
c(
0,0,0,0,1,0,0,0,0,0,#1
0,0,0,0,0,1,1,0,0,#2
1,1,0,0,0,0,0,0,0,#3
0,0,0,1,1,0,1,0,1,#4
1,1,0,0,0,1,0,0,#4
1,1,0,0,1,0,0,0,#4
0,0,0,1,0,0,1,1,#4
1,0,1,0,1,0,0,0,1, #5
1,1,0,0,1,0,0,1,1,#6
1,1,1,0,1,1,0,1,1) #8
**summaryhbreadth**

```r
dat<-array(dim=c(10,10),data=testdata)
dat<-t(dat)
colnames(dat)<-paste("",LETTERS[1:10],sep="")
rownames(dat)<-paste("bug",1:10,sep="")

x<-ordi.breadth(dat)
profPlot(x,5)#profile plot for species 5
```

---

**Description**

This function summarizes the ordinated host breadth from the object created by `ordi.breadth`.

**Usage**

```r
summaryhbreadth(specialization, round = 5, do.order = FALSE, by = "Richness")
```

**Arguments**

- `specialization` The object created by the function `ordi.breadth`.
- `round` The number of digits to round results
- `do.order` Logical indicating whether to sort results
- `by` Indicate which column to sort results by. Can be "Herbivore", "Richness", "Breadth", or "ScaledBreadth"

**Value**

A dataframe showing result summary

**Author(s)**

James Fordyce

**References**


**See Also**

`ordi.breadth`
summaryordi

Examples

testdata <-
  c(
    0,0,0,1,0,0,0,0,0,#1
    0,0,0,0,1,1,0,0,#2
    1,1,0,0,0,0,0,0,#3
    0,0,0,1,1,0,1,0,#4
    1,1,1,0,0,1,0,0,#4
    1,1,0,0,1,0,0,0,#4
    0,0,1,0,0,1,0,1,1,#4
    1,0,1,0,1,1,0,0,1, #5
    1,1,0,0,1,0,0,1,1,1,#6
    1,1,1,0,1,0,1,1,1) #8

dat <- array(dim = c(10, 10), data = testdata)
dat <- t(dat)
colnames(dat) <- paste("", LETTERS[1:10], sep="")
rownames(dat) <- paste("bug", 1:10, sep="")

x <- ordi.breadth(dat)
summaryhbreadth(x)

summaryordi

Description

Summarizes object provided by ordi.focal.drop

Usage

summaryordi(ordi.out, round = 5)

Arguments

ordi.out Object provided by ordi.focal.drop.
round The number of digits to round results.

Value

A dataframe showing result summary

Author(s)

James Fordyce
References

Examples

testdata<- c(
  0,0,0,0,1,0,0,0,0,0,
  0,0,0,0,0,1,1,0,0,0,
  1,1,0,0,0,0,0,0,0,0,
  0,0,0,1,1,0,1,0,1,1,
  1,1,1,0,0,1,0,0,0,0,
  1,1,0,0,1,0,0,0,0,0,
  0,0,0,1,0,0,1,0,1,1,
  1,0,1,0,1,0,0,0,1,1,
  1,0,0,1,0,0,1,1,1,1,
  1,1,1,0,1,1,0,1,1,1)

dat<-array(dim=c(10,10),data=testdata)
dat<-t(dat)
colnames(dat)<-paste("","LETTERS[1:10],sep="")
rownames(dat)<-paste("bug",1:10,sep="")

x<-ordi.focal.drop(dat)
summaryordi(x)
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