

# Package ‘ordiBreadth’

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**Type** Package

**Title** Ordinated Diet Breadth

**Version** 1.0

**Date** 2015-11-11

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**Description** Calculates ordinated diet breadth with some plotting functions.

**License** GPL (>= 3)

**LazyLoad** yes

**Depends** vegan

**NeedsCompilation** no

**Repository** CRAN

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ordiBreadth-package     *Calculates ordinated diet breadth.*

---

### 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

Fordyce, J.A., C.C. Nice, C.A. Hamm, & M.L. Forister. Quantifying diet breadth through ordination of host association. *Ecology*

---

dist.group.plot     *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**

Fordyce, J.A., C.C. Nice, C.A. Hamm, & M.L. Forister. Quantifying diet breadth through ordination of host association. Ecology

**Examples**

```
testdata<-
c(
0,0,0,0,1,0,0,0,0,0,#1
0,0,0,0,0,0,1,1,0,0,#2
1,1,1,0,0,0,0,0,0,0,#3
```

```

0,0,0,0,1,1,0,1,0,1,#4
1,1,1,0,0,0,1,0,0,0,#4
1,1,0,0,1,0,1,0,0,0,#4
0,0,0,1,0,0,1,0,1,1,#4
1,0,1,0,1,1,0,0,0,1, #5
1,1,0,0,1,0,0,1,1,1,#6
1,1,1,0,1,1,0,1,1,1) #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)

dist.group.plot(specialization=x,id=7,cex=1)
dist.group.plot(specialization=x,id=10,cex=1,pt.cex=0.75,plant.plot="points",nrel.pch=1,
nrel.col="black",nrel.cex=0.75)

```

---

focal.profPlot

*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

Fordyce, J.A., C.C. Nice, C.A. Hamm, & M.L. Forister. Quantifying diet breadth through ordination of host association. *Ecology*

## Examples

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

---

hyp.ordi.breadth      *hyp.ordi.breadth*

---

## 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**

Fordyce, J.A., C.C. Nice, C.A. Hamm, & M.L. Forister. Quantifying diet breadth through ordination of host association. *Ecology*

**Examples**

```
testdata<-
c(
0,0,0,0,1,0,0,0,0,0,#1
0,0,0,0,0,0,1,1,0,0,#2
1,1,1,0,0,0,0,0,0,0,#3
0,0,0,0,1,1,0,1,0,1,#4
1,1,1,0,0,0,1,0,0,0,#4
1,1,0,0,1,0,1,0,0,0,#4
0,0,0,1,0,0,1,0,1,1,#4
1,0,1,0,1,1,0,0,0,1,#5
1,1,0,0,1,0,0,1,1,1,#6
1,1,1,0,1,1,0,1,1,1)#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="")

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(1,1,1,1,1,1,1,1,1,1)
hyp.ordi.breadth(dat,group)#extreme generalist
hyp.ordi.breadth(dat,group,distance=TRUE)
```

---

null.breadth	<i>null.breadth</i>
--------------	---------------------

---

### Description

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

### Usage

```
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

Fordyce, J.A., C.C. Nice, C.A. Hamm, & M.L. Forister. Quantifying diet breadth through ordination of host association. Ecology

### Examples

```
testdata<-
c(
0,0,0,0,1,0,0,0,0,0,
0,0,0,0,0,0,1,1,0,0,
1,1,1,0,0,0,0,0,0,0,
0,0,0,0,1,1,0,1,0,1,
1,1,1,0,0,0,1,0,0,0,
1,1,0,0,1,0,1,0,0,0,
0,0,0,1,0,0,1,0,1,1,
1,0,1,0,1,1,0,0,0,1,
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="")

null.breadth(dat)

```

---

```

null.breadth.focal    null.breadth.focal

```

---

### 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

<code>dat</code>	A matrix of diet associations. Rows are herbivores and columns are diet items.
<code>dis.method</code>	Dissimilarity index passed on to <code>vegdist</code> in the <code>vegan</code> package.
<code>reps</code>	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:

<code>species</code>	Name of herbivore species (row name of <code>dat</code> )
<code>observed.breadth</code>	Ordinated diet breadth
<code>scale.factor</code>	Ordinated diet breadth of most extreme generalist herbivore based on ordination
<code>observed.breadth.scaled</code>	Scaled ordinated diet breadth
<code>totalplantrichness</code>	Taxonomic diet richness of focal species
<code>modplantrichness</code>	Modified taxonomic diet richness of focal species (see details)
<code>null</code>	A vector of null ordinated diet values



**Author(s)**

James Fordyce

**References**

Fordyce, J.A., C.C. Nice, C.A. Hamm, & M.L. Forister. Quantifying diet breadth through ordination of host association. *Ecology*

**Examples**

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

**Arguments**

<code>null.breadth.focal.out</code>	Object created by <code>null.breadth.focal</code>
<code>quantiles</code>	A vector length of two indicating the lower and upper quantiles to report for the null distribution.
<code>round</code>	A value indicating the number of digits to round results
<code>scaled</code>	Logical indicating whether to return scaled ordinated host breadth.

**Value**

Returns a dataframe of summarized results.

**Author(s)**

James Fordyce

**References**

Fordyce, J.A., C.C. Nice, C.A. Hamm, & M.L. Forister. Quantifying diet breadth through ordination of host association. *Ecology*

**Examples**

```
testdata<-
c(
0,0,0,0,1,0,0,0,0,0,#1
0,0,0,0,0,0,1,1,0,0,#2
1,1,1,0,0,0,0,0,0,0,#3
0,0,0,0,1,1,0,1,0,1,#4
1,1,1,0,0,0,1,0,0,0,#4
1,1,0,0,1,0,1,0,0,0,#4
0,0,0,1,0,0,1,0,1,1,#4
1,0,1,0,1,1,0,0,0,1, #5
1,1,0,0,1,0,0,1,1,1,#6
1,1,1,0,1,1,0,1,1,1) #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<-null.breadth.focal(dat)
null.breadth.focal.summary(x)
```

---

ordi.breadth	<i>ordi.breadth</i>
--------------	---------------------

---

### Description

This function calculates ordinated diet breadth

### Usage

```
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

Fordyce, J.A., C.C. Nice, C.A. Hamm, & M.L. Forister. Quantifying diet breadth through ordination of host association. Ecology

### See Also

summaryhbreadth

**Examples**

```

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

ordi.breadth(dat)

```

---

```
ordi.focal.drop      ordi.focal.drop
```

---

**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**

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

**Value**

A list containing the following:

<code>species</code>	Name of herbivore species (row name of <code>dat</code> )
<code>ODB</code>	Ordinated diet breadth
<code>ODB.scaled</code>	Scaled ordinated diet breadth

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

Fordyce, J.A., C.C. Nice, C.A. Hamm, & M.L. Forister. Quantifying diet breadth through ordination of host association. *Ecology*

### Examples

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

*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

Fordyce, J.A., C.C. Nice, C.A. Hamm, & M.L. Forister. Quantifying diet breadth through ordination of host association. *Ecology*

### Examples

```
testdata<-
c(
0,0,0,0,1,0,0,0,0,0,#1
0,0,0,0,0,0,1,1,0,0,#2
1,1,1,0,0,0,0,0,0,0,#3
0,0,0,0,1,1,0,1,0,1,#4
1,1,1,0,0,0,1,0,0,0,#4
1,1,0,0,1,0,1,0,0,0,#4
0,0,0,1,0,0,1,0,1,1,#4
1,0,1,0,1,1,0,0,0,1,#5
1,1,0,0,1,0,0,1,1,1,#6
1,1,1,0,1,1,0,1,1,1)#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)
profPlot(x,5)#profile plot for species 5

```

---

summaryhbreadth	<i>summaryhbreadth</i>
-----------------	------------------------

---

### Description

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

### Usage

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

### Arguments

<code>specialization</code>	The object created by the function <code>ordi.breadth</code> .
<code>round</code>	The number of digits to round results
<code>do.order</code>	Logical indicating whether to sort results
<code>by</code>	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

Fordyce, J.A., C.C. Nice, C.A. Hamm, & M.L. Forister. Quantifying diet breadth through ordination of host association. *Ecology*

### See Also

`ordi.breadth`

**Examples**

```

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

*summaryordi*


---

**Description**

Summarizes object provided by `ordi.focal.drop`

**Usage**

```
summaryordi(ordi.out, round = 5)
```

**Arguments**

<code>ordi.out</code>	Object provided by <code>ordi.focal.drop</code> .
<code>round</code>	The number of digits to round results.

**Value**

A dataframe showing result summary

**Author(s)**

James Fordyce



## References

Fordyce, J.A., C.C. Nice, C.A. Hamm, & M.L. Forister. Quantifying diet breadth through ordination of host association. *Ecology*

## Examples

```
testdata<-
c(
0,0,0,0,1,0,0,0,0,0,
0,0,0,0,0,0,1,1,0,0,
1,1,1,0,0,0,0,0,0,0,
0,0,0,0,1,1,0,1,0,1,
1,1,1,0,0,0,1,0,0,0,
1,1,0,0,1,0,1,0,0,0,
0,0,0,1,0,0,1,0,1,1,
1,0,1,0,1,1,0,0,0,1,
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="")

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

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