

Package ‘FuzzyQ’

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Title Fuzzy Quantification of Common and Rare Species in Ecological Communities

Description This package performs fuzzy classification of species in an ecological community as common or rare based on their abundance and occupancy. It also includes functions to compute confidence intervals of classification metrics and plot results.

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antsA	<i>Ant species abundance from Arnan et al. (2011)</i>
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Description

Abundance of 46 ant species from 99 sites sampled in the Northern Territory (Australia). This dataset corresponds to Plot A data in Arnan et al. (2011).

Usage

```
data(antsA)
```

Format

A data frame with 99 rows (sites) and 46 variables (species abundances)

Source

Calatayud, J., Andivia, E., Escudero, A., Melian, C. J., Bernardo-Madrid, R., Stoffel, M., ... , Madrigal-Gonzalez, J.(2019) Positive associations among rare species and their persistence in ecological assemblages. *Nature Ecology & Evolution*, 4: 40-45. doi: 10.6084/m9.figshare.9906092.

References

Arnan, X., Gaucherel, C., Andersen, A. N. (2011) Dominance and species co-occurrence in highly diverse ant communities: a test of the interstitial hypothesis and discovery of a three-tiered competition cascade. *Oecologia*, 166: 783-794. doi: 10.1007/s00442-011-1919-y.

Examples

```
data(antsA)
FQAnts <- fuzzyq(antsA, sorting = TRUE)
```

AOplot	<i>Abundance Occupancy Plot</i>
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Description

Plots the abundance-occupancy relationship of species in a community categorized as common or rare by fuzzyq.

Usage

```
AOplot(
  fq,
  col.rc = c("red", "blue"),
  opacity = 0.1,
  log.x = FALSE,
  log.y = FALSE,
  xLab = "Fraction of sites occupied",
  yLab = "Mean abundance",
  ...
)
```

Arguments

<code>fq</code>	A list of class <code>fuzzyq</code> returned by <code>FuzzyQ</code> : <code>fuzzyq</code> .
<code>col.rc</code>	A vector specifying two colors to be used to plot common and rare species. Accept any valid color specification in R.
<code>opacity</code>	Number within [0,1] specifying the opacity of convex hulls grouping common and rare species.
<code>log.x</code>	Logical. Whether or not the x axis should be in log10 scale.
<code>log.y</code>	Logical. Whether or not the y axis should be in log10 scale.
<code>xLab</code>	String. Title for the x axis.
<code>yLab</code>	String. Title for the y axis.
<code>...</code>	Other graphical parameters to be passed to <code>plot</code> .

Value

A scatter plot of occupancy vs. abundance of species. Convex hulls enclose common and rare species.

Examples

```
data(antsA)
FQAnts <- fuzzyq(antsA, sorting = TRUE)
AOplot(FQAnts) # Plor with default values

# Alternative with colors specified in Hex code, logarithmic axes and other
# point format
AOplot(FQAnts, col.rc = c("#013bad", "#bd5f69"),
       log.x = TRUE, log.y = TRUE, pch = 4)
```

Azov

Helminth communities of so-iuy mullets from the Sea of Azov

Description

Abundance of 25 helminth species from 378 so-iuy mullets collected in the Sea of Azov and the Black Sea. Fish are grouped in 12 surveys.

Usage

```
data(Azov)
```

Format

A data frame with 378 rows and 26 columns. The first column (sample) is a survey identifier. The remaining columns correspond to species abundances. See source for species abbreviations and survey identifiers.

Source

Llopis-Belenguer, C. (2019) Replication data for: Native and invasive hosts play different roles in host-parasite networks, Harvard Dataverse, doi: 10.7910/DVN/IWIKOL.

References

Llopis-Belenguer, C., Blasco-Costa, I., Balbuena, J.A., Sarabeev, V., Stouffer, D.B. (2020), Native and invasive hosts play different roles in host-parasite networks. *Ecography*, 43: 559-568. doi: 10.1111/ecog.04963.

Examples

```
data(Azov)
# Apply the FuzzyQ algorithm to each survey:
fuzzyq.azov <- by(Azov[, -1], Azov[, "sample"], fuzzyq, rm.absent = FALSE)
# Get cluster membership, silhouette widths and commonness indices
# per sp. per survey:
sppsilw.azov <- lapply(fuzzyq.azov, function(x) x$spp)
# Get global silhouette widths, commonness indices and Dunn's normalized
# partition coefficient per survey:
global.azov <- t(sapply(fuzzyq.azov, function(x) x$global))
```

fuzzyq

*Fuzzy Quantification of Common and Rare Species in Ecological Communities***Description**

Perform fuzzy clustering of each species based on their abundance and occupancy.

Usage

```
fuzzyq(
  M,
  diss = "gower",
  rm.absent = FALSE,
  sorting = TRUE,
  keep.Diss = FALSE,
  std = FALSE,
  wgts = c(1, 1),
  ...
)
```

Arguments

M	A matrix or data frame of species abundances (columns). Each row represents a site.
diss	String. Specify the dissimilarity coefficient to be used. Default is "gower". See daisy in package <code>cluster</code> for other choices.
rm.absent	Logical. Whether or not absent species are to be removed from the calculations.
sorting	Logical. If TRUE (the default) species are sorted in the output by ascending silhouette widths within each cluster, else species are arranged in the same order as in the input matrix or data frame.
keep.Diss	Logical. Whether or not the species dissimilarity matrix should be returned. The default is FALSE.
std	Logical. Whether or not the measurements of occupancy and abundance are to be standardized before calculating the dissimilarities. Measurements are standardized for each variable (column), by subtracting the variable's mean value and dividing by the variable's mean absolute deviation. It only takes effect if diss is different from "gower".
wgts	an optional numeric vector of length 2. To be used if diss = "gower", specifying weights for occupancy and abundance, respectively. Default is 1 each as in Gower's original formula.
...	Arguments to be passed to function <code>fanny</code> in package <code>cluster</code> .

Value

A list of class fuzzyq containing the following:

A_O Abundance-occupancy information for each species.

Diss Object of class dist with pairwise dissimilarities among species based on A_O. (only if keep.Diss = TRUE).

spp Clustering metrics per species: Cluster membership (where 0 and 1 denote allocation to the rare and common category, respectively), Silhouette Widths and Commonness Indices).

global Community level clustering metrics: Average silhouette widths per cluster and globally, Mean commonness indices per cluster and Normalized Dunn's coefficient.

See Also

[fanny](#) and [daisy](#) in package cluster

Examples

```
data(antsA)
FQAnts <- fuzzyq(antsA, sorting = TRUE)
```

fuzzyqBoot

Apply Fuzzy Quantification of Common and Rare Species to Bootstrap Replicates

Description

Produce N replicates of the original site by species matrix or dataframe by taking bootstrap samples of sites (rows) and apply fuzzyq to each replicate.

Usage

```
fuzzyqBoot(
  M,
  N = 1000,
  level = "spp",
  std = FALSE,
  rm.absent = FALSE,
  wgts = c(1, 1),
  ...
)
```

Arguments

M	A matrix or dataframe of species abundances (columns). Each row represents a site.
N	Integer. Number of bootstrap replicates desired. Default is 1,000.
level	String. Specify the type of metrics to be computed for each bootstrap replicate. Either "spp" or "global", corresponding to species or community-level metrics, respectively.
std	Logical. Whether or not the measurements of occupancy and abundance are to be standardized before calculating the dissimilarities. Measurements are standardized for each variable (column), by subtracting the variable's mean value and dividing by the variable's mean absolute deviation. It only takes effect if diss is different from "gower".
rm.absent	Logical. Whether or not absent species are to be removed from the calculations.
wgts	an optional numeric vector of length 2. To be used if diss = "gower", specifying weights for occupancy and abundance, respectively. Default is c(1,1) as in Gower's original formula.
...	Arguments to be passed to function fanny in package cluster.

Value

A list consisting of the following:

bs.rep Matrix of estimated metrics. Replicates are arranged in rows. If level = "spp", columns represent estimates of Commonness Indices per species. If level = "global", columns represent estimates of community-level clustering metrics: Average silhouette widths per cluster and globally, Mean commonness indices per cluster and Normalized Dunn's coefficient.

level Flag indicating whether the estimates are taken at species ("spp") or community level ("global").

Examples

```
data(antsA)
FQAnts <- fuzzyq(antsA, sorting = TRUE)

# Compute species Commonness Indices of species of 1,000 bootstrap
# replicates:
## Not run: BS.FQAnts <- fuzzyqBoot (antsA, N = 1e3, level='spp')

# Compute global metrics of 1,000 bootstrap replicates:
## Not run: BS.global <- fuzzyqBoot (antsA, N = 1e3, level='global')
```

fuzzyqCI

*Compute Confidence Intervals of Clustering Metrics***Description**

Computes confidence intervals of clustering metrics based on the bootstrap replicates produced by fuzzyqBoot.

Usage

```
fuzzyqCI(fq.bs, fq = NULL, method = "pct", c.level = 0.95)
```

Arguments

<code>fq.bs</code>	A list returned by FuzzyQ: : fuzzyqBoot.
<code>fq</code>	A list of class fuzzyq returned by FuzzyQ: : fuzzyq. Required only if method = "bc" or method = "bca".
<code>method</code>	String. Specify the method to compute confidence intervals. Any of the following: "pct" (percentile, the default), "bc" (bias corrected), "bca" (bias corrected and accelerated).
<code>c.level</code>	Number within [0,1]. Specify the confidence interval level. Default is 0.95.

Value

A matrix with upper and lower confidence interval limits of clustering metrics.

Examples

```
data(antsA)
FQAnts <- fuzzyq(antsA, sorting = TRUE)

# Compute species Commonness Indices of species of 1,000 bootstrap
# replicates:
## Not run: BS.FQAnts <- fuzzyqBoot (antsA, N = 1e3, level='spp')

# Compute 95 % confidence intervals, percentile method, default values:
## Not run: BS.sppCI1 <- fuzzyqCI(BS.FQAnts)

# Alternatively, 95 % confidence intervals, bias corrected and accelerated
# method:
## Not run: BS.sppCI2 <- fuzzyqCI(BS.FQAnts, fq=FQAnts, method = "bca")

# Compute global metrics of 1,000 bootstrap replicates:
## Not run: BS.global <- fuzzyqBoot (antsA, N = 1e3, level='global')

# Compute 95 % confidence intervals, bias corrected and accelerated method:
## Not run: BS.globalCI <- fuzzyqCI(BS.global, fq=FQAnts, method = "bca")
```

Japan

Helminth communities of so-iuy mullets from the Japan Sea

Description

Abundance of 21 helminth species from 192 so-iuy mullets collected in the Japan Sea. Fish are grouped in seven surveys.

Usage

```
data(Japan)
```

Format

A data frame with 192 rows and 22 columns. The first column (sample) is a survey identifier. The remaining columns correspond to species abundances. See source for species abbreviations and survey identifiers.

Source

Llopis-Belenguer, C. (2019) Replication data for: Native and invasive hosts play different roles in host-parasite networks, Harvard Dataverse, doi: 10.7910/DVN/IWIKOL.

References

Llopis-Belenguer, C., Blasco-Costa, I., Balbuena, J.A., Sarabeev, V., Stouffer, D.B. (2020), Native and invasive hosts play different roles in host-parasite networks. *Ecography*, 43: 559-568. doi: 10.1111/ecog.04963.

Examples

```
data(Azov)
# Apply the FuzzyQ algorithm to each survey:
fuzzyq.japan <- by(Japan[, -1], Japan[, "sample"], fuzzyq, rm.absent = FALSE)
# Get cluster membership, silhouette widths and commonness indices
# per sp. per survey:
spp.japan <- lapply(fuzzyq.japan, function(x) x$spp)
# Get global silhouette widths, commonness indices and Dunn's normalized
# partition coefficient per survey:
global.japan <- t(sapply(fuzzyq.japan, function(x) x$global))
```

sortClus

*Sort Species by fuzzyq Clustering***Description**

Sort species in a matrix or data frame to match the resulting species order of a fuzzyq object. This is useful prior to plotting Commonness Indices derived from bootstrap replicates.

Usage

```
sortClus(M, fq)
```

Arguments

M A matrix or data frame with information of species in columns.

fq A list of class fuzzyq returned by FuzzyQ: : fuzzyq.

Value

A matrix or data frame with information of species in columns sorted according to fq\$spp.

Examples

```
data(antsA)
FQAnts <- fuzzyq(antsA, sorting = TRUE)
# Compute species Commonness Indices of species of 1,000 bootstrap
# replicates:
## Not run: BS.FQAnts <- fuzzyqBoot (antsA, N = 1e3, level='spp')

# Compute 95 % confidence intervals, percentile method, default values:
## Not run: BS.sppCI1 <- fuzzyqCI(BS.FQAnts)

# Plot Commonness Indices and their respective confidence intervals:
## Not run: BS.sppCI1 <- sortClus(BS.sppCI1, FQAnts)
spp <- FQAnts$spp
col.RC <- c("brown2", "turquoise3") # two colors to plot rare and common

# species
## Not run: plot(spp[, 3], cex.axis = 0.8, xaxt= 'n', ylab = "Commonness index",
  ylim = c(0, max(BS.sppCI1)), xlab = "Species", col = col.RC[spp[, 1] + 1],
  pch = 16, cex = 0.8, las = 1)
ebar.int <- seq_len(nrow(spp))
arrows(ebar.int, BS.sppCI1["Lower", ], ebar.int, BS.sppCI1["Upper", ],
  length= 0, col = col.RC[spp[, 1] + 1])
axis(1, at = ebar.int, labels = rownames(spp), las = 2, cex.axis = 0.6)
## End(Not run)
```

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