Package ‘hierDiversity’

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Title Hierarchical Multiplicative Partitioning of Complex Phenotypes

Author Zachary Marion, James Fordyce, and Benjamin Fitzpatrick

Maintainer Zachary Marion `<zmarion@vols.utk.edu>`

Description Hierarchical group-wise partitioning of phenotypic diversity into within-group (alpha), among-group (beta), and pooled-total (gamma) components using Hill numbers.
Turnover and overlap are also calculated as standardized alternatives to beta diversity. Hierarchical bootstrapping is used to approximate uncertainty around each diversity component.

License GPL (>= 2)

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`hierDiversity-package` *Hierarchical Multiplicative Partitioning of Diversity and Complexity*

Description

Computes the diversity of multivariate phenotypic or species composition datasets in a group-wise hierarchical framework (Marion et al. *in press*). The method provides several benefits. First, partitioning complexity in terms of Hill numbers (Hill 1973) or the 'effective number' of parts (Jost 2006, 2007) offers biologically interpretable and relevant estimates of phenotypic or species complexity. Second, diversities can be calculated for any order (q) as a continuous estimate of disparity in the abundances, counts, or concentrations of phenotypic parts. Third, for a given hierarchical level, the pooled total phenotypic complexity (gamma) is multiplicatively partitioned into two components: 1) a within-group component (alpha), the average effective number of phenotypic subunits expected within a sample from the group; and 2) an among-group component (beta), the effective number of completely distinct phenotypic combinations found within the group. Finally, uncertainty around diversity estimates is approximated using hierarchical bootstrapping.

Details

Package:	hierDiversity
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License:	GPL >= 2

The package contains two functions. The first function, `dz`, computes alpha, beta, and gamma diversity as 'effective numbers' for any order of q. The second function, $hierDiversity$, uses group-wise hierarchical partitioning (Marion et al. *in press*) to calculate phenotypic diversity for each group within a hierarchical level. Proportional turnover and homogeneity are also provided as standardized alternatives to beta diversity for comparisons among groups when sample sizes are uneven. Hierarchical bootstrapping approximates uncertainty by resampling appropriate subgroups within a level. Although designed for phenotypic complexity, the package is all appropriate for community composition data as well. Group-wise partitioning provides a complement to the level-wise partitioning approach proposed by Crist et al. (2003).

Author(s)

Zachary Marion <`zmarion@vols.utk.edu`>, James Fordyce <`jfordyce@utk.edu`>, and Benjamin Fitzpatrick <`benfitz@utk.edu`>

References

Crist, T.O., J.A. Veech, J.C. Gering, and K.S. Summerville (2003). Partitioning species diversity across landscapes and regions: a hierarchical analysis of α, β, and γ-diversity. *Am. Nat.*, 162(6): 734–743.

Hill, M.O. (1973). Diversity and evenness: a unifying notation and its consequences. *Ecology*, 54(2): 427–432.

Jost, L. (2006). Entropy and diversity. *Oikos*, 113(2): 363–375.

Jost, L. (2007). Partitioning diversity into independent alpha and beta components. *Ecology*, 88(10): 2427–2439.

Marion, Z.H., J.A. Fordyce, and B.M. Fitzpatrick. Extending the concept of diversity partitioning to characterize complex phenotypes. *Am. Nat.. in press*.

See Also

`vegetarian-package`

Examples

```
set.seed(2)
dat <- matrix(rpois(100, lambda = 3), nrow = 10)
dz(abundances = dat, lev = "beta", q = 2)
#1.336

#Create Grouping Matrix
group <- as.matrix(data.frame(
  L1 = rep(c("A","B","C","D","E"), each=2),
  L2 = rep(c("AB", "CDE"), times=c(4,6)),
  L3 = rep("total",10)))

hierDiversity(dat, group, reps=9)
```

`dz` *Effective Numbers for Alpha, Beta, and Gamma Diversity Indices*

Description

The function `dz` calculates the 'effective number' of traits or species in terms of multiplicative alpha, beta, or gamma diversity for any order of q (Hill 1973; Jost 2006, 2007). As the order q increases, the diversity calculated by `dz` becomes increasingly sensitive to differential abundance or amount; rare or low-abundance traits/species become downweighted in importance.

Usage

```
dz(abundances, lev = "beta", q = 1)
```

Arguments

`abundances`	A matrix of community or phenotypic data where columns are individual species or traits and rows are replicates (e.g., sites, individuals, groups). Matrix elements are abundances or amounts (e.g., concentrations, counts).
`lev`	Partitioning level of diversity. Can be "alpha," "beta," or "gamma".
`q`	Order of diversity. Default is the exponential of Shannon's entropy where q = 1.

Details

`dz` is a direct modification of the `d` function from the `vegetarian` package (Charney & Record 2012). The function was optimized to work with `hierDiversity` to return the desired multiplicative diversity partition of interest for a given order q.

The diversity orders most familiar to ecologists are q = 0 (richness), q = 1 (Shannon entropy), and q = 2 (Simpson's probability of identity). As q increases, the diversity measure becomes less sensitive to rare subcomponents of low amount, while components of high abundance are increasingly upweighted (Jost 2006, 2007).

Value

`D.VALUE`	A scalar that gives the effective number of alpha, beta, or gamma diversity for the desired order of q.

Note

If `abundances` is a class other than a matrix or vector, `dz` will return an error.

Author(s)

Zachary Marion <`zmarion@vols.utk.edu`>, James Fordyce <`jfordyce@utk.edu`>, and Benjamin Fitzpatrick <`benfitz@utk.edu`>

References

Charney, N. and S. Record. (2012). *vegetarian: Jost Diversity Measures for Community Data.* R package version 1.2.

Hill, M.O. (1973). Diversity and evenness: a unifying notation and its consequences. *Ecology*, 54(2):427–432.

Jost, L. (2006). Entropy and diversity. *Oikos*, 113(2):363–375.

Jost, L. (2007). Partitioning diversity into independent alpha and beta components. *Ecology*, 88(10):2427–2439.

See Also

`hierDiversity`, `d`

Examples

```
set.seed(2)
dat <- matrix(rpois(100, lambda = 3), nrow = 10)
dz(abundances = dat, lev = "beta", q = 2)
#1.336
```

`hierDiversity` *Hierarchical Group-wise Diversity Partitioning*

Description

Group-wise diversity partitioning (Marion et al. *in press*) summarizes diversity for each group using the framework of effective or Hill numbers at each hierarchical level for any order q (Hill 1973; Jost 2006, 2007). This approach facilitates comparisons among groups at each level. Hierarchical bootstrapping is then used to approximate uncertainty around diversity estimates.

Usage

```
hierDiversity(dat, group, replace = NULL, reps = 99, q = 1,
quant = c(0.025, 0.975), sims = FALSE)
```

Arguments

`dat`	A matrix of community or phenotypic data where columns are individual species or traits and rows are replicates (e.g., sites, individuals, groups). Matrix elements are abundances or amounts (e.g., concentrations, counts).
`group`	A matrix with the same number of rows as in `dat`, where columns code the levels of the sampling hierarchy that DO NOT include the individual level (this is added by the function). The column groupings should—from left to right—go from least inclusive to most inclusive, with the highest level containing only one grouping; i.e., the number of groups within the hierarchy should decrease from left to right.
`replace`	A vector of logicals to indicate whether resampling is done with replacement at each level. If `NULL`, bootstrapping is automatically done for all levels.
`reps`	Numeric indicating the number of bootstrap replicates to conduct for approximating uncertainty.
`q`	Order of diversity. Default is the exponential of Shannon's entropy where q = 1.
`quant`	Numeric vector of probabilities with values in $[0, 1]$ for bootstrapped sample quantiles. Defaults to `c(0.025, 0.975)`.
`sims`	Logical to save each bootstrapped diversity estimate.

Details

`hierDiversity` uses group-wise hierarchical partitioning (Marion et al. *in press*) to summarize community or phenotypic complexity as the 'effective number' (Hill 1973; Jost 2006, 2007) of parts within and among groups.

For each level of the hierarchial sampling design with $i = 1, 2, 3, \ldots, m$ levels of sampling (e.g., individuals, demes, regions, ..., continents), the total (gamma) diversity of each group within a level is multiplicatively partitioned (Whittaker 1972; Jost 2006, 2007) into two components: (1) `alpha`, the within-group component, is the average effective number of individual phenotypic elements within a sample; and (2) `beta`, the among-group component, is the effective number of completely distinct phenotypic combinations present and estimates the extent of differentiation among phenotypes (Jost 2006).

Group-wise partitioning (Marion et al. *in press*) uniquely differs from the level-wise partitioning approach proposed by Crist et al. (2003). Instead of a single α_i and β_i at level *i*, separate estimates are provided for each of the n_{i+1} groups at the next level up. This method facilitates comparisons among groups at each hierarchical level; level-wise partitioning highlights comparisons among i levels in the hierarchy.

To enable comparisons when there are unequal sample sizes among levels, this function also provides two standardized estimates of beta diversity: turnover and homogeneity (Jost 2007). Turnover is the proportional turnover rate per sample ranging from 0 (all samples are identical) to unity (all samples are completely distinct). Homogeneity is interpreted as the inverse of turnover. See Jost (2007) for a more complete mathmatical description.

To approximate uncertainty around the diversity estimates, hierarchical bootstrapping is used. In each iteration, the appropriate subgroups in a level are re-sampled, the groups within those subgroups are resampled, etc. down to the lowest level of replication.

Value

`hierDiversity` returns a list of diversity estimates for each group within each hierarchical level. For each group, a dataframe is provided. The first row returns the true estimates of diversity. The second returns the standard error (standard deviation of bootstrap replicates). Subsequent rows return the quantiles specified in the `quant` arguement. The dataframe returns the following columns:

`alpha`	A scalar, alpha diversity, is the average effective number of parts within a group-level replicate.
`beta`	A scalar, beta diversity, is the effective number of completely distinct combinations within a group. Ranges from unity, when all group members are identical, to N when all group members are distinct.
`gamma`	A scalar, gamma diversity, is the pooled total effective number of parts overall.
`turnover`	A scalar that gives the proportional turnover among group replicates. The lower limit is 0 when all group members are identical, and the upper limit is unity when all members are distinct.
`homogeneity`	A scalar where the lower limit is 0 when all N group members are completely distinct, and the upper limit is unity when all members are identical.

If `sims`=TRUE, a separate dataframe is provided for each group returning the saved bootstrapped diversity replicates for each iteration of `rep`.

Note

If groupings among levels are not unique (i.e., group "A" appears in both level 1 and level 2), only the diversity estimates from the lowest (least inclusive) should be interpreted. For higher levels, alpha will equal gamma, beta diversity will be one, and there will be no error due to the hierarchical nature of the sampling.

Author(s)

Zachary Marion <`zmarion@vols.utk.edu`>, James Fordyce <`jfordyce@utk.edu`>, and Benjamin Fitzpatrick <`benfitz@utk.edu`>

References

Crist, T.O., J.A. Veech, J.C. Gering, and K.S. Summerville (2003). Partitioning species diversity across landscapes and regions: a hierarchical analysis of α, β, and γ-diversity. *Am. Nat.*, 162(6): 734–743.

Fordyce, J.A. and S.B. Malcolm (2000). Specialist weevil, *Rhyssomatus lineaticollis*, does not spatially avoid cardenolide defenses of common milkweed by ovipositing into pith tissue. *J. Chem. Ecol.*. 26(12): 2857–2874.

Hill, M.O. (1973). Diversity and evenness: a unifying notation and its consequences. *Ecology*, 54(2): 427–432.

Jost, L. (2006). Entropy and diversity. *Oikos*, 113(2): 363–375.

Jost, L. (2007). Partitioning diversity into independent alpha and beta components. *Ecology*, 88(10): 2427–2439.

Marion, Z.H., J.A. Fordyce, and B.M. Fitzpatrick. Extending the concept of diversity partitioning to characterize complex phenotypes. *Am. Nat.*. *in press*.

Whittaker R.H. (1972.) Evolution and measurement of species diversity. *Taxon*, 21, 213–251.

Examples

```
## NOTE: 'reps' argument usually needs to be >= 99.
## The lower values used here are for demonstration.

set.seed(2)
## Create Data Matrix
dat <- matrix(rpois(1000, 3), nrow=100)
#Create Grouping Matrix
group <- as.matrix(data.frame(
  L1 = rep(c("A","B","C","D","E"), each=20),
  L2 = rep(c("AB", "CDE"), times=c(40,60)),
  L3 = rep("total",100)))

hierDiversity(dat, group, reps=9)
replace <- c(FALSE, rep(TRUE, 3))
hierDiversity(dat, group, replace=replace, reps=9, q=2)
div <- hierDiversity(dat, group, reps=9, q=2,
  quant=c(0.25, 0.75), sims=TRUE)
div$L2$CDE


##### Example data from Fordyce & Malcolm (2000)
data(milkweedData)
data(milkweedVars)
milkDat <- as.matrix(milkweedData)
milkVars <- as.matrix(milkweedVars)
```

```
milkDiv <- hierDiversity(milkDat, milkVars, reps=5, q=3,
  sims=TRUE)
milkDiv$infectstatus
turnover <- c(milkDiv$infectstatus$I[[2]][,5],
  milkDiv$infectstatus$U[[2]][,5])
infectionStatus <- rep(c("infected","uninfected"), each=6)
boxplot(turnover~infectionStatus, las = 1,
  ylab = "Turnover", xlab = "Infection Status")
```

`milkweedData` *Milkweed Chemical Defense Data*

Description

The milkweed (*Asclepius syriaca*) chemical defense data, `milkweedData`, has concentrations for 12 cardenolides from multiple tissues and plants with and without evidence of herbivorous weevil damage. These correspond to the `milkweedVars` dataframe, which contains the plant variables.

Usage

```
data("milkweedData")
data("milkweedVars")
```

Format

`milkweedData` is a data frame with 101 observations of concentrations (μg per 0.1 g dry wt) for 12 cardenolides. Column names indicate the HPLC retention times for each compound (earlier RTs are more polar).

`milkweedVars` is a dataframe of 101 observations on the following 4 variables:

`tissue`	a character vector of five tissues analyzed: `cortex`, `epidermis`, `leaf`, `pith`, and `vascular` tissue
`PlantID`	a character vector of unique plant IDs
`infectstatus`	a character vector identifying whether a plant had weevil oviposition damage (`D`) or was undamaged (`U`)
`total`	a character vector indicating the highest hierarchical level

Source

Fordyce, J.A. and S.B. Malcolm (2000). Specialist weevil, *Rhyssomatus lineaticollis*, does not spatially avoid cardenolide defenses of common milkweed by oviposition into pith tissue. *J. Chem. Ecol.*. 26(12):2857–2874.

Examples

```
data(milkweedData)
str(milkweedData)

data(milkweedVars)
str(milkweedVars)
```

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