

Package ‘hillR’

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Type Package

Title Diversity Through Hill Numbers

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Description Calculate taxonomic, functional and phylogenetic diversity measures through Hill Numbers proposed by Chao, Chiu and Jost (2014) <doi:10.1146/annurev-ecolsys-120213-091540>.

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LazyData TRUE

Depends R (>= 3.1)

Imports FD, plyr, ade4, ape, tibble, geiger

RoxygenNote 7.1.1

Suggests testthat, covr, betapart

URL <https://github.com/daijiang/hillR>

BugReports <https://github.com/daijiang/hillR/issues>

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hillR	<i>hillR: Diversity Through Hill Numbers</i>
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Description

The R package ‘hillR’ implements the framework proposed by Chao, et al. 2014 and makes it easy to calculate taxonomic, functional, and phylogenetic diversity of ecological communities as Hill numbers. For each facet of diversity, ‘hillR’ has three functions. The first set of functions (hill_taxa, hill_func, and hill_phylo) calculates alpha diversity of each site. The second set of functions (hill_taxa_parti, hill_func_parti, and hill_phylo_parti) calculates diversity across all sites. The third set of functions (hill_taxa_parti_pairwise, hill_func_parti_pairwise, and hill_phylo_parti_pairwise) calculates all possible pairwise diversity across all sites. Users can set the argument `_q_` to control the weight of species abundance.

Details

Users may be interested in other similar packages such as [vegetarian](#) and [iNEXT](#).

Taxonomic Hill Numbers

[hill_taxa](#), [hill_taxa_parti](#), [hill_taxa_parti_pairwise](#)

Functional Hill Numbers

[hill_func](#), [hill_func_parti](#), [hill_func_parti_pairwise](#)

Phylogenetic Hill Numbers

[hill_phylo](#), [hill_phylo_parti](#), [hill_phylo_parti_pairwise](#)

References

Chao, Anne, Chun-Huo Chiu, and Lou Jost. Unifying Species Diversity, Phylogenetic Diversity, Functional Diversity, and Related Similarity and Differentiation Measures Through Hill Numbers. *Annual Review of Ecology, Evolution, and Systematics* 45, no. 1 (2014): 297–324. <doi:10.1146/annurev-ecolsys-120213-091540>.

hill_func

Functional diversity through Hill Numbers

Description

Calculate functional diversity for each site (alpha diversity).

Usage

```
hill_func(
  comm,
  traits,
  traits_as_is = FALSE,
  q = 0,
  base = exp(1),
  check_data = TRUE,
  div_by_sp = FALSE,
  ord = c("podani", "metric"),
  fdis = TRUE,
  stand_dij = FALSE
)
```

Arguments

comm	A data frame of vegetation data. Sites as rows, species as columns.
traits	A data frame of species functional traits data. Species as rows, traits as columns. It can include both continuous and categorical data. It will be transformed into a distance matrix using 'FD::gowdis(traits)'. If all traits are numeric, then it will use Euclidean distance.
traits_as_is	if FALSE (default) traits data frame will be transformed into a distance matrix. Otherwise, will use as is (i.e. traits is a symmetric distance matrix).
q	Hill number, q = 0 (default) to get species richness, q = 1 to get shannon entropy, q = 2 will give inverse Simpson.
base	default is exp(1), the base of log.
check_data	whether to check data first? Default is TRUE.
div_by_sp	as FD calculated in this way will be highly correlated with taxonomic diversity, one potential simple way to correct this is to divide the results by the number of species. However, a more common way to deal with correlations is to use null models and calculate standardized effect sizes. Therefore, I set the default to be FALSE.
ord	ord in FD: :gowdis.
fdis	whether to calculated FDis, default is TRUE
stand_dij	whether to standardize distance matrix to have max value of 1? Default is FALSE.

Value

A matrix, with these information for each site: Q (Rao's Q); D_q (functional hill number, the effective number of equally abundant and functionally equally distinct species); MD_q (mean functional diversity per species, the effective sum of pairwise distances between a fixed species and all other species); FD_q (total functional diversity, the effective total functional distance between species of the assemblage). See Chiu and Chao 2014 page 4 for more information.

References

Chao, Anne, Chun-Huo Chiu, and Lou Jost. Unifying Species Diversity, Phylogenetic Diversity, Functional Diversity, and Related Similarity and Differentiation Measures Through Hill Numbers. *Annual Review of Ecology, Evolution, and Systematics* 45, no. 1 (2014): 297–324. <doi:10.1146/annurev-ecolsys-120213-091540>.

Chiu, Chun-Huo, and Anne Chao. Distance-Based Functional Diversity Measures and Their Decomposition: A Framework Based on Hill Numbers. *PLoS ONE* 9, no. 7 (July 7, 2014): e100014. <doi:10.1371/journal.pone.0100014>.

Examples

```
dummy = FD::dummy
hill_func(comm = dummy$abun, traits = dummy$trait, q = 0)
hill_func(comm = dummy$abun, traits = dummy$trait, q = 1)
hill_func(comm = dummy$abun, traits = dummy$trait, q = 0.9999)
hill_func(comm = dummy$abun, traits = dummy$trait, q = 2)
hill_func(comm = dummy$abun, traits = dummy$trait, q = 3)
```

hill_func_parti

Decomposition of functional diversity through Hill Numbers

Description

Calculate functional gamma, alpha, and beta diversity for all communities, as well as site similarity. These values are based on ALL communities.

Usage

```
hill_func_parti(
  comm,
  traits,
  traits_as_is = FALSE,
  q = 0,
  base = exp(1),
  check_data = TRUE,
  rel_then_pool = TRUE,
  ord = c("podani", "metric"),
  stand_dij = FALSE,
  show_warning = TRUE
)
```

Arguments

comm	A data frame of vegetation data. Sites as rows, species as columns.
traits	A data frame of species functional traits data. Species as rows, traits as columns. It can include both continuous and categorical data. It will be transformed into a distance matrix using 'FD::gowdis(traits)'. If all traits are numeric, then it will use Euclidean distance.
traits_as_is	if FALSE (default) traits data frame will be transformed into a distance matrix. Otherwise, will use as is (i.e. traits is a symmetric distance matrix).
q	Hill number, q = 0 (default) to get species richness, q = 1 to get shannon entropy, q = 2 will give inverse Simpson.
base	default is exp(1), the base of log.
check_data	whether to check data first? Default is TRUE.
rel_then_pool	default is TRUE. Abundance of species are first changed to relative abundance within sites, then pooled into one assemblage. If FALSE, sites are pooled first, then change abundance of species to relative abundance.
ord	ord in FD: :gowdis.
stand_dij	whether to standardize distance matrix to have max value of 1? Default is FALSE.
show_warning	whether to print warning, default is TRUE.

Value

a data frame with one row (across all sites), including these columns: q, RaoQ of pooled assemblage, gamma diversity, alpha diversity, beta diversity, local species overlap (similar to Sorensen), and region species overlap (similar to Jaccard). See Chiu and Chao 2014 Table 3 for more information.

References

Chao, Anne, Chun-Huo Chiu, and Lou Jost. Unifying Species Diversity, Phylogenetic Diversity, Functional Diversity, and Related Similarity and Differentiation Measures Through Hill Numbers. *Annual Review of Ecology, Evolution, and Systematics* 45, no. 1 (2014): 297–324. <doi:10.1146/annurev-ecolsys-120213-091540>.

Chiu, Chun-Huo, and Anne Chao. Distance-Based Functional Diversity Measures and Their Decomposition: A Framework Based on Hill Numbers. *PLoS ONE* 9, no. 7 (July 7, 2014): e100014. <doi:10.1371/journal.pone.0100014>.

See Also

[hill_taxa_parti](#), [hill_func](#)

Examples

```
dummy = FD::dummy
hill_func_parti(comm = dummy$abun, traits = dummy$trait, q = 0)
hill_func_parti(comm = dummy$abun, traits = dummy$trait, q = 1)
hill_func_parti(comm = dummy$abun, traits = dummy$trait, q = 0.9999)
```

```
hill_func_parti(comm = dummy$abun, traits = dummy$trait, q = 2)
hill_func_parti(comm = dummy$abun, traits = dummy$trait, q = 3)
```

```
hill_func_parti_pairwise
```

Pairwise comparisons for all sites.

Description

Calculate pairwise functional gamma, alpha, and beta diversity for communities, as well as site similarity. It is based on [hill_func_parti](#). If comm has >2 sites, this function will give results for all pairwise comparisons.

Usage

```
hill_func_parti_pairwise(
  comm,
  traits,
  traits_as_is = FALSE,
  q = 0,
  rel_then_pool = TRUE,
  output = c("data.frame", "matrix"),
  pairs = c("unique", "full"),
  .progress = TRUE,
  show_warning = TRUE,
  ...
)
```

Arguments

comm	A data frame of vegetation data. Sites as rows, species as columns.
traits	A data frame of species functional traits data. Species as rows, traits as columns. It can include both continuous and categorical data. It will be transformed into a distance matrix using 'FD::gowdis(traits)'. If all traits are numeric, then it will use Euclidean distance.
traits_as_is	if FALSE (default) traits data frame will be transformed into a distance matrix. Otherwise, will use as is (i.e. traits is a symmetric distance matrix).
q	Hill number, q = 0 (default) to get species richness, q = 1 to get shannon entropy, q = 2 will give inverse Simpson.
rel_then_pool	default is TRUE. Abundance of species are first changed to relative abundance within sites, then pooled into one assemblage. If FALSE, sites are pooled first, then change abundance of species to relative abundance.
output	output type: data.frame (default) or matrix. If matrix, then this function will return a list of matrices.

pairs	full or unique (default). Do you want to compare all possible pairs (i.e. n^2) or just unique pairs (i.e. $\text{choose}(n, 2)$)?
.progress	Whether to show progress bar. Default is 'TRUE'.
show_warning	whether to print warning, default is TRUE.
...	additional arguments for hill_func_parti.

Value

a data frame with results for all pairwise comparisons.

References

Chao, Anne, Chun-Huo Chiu, and Lou Jost. Unifying Species Diversity, Phylogenetic Diversity, Functional Diversity, and Related Similarity and Differentiation Measures Through Hill Numbers. *Annual Review of Ecology, Evolution, and Systematics* 45, no. 1 (2014): 297–324. <doi:10.1146/annurev-ecolsys-120213-091540>.

Chiu, Chun-Huo, and Anne Chao. Distance-Based Functional Diversity Measures and Their Decomposition: A Framework Based on Hill Numbers. *PLoS ONE* 9, no. 7 (July 7, 2014): e100014. <doi:10.1371/journal.pone.0100014>.

See Also

[hill_func_parti](#)

Examples

```
## Not run:
dummy = FD::dummy
hill_func_parti_pairwise(comm = dummy$abun, traits = dummy$trait, q = 0)
hill_func_parti_pairwise(comm = dummy$abun, traits = dummy$trait, q = 0,
  output = 'matrix')
hill_func_parti_pairwise(comm = dummy$abun, traits = dummy$trait, q = 0,
  output = 'matrix', pairs = 'full')
hill_func_parti_pairwise(comm = dummy$abun, traits = dummy$trait, q = 1)
hill_func_parti_pairwise(comm = dummy$abun, traits = dummy$trait, q = 0.9999)
hill_func_parti_pairwise(comm = dummy$abun, traits = dummy$trait, q = 2)
hill_func_parti_pairwise(comm = dummy$abun, traits = dummy$trait, q = 3)

## End(Not run)
```

hill_phylo

Phylogenetic diversity through Hill Numbers

Description

Calculate alpha phylogenetic diversity based on Hill numbers

Usage

```
hill_phylo(
  comm,
  tree,
  q = 0,
  base = exp(1),
  rel_then_pool = TRUE,
  show_warning = TRUE,
  return_dt = FALSE
)
```

Arguments

comm	A data frame of vegetation data. Sites as rows, species as columns.
tree	A phylogeny with class 'phylo'.
q	Hill number, q = 0 (default) to get species richness, q = 1 to get shannon entropy, q = 2 will give inverse Simpson.
base	default is exp(1), the base of log.
rel_then_pool	default is TRUE. Abundance of species are first changed to relative abundance within sites, then pooled into one assemblage. If FALSE, sites are pooled first, then change abundance of species to relative abundance.
show_warning	whether to print warning, default is TRUE.
return_dt	Whether to return the Phylogenetic Hill numbers Dt, default is 'FALSE'.

Value

A vector of hill number based phylogenetic diversity ('PD(T)', effective total branch length) for all sites.

Author(s)

Chiu & Chao & Daijiang Li

References

Chao, Anne, Chun-Huo Chiu, and Lou Jost. Unifying Species Diversity, Phylogenetic Diversity, Functional Diversity, and Related Similarity and Differentiation Measures Through Hill Numbers. *Annual Review of Ecology, Evolution, and Systematics* 45, no. 1 (2014): 297–324. <doi:10.1146/annurev-ecolsys-120213-091540>.

Examples

```
comm = dummy = FD::dummy$abun
tree = ape::rtree(n = ncol(comm), tip.label = paste0('sp', 1:8))
hill_phylo(comm, tree, q = 0)
hill_phylo(comm, tree, q = 0.999)
hill_phylo(comm, tree, q = 1)
hill_phylo(comm, tree, q = 2)
```

hill_phylo_parti *Phylogenetic diversity of multiple sites*

Description

Calculate overall phylogenetic diversity and site similarity across multiple sites.

Usage

```
hill_phylo_parti(
  comm,
  tree,
  q = 0,
  base = exp(1),
  rel_then_pool = TRUE,
  show_warning = TRUE,
  phy_abund = NULL,
  check_data = TRUE
)
```

Arguments

comm	A data frame of vegetation data. Sites as rows, species as columns.
tree	A phylogeny with class 'phylo'.
q	Hill number, q = 0 (default) to get species richness, q = 1 to get shannon entropy, q = 2 will give inverse Simpson.
base	default is exp(1), the base of log.
rel_then_pool	default is TRUE. Abundance of species are first changed to relative abundance within sites, then pooled into one assemblage. If FALSE, sites are pooled first, then change abundance of species to relative abundance.
show_warning	whether to print warning, default is TRUE.
phy_abund	A matrix of phylogeny node and tips by community matrix derived from 'dat_prep_phylo()'. Can be specified to speed up 'hill_phylo_parti_pairwise()'.
check_data	Whether to check the community data and phylogeny. Default is 'TRUE'. Can be set to 'FALSE' to speed up 'hill_phylo_parti_pairwise()'.

Value

A data frame with one row (across all sites) and six columns: q, gamma diversity, alpha diversity, beta diversity, local similarity (similar to Sorensen), and region similarity (similar to Jaccard).

Author(s)

Chiu & Chao, Daijiang Li

References

Chao, Anne, Chun-Huo Chiu, and Lou Jost. Unifying Species Diversity, Phylogenetic Diversity, Functional Diversity, and Related Similarity and Differentiation Measures Through Hill Numbers. *Annual Review of Ecology, Evolution, and Systematics* 45, no. 1 (2014): 297–324. <doi:10.1146/annurev-ecolsys-120213-091540>.

Examples

```
comm = dummy = FD::dummy$abun
tree = ape::rtree(n = ncol(comm), tip.label = paste0('sp', 1:8))
hill_phylo_parti(comm, tree, q = 0)
hill_phylo_parti(comm, tree, q = 0.999)
hill_phylo_parti(comm, tree, q = 1)
hill_phylo_parti(comm, tree, q = 2)
```

hill_phylo_parti_pairwise

Pairwise phylogenetic diversity through Hill numbers

Description

Calculate pairwise phylogenetic diversity.

Usage

```
hill_phylo_parti_pairwise(
  comm,
  tree,
  q = 0,
  output = c("data.frame", "matrix"),
  pairs = c("unique", "full"),
  rel_then_pool = TRUE,
  .progress = TRUE,
  show_warning = TRUE,
  ...
)
```

Arguments

comm	A data frame of vegetation data. Sites as rows, species as columns.
tree	A phylogeny with class 'phylo'.
q	Hill number, q = 0 (default) to get species richness, q = 1 to get shannon entropy, q = 2 will give inverse Simpson.
output	output type: data.frame (default) or matrix. If matrix, then this function will return a list of matrices.

pairs	full or unique (default). Do you want to compare all possible pairs (i.e. n^2) or just unique pairs (i.e. $\text{choose}(n, 2)$)?
rel_then_pool	default is TRUE. Abundance of species are first changed to relative abundance within sites, then pooled into one assemblage. If FALSE, sites are pooled first, then change abundance of species to relative abundance.
.progress	Whether to show progress bar. Default is 'TRUE'.
show_warning	whether to print warning, default is TRUE.
...	additional arguments for hill_func_parti.

Value

A data frame or a matrix with results for all pairwise comparisons.

References

Chao, Anne, Chun-Huo Chiu, and Lou Jost. Unifying Species Diversity, Phylogenetic Diversity, Functional Diversity, and Related Similarity and Differentiation Measures Through Hill Numbers. *Annual Review of Ecology, Evolution, and Systematics* 45, no. 1 (2014): 297–324. <doi:10.1146/annurev-ecolsys-120213-091540>.

See Also

[hill_phylo_parti](#)

Examples

```
## Not run:
comm = dummy = FD::dummy$abun
tree = ape::rtree(n = ncol(comm), tip.label = paste0('sp', 1:8))
hill_phylo_parti_pairwise(comm, tree, q = 0, show_warning = FALSE)
hill_phylo_parti_pairwise(comm, tree, q = 0.999, show_warning = FALSE)
hill_phylo_parti_pairwise(comm, tree, q = 1, show_warning = FALSE)
hill_phylo_parti_pairwise(comm, tree, q = 2, show_warning = FALSE)

## End(Not run)
```

hill_taxa

Taxonomic diversity through Hill Numbers

Description

Calculate taxonomic diversity for each site (alpha diversity).

Usage

```
hill_taxa(comm, q = 0, MARGIN = 1, base = exp(1))
```

Arguments

comm	A data frame of vegetation data. Sites as rows, species as columns.
q	Hill number, q = 0 (default) to get species richness, q = 1 to get shannon entropy, q = 2 will give inverse Simpson.
MARGIN	default is 1, if sites are columns, set MARGIN to 2.
base	default is exp(1), the base of log.

Value

A named vector, diversity values for each site in the comm.

References

Chao, Anne, Chun-Huo Chiu, and Lou Jost. Unifying Species Diversity, Phylogenetic Diversity, Functional Diversity, and Related Similarity and Differentiation Measures Through Hill Numbers. *Annual Review of Ecology, Evolution, and Systematics* 45, no. 1 (2014): 297–324. <doi:10.1146/annurev-ecolsys-120213-091540>.

Jost, Lou. Entropy and diversity. *Oikos* 113, no. 2 (2006): 363-375. <doi:10.1111/j.2006.0030-1299.14714.x>.

Examples

```
dummy = FD::dummy
hill_taxa(comm = dummy$abun, q = 0)
# same as: vegan::specnumber(dummy$abun)
hill_taxa(comm = dummy$abun, q = 1)
# same as: exp(vegan::diversity(x = dummy$abun, index = 'shannon'))
hill_taxa(comm = dummy$abun, q = 2)
# same as: vegan::diversity(x = dummy$abun, index = 'invsimpson')
hill_taxa(comm = dummy$abun, q = 0.999)
```

hill_taxa_parti

Decomposition of Taxonomic diversity through Hill Numbers

Description

Calculate taxonomic gamma, alpha, and beta diversity across all communities, as well as site similarity. If comm has 2 sites, this function gives pair comparison. If comm has >2 sites, gamma diversity is the diversity of the pooled assemblage, alpha is the average diversity across all site, beta is across all communities.

Usage

```
hill_taxa_parti(
  comm,
  q = 0,
  base = exp(1),
  rel_then_pool = TRUE,
  show_warning = TRUE,
  check_data = TRUE
)
```

Arguments

comm	A data frame of vegetation data. Sites as rows, species as columns.
q	Hill number, q = 0 (default) to get species richness, q = 1 to get shannon entropy, q = 2 will give inverse Simpson.
base	default is exp(1), the base of log.
rel_then_pool	default is TRUE. Abundance of species are first changed to relative abundance within sites, then pooled into one assemblage. If FALSE, sites are pooled first, then change abundance of species to relative abundance.
show_warning	whether to print warning, default is TRUE.
check_data	whether to check data first? Default is TRUE.

Value

A data frame with one row (across all sites), including these columns: q, gamma diversity, alpha diversity, beta diversity, MacArthur's homogeneity measure, local similarity (species overlap, similar to Sorensen), and region similarity (species overlap, similar to Jaccard). See Chao, Chiu and Jost 2014 Table 2 for more information.

References

Chao, Anne, Chun-Huo Chiu, and Lou Jost. Unifying Species Diversity, Phylogenetic Diversity, Functional Diversity, and Related Similarity and Differentiation Measures Through Hill Numbers. *Annual Review of Ecology, Evolution, and Systematics* 45, no. 1 (2014): 297–324. <doi:10.1146/annurev-ecolsys-120213-091540>.

Jost, Lou. Entropy and diversity. *Oikos* 113, no. 2 (2006): 363-375. <doi:10.1111/j.2006.0030-1299.14714.x>.

See Also

[hill_taxa](#)

Examples

```
dummy = FD::dummy
hill_taxa_parti(comm = dummy$abun, q = 0)
hill_taxa_parti(comm = dummy$abun, q = 1)
```

```

hill_taxa_parti(comm = dummy$abun, q = 0.9999999)
hill_taxa_parti(comm = dummy$abun, q = 0.9999999, rel_then_pool = FALSE)
hill_taxa_parti(comm = dummy$abun, q = 1, rel_then_pool = FALSE)
hill_taxa_parti(comm = dummy$abun, q = 2)
hill_taxa_parti(comm = dummy$abun, q = 3)

```

hill_taxa_parti_pairwise

Pairwise comparisons for all sites

Description

Calculate pairwise taxonomic gamma, alpha, and beta diversity for communities, as well as site similarity. It is based on [hill_taxa_parti](#). If comm has >2 sites, this function will give results for all pairwise comparisons.

Usage

```

hill_taxa_parti_pairwise(
  comm,
  q = 0,
  rel_then_pool = TRUE,
  output = c("data.frame", "matrix"),
  pairs = c("unique", "full"),
  .progress = TRUE,
  show_warning = TRUE,
  ...
)

```

Arguments

comm	A data frame of vegetation data. Sites as rows, species as columns.
q	Hill number, q = 0 (default) to get species richness, q = 1 to get shannon entropy, q = 2 will give inverse Simpson.
rel_then_pool	default is TRUE. Abundance of species are first changed to relative abundance within sites, then pooled into one assemblage. If FALSE, sites are pooled first, then change abundance of species to relative abundance.
output	output type: data.frame (default) or matrix. If matrix, then this function will return a list of matrices.
pairs	full or unique (default). Do you want to compare all possible pairs (i.e. n^2) or just unique pairs (i.e. $\text{choose}(n, 2)$)?
.progress	Whether to show progress bar. Default is 'TRUE'.
show_warning	whether to print warning, default is TRUE.
...	other arguments in <code>hill_taxa_parti()</code> .

Value

A data frame with results for all pairwise comparisons.

References

Chao, Anne, Chun-Huo Chiu, and Lou Jost. Unifying Species Diversity, Phylogenetic Diversity, Functional Diversity, and Related Similarity and Differentiation Measures Through Hill Numbers. *Annual Review of Ecology, Evolution, and Systematics* 45, no. 1 (2014): 297–324. <doi:10.1146/annurev-ecolsys-120213-091540>.

Jost, Lou. Entropy and diversity. *Oikos* 113, no. 2 (2006): 363-375. <doi:10.1111/j.2006.0030-1299.14714.x>.

See Also

[hill_taxa_parti](#)

Examples

```
## Not run:
dummy = FD::dummy
hill_taxa_parti_pairwise(comm = dummy$abun, q = 0)
hill_taxa_parti_pairwise(comm = dummy$abun, q = 0, output = 'matrix')
hill_taxa_parti_pairwise(comm = dummy$abun, q = 1)
hill_taxa_parti_pairwise(comm = dummy$abun, q = 0.9999999)
hill_taxa_parti_pairwise(comm = dummy$abun, q = 0.9999999, rel_then_pool = FALSE)
hill_taxa_parti_pairwise(comm = dummy$abun, q = 1, rel_then_pool = FALSE)
hill_taxa_parti_pairwise(comm = dummy$abun, q = 2)
hill_taxa_parti_pairwise(comm = dummy$abun, q = 3)

## End(Not run)
```

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