Package ‘BAT’

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Title Biodiversity Assessment Tools

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Description Includes algorithms to assess alpha and beta diversity in all their dimensions (taxon, phylogenetic and functional diversity), whether communities are completely sampled or not. It allows performing a number of analyses based on either species identities or phylogenetic/functional trees depicting species relationships.

Depends R (>= 3.0.0)

Imports graphics, nls2, raster, spatstat, stats, utils, vegan

License GPL-3

LazyData true

RoxygenNote 6.0.1

NeedsCompilation no

Repository CRAN

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R topics documented:

`accuracy` *Scaled mean squared error of accumulation curves.*

Description

Accuracy (scaled mean squared error) of accumulation curves compared with a known true diversity value (target).

Usage

```
accuracy(accum, target = -1)
```

Arguments

`accum`	A matrix resulting from the alpha.accum or beta.accum functions (sampling units x diversity values).
`target`	The true known diversity value, with which the curve will be compared. If not specified, default is the diversity observed with all sampling units.

Details

Among multiple measures of accuracy (Walther & Moore 2005) the SMSE presents several advantages, as it is (Cardoso et al. 2014): (i) scaled to true diversity, so that similar absolute differences are weighted according to how much they represent of the real value; (ii) scaled to the number of sampling units, so that values are independent of sample size; (iii) squared, so that small, mostly meaningless fluctuations around the true value are down-weighted; and (iv) independent of positive or negative deviation from the real value, as such differentiation is usually not necessary. For alpha diversity accuracy may also be weighted according to how good the data is predicted to be. The weight of each point in the curve is proportional to its sampling intensity (i.e. n/Sobs).

Value

Accuracy values (both raw and weighted) for all observed and estimated curves.

References

Cardoso, P., Rigal, F., Borges, P.A.V. & Carvalho, J.C. (2014) A new frontier in biodiversity inventory: a proposal for estimators of phylogenetic and functional diversity. Methods in Ecology and Evolution, in press.

Walther, B.A. & Moore, J.L. (2005) The concepts of bias, precision and accuracy, and their use in testing the performance of species richness estimators, with a literature reviewof estimator performance. Ecography, 28, 815-829.

Examples

```
comm1 <- matrix(c(2,2,0,0,0,1,1,0,0,0,0,2,2,0,0,0,0,0,2,2), nrow = 4, ncol = 5, byrow = TRUE)
comm2 <- matrix(c(1,1,0,0,0,0,2,1,0,0,0,0,2,1,0,0,0,0,2,1), nrow = 4, ncol = 5, byrow = TRUE)
tree <- hclust(dist(c(1:5), method="euclidean"), method="average")
acc.alpha = alpha.accum(comm1)
accuracy(acc.alpha)
accuracy(acc.alpha, 10)
acc.beta = beta.accum(comm1, comm2, tree)
accuracy(acc.beta)
accuracy(acc.beta, c(1,1,0))
```

---

alpha — *Alpha diversity (Taxon, Phylogenetic or Functional Diversity - TD, PD, FD).*

Description

Observed alpha diversity with possible rarefaction, multiple sites simultaneously.

Usage

```
alpha(comm, tree, raref = 0, runs = 100)
```

Arguments

`comm`	A sites x species matrix, with either abundance or incidence data.
`tree`	An hclust or phylo object (used only for PD or FD).
`raref`	An integer specifying the number of individuals for rarefaction (individual based). If raref < 1 no rarefaction is made. If raref = 1 rarefaction is made by the minimum abundance among all sites. If raref > 1 rarefaction is made by the abundance indicated. If not specified, default is 0.
`runs`	Number of resampling runs for rarefaction. If not specified, default is 100.

Details

TD is equivalent to species richness. Calculations of PD and FD are based on Faith (1992) and Petchey & Gaston (2002, 2006), which measure PD and FD of a community as the total branch length of a tree linking all species represented in such community. PD and FD are calculated based on a tree (hclust or phylo object, no need to be ultrametric). The path to the root of the tree is always included in calculations of PD and FD. The number and order of species in comm must be the same as in tree. The rarefaction option is useful to compare communities with much different numbers of individuals sampled, which might bias diversity comparisons (Gotelli & Colwell 2001)

Value

A matrix of sites x diversity values (either "Obs" OR "Median, Min, LowerCL, UpperCL and Max").

References

Faith, D.P. (1992) Conservation evaluation and phylogenetic diversity. Biological Conservation, 61, 1-10.

Gotelli, N.J. & Colwell, R.K. (2001) Quantifying biodiversity: procedures and pitfalls in the measurement and comparison of species richness. Ecology Letters, 4, 379-391.

Petchey, O.L. & Gaston, K.J. (2002) Functional diversity (FD), species richness and community composition. Ecology Letters, 5, 402-411.

Petchey, O.L. & Gaston, K.J. (2006) Functional diversity: back to basics and looking forward. Ecology Letters, 9, 741-758.

Examples

```
comm <- matrix(c(0,0,1,1,0,0,2,1,0,0), nrow = 2, ncol = 5, byrow = TRUE)
tree <- hclust(dist(c(1:5), method="euclidean"), method="average")
alpha(comm)
alpha(comm, raref = 0)
alpha(comm, tree, 2, 100)
```

`alpha.accum` *Alpha diversity accumulation curves (observed and estimated).*

Description

Estimation of alpha diversity of a single site with accumulation of sampling units.

Usage

```
alpha.accum(comm, tree, func = "nonparametric", target = -2, runs = 100,
  prog = TRUE)
```

Arguments

`comm`	A sampling units x species matrix, with either abundance or incidence data.
`tree`	An hclust or phylo object (used only for Phylogenetic (PD) or Functional (FD) Diversity, not for Taxon Diversity (TD)).
`func`	The class of estimators to be used: If func is partial match of "curve", TD, PD or FD are based on extrapolating the accumulation curve of observed diversity. If func is partial match of "nonparametric", TD, PD or FD are based on non-parametric estimators. If func is partial match of "completeness", PD or FD estimates are based on the completeness of TD (requires a tree to be used). If not specified, default is "nonparametric.
`target`	True diversity value to calculate the accuracy of curves (scaled mean squared error). If not specified do not calculate accuracy (default), -1 uses the total observed diversity as true diversity and any other value is the true known diversity.
`runs`	Number of random permutations to be made to the sampling order. If not specified, default is 100.
`prog`	Present a text progress bar in the R console.

Details

Observed diversity often is an underestimation of true diversity. Several approaches have been devised to estimate species richness (TD) from incomplete sampling. These include: (1) fitting asymptotic functions to randomised accumulation curves (Soberon & Llorente 1993; Flather 1996; Cardoso et al. in prep.) (2) the use of non-parametric estimators based on the incidence or abundance of rare species (Heltshe & Forrester 1983; Chao 1984, 1987; Colwell & Coddington 1994). A correction to non-parametric estimators has also been recently proposed, based on the proportion of singleton or unique species (species represented by a single individual or in a single sampling unit respectively; Lopez et al. 2012). Cardoso et al. (2014) have proposed a way of adapting these approaches to estimate PD and FD, also adding a third possible approach for these dimensions of diversity: (3) correct PD and FD values based on the completeness of TD, where completeness equals the proportion of estimated true diversity that was observed. Calculations of PD and FD are based on Faith (1992) and Petchey & Gaston (2002, 2006), which measure PD and FD of a community as the total branch length of a tree linking all species represented in such community. PD and FD are calculated based on a tree (hclust or phylo object, no need to be ultrametric). The path to the root of the tree is always included in calculations of PD and FD. The number and order of species in comm must be the same as in tree.

Value

A matrix of sampling units x diversity values (sampling units, individuals, observed and estimated diversity). The values provided by this function are:

Sampl - Number of sampling units;

Ind - Number of individuals;

Obs - Observed diversity;

S1 - Singletons;

S2 - Doubletons;

Q1 - Uniques;

Q2 - Duplicates;

Jack1ab - First order jackknife estimator for abundance data;

Jack1in - First order jackknife estimator for incidence data;

Jack2ab - Second order jackknife estimator for abundance data;

Jack2in - Second order jackknife estimator for incidence data;

Chao1 - Chao estimator for abundance data;

Chao2 - Chao estimator for incidence data;

Clench - Clench or Michaelis-Menten curve;

Exponential - Exponential curve;

Rational - Rational function;

Weibull - Weibull curve;

The P-corrected version of all non-parametric estimators is also provided.

Accuracy - if accuracy is to be calculated a list is returned instead, with the second element being the scaled mean squared error of each estimator.

References

Cardoso, P., Rigal, F., Borges, P.A.V. & Carvalho, J.C. (2014) A new frontier in biodiversity inventory: a proposal for estimators of phylogenetic and functional diversity. Methods in Ecology and Evolution, in press.

Chao, A. (1984) Nonparametric estimation of the number of classes in a population. Scandinavian Journal of Statistics, 11, 265-270.

Chao, A. (1987). Estimating the population size for capture-recapture data with unequal catchability. Biometrics 43, 783-791.

Colwell, R.K. & Coddington, J.A. (1994). Estimating terrestrial biodiversity through extrapolation. Phil. Trans. Roy. Soc. London B 345, 101-118.

Faith, D.P. (1992) Conservation evaluation and phylogenetic diversity. Biological Conservation, 61, 1-10.

Flather, C. (1996) Fitting species-accumulation functions and assessing regional land use impacts on avian diversity. Journal of Biogeography, 23, 155-168.

Heltshe, J. & Forrester, N.E. (1983) Estimating species richness using the jackknife procedure. Biometrics, 39, 1-11.

Lopez, L.C.S., Fracasso, M.P.A., Mesquita, D.O., Palma, A.R.T. & Riul, P. (2012) The relationship between percentage of singletons and sampling effort: a new approach to reduce the bias of richness estimates. Ecological Indicators, 14, 164-169.

Petchey, O.L. & Gaston, K.J. (2002) Functional diversity (FD), species richness and community composition. Ecology Letters, 5, 402-411.

Petchey, O.L. & Gaston, K.J. (2006) Functional diversity: back to basics and looking forward. Ecology Letters, 9, 741-758.

Soberon, M.J. & Llorente, J. (1993) The use of species accumulation functions for the prediction of species richness. Conservation Biology, 7, 480-488.

Examples

```
comm <- matrix(c(1,1,0,0,0,0,2,1,0,0,0,0,2,1,0,0,0,0,2,1), nrow = 4, ncol = 5, byrow = TRUE)
tree <- hclust(dist(c(1:5), method="euclidean"), method="average")
alpha.accum(comm)
alpha.accum(comm, func = "nonparametric")
alpha.accum(comm, tree, "completeness")
alpha.accum(comm, tree, "curve", runs = 1000)
alpha.accum(comm, target = -1)
```

`alpha.estimate` *Alpha diversity estimates.*

Description

Estimation of alpha diversity of multiple sites simultaneously.

Usage

```
alpha.estimate(comm, tree, func = "nonparametric")
```

Arguments

`comm`	A sites x species matrix, with either abundances or number of incidences.
`tree`	An hclust or phylo object (used only for Phylogenetic (PD) or Functional (FD) Diversity, not for Taxon Diversity (TD)).
`func`	The class of estimators to be used: If func is partial match of "nonparametric", TD, PD or FD are based on non-parametric estimators. If func is partial match of "completeness", PD or FD estimates are based on the completeness of TD (requires a tree to be used). If not specified, default is "nonparametric".

Details

Observed diversity often is an underestimation of true diversity. Non-parametric estimators based on the incidence or abundance of rare species have been proposed to overcome the problem of undersampling (Heltshe & Forrester 1983; Chao 1984, 1987; Colwell & Coddington 1994). A correction to non-parametric estimators has also been recently proposed, based on the proportion (P) of singleton or unique species (species represented by a single individual or in a single sampling unit respectively; Lopez et al. 2012). Cardoso et al. (2014) have proposed a way of adapting non-parametric species richness estimators to PD and FD. They have also proposed correcting PD and FD values based on the completeness of TD, where completeness equals the proportion of estimated true diversity that was observed. Calculations of PD and FD are based on Faith (1992) and Petchey & Gaston (2002, 2006), which measure PD and FD of a community as the total branch length of a tree linking all species represented in such community. PD and FD are calculated based on a tree (hclust or phylo object, no need to be ultrametric). The path to the root of the tree is always included in calculations of PD and FD. The number and order of species in comm must be the same as in tree.

Value

A matrix of sites x diversity values (individuals, observed and estimated diversity). The values provided by this function are:

Ind - Number of individuals;

Obs - Observed diversity;

S1 - Singletons;

S2 - Doubletons;

Jack1ab - First order jackknife estimator for abundance data;

Jack2ab - Second order jackknife estimator for abundance data;

Chao1 - Chao estimator for abundance data.

The P-corrected version of all estimators is also provided.

References

Cardoso, P., Rigal, F., Borges, P.A.V. & Carvalho, J.C. (2014) A new frontier in biodiversity inventory: a proposal for estimators of phylogenetic and functional diversity. Methods in Ecology and Evolution, in press.

Chao, A. (1984) Nonparametric estimation of the number of classes in a population. Scandinavian Journal of Statistics, 11, 265-270.

Chao, A. (1987). Estimating the population size for capture-recapture data with unequal catchability. Biometrics 43, 783-791.

Colwell, R.K. & Coddington, J.A. (1994). Estimating terrestrial biodiversity through extrapolation. Phil. Trans. Roy. Soc. London B 345, 101-118.

Faith, D.P. (1992) Conservation evaluation and phylogenetic diversity. Biological Conservation, 61, 1-10.

Heltshe, J. & Forrester, N.E. (1983) Estimating species richness using the jackknife procedure. Biometrics, 39, 1-11.

Lopez, L.C.S., Fracasso, M.P.A., Mesquita, D.O., Palma, A.R.T. & Riul, P. (2012) The relationship between percentage of singletons and sampling effort: a new approach to reduce the bias of richness estimates. Ecological Indicators, 14, 164-169.

Petchey, O.L. & Gaston, K.J. (2002) Functional diversity (FD), species richness and community composition. Ecology Letters, 5, 402-411.

Petchey, O.L. & Gaston, K.J. (2006) Functional diversity: back to basics and looking forward. Ecology Letters, 9, 741-758.

Examples

```
comm <- matrix(c(1,1,0,0,0,0,2,1,0,0,0,0,2,1,0,0,0,0,2,1), nrow = 4, ncol = 5, byrow = TRUE)
tree <- hclust(dist(c(1:5), method="euclidean"), method="average")
alpha.estimate(comm)
alpha.estimate(comm, tree)
alpha.estimate(comm, tree, func = "completeness")
```

`arrabida` *Sample data of spiders in Arrabida (Portugal)*

Description

A dataset containing the abundance of 338 spider species in each of 320 sampling units. Details are described in: Cardoso, P., Gaspar, C., Pereira, L.C., Silva, I., Henriques, S.S., Silva, R.R. & Sousa, P. (2008) Assessing spider species richness and composition in Mediterranean cork oak forests. Acta Oecologica, 33: 114-127.

Usage

```
data(arrabida)
```

Format

A data frame with 320 sampling units (rows) and 338 species (variables).

`beta` *Beta diversity (Taxon, Phylogenetic or Functional Diversity - TD, PD, FD).*

Description

Beta diversity with possible rarefaction, multiple sites simultaneously.

Usage

```
beta(comm, tree, abund = FALSE, func = "jaccard", raref = 0, runs = 100)
```

Arguments

- `comm` — A sites x species matrix, with either abundance or incidence data.
- `tree` — An hclust or phylo object (used only for PD or FD).
- `abund` — A boolean (T/F) indicating whether abundance data should be used or converted to incidence before analysis. If not specified, default is FALSE.
- `func` — Partial match indicating whether the Jaccard or Soerensen family of beta diversity measures should be used. If not specified, default is Jaccard.
- `raref` — An integer specifying the number of individuals for rarefaction (individual based). If raref < 1 no rarefaction is made. If raref = 1 rarefaction is made by the minimum abundance among all sites. If raref > 1 rarefaction is made by the abundance indicated. If not specified, default is 0.
- `runs` — Number of resampling runs for rarefaction. If not specified, default is 100.

Details

The beta diversity measures used here follow the partitioning framework independently developed by Podani & Schmera (2011) and Carvalho et al. (2012) and later expanded to PD and FD by Cardoso et al. (2014), where Btotal = Brepl + Brich. Btotal = total beta diversity, reflecting both species replacement and loss/gain; Brepl = beta diversity explained by replacement of species alone; Brich = beta diversity explained by species loss/gain (richness differences) alone. PD and FD are calculated based on a tree (hclust or phylo object, no need to be ultrametric). The path to the root of the tree is always included in calculations of PD and FD. The number and order of species in comm must be the same as in tree. The rarefaction option is useful to compare communities with much different numbers of individuals sampled, which might bias diversity comparisons (Gotelli & Colwell 2001)

Value

Three distance matrices between sites, one per each of the three beta diversity measures (either "Obs" OR "Median, Min, LowerCL, UpperCL and Max").

References

Cardoso, P., Rigal, F., Carvalho, J.C., Fortelius, M., Borges, P.A.V., Podani, J. & Schmera, D. (2014) Partitioning taxon, phylogenetic and functional beta diversity into replacement and richness difference components. Journal of Biogeography, 41, 749-761.

Carvalho, J.C., Cardoso, P. & Gomes, P. (2012) Determining the relative roles of species replacement and species richness differences in generating beta-diversity patterns. Global Ecology and Biogeography, 21, 760-771.

Gotelli, N.J. & Colwell, R.K. (2001) Quantifying biodiversity: procedures and pitfalls in the measurement and comparison of species richness. Ecology Letters, 4, 379-391.

Podani, J. & Schmera, D. (2011) A new conceptual and methodological framework for exploring and explaining pattern in presence-absence data. Oikos, 120, 1625-1638.

Examples

```
comm <- matrix(c(2,2,0,0,0,1,1,0,0,0,0,2,2,0,0,0,0,0,2,2), nrow = 4, ncol = 5, byrow = TRUE)
tree <- hclust(dist(c(1:5), method="euclidean"), method="average")
beta(comm)
beta(comm, func = "Soerensen")
beta(comm, tree)
beta(comm, raref = 1)
beta(comm, tree, abund = TRUE, "s", raref = 2)
```

---

beta.accum — *Beta diversity accumulation curves.*

Description

Beta diversity between two sites with accumulation of sampling units.

Usage

```
beta.accum(comm1, comm2, tree, abund = FALSE, func = "jaccard",
  runs = 100, prog = TRUE)
```

Arguments

comm1	A sampling units x species matrix for the first site, with either abundance or incidence data.
comm2	A sampling units x species matrix for the second site, with either abundance or incidence data.
tree	An hclust or phylo object (used only for Phylogenetic (PD) or Functional (FD) Diversity, not for Taxon Diversity (TD)).
abund	A boolean (T/F) indicating whether abundance data should be used or converted to incidence before analysis. If not specified, default is FALSE.
func	Partial match indicating whether the Jaccard or Soerensen family of beta diversity measures should be used. If not specified, default is jaccard.
runs	Number of random permutations to be made to the sampling order. If not specified, default is 100.
prog	Present a text progress bar in the R console.

Details

As widely recognized for species richness, beta diversity is also biased when communities are undersampled. Beta diversity accumulation curves have been proposed by Cardoso et al. (2009) to test if beta diversity has approached an asymptote when comparing two undersampled sites. The beta diversity measures used here follow the partitioning framework independently developed by Podani & Schmera (2011) and Carvalho et al. (2012) and later expanded to PD and FD by Cardoso et al. (2014), where Btotal = Brepl + Brich. Btotal = total beta diversity, reflecting both species replacement and loss/gain; Brepl = beta diversity explained by replacement of species alone; Brich =

beta diversity explained by species loss/gain (richness differences) alone. PD and FD are calculated based on a tree (hclust or phylo object, no need to be ultrametric). The path to the root of the tree is always included in calculations of PD and FD. The number and order of species in comm1 and comm2 must be the same as in tree. Also, the number of sampling units should be similar in both sites.

Value

Three matrices of sampling units x diversity values, one per each of the three beta diversity measures (sampling units, individuals and observed diversity).

References

Cardoso, P., Borges, P.A.V. & Veech, J.A. (2009) Testing the performance of beta diversity measures based on incidence data: the robustness to undersampling. Diversity and Distributions, 15, 1081-1090.

Cardoso, P., Rigal, F., Carvalho, J.C., Fortelius, M., Borges, P.A.V., Podani, J. & Schmera, D. (2014) Partitioning taxon, phylogenetic and functional beta diversity into replacement and richness difference components. Journal of Biogeography, 41, 749-761.

Carvalho, J.C., Cardoso, P. & Gomes, P. (2012) Determining the relative roles of species replacement and species richness differences in generating beta-diversity patterns. Global Ecology and Biogeography, 21, 760-771.

Podani, J. & Schmera, D. (2011) A new conceptual and methodological framework for exploring and explaining pattern in presence-absence data. Oikos, 120, 1625-1638.

Examples

```
comm1 <- matrix(c(2,2,0,0,0,1,1,0,0,0,0,2,2,0,0,0,0,0,2,2), nrow = 4, byrow = TRUE)
comm2 <- matrix(c(1,1,0,0,0,0,2,1,0,0,0,0,2,1,0,0,0,0,2,1), nrow = 4, byrow = TRUE)
tree <- hclust(dist(c(1:5), method="euclidean"), method="average")
beta.accum(comm1, comm2)
beta.accum(comm1, comm2, func = "Soerensen")
beta.accum(comm1, comm2, tree)
beta.accum(comm1, comm2, abund = TRUE)
beta.accum(comm1, comm2, tree, TRUE)
```

---

beta.multi *Beta diversity among multiple communities.*

Description

Beta diversity with possible rarefaction - multiple sites measure calculated as the average or variance of all pairwise values.

Usage

```
beta.multi(comm, tree, abund = FALSE, func = "jaccard", raref = 0,
  runs = 100)
```

Arguments

comm	A sites x species matrix, with either abundance or incidence data.
tree	An hclust or phylo object (used only for Phylogenetic (PD) or Functional (FD) Diversity, not for Taxon Diversity (TD)).
abund	A boolean (T/F) indicating whether abundance data should be used or converted to incidence before analysis. If not specified, default is FALSE.
func	Indicates whether the Jaccard or Soerensen family of beta diversity measures should be used. If not specified, default is jaccard.
raref	An integer specifying the number of individuals for rarefaction (individual based). If raref < 1 no rarefaction is made. If raref = 1 rarefaction is made by the minimum abundance among all sites. If raref > 1 rarefaction is made by the abundance indicated. If not specified, default is 0.
runs	Number of resampling runs for rarefaction. If not specified, default is 100.

Details

Beta diversity of multiple sites simultaneously is calculated as either the average or the variance among all pairwise comparisons (Legendre, 2014). The beta diversity measures used here follow the partitioning framework independently developed by Podani & Schmera (2011) and Carvalho et al. (2012) and later expanded to PD and FD by Cardoso et al. (2014), where Btotal = Brepl + Brich. Btotal = total beta diversity, reflecting both species replacement and loss/gain; Brepl = beta diversity explained by replacement of species alone; Brich = beta diversity explained by species loss/gain (richness differences) alone. PD and FD are calculated based on a tree (hclust or phylo object, no need to be ultrametric). The path to the root of the tree is always included in calculations of PD and FD. The number and order of species in comm must be the same as in tree.

Value

A matrix of beta measures x diversity values (average and variance).

References

Cardoso, P., Rigal, F., Carvalho, J.C., Fortelius, M., Borges, P.A.V., Podani, J. & Schmera, D. (2014) Partitioning taxon, phylogenetic and functional beta diversity into replacement and richness difference components. Journal of Biogeography, 41, 749-761.

Carvalho, J.C., Cardoso, P. & Gomes, P. (2012) Determining the relative roles of species replacement and species richness differences in generating beta-diversity patterns. Global Ecology and Biogeography, 21, 760-771.

Legendre, P. (2014) Interpreting the replacement and richness difference components of beta diversity. Global Ecology and Biogeography, in press.

Podani, J. & Schmera, D. (2011) A new conceptual and methodological framework for exploring and explaining pattern in presence-absence data. Oikos, 120, 1625-1638.

Examples

```
comm <- matrix(c(2,2,0,0,0,1,1,0,0,0,0,2,2,0,0,0,0,0,2,2), nrow = 4, ncol = 5, byrow = TRUE)
tree <- hclust(dist(c(1:5), method="euclidean"), method="average")
beta.multi(comm)
beta.multi(comm, func = "Soerensen")
beta.multi(comm, tree)
beta.multi(comm, raref = 1)
beta.multi(comm, tree, TRUE, "s", raref = 2)
```

`contribution` *Contribution of species or individuals to total PD or FD.*

Description

Contribution of each species or individuals to the total PD or FD of a number of communities.

Usage

```
contribution(comm, tree, abund = FALSE, relative = FALSE)
```

Arguments

`comm`	A sites x species matrix, with either abundance or incidence data.
`tree`	An hclust or phylo object.
`abund`	A boolean (T/F) indicating whether contribution should be calculated per individual (T) or species (F). If not specified, default is FALSE.
`relative`	A boolean (T/F) indicating whether contribution should be relative to total PD or FD (proportional contribution per individual or species). If False, the sum of contributions for each site is equal to total PD/FD, if True it is 1.

Details

Contribution is equivalent to the evolutionary distinctiveness index (ED) of Isaac et al. (2007) if done by species and to the abundance weighted evolutionary distinctiveness (AED) of Cadotte et al. (2010) if done by individual.

Value

A matrix of sites x species values.

References

Isaac, N.J.B., Turvey, S.T., Collen, B., Waterman, C. & Baillie, J.E.M. (2007) Mammals on the EDGE: conservation priorities based on threat and phylogeny. PLoS One, 2: e296.

Cadotte, M.W., Davies, T.J., Regetz, J., Kembel, S.W., Cleland, E. & Oakley, T.H. (2010) Phylogenetic diversity metrics for ecological communities: integrating species richness, abundance and evolutionary history. Ecology Letters, 13: 96-105.

Examples

```
comm <- matrix(c(1,2,0,0,0,1,1,0,0,0,0,2,2,0,0,0,0,0,2,2), nrow = 4, byrow = TRUE)
tree <- hclust(dist(c(1:5), method="euclidean"), method="average")
contribution(comm, tree)
contribution(comm, tree, FALSE)
contribution(comm, tree, abund = TRUE, relative = TRUE)
```

`dispersion` *Phylogenetic/functional dispersion of species or individuals.*

Description

Average dissimilarity between any two species or individuals randomly chosen in a community with replacement.

Usage

```
dispersion(comm, tree, abund = FALSE, relative = FALSE)
```

Arguments

`comm`	A sites x species matrix, with either abundance or incidence data.
`tree`	An hclust or phylo object.
`abund`	A boolean (T/F) indicating whether dispersion should be calculated per individual (T) or species (F). If not specified, default is FALSE.
`relative`	A boolean (T/F) indicating whether dispersion should be relative to the maximum distance between any two species in the tree.

Details

If abundance data is used and a tree is given, dispersion is the quadratic entropy of Rao (1982). If abundance data is not used but a tree is given, dispersion is the phylogenetic dispersion measure of Webb et al. (2002) although with replacement. If abundance data is used but no tree is given, dispersion is 1 - Simpson's index (Simpson 1949).

Value

A vector of values per site.

References

Rao, C.R. (1982) Diversity and dissimilarity coefficients: a unified approach. Theoretical Population Biology, 21: 24-43.

Simpson, E.H. (1949) Measurement of diversity. Nature 163: 688.

Webb, C.O., Ackerly, D.D., McPeek, M.A. & Donoghue, M.J. (2002) Phylogenies and community ecology. Annual Review of Ecology and Systematics, 33: 475-505.

Examples

```
comm <- matrix(c(1,2,0,0,0,1,1,0,0,0,0,2,2,0,0,0,0,0,2,2), nrow = 4, byrow = TRUE)
tree <- hclust(dist(c(1:5), method="euclidean"), method="average")
dispersion(comm)
dispersion(comm, tree)
dispersion(comm, tree, abund = TRUE)
dispersion(comm, tree, abund = TRUE, relative = TRUE)
```

---

functree *Functional tree for 338 species of spiders*

Description

A dataset representing the functional tree for 338 species of spiders captured in Portugal. For each species were recorded: average size, type of web, type of hunting, stenophagy, vertical stratification in vegetation and circadial activity. Details are described in: Cardoso, P., Pekar, S., Jocque, R. & Coddington, J.A. (2011) Global patterns of guild composition and functional diversity of spiders. PLoS One, 6: e21710.

Usage

```
data(functree)
```

Format

An hclust object with 338 species.

---

gdm *General dynamic model of oceanic island biogeography (GDM).*

Description

Fits and compares several of the most supported models for the GDM (using TD, PD or FD).

Usage

```
gdm(comm, tree, area, time)
```

Arguments

comm	Either a vector with the diversity values per island, or an island x species matrix.
tree	An hclust or phylo object (used only to fit the PD or FD GDM, requires comm to be a sites x species matrix).
area	A vector with the area of islands.
time	A vector with the age of islands. If not given, the species-area relationship is returned instead.

Details

The general dynamic model of oceanic island biogeography was proposed to account for diversity patterns within and across oceanic archipelagos as a function of area and age of the islands (Whittaker et al. 2008). Several different equations have been found to describe the GDM, extending the different SAR models with the addition of a polynomial term using island age and its square (TT2), depicting the island ontogeny. The first to be proposed was an extension of the exponential model (Whittaker et al. 2008), the power model extensions following shortly after (Fattorini 2009; Steinbauer et al. 2013), as was the linear model (Cardoso et al. subm.). The relationships for PD and FD are calculated based on a tree (hclust or phylo object, no need to be ultrametric).

Value

A matrix with the different model parameters and explanatory power.

References

Cardoso, P., Borges, P.A.V., Carvalho, J.C., Rigal, F., Gabriel, R., Cascalho, J. & Correia, L. (subm.) Automated discovery of relationships, models and principles in ecology. Pre-print available from bioRxiv doi: http://dx.doi.org/10.1101/027839

Fattorini, S. (2009) On the general dynamic model of oceanic island biogeography. Journal of Biogeography, 36: 1100-1110.

Steinbauer, M.J, Klara, D., Field, R., Reineking, B. & Beierkuhnlein, C. (2013) Re-evaluating the general dynamic theory of oceanic island biogeography. Frontiers of Biogeography, 5: 185-194.

Whittaker, R.J., Triantis, K.A. & Ladle, R.J. (2008) A general dynamic theory of oceanic island biogeography. Journal of Biogeography, 35: 977-994.

Examples

```
div <- c(1,3,5,8,10)
comm <- matrix(c(2,0,0,0,3,1,0,0,2,4,5,0,1,3,2,5,1,1,1,1), nrow = 5, ncol = 4, byrow = TRUE)
tree <- hclust(dist(c(1:4), method="euclidean"), method="average")
area <- c(10,40,80,160,160)
time <- c(1,2,3,4,5)
gdm(div,,area,time)
gdm(comm,tree,area,time)
gdm(div,,area)
```

---

geres *Sample data of spiders in Geres (Portugal)*

Description

A dataset containing the abundance of 338 spider species in each of 320 sampling units. Details are described in: Cardoso, P., Scharff, N., Gaspar, C., Henriques, S.S., Carvalho, R., Castro, P.H., Schmidt, J.B., Silva, I., Szuts, T., Castro, A. & Crespo, L.C. (2008) Rapid biodiversity assessment of spiders (Araneae) using semi-quantitative sampling: a case study in a Mediterranean forest. Insect Conservation and Diversity, 1: 71-84.

Usage

```
data(geres)
```

Format

A data frame with 320 sampling untis (rows) and 338 species (variables).

---

guadiana — *Sample data of spiders in Guadiana (Portugal)*

Description

A dataset containing the abundance of 338 spider species in each of 320 sampling units. Details are described in: Cardoso, P., Henriques, S.S., Gaspar, C., Crespo, L.C., Carvalho, R., Schmidt, J.B., Sousa, P. & Szuts, T. (2009) Species richness and composition assessment of spiders in a Mediterranean scrubland. Journal of Insect Conservation, 13: 45-55.

Usage

```
data(guadiana)
```

Format

A data frame with 192 sampling units (rows) and 338 species (variables).

---

iaor — *Interspecific abundance-occupancy relationship (IAOR).*

Description

Fits and compares several of the most supported models for the IAOR.

Usage

```
iaor(comm)
```

Arguments

`comm`	A sites x species matrix with abundance values.

Details

Locally abundant species tend to be widespread while locally rare species tend to be narrowly distributed. That is, for a given species assemblage, there is a positive interspecific abundance-occupancy relationship (Brown 1984). This function compares some of the most commonly used and theoretically or empirically suported models (Nachman 1981; He & Gaston 2000; Cardoso et al. subm.).

Value

A matrix with the different model parameters and explanatory power.

References

Brown, J.H. (1984) On the relationship between abundance and distribution of species. American Naturalist, 124: 255-279.

Cardoso, P., Borges, P.A.V., Carvalho, J.C., Rigal, F., Gabriel, R., Cascalho, J. & Correia, L. (subm.) Automated discovery of relationships, models and principles in ecology. Pre-print available from bioRxiv doi: http://dx.doi.org/10.1101/027839

He, F.L. & Gaston, K.J. (2000) Estimating species abundance from occurrence. American Naturalist, 156: 553-559.

Nachman, G. (1981) A mathematical model of the functional relationship between density and spatial distribution of a population. Journal of Animal Ecology, 50: 453-460.

Examples

```
comm <- matrix(c(4,3,2,1,5,4,3,2,3,2,1,0,6,3,0,0,0,0,0,0), nrow = 5, ncol = 4, byrow = TRUE)
iaor(comm)
```

---

optim.alpha — *Optimization of alpha diversity sampling protocols.*

Description

Optimization of alpha diversity sampling protocols when different methods and multiple samples per method are available.

Usage

```
optim.alpha(comm, tree, methods, base, runs = 1000, prog = TRUE)
```

Arguments

`comm`	A samples x species x sites array, with either abundance or incidence data.
`tree`	An hclust or phylo object (used only to optimize PD or FD sampling).
`methods`	A vector specifying the method of each sample (length must be equal to nrow(comm))
`base`	A vector defining a base protocol from which to build upon (complementarity analysis) (length must be equal to number of methods).
`runs`	Number of random permutations to be made to the sample order. Default is 1000.
`prog`	Present a text progress bar in the R console.

Details

Often a combination of methods allows sampling maximum plot diversity with minimum effort, as it allows sampling different sub-communities, contrary to using single methods. Cardoso (2009) proposed a way to optimize the number of samples per method when the target is to maximize sampled alpha diversity. It is applied here for TD, PD and FD, and for one or multiple sites simultaneously. PD and FD are calculated based on a tree (hclust or phylo object, no need to be ultrametric).

Value

A matrix of samples x methods (values being optimum number of samples per method). The last column is the average alpha diversity value, rescaled to 0-1 if made for several sites, where 1 is the true diversity of each site.

References

Cardoso, P. (2009) Standardization and optimization of arthropod inventories - the case of Iberian spiders. Biodiversity and Conservation, 18, 3949-3962.

Examples

```
comm1 <- matrix(c(1,1,0,2,4,0,0,1,2,0,0,3), nrow = 4, ncol = 3, byrow = TRUE)
comm2 <- matrix(c(2,2,0,3,1,0,0,0,5,0,0,2), nrow = 4, ncol = 3, byrow = TRUE)
comm <- array(c(comm1, comm2), c(4,3,2))
colnames(comm) <- c("Sp1","Sp2","Sp3")
methods <- c("Met1","Met2","Met2","Met3")
tree <- hclust(dist(c(1:3), method="euclidean"), method="average")
optim.alpha(comm,,methods)
optim.alpha(comm, tree, methods)
optim.alpha(comm,, methods = methods, base = c(0,0,1), runs = 100)
```

`optim.alpha.stats` *Efficiency statistics for alpha-sampling.*

Description

Average alpha diversity observed with a given number of samples per method.

Usage

```
optim.alpha.stats(comm, tree, methods, samples, runs = 1000)
```

Arguments

`comm`	A samples x species x sites array, with either abundance or incidence data.
`tree`	An hclust or phylo object (used only to optimize PD or FD sampling).
`methods`	A vector specifying the method of each sample (length must be equal to nrow(comm))

samples — A vector defining the number of samples per method to be evaluated (length must be equal to number of methods).

runs — Number of random permutations to be made to the sample order. Default is 1000.

Details

Different combinations of samples per method allow sampling different sub-communities. This function allows knowing the average TD, PD or FD values for a given combination, for one or multiple sites simultaneously. PD and FD are calculated based on a tree (hclust or phylo object, no need to be ultrametric).

Value

A single average alpha diversity value. Rescaled to 0-1 if made for several sites, where 1 is the true diversity of each site.

Examples

```
comm1 <- matrix(c(1,1,0,2,4,0,0,1,2,0,0,3), nrow = 4, ncol = 3, byrow = TRUE)
comm2 <- matrix(c(2,2,0,3,1,0,0,0,5,0,0,2), nrow = 4, ncol = 3, byrow = TRUE)
comm <- array(c(comm1, comm2), c(4,3,2))
colnames(comm) <- c("Sp1","Sp2","Sp3")
methods <- c("Met1","Met2","Met2","Met3")
tree <- hclust(dist(c(1:3), method="euclidean"), method="average")
optim.alpha.stats(comm,,methods, c(1,1,1))
optim.alpha.stats(comm, tree, methods = methods, samples = c(0,0,1), runs = 100)
```

---

optim.beta — *Optimization of beta diversity sampling protocols.*

Description

Optimization of beta diversity sampling protocols when different methods and multiple samples per method are available.

Usage

```
optim.beta(comm, tree, methods, base, abund = FALSE, runs = 1000,
  prog = TRUE)
```

Arguments

comm — A samples x species x sites array, with either abundance or incidence data.

tree — An hclust or phylo object (used only to optimize PD or FD sampling).

methods — A vector specifying the method of each sample (length must be equal to nrow(comm))

base — Allows defining a base mandatory protocol from which to build upon (complementarity analysis). It should be a vector with length = number of methods.

abund	A boolean (T/F) indicating whether abundance data should be used or converted to incidence before analysis.
runs	Number of random permutations to be made to the sample order. Default is 1000.
prog	Present a text progress bar in the R console.

Details

Often, comparing differences between sites or the same site along time (i.e. measure beta diversity) it is not necessary to sample exhaustively. A minimum combination of samples targeting different sub-communities (that may behave differently) may be enough to perceive such differences, for example, for monitoring purposes. Cardoso et al. (in prep.) introduce and differentiate the concepts of alpha-sampling and beta-sampling. While alpha-sampling optimization implies maximizing local diversity sampled (Cardoso 2009), beta-sampling optimization implies minimizing differences in beta diversity values between partially and completely sampled communities. This function uses as beta diversity measures the Btotal, Brepl and Brich partitioning framework (Carvalho et al. 2012) and respective generalizations to PD and FD (Cardoso et al. 2014). PD and FD are calculated based on a tree (hclust or phylo object, no need to be ultrametric).

Value

A matrix of samples x methods (values being optimum number of samples per method). The last column is the average absolute difference from real beta.

References

Cardoso, P. (2009) Standardization and optimization of arthropod inventories - the case of Iberian spiders. Biodiversity and Conservation, 18, 3949-3962.

Cardoso, P., Rigal, F., Carvalho, J.C., Fortelius, M., Borges, P.A.V., Podani, J. & Schmera, D. (2014) Partitioning taxon, phylogenetic and functional beta diversity into replacement and richness difference components. Journal of Biogeography, 41, 749-761.

Cardoso, P., et al. (in prep.) Optimal inventorying and monitoring of taxon, phylogenetic and functional diversity.

Carvalho, J.C., Cardoso, P. & Gomes, P. (2012) Determining the relative roles of species replacement and species richness differences in generating beta-diversity patterns. Global Ecology and Biogeography, 21, 760-771.

Examples

```
comm1 <- matrix(c(1,1,0,2,4,0,0,1,2,0,0,3), nrow = 4, ncol = 3, byrow = TRUE)
comm2 <- matrix(c(2,2,0,3,1,0,0,0,5,0,0,2), nrow = 4, ncol = 3, byrow = TRUE)
comm3 <- matrix(c(2,0,0,3,1,0,0,0,5,0,0,2), nrow = 4, ncol = 3, byrow = TRUE)
comm <- array(c(comm1, comm2, comm3), c(4,3,3))
colnames(comm) <- c("sp1","sp2","sp3")
methods <- c("Met1","Met2","Met2","Met3")
tree <- hclust(dist(c(1:3), method="euclidean"), method="average")
optim.beta(comm, methods = methods, runs = 100)
optim.beta(comm, tree, methods = methods, abund = TRUE, base = c(0,0,1), runs = 100)
```

optim.beta.stats *Efficiency statistics for beta-sampling.*

Description

Average absolute difference between sampled and real beta diversity when using a given number of samples per method.

Usage

```
optim.beta.stats(comm, tree, methods, samples, abund = FALSE, runs = 1000)
```

Arguments

comm	A samples x species x sites array, with either abundance or incidence data.
tree	An hclust or phylo object (used only to optimize PD or FD sampling).
methods	A vector specifying the method of each sample (length must be equal to nrow(comm))
samples	The combination of samples per method we want to test. It should be a vector with length = number of methods.
abund	A boolean (T/F) indicating whether abundance data should be used or converted to incidence before analysis.
runs	Number of random permutations to be made to the sample order. Default is 1000.

Details

Different combinations of samples per method allow sampling different sub-communities. This function allows knowing the average absolute difference between sampled and real beta diversity for a given combination, for one or multiple sites simultaneously. PD and FD are calculated based on a tree (hclust or phylo object, no need to be ultrametric).

Value

A single average absolute beta diversity difference value.

Examples

```
comm1 <- matrix(c(1,1,0,2,4,0,0,1,2,0,0,3), nrow = 4, ncol = 3, byrow = TRUE)
comm2 <- matrix(c(2,2,0,3,1,0,0,0,5,0,0,2), nrow = 4, ncol = 3, byrow = TRUE)
comm3 <- matrix(c(2,0,0,3,1,0,0,0,5,0,0,2), nrow = 4, ncol = 3, byrow = TRUE)
comm <- array(c(comm1, comm2, comm3), c(4,3,3))
colnames(comm) <- c("sp1","sp2","sp3")
methods <- c("Met1","Met2","Met2","Met3")
tree <- hclust(dist(c(1:3), method="euclidean"), method="average")
optim.beta.stats(comm,,methods, c(1,1,1))
optim.beta.stats(comm, tree, methods = methods, samples = c(0,0,1), runs = 100)
```

`optim.spatial` *Optimization of spatial sampling.*

Description

Optimization of sampling site distribution in space based on environmental (or other) variables.

Usage

```
optim.spatial(layers, n, latlong = TRUE, clusterMap = TRUE)
```

Arguments

`layers`	A Raster* object (typically a multi-layer type: RasterStack or RasterBrick).
`n`	The number of intended sampling sites (clusters).
`latlong`	Boolean indicating whether latitude and longitude should be taken into account when clustering.
`clusterMap`	Boolean indicating whether to build a new raster with clusters.

Details

Optimizing the selection of sampling sites often requires maximizing the environmental diversity covered by them. One possible solution to this problem, here adopted, is performing a k-means clustering using environmental data and choosing the sites closest to the multidimensional environmental centroid of each cluster for sampling (Jimenez-Valverde & Lobo 2004)

Value

Either a matrix of cells x clusters (also indicating distance to centroid, longitude and latitude of each cell) or a list with such matrix plus the clusterMap.

References

Jimenez-Valverde, A., & Lobo, J. M. (2004). Un metodo sencillo para seleccionar puntos de muestreo con el objetivo de inventariar taxones hiperdiversos: el caso practico de las familias Araneidae y Thomisidae (Araneae) en la comunidad de Madrid, Espana. Ecologia, 18: 297-305.

`phylotree` *Taxonomic tree for 338 species of spiders (surrogate for phylogeny)*

Description

A dataset representing an approximation to the phylogenetic tree for 338 species of spiders captured in Portugal. The tree is based on the linnean hierarchy, with different suborders separated by 1 unit, families by 0.75, genera by 0.5 and species by 0.25.

Usage

```
data(phylotree)
```

Format

An hclust object with 338 species.

`sar` *Species-area relationship (SAR).*

Description

Fits and compares several of the most supported models for the species (or PD, or FD) -area relationship.

Usage

```
sar(comm, tree, area)
```

Arguments

`comm`	Either a vector with the diversity values per site, or a sites x species matrix.
`tree`	An hclust or phylo object (used only to fit the PD or FD-area relationships, requires comm to be a sites x species matrix).
`area`	A vector with the area per site.

Details

Larger areas (often islands) usually carry more species. Several formulas were proposed in the past to describe this relationship (Arrhenius 1920, 1921; Gleason 1922). Recently, the same approach began to be used for other measures of diversity, namely phylogenetic (PD) and functional (FD) diversity (Whittaker et al. 2014). The function compares some of the most commonly used and theoretically or empirically suported models. The relationships for PD and FD are calculated based on a tree (hclust or phylo object, no need to be ultrametric).

Value

A matrix with the different model parameters and explanatory power.

References

Arrhenius, O. (1920) Distribution of the species over the area. Meddelanden fran Vetenskapsakadmiens Nobelinstitut, 4: 1-6.

Arrhenius, O. (1921) Species and area. Journal of Ecology, 9: 95-99.

Gleason, H.A. (1922) On the relation between species and area. Ecology, 3: 158-162.

Whittaker, R.J., Rigal, F., Borges, P.A.V., Cardoso, P., Terzopoulou, S., Casanoves, F., Pla, L., Guilhaumon, F., Ladle, R. & Triantis, K.A. (2014) Functional biogeography of oceanic islands and the scaling of functional diversity in the Azores. Proceedings of the National Academy of Sciences USA, 111: 13709-13714.

Examples

```
div <- c(1,2,3,4,4)
comm <- matrix(c(2,0,0,0,3,1,0,0,2,4,5,0,1,3,2,5,1,1,1,1), nrow = 5, ncol = 4, byrow = TRUE)
tree <- hclust(dist(c(1:4), method="euclidean"), method="average")
area <- c(10,40,80,160,160)
sar(div,,area)
sar(comm,,area)
sar(comm,tree,area)
```

`sim.plot` *Plots of simulated species spatial distributions.*

Description

Plots individuals from artificial communities with given SAD and spatial clustering.

Usage

```
sim.plot(comm, sad = FALSE, s = 0)
```

Arguments

`comm`	artificial community data from function sim.spatial.
`sad`	boolean indicating if the SAD plot should also be shown. Default is FALSE.
`s`	number of species to plot simultaneously. Default is the number of species in comm.

Details

Function useful for visualizing the results of sim.spatial.

Examples

```
comm <- sim.spatial(1000, 24)
sim.plot(comm)
sim.plot(comm, sad = TRUE)
sim.plot(comm, s = 9)
```

---

sim.sad *Simulation of species abundance distributions (SAD).*

Description

Creates artificial communities following given SADs.

Usage

```
sim.sad(n, s, sad = "lognormal", sd = 1)
```

Arguments

`n`	total number of individuals.
`s`	number of species.
`sad`	The SAD distribution type (lognormal, uniform, broken stick or geometric). Default is lognormal.
`sd`	The standard deviation of lognormal distributions. Default is 1.

Details

Species Abundance Distributions may take a number of forms. A lognormal SAD probably is the most supported by empirical data, but we include other common types useful for testing multiple algorithms including several of the functions in BAT.

Value

A matrix of species x abundance per species.

Examples

```
comm1 <- sim.sad(10000, 100)
comm2 <- sim.sad(10000, 100, sd = 2)
comm3 <- sim.sad(10000, 100, sad = "uniform")
par(mfrow=c(1,3))
hist(log(comm1$Freq))
hist(log(comm2$Freq))
hist(log(comm3$Freq))
```

`sim.sample` *Simulation of sampling from artificial communities.*

Description

Simulates a sampling process from artificial communities.

Usage

```
sim.sample(comm, cells = 100, samples = 0)
```

Arguments

`comm`	simulated community data from function sim.spatial.
`cells`	number of cells to divide the simulated space into. Default is 100.
`samples`	number of samples (cells) to randomly extract. Default is the number of cells (the entire community).

Details

The space will be divided in both dimensions by sqrt(cells).

Function useful for simulating sampling processes from the results of sim.spatial.

May be used as direct input to other functions (e.g. alpha, alpha.accum, beta, beta.accum) to test the behavior of multiple descriptors and estimators.

Value

A matrix of samples x species (values are abundance per species per sample).

Examples

```
comm <- sim.spatial(1000, 10)
sim.sample(comm)
sim.sample(comm, cells = 10, samples = 5)
```

sim.spatial *Simulation of species spatial distributions.*

Description

Creates artificial communities with given SAD and spatial clustering.

Usage

```
sim.spatial(n, s, sad = "lognormal", sd = 1, distribution = "aggregated",
  clust = 1)
```

Arguments

n	total number of individuals.
s	number of species.
sad	The SAD distribution type (lognormal, uniform, broken stick or geometric). Default is lognormal.
sd	The standard deviation of lognormal distributions. Default is 1.
distribution	The spatial distribution of individual species populations (aggregated, random, uniform or gradient). Default is aggregated.
clust	The clustering parameter if distribution is either aggregated or gradient (higher values create more clustered populations). Default is 1.

Details

The spatial distribution of individuals of given species may take a number of forms. Competitive exclusion may cause overdispersion, specific habitat needs or cooperation may cause aggregation and environmental gradients may cause abundance gradients.

Value

A matrix of individuals x (species, x coords and y coords).

Examples

```
par(mfrow = c(3 ,3))
comm = sim.spatial(100, 9, distribution = "uniform")
for(i in 1:9){
sp <- comm[comm[1] == paste("Sp", i, sep = ""), ]
plot(sp$x, sp$y, main = paste("Sp", i), xlim = c(0,1), ylim = c(0,1))
}
comm = sim.spatial(1000, 9, sad = "lognormal", sd = 0.5, distribution = "aggregated", clust = 2)
for(i in 1:9){
sp <- comm[comm[1] == paste("Sp", i, sep=""), ]
plot(sp$x, sp$y, main = paste("Sp", i), xlim = c(0,1), ylim = c(0,1))
}
```

sim.tree *Simulation of phylogenetic or functional tree.*

Description

Simulates a random tree.

Usage

```
sim.tree(s, m = 100)
```

Arguments

s	number of species.
m	a structural parameter defining the average difference between species. Default is 100. Lower numbers create trees dominated by increasingly similar species, higher numbers by increasingly dissimilar species.

Details

A very simple tree based on random genes/traits.

Value

An hclust object.

Examples

```
tree <- sim.tree(10)
plot(as.dendrogram(tree))
tree <- sim.tree(100,10)
plot(as.dendrogram(tree))
tree <- sim.tree(100,1000)
plot(as.dendrogram(tree))
```

slope *Slope of accumulation curves.*

Description

This is similar to the first derivative of the curves at each of its points.

Usage

```
slope(accum)
```

Arguments

accum — A matrix resulting from the alpha.accum or beta.accum functions (sampling units x diversity values).

Details

Slope is the expected gain in diversity when sampling a new individual. The slope of an accumulation curve, of either observed or estimated diversity, allows verifying if the asymptote has been reached (Cardoso et al. 2011). This is an indication of either the completeness of the inventory (low final slopes of the observed curve indicate high completeness) or reliability of the estimators (stability of the slope around a value of 0 along the curve indicates reliability).

Value

A matrix of sampling units x slope values.

References

Cardoso, P., Pekar, S., Jocque, R. & Coddington, J.A. (2011) Global patterns of guild composition and functional diversity of spiders. PLoS One, 6, e21710.

Examples

```
comm1 <- matrix(c(2,2,0,0,0,1,1,0,0,0,0,2,2,0,0,0,0,0,2,2), nrow = 4, ncol = 5, byrow = TRUE)
comm2 <- matrix(c(1,1,0,0,0,0,2,1,0,0,0,0,2,1,0,0,0,0,2,1), nrow = 4, ncol = 5, byrow = TRUE)
tree <- hclust(dist(c(1:5), method="euclidean"), method="average")
acc.alpha = alpha.accum(comm1)
slope(acc.alpha)
acc.beta = beta.accum(comm1, comm2, tree)
slope(acc.beta)
```

---

uniqueness — *Phylogenetic/functional uniqueness of species or individuals.*

Description

Average dissimilarity between a species or individual and all others in a community with replacement.

Usage

```
uniqueness(comm, tree, abund = FALSE, relative = FALSE)
```

Arguments

- `comm` — A sites x species matrix, with either abundance or incidence data.
- `tree` — An hclust or phylo object.
- `abund` — A boolean (T/F) indicating whether uniqueness should be calculated per individual (T) or species (F). If not specified, default is FALSE.
- `relative` — A boolean (T/F) indicating whether uniqueness should be relative to the maximum distance between any two species in the tree.

Details

Uniqueness is the originality measure of Pavoine et al. (2005).

Value

A matrix of sites x species values.

References

Pavoine, S., Ollier, S. & Dufour, A.-B. (2005) Is the originality of a species measurable? Ecology Letters, 8: 579-586.

Examples

```
comm <- matrix(c(1,2,0,0,0,1,1,0,0,0,0,2,2,0,0,0,0,0,2,2), nrow = 4, byrow = TRUE)
tree <- hclust(dist(c(1:5), method="euclidean"), method="average")
uniqueness(comm, tree)
uniqueness(comm, tree, abund = TRUE)
uniqueness(comm, tree, abund = TRUE, relative = TRUE)
```

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