Package 'NST'

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Type Package

Title Normalized Stochasticity Ratio

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Imports vegan,parallel,permute,ape,bigmemory,iCAMP,DirichletReg

Depends R (>= 3.5.0)

Description To estimate ecological stochasticity in community assembly. Understanding the community assembly mechanisms controlling biodiversity patterns is a central issue in ecology. Although it is generally accepted that both deterministic and stochastic processes play important roles in community assembly, quantifying their relative importance is challenging. The new index, normalized stochasticity ratio (NST), is to estimate ecological stochasticity, i.e. relative importance of stochastic processes, in community assembly. With functions in this package, NST can be calculated based on different similarity metrics and/or different null model algorithms, as well as some previous indexes, e.g. previous Stochasticity Ratio (ST), Standard Effect Size (SES), modified Raup-Crick metrics (RC). Functions for permutational test and bootstrapping analysis are also included. Previous ST is published by Zhou et al (2014) <doi:10.1073/pnas.1324044111>. NST is modified from ST by considering two alternative situations and normalizing the index to range from 0 to 1 (Ning et al 2019) <doi:10.1073/pnas.1904623116>. A modified version, MST, is a special case of NST, used in some recent or upcoming publications, e.g. Liang et al (2020) <doi:10.1016/j.soilbio.2020.108023>. SES is calculated as described in Kraft et al (2011) <doi:10.1126/science.1208584>. RC is calculated as reported by Chase et al (2011) <doi:10.1890/ES10-00117.1> and Stegen et al (2013) <doi:10.1038/ismej.2013.93>. Version 3 added NST based on phylogenetic beta diversity, used by Ning et al (2020) <doi:10.1038/s41467-020-18560-z>.

License GPL-2

URL https://github.com/DaliangNing/NST

NeedsCompilation no

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R topics documented:

NST-package   *Normalized Stochasticity Ratio*

Description

This package is to estimate ecological stochasticity in community assembly based on beta diversity. Various indexes can be calculated, including Stochasticity Ratio (ST), Normalized Stochasticity Ratio (NST), Modified Stochasticity Ratio (MST), Standard Effect Size (SES), and modified Raup-Crick metrics (RC), based on various taxonomic and phylogenetic dissimilarity metrics and different null model algorithms. All versions and examples are available from GitHub. URL: https://github.com/DaliangNing/NST

Version 2.0.4: Update citation and references. Emphasize that NST variation should be calculated from nst.boot rather than pairwise NST.ij from tNST. Emphasize that different group setting in tNST may lead to different NST results. Version 3.0.1: Add NST based on phylogenetic beta diversity (pNST). Version 3.0.2: debug pNST. Version 3.0.3: remove setwd in functions; change dontrun to donttest and revise save.wd in help doc. Version 3.0.4: update github link of NST; update nst.boot and nst.panova to include MST results. Version 3.0.5: debug nst.panova. Version 3.0.6: update references. Version 3.1.1: add options to allow input propotional data (rather than counts) as community matrix, as well as community data transformation before dissimilarity calculation. Version 3.1.2: provide temporary solution for the failure of makeCluster in some OS. Version 3.1.3: add options to specify occurrence frequency in regional pool. Version 3.1.4: debug ab.assign. Version 3.1.5: add function cNST to calculate NST using user customized beta diversity and the null results. Version 3.1.6: revise functions tNST, pNST, cNST, nst.boot, and nst.panova to avoid error for special cases in MST calculation. Version 3.1.7(20210928): revise function nst.panova to avoid error for special cases in permutation. Version 3.1.8(20211029): add summary and test for SES and RC in functions tNST, pNST, cNST, nst.boot, and nst.panova. Version 3.1.9(20220410):

address notes from package check. Version 3.1.10(20220603): tested with the latest version of package iCAMP.

Details

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Author(s)

Daliang Ning <ningdaliang@ou.edu>

References

Ning D., Deng Y., Tiedje J.M. & Zhou J. (2019) A general framework for quantitatively assessing ecological stochasticity. Proceedings of the National Academy of Sciences 116, 16892-16898. doi:10.1073/pnas.1904623116.

Zhou J, Deng Y, Zhang P, Xue K, Liang Y, Van Nostrand JD, Yang Y, He Z, Wu L, Stahl DA, Hazen TC, Tiedje JM, and Arkin AP. (2014) Stochasticity, succession, and environmental perturbations in a fluidic ecosystem. Proceedings of the National Academy of Sciences of the United States of America 111, E836-E845. doi:10.1073/pnas.1324044111.

Examples

```
data(tda)
comm=tda$comm
group=tda$group
tnst=tNST(comm=comm, group=group, dist.method="jaccard",
          abundance.weighted=TRUE, rand=100,
          nworker=1, null.model="PF", between.group=TRUE,
          SES=TRUE, RC=TRUE)
```

---

ab.assign	*Randomly draw individuals into species according to specified probabilities*

Description

This funciton is to assign abundances to species when randomizing communities based on null models considering abundances. Individuals are randomly drawn into species according to the specified probabilities.

Usage

```
ab.assign(comm.b, samp.ab=NULL, prob.ab)
```

Arguments

comm.b	numeric matrix, binary (present/absent) community data, rownames are sample/site names, colnames are species names.
samp.ab	numeric vector, total abundances (total individual numbers) in each sample. If samp.ab=NULL, Dirichlet distribution will be used to generate randomized community matrix with relative abundance (proportion) of each taxon in each sample.
prob.ab	numeric matrix, probability of each species into which the individuals in a certain sample are drawn.

Details

This function is called by the function [`taxo.null`](#) to generate randomized communities.

Value

A matrix of community data with abundances (or relative abundance) is returned. rownames are sample/site names, and colnames are species names.

Note

Version 3: 2021.7.27, debug, if samp.ab is lower than samp.rich, no need to assign abundance. Version 2: 2021.4.16, add new algorithm based on Dirichlet distribution. Version 1: 2015.10.22.

Author(s)

Daliang Ning

References

Stegen JC, Lin X, Fredrickson JK, Chen X, Kennedy DW, Murray CJ, Rockhold ML, and Konopka A. Quantifying community assembly processes and identifying features that impose them. Isme Journal 7, 2069-2079 (2013).

See Also

[`taxo.null`](#)

Examples

```
data(tda)
comm=tda$comm
comm.b=comm
comm.b[comm.b>0]=1
samp.ab=rowSums(comm)
prob.ab=matrix(colSums(comm),nrow=nrow(comm),ncol=ncol(comm),byrow=TRUE)
```

```
comm.rand=ab.assign(comm.b,samp.ab,prob.ab)
```

---

beta.g   *Various taxonomic beta diversity indexes*

Description

This function can simultaneously calculate various taxonomic dissimilarity indexes, mainly based on vegdist from package vegan.

Usage

```
beta.g(comm, dist.method="bray", abundance.weighted=TRUE,
       as.3col=FALSE,out.list=TRUE, transform.method=NULL, logbase=2)
chaosorensen(comm, dissimilarity=TRUE, to.dist=TRUE)
chaojaccard(comm, dissimilarity=TRUE, to.dist=TRUE)
```

Arguments

comm	Community data matrix. rownames are sample names. colnames are species names.
dist.method	A character or vector indicating one or more index(es). match to "manhattan", "euclidean", "canberra", "bray", "kulczynski", "jaccard", "gower", "altGower", "morisita", "horn", "mountford", "raup" , "binomial", "chao", "cao", "mahalanobis", "mGower", "mEuclidean", "mManhattan", "chao.jaccard", "chao.sorensen". default is "bray"
abundance.weighted	
	Logic, consider abundances or not (just presence/absence). default is TRUE.
as.3col	Logic, output a 3-column matrix (TRUE) or a square matrix (FALSE) for each index. default is FALSE.
out.list	Logic, if using multiple indexes, output their results as a list (TRUE) or a matrix combining all 3-column matrixes (FALSE). if out.list=FALSE, as.3col will be forced to be TRUE. default is TRUE.
dissimilarity	Logic, calculate dissimilarity or similarity. default is TRUE, means to return dissimilarity.
to.dist	Logic, return distance object or squared matrix. default is TRUE, means to return distance object.
transform.method	
	character or a defined function, to specify how to transform community matrix before calculating dissimilarity. if it is a characher, it should be a method name as in the function 'decostand' in package 'vegan', including 'total','max','freq','normalize','range','standa
logbase	numeric, the logarithm base used when transform.method='log'.

Details

All the taxonomic beta diversity indexes are mainly calculated by vegdist in package vegan, except following methods:

mGower, mEuclidean, and mManhattan are modified from Gower, Euclidean, and Manhattan, respectively, according to the method reported previously (Anderson et al 2006).

chao.jaccard and chao.sorensen are calculated as described previously (Chao et al 2005), using open-source code from R package "fossil" (Vavrek 2011), but output as dissimilarity for each pairwise comparison.

Value

beta.g will return a square matrix of each index if as.3col=FALSE, and combined as a list if out.list=TRUE (default). A 3-column matrix with first 2 columns indicating the pairwised samples will be output for each index if as.3col=TRUE, and combined as a list if out.list=TRUE or integrated into one matrix if out.list=FALSE.

chaosorensen and chaojaccard will return a distance object (if to.dist=TRUE) or a squared matrix (if to.dist=FALSE).

Note

Version 3: 2021.4.16, add option to transform community matrix. Version 2: 2019.5.10. Version 1: 2015.9.25.

Author(s)

Daliang Ning

References

Jari Oksanen, F. Guillaume Blanchet, Michael Friendly, Roeland Kindt, Pierre Legendre, Dan McGlinn, Peter R. Minchin, R. B. O'Hara, Gavin L. Simpson, Peter Solymos, M. Henry H. Stevens, Eduard Szoecs and Helene Wagner (2019). vegan: Community Ecology Package. R package version 2.5-4.

Anderson MJ, Ellingsen KE, & McArdle BH (2006) Multivariate dispersion as a measure of beta diversity. Ecol Lett 9(6):683-693.

Chao, A., R. L. Chazdon, et al. (2005) A new statistical approach for assessing similarity of speciescomposition with incidence and abundance data. Ecology Letters 8: 148-159

Vavrek, Matthew J. 2011. fossil: palaeoecological and palaeogeographical analysis tools. Palaeontologia Electronica, 14:1T.

Legendre, P. & Gallagher, E.D. (2001) Ecologically meaningful transformations for ordination of species data. Oecologia 129, 271–280.

Others cited in the help document of vegdist in R package vegan.

See Also

tNST

Examples

```
data(tda)
comm=tda$comm
# calculate one index
beta.bray=beta.g(comm=comm,as.3col=TRUE)

# calculate multiple indexes
beta.td=beta.g(comm=comm,dist.method=c("bray","jaccard","euclidean",
              "manhattan","binomial","chao","cao"),
              abundance.weighted = TRUE,out.list=FALSE)
```

---

beta.limit	*Upper limit of different beta diversity (dissimilarity) indexes*

Description

Upper limit value of each abundance-based or incidence-based dissimilarity index.

Usage

```
data("beta.limit")
```

Format

A data frame with 18 observations on the following 2 variables.

Dmax.in numeric, upper limit of incidence-based dissimilarity

Dmax.ab numeric, upper limit of abundance-based dissimilarity

Examples

```
data(beta.limit)
```

---

beta.obs.rand	*Test data B observed and null beta diversity*

Description

A simple dataset of observed and null beta diversity values, with sample grouping information.

Usage

```
data("beta.obs.rand")
```

Format

A list object with 3 elements.

obs matrix, pairwise values of beta diversity (dissimilarity).

rand list, each element shows the beta diversity of randomized communities from a null model algorithm.

group data.frame, only one column showing which samples are controls and which are under treatment.

Examples

```
data(beta.obs.rand)
beta.obs=beta.obs.rand$obs
beta.rand.list=beta.obs.rand$rand
group=beta.obs.rand$group
```

---

bmntd.big   *beta mean nearest taxon distance (betaMNTD) from big data*

Description

Calculates beta MNTD (beta mean nearest taxon distance, Webb et al 2008) for taxa in each pair of communities in a givern community matrix, using bigmemory (Kane et al 2013) to deal with too large dataset.

Usage

```
bmntd.big(comm, pd.desc = "pd.desc", pd.spname, pd.wd,
          spname.check = FALSE, abundance.weighted = TRUE,
          exclude.conspecifics = FALSE, time.output = FALSE)
```

Arguments

comm	matrix or data.frame, community data matrix, rownames are sample names, colnames are taxa ids.
pd.desc	character, the name to describe bigmemory file of phylogenetic distance matrix, default is "pd.desc".
pd.spname	vector, the OTU ids (species names) in exactly the same order as the phylogenetic matrix rows or columns
pd.wd	the path of the folder saving the phylogenetic distance matrix.
spname.check	logic, whether to check the OTU ids (species names) in community matrix and phylogenetic distance matrix are the same.
abundance.weighted	
	logic, whether weighted by species abundance, default is TRUE, means weighted.
exclude.conspecifics	
	logic, whether conspecific taxa in different communities be exclude from beta MNTD calculations, default is FALSE.
time.output	logic, whether to count calculation time, default is FALSE.

Details

beta mean nearest taxon distance for taxa in each pair of communities. Improved from 'comdistnt' in package 'picante'(Kembel et al 2010). This function adds bigmemory part (Kane et al 2013) to deal with large dataset.

Value

result is a distance object.

Note

Version 3: 2020.9.9, remove setwd; change dontrun to donttest and revise save.wd in help doc. Version 2: 2020.8.22, add to NST package, update help document. Version 1: 2017.3.13

Author(s)

Daliang Ning (ningdaliang@ou.edu)

References

Webb, C.O., Ackerly, D.D. & Kembel, S.W. (2008). Phylocom: software for the analysis of phylogenetic community structure and trait evolution. Bioinformatics, 24, 2098-2100.

Kembel, S.W., Cowan, P.D., Helmus, M.R., Cornwell, W.K., Morlon, H., Ackerly, D.D. et al. (2010). Picante: R tools for integrating phylogenies and ecology. Bioinformatics, 26, 1463-1464.

Kane, M.J., Emerson, J., Weston, S. (2013). Scalable Strategies for Computing with Massive Data. Journal of Statistical Software, 55(14), 1-19. URL http://www.jstatsoft.org/v55/i14/.

Examples

```
data("tda")
comm=tda$comm
tree=tda$tree
# since it needs to save some file to a certain folder,
# the following code is set as 'not test'.
# but you may test the code on your computer
# after change the folder path for 'save.wd'.

  save.wd=tempdir() # please change to the folder you want to use.
  nworker=2 # parallel computing thread number
  pd.big=iCAMP::pdist.big(tree = tree,wd = save.wd, nworker = nworker)
  bmntd.wt=bmntd.big(comm=comm, pd.desc = pd.big$pd.file,
                     pd.spname = pd.big$tip.label, pd.wd = pd.big$pd.wd,
                     abundance.weighted = TRUE)
```

---

cNST   *Normalized Stochasticity Ratio based on customized metrics and null results*

Description

Calculate normalized stochasticity ratio (NST) based on given values of observed and null beta diveresity metrics.

Usage

```
cNST(beta.obs, beta.rand.list, group,
     Dmax = 1, between.group = FALSE,
     SES = FALSE, RC = FALSE, output.detail = FALSE)
```

Arguments

beta.obs	square matrix or distance object, to provide the observed pairwise values of beta diversity (dissimilarity).
beta.rand.list	a list object. Each element of the list is a square matrix or a distance object, to provide null values of beta diversity from a null model.
group	matrix or data.frame, a one-column (n x 1) matrix indicating the group or treatment of each sample, rownames are sample IDs. if input a n x m matrix, only the first column is used. Attention: different group setting will change NST values.
Dmax	The maximum or upper limit of dissimilarity before standardized, which is used to standardize the dissimilarity with upper limit not equal to one.
between.group	Logic, whether to calculate stochasticity for between-group turnovers. default is FALSE.
SES	Logic, whether to calculate standardized effect size, which is (observed dissimilarity - mean of null dissimilarity)/standard deviation of null dissimilarity. default is FALSE.
RC	Logic, whether to calculate modified Raup-Crick metric, which is percentage of null dissimilarity lower than observed dissimilarity x 2 - 1. default is FALSE.
output.detail	Logic, whether to output some details, including dissimilarity results of each randomization. Default is FALSE.

Details

NST is a metric to estimate ecological stochasticity based on null model analysis of dissimilarity. When using the function tNST or pNST, you can only select the metrics or null model from the given options. This function gives more flexibility if your beta diversity metric or null model algorithm is not included in tNST or pNST's options.

Value

Output is a list. Please DO NOT use NST.ij values in index.pair.grp and index.between.grp which can be out of [0,1] without ecologcial meanning. Please use `nst.boot` to get variation of NST.

index.pair   indexes for each pairwise comparison. D.ij, observed dissimilarity, not standardized; G.ij, average null expectation of dissimilarity, not standardized; Ds.ij, observed dissimilarity, standardized to range from 0 to 1; Gs.ij, average null expectation of dissimilarity, standardized; C.ij and E.ij are similarity and average null expectation of simmilarity, standardized if the dissimilarity has no fixed upper limit; ST.ij, stochasticity ratio calculated by previous method (Zhou et al 2014); MST.ij, modified stochasticity ratio calculated by a modified method (Liang et al 2020; Guo et al 2018); SES.ij, standard effect size of difference between observed and null dissimilarity (Kraft et al 2011); RC.ij, modified Roup-Crick metrics (Chase et al 2011, Stegen et al 2013).

index.grp   mean value of each index in each group. group, group name; size, number of pairwise comparisons in this group; ST.i, group mean of stochasticity ratio, not normalized; NST.i, group mean of normalized stochasticity ratio; MST.i, group mean of modified stochasticity ratio; SES.i, group mean of standard effect size; RC.i, group mean of modified Roup-Crick metric.

index.pair.grp   pairwise values of each index in each group. group, group name; C.ij, E.ij, ST.ij, MST.ij, SES.ij, and RC.ij have the same meaning as in index.pair; NST.ij, the pairwise values of NST, for reference only, DO NOT use. Since NST is normalized ST calculated from ST.ij, NST pairwise values NST.ij have no ecological meaning. Variation of NST from bootstrapping test is preferred, see `nst.boot`.

index.between   mean value of each index between each two groups. Similar to index.grp, but calcualted from comparisons between each two groups.

index.pair.between
                    pairwise values of each index between each two groups. Similar to index.pair.grp, but calcualted from comparisons between each two groups.

Dmax   The maximum or upper limit of dissimilarity before standardized, which is used to standardize the dissimilarity with upper limit not equal to one. See `beta.limit` for details.

details   detailed results. rand.mean, mean of null dissimilarity for each pairwise comparison, not standardized; Dmax, the maximum or upper limit of dissimilarity before standardized; obs3, observed dissimilarity, not standardized; dist.ran, alll null dissimilarity values, each row is a pairwise comparison, each column is results from one randomization; group, input group informaiton; meta.group, input metacommunity information.

Note

Version 3: 2021.10.29, add summary of SES and RC. Version 2: 2021.8.25, revised to avoid error for special cases in MST calculation. Version 1: 2021.7.29

Author(s)

Daliang Ning

References

Ning D., Deng Y., Tiedje J.M. & Zhou J. (2019) A general framework for quantitatively assessing ecological stochasticity. Proceedings of the National Academy of Sciences 116, 16892-16898. doi:10.1073/pnas.1904623116.

Zhou J, Deng Y, Zhang P, Xue K, Liang Y, Van Nostrand JD, Yang Y, He Z, Wu L, Stahl DA, Hazen TC, Tiedje JM, and Arkin AP. (2014) Stochasticity, succession, and environmental perturbations in a fluidic ecosystem. Proceedings of the National Academy of Sciences of the United States of America 111, E836-E845. doi:10.1073/pnas.1324044111.

Liang Y, Ning D, Lu Z, Zhang N, Hale L, Wu L, Clark IM, McGrath SP, Storkey J, Hirsch PR, Sun B, and Zhou J. (2020) Century long fertilization reduces stochasticity controlling grassland micro-bial community succession. Soil Biology and Biochemistry 151, 108023. doi:10.1016/j.soilbio.2020.108023.

Guo X, Feng J, Shi Z, Zhou X, Yuan M, Tao X, Hale L, Yuan T, Wang J, Qin Y, Zhou A, Fu Y, Wu L, He Z, Van Nostrand JD, Ning D, Liu X, Luo Y, Tiedje JM, Yang Y, and Zhou J. (2018) Climate warming leads to divergent succession of grassland microbial communities. Nature Climate Change 8, 813-818. doi:10.1038/s41558-018-0254-2.

Kraft NJB, Comita LS, Chase JM, Sanders NJ, Swenson NG, Crist TO, Stegen JC, Vellend M, Boyle B, Anderson MJ, Cornell HV, Davies KF, Freestone AL, Inouye BD, Harrison SP, and Myers JA. (2011) Disentangling the drivers of beta diversity along latitudinal and elevational gradients. Science 333, 1755-1758. doi:10.1126/science.1208584.

Chase JM, Kraft NJB, Smith KG, Vellend M, and Inouye BD. (2011) Using null models to disen-tangle variation in community dissimilarity from variation in alpha-diversity. Ecosphere 2, art24. doi:10.1890/es10-00117.1.

Stegen JC, Lin X, Fredrickson JK, Chen X, Kennedy DW, Murray CJ, Rockhold ML, and Konopka A. (2013) Quantifying community assembly processes and identifying features that impose them. The Isme Journal 7, 2069. doi:10.1038/ismej.2013.93.

See Also

nst.boot, nst.panova, taxo.null, tNST, pNST

Examples

```
data(beta.obs.rand)
beta.obs=beta.obs.rand$obs
beta.rand.list=beta.obs.rand$rand
group=beta.obs.rand$group
nst=cNST(beta.obs=beta.obs, beta.rand.list=beta.rand.list,
        group=group,Dmax = 1,between.group = TRUE,
        SES = TRUE, RC = TRUE, output.detail = FALSE)
```

---

dist.3col   *Transform distance matrix to 3-column matrix*

Description

Transform a distance matrix to a 3-column matrix in which the first 2 columns indicate the pairwised samples/species names.

Usage

```
dist.3col(dist)
```

Arguments

dist   a square matrix or distance object with column names and row names.

Details

In many cases, a 3-column matrix is easier to use than a distance matrix.

Value

name1   1st column, the first item of pairwised two items

name2   2nd column, the second item of pairwised two items

dis   3rd column, distance value of the pairwised two itmes

Note

Version 1: 2015.5.17

Author(s)

Daliang Ning

Examples

```
data(tda)
comm=tda$comm
bray=beta.g(comm,dist.method="bray")
bray.3col=dist.3col(bray)
```

---

match.name	*Check and ensure the consistency of IDs in different objects.*

Description

This function is usually used to check the consistency of species or samples names in different data table (e.g. OTU table and phylogenetic distance matrix). it can be used to check row names and/or column names of different matrixes, names in vector(s) or list(s), and tip.lable in tree(s)

Usage

```
match.name(name.check=integer(0), rn.list=list(integer(0)),
           cn.list=list(integer(0)), both.list=list(integer(0)),
           v.list=list(integer(0)), lf.list=list(integer(0)),
           tree.list=list(integer(0)), group=integer(0),
           rerank=TRUE, silent=FALSE)
```

Arguments

name.check	A character vector, indicating reference name list or the names you would like to keep. If not available, a union of all names is set as reference name list.
rn.list	A list object, including the matrix(es) of which the row names will be check. rn.list must be set in a format like "rn.list=list(A=A,B=B)". default is nothing.
cn.list	A list object, including the matrix(es) of which the column names will be check. cn.list must be set in a format like "cn.list=list(A=A,B=B)". default is nothing.
both.list	A list object, including the matrix(es) of which both column and row names will be check. both.list must be set in a format like "both.list=list(A=A,B=B)". default is nothing.
v.list	A list object, including the vector(s) of which the names will be check. v.list must be set in a format like "v.list=list(A=A,B=B)".default is nothing.
lf.list	A list object, including the list(s) of which the names will be check. lf.list must be set in a format like "lf.list=list(A=A,B=B)".default is nothing.
tree.list	A list object, including the tree(s) of which the tip.label names will be check. tree.list must be set in a format like "tree.list=list(A=A,B=B)".default is nothing.
group	a vector or one-column matrix/data.frame indicating the grouping information of samples or species, of which the sample/species names will be check.
rerank	Logic, make all names in the same rank or not. Default is TRUE
silent	Logic, whether to show messages. Default is FALSE, thus all messages will be showed.

Details

In many cases and functions, species names and samples names must be checked and set in the same rank. Sometimes, we also need to select some samples or species as necessary. This function can help.

Value

Return a list object, new matrixes with the same row/column names in the same rank. Some messages will return if some names are removed or all names matches very well.

Note

Version 3: 2017.3.13 Version 2: 2015.9.25

Author(s)

Daliang Ning

Examples

```
data(tda)
comm=tda$comm
group=tda$group
# check sample IDs
sampc=match.name(rn.list=list(com=comm,grp=group))
# output comm and group with consitent IDs.
comc=sampc$com
grpc=sampc$grp
```

---

nst.boot   *Bootstrapping test for ST and NST*

Description

To test the distribution of ST and NST in each group, and the significance of ST and NST difference between each pair of groups.

Usage

```
nst.boot(nst.result, group=NULL, rand=999, trace=TRUE,
         two.tail=FALSE, out.detail=FALSE, between.group=FALSE,
         nworker=1, SES=FALSE, RC=FALSE)
```

Arguments

nst.result	list object, the output of tNST, must have "details", thus the output.rand must be TRUE in tNST function.
group	n x 1 matrix, if the grouping is different from the nst.result. default is NULL, means to use the grouping in nst.result.
rand	integer, random draw times for bootstrapping test.
trace	logic, whether to show message when randomizing.
two.tail	logic, the p value is two-tail or one-tail.
out.detail	logic, whether to output details rather than just summarized results.
between.group	Logic, whether to calculate for between-group turnovers. default is FALSE.
nworker	for parallel computing. Either a character vector of host names on which to run the worker copies of R, or a positive integer (in which case that number of copies is run on localhost). default is 1, means not to use parallel computing.
SES	Logic, whether to perform bootstrapping test for standardized effect size (SES). SES is (observed dissimilarity - mean of null dissimilarity)/standard deviation of null dissimilarity. default is FALSE.

RC   Logic, whether to perform bootstrapping test for modified Raup-Crick metric
                                (RC). RC is percentage of null dissimilarity lower than observed dissimilarity x
                                2 - 1. default is FALSE.

Details

Normalized stochasticity ratio (NST, Ning et al 2019) is a index to estimate average stochasticity
within a group of samples. Bootstrapping is an excellent method to evaluate the statistical vari-
ation. Since the observed/null dissimilarity values are not independent (pairwise comparisons),
bootstrapping should be random draw of samples rather than the pairwise values. Bootstrapping for
stochasticity ratio (ST, Zhou et al 2014) or SES or RC can also be performed.

Value

Output is a list object, includes

summary   Index, based on ST, NST, or MST; Group, group/treatment; obs, the index value
                            of observed samples; mean, mean value of bootstrapping results; stdev, stan-
                            dard deviation; Min, minimal value; Quantile25, quantile of 25 percent; Me-
                            dian, median value; Quantile75, 75 percent quantile; Max, maximum value;
                            LowerWhisker, LowerHinge, Median, HigherHinge, HigherWhisker, values for
                            box-and-whisker plot; Outliers, outliers in bootstrapping values which out of the
                            range of 1.5 fold of IQR.

compare   Comparison between each pair of groups, and p values. p.wtest, p value from
                            wilcox.test; w.value, w value from wilcom.test; p.count, p value calculated by
                            directly comparing all values in two groups; ..noOut, means outliers were not
                            included for significance test. In principle, p.count or p.count.noOutis preferred,
                            and others have defects.

detail   a list object. ST.boot, a list of bootstrapping detail results of ST for each group,
                            each element in the list means the result of one random draw; NST.boot and
                            MST.boot, bootstrapping results of NST and MST; ST.boot.rmout, bootstrap-
                            ping results of ST without outliers; NST.boot.rmout and MST.boot.rmout, boot-
                            strapping results of NST and MST without outliers; STb.boot, NSTb.boot, MSTb.boot,
                            STb.boot.rmout, NSTb.boot.rmout, and MSTb.boot.rmout have the same mean-
                            ning but for between-group comparisons.

Note

Version 6: 2021.10.29, add bootstrapping test for SES and RC. Version 5: 2021.8.25, revised to
avoid error for special cases in MST calculation. Version 4: 2020.9.19, Add MST results into
output. Version 3: 2019.10.8, Update reference. Version 2: 2019.5.10 Version 1: 2018.1.9

Author(s)

Daliang Ning

References

Ning D., Deng Y., Tiedje J.M. & Zhou J. (2019) A general framework for quantitatively assessing ecological stochasticity. Proceedings of the National Academy of Sciences 116, 16892-16898. doi:10.1073/pnas.1904623116.

See Also

[tNST](), [nst.panova]()

Examples

```
data(tda)
comm=tda$comm
group=tda$group
tnst=tNST(comm=comm, group=group, rand=20,
          output.rand=TRUE, nworker=1)
# rand is usually set as 1000, here set rand=20 to save test time.

nst.bt=nst.boot(nst.result=tnst, group=NULL, rand=99,
                trace=TRUE, two.tail=FALSE, out.detail=FALSE,
                between.group=FALSE, nworker=1)
# rand is usually set as 999, here set rand=99 to save test time.
```

---

nst.panova	*Permutational multivariate ANOVA test for ST and NST*

Description

Permutational multivariate ANOVA test for stochasticity ratio and normalized stochasticity ratio between treatments

Usage

```
nst.panova(nst.result, group=NULL, rand=999, trace=TRUE, SES=FALSE, RC=FALSE)
```

Arguments

nst.result	list object, the output of nsto, must have "details"
group	nx1 matrix, if the grouping is different from the nst.result. default is NULL, means to use the grouping in nst.result.
rand	integer, randomization times for permuational test
trace	logic, whether to show message when randomizing.
SES	Logic, whether to perform the test for standardized effect size (SES). SES is (observed dissimilarity - mean of null dissimilarity)/standard deviation of null dissimilarity. default is FALSE.
RC	Logic, whether to perform the test for modified Raup-Crick metric (RC). RC is percentage of null dissimilarity lower than observed dissimilarity x 2 - 1. default is FALSE.

Details

PERMANOVA for stochasticity ratio (ST or NST or MST) or SES or RC is based on the comparison of F values between observed pattern and the permutated patterns where samples are randomly shuffled regardless of treatments. However, it is a bit different from PERMANOVA for dissimilarity. The PERMANOVA of stochasticity ratio here is to ask whether the ST values within a group is higher than those within another group. But the PERMANOVA of dissimilarity is to ask whether the between-group dissimilarity is higher than within-group dissimilarity.

Value

Output is a data.frame object.

index	name of index
group1	treatment/group name
group2	treatment/group name
Index.group1	index value in group1
Index.group2	index value in group2
Difference	index.group1 - index.group2
F.obs	F value
P.anova	P value of parametric ANOVA test
P.panova	P value of permutational ANOVA test
P.perm	P value of permutational test of the difference

Note

Version 7: 2021.10.29, add PERMANOVA test for SES and RC. Version 6: 2021.9.28, avoid error for special cases in permutation. Version 5: 2021.8.25, revised to avoid error for special cases in MST calculation. Version 4: 2020.10.14, debug some error when replecate number is low and edit details in help. Version 3: 2019.10.8, Update reference. Version 2: 2019.5.10 Version 1: 2017.12.30

Author(s)

Daliang Ning

References

Ning D., Deng Y., Tiedje J.M. & Zhou J. (2019) A general framework for quantitatively assessing ecological stochasticity. Proceedings of the National Academy of Sciences 116, 16892-16898. doi:10.1073/pnas.1904623116.

See Also

tNST, nst.boot

Examples

```
data(tda)
comm=tda$comm
group=tda$group
tnst=tNST(comm=comm, group=group, rand=20,
          output.rand=TRUE, nworker=1)
# rand is usually set as 1000, here set rand=20 to save test time.

nst.pova=nst.panova(nst.result=tnst, rand=99)
# rand is usually set as 999, here set rand=99 to save test time.
```

---

null.models   *Options of null model algorithms*

Description

The parameters passing to function `taxo.null` for each null model algorithm

Usage

```
data("null.models")
```

Format

A data frame with 13 rows on the following 3 variables. Rownames are null model algorithm IDs.

sp.freq character, how the species occurrence frequency will be constrainted in the null model.

samp.rich character, how the species richness in each sample will be constrainted in the null model.

swap.method character, method for fixed sp.freq and fixed samp.rich.

References

Gotelli NJ. Null model analysis of species co-occurrence patterns. Ecology 81, 2606-2621 (2000) doi:10.1890/0012-9658(2000)081[2606:nmaosc]2.0.co;2.

Examples

```
data(null.models)
```

---

pNST   *Normalized Stochasticity Ratio based on phylogenetic beta diversity*

Description

Calculate normalized stochasticity ratio according to method improved from Zhou et al (2014, PNAS), based on phylogenetic beta diversity index.

Usage

```
pNST(comm, tree=NULL, pd=NULL,pd.desc=NULL,pd.wd=NULL,pd.spname=NULL,
     group, meta.group=NULL, abundance.weighted=TRUE, rand=1000,
     output.rand=FALSE, taxo.null.model=NULL, phylo.shuffle=TRUE,
     exclude.conspecifics=FALSE, nworker=4, LB=FALSE,
     between.group=FALSE, SES=FALSE, RC=FALSE, dirichlet=FALSE)
```

Arguments

comm	matrix or data.frame, community data, rows are samples/sites, colnames are taxa (species/OTUs/ASVs)
tree	phylogenetic tree, an object of class "phylo".
pd	matrix, phylogenetic distance matrix.
pd.desc	character, the name of the file to hold the backingfile description of the phylogenetic distance matrix, it is usually "pd.desc" if using default setting in pdist.big function. If it is NULL and 'pd' is not given either, the fucntion pd.big will be used to calculate the phylogenetic distance matrix from tree, and save it in pd.wd as a big.memory file..
pd.wd	folder path, where the bigmemmory file of the phylogenetic distance matrix are saved.
pd.spname	character vector, taxa id in the same rank as the big matrix of phylogenetic distances.
group	a n x 1 matrix indicating the group or treatment of each sample, rownames are sample names. if input a n x m matrix, only the first column is used.
meta.group	a n x 1 matrix, to specify the metacommunity ID that each sample belongs to. NULL means the samples are from the same metacommunity.
abundance.weighted	
	Logic, consider abundances or not (just presence/absence). default is TRUE.
rand	integer, randomization times. default is 1000.
output.rand	Logic, whether to output dissimilarity results of each randomization. Default is FALSE.
taxo.null.model	
	Character, indicates null model algorithm to randomize the community matrix 'comm', including "EE", "EP", "EF", "PE", "PP", "PF", "FE", "FP", "FF", etc.

The first letter indicate how to constraint species occurrence frequency, the second letter indicate how to constraint richness in each sample. see null.models for details. default is NULL, means not to randomze community but just randomize the tips, i.e. phylogeny shuffle, also named taxa shuffle.

phylo.shuffle   Logic, if TRUE, the null model algorithm "taxa shuffle" (Kembel 2009) is used, i.e. shuffling taxa labels across the tips of the phylogenetic tree to randomize phylogenetic relationships among species.

exclude.conspecifics
    Logic, should conspecific taxa in different communities be exclude from MNTD calculations? default is FALSE.

nworker   for parallel computing. Either a character vector of host names on which to run the worker copies of R, or a positive integer (in which case that number of copies is run on localhost). default is 4, means 4 threads will be run.

LB   logic, whether to use a load balancing version of parallel computing code.

between.group   Logic, whether to calculate stochasticity for between-group turnovers. default is FALSE.

SES   Logic, whether to calculate standardized effect size, which is (observed dissimilarity - mean of null dissimilarity)/standard deviation of null dissimilarity. default is FALSE.

RC   Logic, whether to calculate modified Raup-Crick metric, which is percentage of null dissimilarity lower than observed dissimilarity x 2 - 1. default is FALSE.

dirichlet   Logic. If TRUE, the taxonomic null model will use Dirichlet distribution to generate relative abundances in randomized community matrix. If the input community matrix has all row sums no more than 1, the function will automatically set dirichlet=TRUE. default is FALSE.

Details

NST is a metric to estimate ecological stochasticity based on null model analysis of dissimilarity (Ning et al 2019). NST is improved from previous index ST (Zhou et al 2014). Modified stochasticity ratio (MST) is also calculated (Liang et al 2020; Guo et al 2018), which can be regarded as a spcial transformation of NST under assumption that observed similarity can be equal to mean of null similarity under pure stochastic assembly.

pNST is NST based on phylogenetic beta diversity (Ning et al 2019, Guo et al 2018), here, beta mean nearest taxon distance (bMNTD). pNST showed better performance in stochasticity estimation than tNST in some cases (Ning et al 2020).

Value

Output is a list. Please DO NOT use NST.ij values in index.pair.grp and index.between.grp which can be out of [0,1] without ecologcial meanning. Please use nst.boot to get variation of NST.

index.pair   indexes for each pairwise comparison. D.ij, observed dissimilarity, not standardized; G.ij, average null expectation of dissimilarity, not standardized; Ds.ij, observed dissimilarity, standardized to range from 0 to 1; Gs.ij, average null expectation of dissimilarity, standardized; C.ij and E.ij are similarity and average

null expectation of simmilarity, standardized if the dissimilarity has no fixed upper limit; ST.ij, stochasticity ratio calculated by previous method (Zhou et al 2014); MST.ij, modified stochasticity ratio calculated by a modified method (Liang et al 2020; Guo et al 2018); bNTI, beta nearest taxon index, i.e. standard effect size of difference between observed and null betaMNTD (Webb et al 2008); RC.bMNTD, modified Roup-Crick metrics (Chase et al 2011) but based on betaMNTD.

index.grp   mean value of each index in each group. group, group name; size, number of pairwise comparisons in this group; ST.i, group mean of stochasticity ratio, not normalized; NST.i, group mean of normalized stochasticity ratio; MST.i, group mean of modified stochasticity ratio; SES.i, group mean of standard effect size (bataNTI); RC.i, group mean of modified Roup-Crick metric.

index.pair.grp   pairwise values of each index in each group. group, group name; C.ij, E.ij, ST.ij, MST.ij, SES.ij (i.e. bNTI), and RC.ij have the same meaning as in index.pair; NST.ij, the pairwise values of NST, for reference only, DO NOT use. Since NST is normalized ST calculated from ST.ij, NST pairwise values NST.ij have no ecological meaning. Variation of NST from bootstrapping test is preferred, see nst.boot.

index.between   mean value of each index between each two groups. Similar to index.grp, but calcualted from comparisons between each two groups.

index.pair.between
                 pairwise values of each index between each two groups. Similar to index.pair.grp, but calcualted from comparisons between each two groups.

Dmax   The maximum or upper limit of dissimilarity before standardized, which is used to standardize the dissimilarity with upper limit not equal to one.

dist.method   dissimilarity index name.

details   detailed results. rand.mean, mean of null dissimilarity for each pairwise comparison, not standardized; Dmax, the maximum or upper limit of dissimilarity before standardized; obs3, observed dissimilarity, not standardized; dist.ran, alll null dissimilarity values, each row is a pairwise comparison, each column is results from one randomization; group, input group informaiton; meta.group, input metacommunity information.

Note

Version 6: 2021.10.29, add summary of SES (i.e. betaNTI) and RC. Version 5: 2021.8.25, revised to avoid error for special cases in MST calculation. Version 4: 2021.4.16, add option dirichlet, to allow input community matrix with relative abundances (proportion) rather than integer counts. Version 3: 2020.9.9, remove setwd; change dontrun to donttest and revise save.wd in help doc. Version 2: 2020.8.22, add to NST package, update help document. Version 1: 2018.1.9

Author(s)

Daliang Ning

References

Ning D., Deng Y., Tiedje J.M. & Zhou J. (2019) A general framework for quantitatively assessing ecological stochasticity. Proceedings of the National Academy of Sciences 116, 16892-16898. doi:10.1073/pnas.1904623116.

Zhou J, Deng Y, Zhang P, Xue K, Liang Y, Van Nostrand JD, Yang Y, He Z, Wu L, Stahl DA, Hazen TC, Tiedje JM, and Arkin AP. (2014) Stochasticity, succession, and environmental perturbations in a fluidic ecosystem. Proceedings of the National Academy of Sciences of the United States of America 111, E836-E845. doi:10.1073/pnas.1324044111.

Liang Y, Ning D, Lu Z, Zhang N, Hale L, Wu L, Clark IM, McGrath SP, Storkey J, Hirsch PR, Sun B, and Zhou J. (2020) Century long fertilization reduces stochasticity controlling grassland microbial community succession. Soil Biology and Biochemistry 151, 108023. doi:10.1016/j.soilbio.2020.108023.

Guo X, Feng J, Shi Z, Zhou X, Yuan M, Tao X, Hale L, Yuan T, Wang J, Qin Y, Zhou A, Fu Y, Wu L, He Z, Van Nostrand JD, Ning D, Liu X, Luo Y, Tiedje JM, Yang Y, and Zhou J. (2018) Climate warming leads to divergent succession of grassland microbial communities. Nature Climate Change 8, 813-818. doi:10.1038/s41558-018-0254-2.

Webb, C.O., Ackerly, D.D. & Kembel, S.W. (2008). Phylocom: software for the analysis of phylogenetic community structure and trait evolution. Bioinformatics, 24, 2098-2100.

Chase JM, Kraft NJB, Smith KG, Vellend M, and Inouye BD. (2011) Using null models to disentangle variation in community dissimilarity from variation in alpha-diversity. Ecosphere 2, art24. doi:10.1890/es10-00117.1.

Ning, D., Yuan, M., Wu, L., Zhang, Y., Guo, X., Zhou, X. et al. (2020). A quantitative framework reveals ecological drivers of grassland microbial community assembly in response to warming. Nature Communications, 11, 4717.

See Also

tNST, nst.boot, nst.panova

Examples

```
data("tda")
comm=tda$comm
group=tda$group
tree=tda$tree

# since it needs to save some file to a certain folder,
# the following code is set as 'not test'.
# but you may test the code on your computer
# after change the folder path for 'save.wd'.

  save.wd=tempdir() # please change to the folder you want to use.
  nworker=2 # parallel computing thread number
  rand.time=20 # usually use 1000 for real data.
  pnst=pNST(comm=comm, tree=tree, group=group,
            pd.wd=save.wd, rand=rand.time, nworker=nworker)
```

taxo.null	*Null models of taxonomic beta diversity*

Description

to randomize the taxonomic structures based on one of various null model algorithms.

Usage

```
taxo.null(comm,sp.freq=c("not","equip","prop","prop.ab","fix"),
          samp.rich=c("not","equip","prop","fix"),
          swap.method=c("not","swap","tswap","quasiswap",
                        "backtrack"),burnin=0,
          abundance=c("not","shuffle","local","region"),
          region.meta=NULL,region.freq=NULL,dirichlet=FALSE)
```

Arguments

comm	matrix, community data, rownames are sample/site names, colnames are species names
sp.freq	character, the constraint of species occurrence frequency when randomizing taxonomic structures, see details.
samp.rich	character, the constraint of sample richness when randomizing taxonomic structures, see details.
swap.method	character, the swap method for fixed sp.freq and fixed samp.rich, see [commsim](#) for details.
burnin	Nonnegative integer, specifying the number of steps discarded before starting simulation. Active only for sequential null model algorithms. Ignored for non-sequential null model algorithms. also see [nullmodel](#).
abundance	character, the method to draw individuals (abundance) into present species when randomizing taxonomic structures, see details.
region.meta	a numeric vector, to define the (relative) abundance of each species in metacommunity/regional pool. The names should be species IDs. If no name, it should be in exact the same order as columns of comm. Default is NULL, the relative abundance in metacommunity will be calculated from comm.
region.freq	a numeric vector, to define the occurrence frequency of each species in metacommunity/regional pool. The names should be species IDs. If no name, it should be in exact the same order as columns of comm. Default is NULL, the occurrence frequency in metacommunity will be calculated from comm. If sp.freq='fix', the input region.freq must be integers. If sp.freq='fix' and samp.rich='fix', since no applicable algorithm now, region.freq will be ignored.
dirichlet	Logic. If TRUE, the taxonomic null model will use Dirichlet distribution to generate relative abundances in randomized community matrix. If the input community matrix has all row sums no more than 1, the function will automatically set dirichlet=TRUE. default is FALSE.

Details

This function returns a randomized community dataset (one time randomization), used by the function tNST. The null models differentiated by how to deal with species occurrence frequency (sp.freq), species richness in each sample (samp.rich), relative abundances (abundance), and which swap method used if both sp.freq and samp.rich are fixed.

Options of sp.freq and samp.rich (Gotelli 2000): not: the whole co-occurrence pattern (present/absent) is not randomized; equip: all the species or samples have equal probability when randomizing; prop: randomization according to probability proportional to observed species occurrence frequency or sample richness; prop.ab: randomization according to probability proportional to observed regional abundance sum of each species, only for sp.freq; fix: randomization maintains the species occurrence frequency or sample richness exactly the same as observed.

Options of abundance: not: not abundance weighted; shuffle: randomly assign observed abundance values of observed species in a sample to species in this sample after the present/absent pattern has been randomized, thus shuffle can only be used if the richness is fixed. Similar to "richness" algorithm in R package picante (Kembel et al 2010); local: randomly draw individuals into randomized species in a sample on the probablities proportional to observed species-abundance-rank curve in this sample. If randomized species number in this sample is more than observed, the probabilities of exceeding species will be proportional to observed minimum abundance. If randomized species number (rN) in this sample is less than observed, the probabilities will be proportional to the observed abundances of top rN observed species. The rank of randomized species in a sample is randomly assigned. region: randomly draw individuals into each ranodmized species in each sample on the probabilities proportional to observed relative abundances of each species in the whole region, as described previously (Stegen et al 2013).

Value

a matrix of community data, e.g. an randomized OTU table, is returned. Rownames are sample/site names, and colnames are species names.

Note

Version 3: 2021.5.11, add option region.freq to specify occurrence frequency in regional pool. Version 2: 2021.4.16, add option dirichlet to handle community matrix with relative abundance values rather than counts. Version 1: 2015.10.22

Author(s)

Daliang Ning

References

Gotelli NJ. Null model analysis of species co-occurrence patterns. Ecology 81, 2606-2621 (2000) doi:10.1890/0012-9658(2000)081[2606:nmaosc]2.0.co;2.

Kembel SW, Cowan PD, Helmus MR, Cornwell WK, Morlon H, Ackerly DD, Blomberg SP, and Webb CO. Picante: R tools for integrating phylogenies and ecology. Bioinformatics 26, 1463-1464 (2010) doi:10.1093/bioinformatics/btq166.

Stegen JC, Lin X, Fredrickson JK, Chen X, Kennedy DW, Murray CJ, Rockhold ML, and Konopka A. Quantifying community assembly processes and identifying features that impose them. Isme Journal 7, 2069-2079 (2013).

Others cited in `commsim`.

See Also

`tNST`, `ab.assign`, `null.models`

Examples

```
data(tda)
comm=tda$comm
comm.rand=taxo.null(comm,sp.freq="prop",samp.rich="fix",abundance="region")
```

---

tda   *Test dataset A*

Description

A simple test data with a community matrix and treatment information

Usage

```
data("tda")
```

Format

A list object with 3 elements.

comm matrix, community table; each row is a sample, thus rownames are sample IDs; each column is a taxon, thus colnames are OTU IDs.

group matrix with only one column. treatment information; rownames are sample IDs; the only column shows treatment IDs.

tree phylogenetic tree.

Examples

```
data(tda)
comm=tda$comm
group=tda$group
```

---

tNST | *Taxonomic Normalized Stochasticity Ratio (tNST)*

Description

Calculate normalized stochasticity ratio (NST) based on specified taxonomic dissimilarity index and null model algorithm.

Usage

```
tNST(comm, group, meta.group=NULL,
     meta.com=NULL,meta.frequency=NULL,
     dist.method="jaccard", abundance.weighted=TRUE,
     rand=1000, output.rand=FALSE, nworker=4,
     LB=FALSE, null.model="PF", dirichlet=FALSE,
     between.group=FALSE, SES=FALSE, RC=FALSE,
     transform.method=NULL, logbase=2)
```

Arguments

comm
: matrix or data.frame, local community data, each row is a sample or site, each colname is a species or OTU or gene, thus rownames should be sample IDs, colnames should be taxa IDs.

group
: matrix or data.frame, a one-column (n x 1) matrix indicating the group or treatment of each sample, rownames are sample IDs. if input a n x m matrix, only the first column is used. Attention: different group setting will change NST values.

meta.group
: matrix or data.frame, a one-column (n x 1) matrix indicating which metacommunity each sample belongs to. rownames are sample IDs. first column is metacommunity IDs. Such that different samples can belong to different metacommunities. If input a n x m matrix, only the first column is used. NULL means all samples belong to the same metacommunity. Default is NULL.

meta.com
: matrix or data.frame, metacommunity relative abundance data. Each row can be a sample or a metacommunity, thus rownames are sample IDs or metacommunity IDs. Such that the relative abundance of each taxa in metacommunity can be set different from the average relative abundance in the observed samples. This can be useful for uneven sampling design. NULL means the relative abundance of each taxa in the metacommunity can be directly calculated from the local community data (comm). Default is NULL.

meta.frequency
: matrix or data.frame, metacommunity occurrence frequency data. Each row can be a samlple or a metacommunity, thus rownames are sample IDs or metacommunity IDs. Such that the occurrence frequency of each taxa in metacommunity can be set different from the occurrence frequency in the observed samples. This can be useful for uneven sampling design. If null.model is "FE" or "FP", the values in meta.frequency must be integers. If null.model is "FF", since no applicable algorithm now, meta.frequency will be ignored. Default is NULL, means the occurrence frequency of each taxa in the metacommunity can be directly calculated from the observed data (comm).

dist.method   A character indicating dissimilarity index, including "manhattan","mManhattan",
                "euclidean","mEuclidean", "canberra", "bray", "kulczynski", "jaccard", "gower",
                "altGower", "mGower", "morisita", "horn", "binomial", "chao", "cao". default
                is "jaccard"

abundance.weighted
                Logic, consider abundances or not (just presence/absence). default is TRUE.

rand   integer, randomization times. default is 1000

output.rand   Logic, whether to output dissimilarity results of each randomization. Default is
                FALSE.

nworker   for parallel computing. Either a character vector of host names on which to run
                the worker copies of R, or a positive integer (in which case that number of copies
                is run on localhost). default is 4, means 4 threads will be run.

LB   Logic, whether to use a load balancing version for parallel computation. If
                TRUE, this can result in better cluster utilization, but increased communication
                can reduce performance. default is FALSE.

null.model   Character, indicates null model algorithm, including "EE", "EP", "EF", "PE",
                "PP", "PF", "FE", "FP", "FF", etc. The first letter indicate how to constraint
                species occurrence frequency, the second letter indicate how to constraint rich-
                ness in each sample. see null.models for details. default is "PF".

dirichlet   Logic. If TRUE, the taxonomic null model will use Dirichlet distribution to gen-
                erate relative abundances in randomized community matrix. If the input com-
                munity matrix has all row sums no more than 1, the function will automatically
                set dirichlet=TRUE. default is FALSE.

between.group   Logic, whether to calculate stochasticity for between-group turnovers. default
                is FALSE.

SES   Logic, whether to calculate standardized effect size, which is (observed dis-
                similarity - mean of null dissimilarity)/standard deviation of null dissimilarity.
                default is FALSE.

RC   Logic, whether to calculate modified Raup-Crick metric, which is percentage of
                null dissimilarity lower than observed dissimilarity x 2 - 1. default is FALSE.

transform.method
                character or a defined function, to specify how to transform community matrix
                before calculating dissimilarity. if it is a characher, it should be a method name
                as in the function 'decostand' in package 'vegan', including 'total','max','freq','normalize','range','standa

logbase   numeric, the logarithm base used when transform.method='log'.

Details

NST is a metric to estimate ecological stochasticity based on null model analysis of dissimilarity. It
is improved from previous index ST (Zhou et al 2014). Detailed description is in Ning et al (2019).
Modified stochasticity ratio (MST) is also calculated (Liang et al 2020; Guo et al 2018), which can
be regarded as a spcial transformation of NST under assumption that observed similarity can be
equal to mean of null similarity under pure stochastic assembly.

Value

Output is a list. Please DO NOT use NST.ij values in index.pair.grp and index.between.grp which can be out of [0,1] without ecologcial meanning. Please use nst.boot to get variation of NST.

index.pair   indexes for each pairwise comparison. D.ij, observed dissimilarity, not standardized; G.ij, average null expectation of dissimilarity, not standardized; Ds.ij, observed dissimilarity, standardized to range from 0 to 1; Gs.ij, average null expectation of dissimilarity, standardized; C.ij and E.ij are similarity and average null expectation of simmilarity, standardized if the dissimilarity has no fixed upper limit; ST.ij, stochasticity ratio calculated by previous method (Zhou et al 2014); MST.ij, modified stochasticity ratio calculated by a modified method (Liang et al 2020; Guo et al 2018); SES.ij, standard effect size of difference between observed and null dissimilarity (Kraft et al 2011); RC.ij, modified Roup-Crick metrics (Chase et al 2011, Stegen et al 2013).

index.grp   mean value of each index in each group. group, group name; size, number of pairwise comparisons in this group; ST.i, group mean of stochasticity ratio, not normalized; NST.i, group mean of normalized stochasticity ratio; MST.i, group mean of modified stochasticity ratio; SES.i, group mean of standard effect size; RC.i, group mean of modified Roup-Crick metric.

index.pair.grp   pairwise values of each index in each group. group, group name; C.ij, E.ij, ST.ij, MST.ij, SES.ij, and RC.ij have the same meaning as in index.pair; NST.ij, the pairwise values of NST, for reference only, DO NOT use. Since NST is normalized ST calculated from ST.ij, NST pairwise values NST.ij have no ecological meaning. Variation of NST from bootstrapping test is preferred, see nst.boot.

index.between   mean value of each index between each two groups. Similar to index.grp, but calcualted from comparisons between each two groups.

index.pair.between

pairwise values of each index between each two groups. Similar to index.pair.grp, but calcualted from comparisons between each two groups.

Dmax   The maximum or upper limit of dissimilarity before standardized, which is used to standardize the dissimilarity with upper limit not equal to one. See beta.limit for details.

dist.method   dissimilarity index name.

details   detailed results. rand.mean, mean of null dissimilarity for each pairwise comparison, not standardized; Dmax, the maximum or upper limit of dissimilarity before standardized; obs3, observed dissimilarity, not standardized; dist.ran, alll null dissimilarity values, each row is a pairwise comparison, each column is results from one randomization; group, input group informaiton; meta.group, input metacommunity information.

Note

Version 6: 2021.10.29, add summary of SES and RC. Version 5: 2021.8.25, revised to avoid error for special cases in MST calculation. Version 4: 2021.5.11, add option meta.frequency, to specify occurrence frequency in regional pool. Version 3: 2021.4.16, add option dirichlet, transform.method, and logbase, to allow input community matrix with relative abundances (value<1)

and community data transformation before dissimilarity calculation. Version 2: 2019.10.8, Updated references. Emphasize that NST variation should be calculated from nst.boot rather than pairwise NST.ij from tNST. Emphasize that different group setting may lead to different NST results. Version 1: 2019.5.10

Author(s)

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See Also

nst.boot, nst.panova, taxo.null, beta.limit, pNST

Examples

```
data(tda)
comm=tda$comm
group=tda$group
tnst=tNST(comm=comm, group=group, meta.group=NULL, meta.com=NULL,
        dist.method="jaccard", abundance.weighted=TRUE, rand=20,
        output.rand=FALSE, nworker=1, LB=FALSE, null.model="PF",
```

```
          between.group=TRUE, SES=TRUE, RC=TRUE)
# rand is usually set as 1000, here set rand=20 to save test time.
tnst.sum=tnst$NSTi
```

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