

rich

September 29, 2010

comp2cv

Compare 2 cumulated values %% ~~function to do ... ~~

Description

Compares 2 cumulated richnesses using a randomization test

Usage

```
comp2cv(pop1, pop2, nrandom, pr1 = 0.025, pr2 = 0.975, name.session = "session",  
        verbose = TRUE)
```

Arguments

pop1	A matrix for population 1.
pop2	A matrix for population 2.
nrandom	Number of randomizations to perform.
pr1	Lower probability level for quantile computations (default=0.025).
pr2	Higher probability level for quantile computations (default=0.975).
name.session	A name for the session (optional).
verbose	If TRUE, the function returns the randomized values.

Details

If the observed value for population 1 *latex* observed value for population 2, `comp2mean` returns a probability `p` estimated as the number of randomizations for which the observed value for population 1 *latex* observed value for population 2 divided by the number of randomization + 1. Similarly, if the observed value for population 1 *latex* observed value for population 2, `p` corresponds to the frequency of such situation in the randomizations.

Value

`res` A data frame showing the outputs of the randomization test:

- `obs. cv pop1` Observed cumulated richness for population 1.
- `obs. cv pop2` Observed cumulated richness for population 2.
- `cv1-cv2` Difference between observed cumulated richness of population 1 and population 2.
- `p` Probability of encountering such a `cv1-cv2` (see details above).
- `quantile for pr1` Quantile value for probability level `pr1`. If `obs. cv pop1` *latex* `obs. cv pop2`.
- `quantile for pr2` Quantile value for probability level `pr2`.
- `randomized cv1-cv2` Mean values of randomized and the observed values.
- `nrandom` Number of randomizations used in the test.

`rand` A vector of `nrandom+1` values corresponding to the `Nrandom` randomized values of `cv1-cv2` *plus* the corresponding observed value. `rand` is available if `verbose == TRUE`.

Author(s)

Jean-Pierre Rossi, <jean-pierre.rossi@supagro.inra.fr>

See Also

[comp2mean](#), [rich](#), [compshared](#)

Examples

```
##Random data matrix
a<-matrix(data=rpois(80,0.45), ncol=8, nrow=10)
colnames(a) <- c("a","b","c","d","e","f","g","h")
rownames(a) <- c("unit01","unit02","unit03","unit04",
"unit05","unit06","unit07","unit08","unit09","unit10")
pop1<-a[1:6,] ; pop2<-a[7:10,]
#compare population 1 and population 2
comp2cv(pop1=pop1,pop2=pop2,nrandom=10,pr1=0.025,
pr2=0.975,name.session="session",verbose=TRUE)

#comparison of species richness of 2 populations
a<-matrix(data=c(1,0,1,2,2,1,1,2,0,3,0,0,0,0,1,0,0,0,
0,0,2,0,1,0,1,1,0,1,0,0,0,1,0,0,0,1,2,1,0,0,0,0,0,0,
0,0,2,0,0,0,0,0,1,0,1,0,0,0,0,0,0,0,2,0,0,0,0,0,0,0,0,
1,0,0,0,0,0,
0,0,0,0,1), ncol=8, nrow=10)
colnames(a) <- c("a","b","c","d","e","f","g","h")
rownames(a) <- c("unit01","unit02","unit03","unit04",
"unit05","unit06","unit07","unit08","unit09","unit10")
pop1<-a[1:6,] ; pop2<-a[7:10,]
#compare population 1 and population 2
compare2vc_random(pop1=pop1,pop2=pop2,Nrandom=10,pr1=0.025,
```

```

pr2=0.975,name.session="session",verbose=TRUE)
##end

#comparison of allelic richness of 2 populations
## construct population 1
#locus 1
l1a1<-c(10,10,10,20)
l1a2<-c(20,10,30,30)
#locus 2
l2a1<-c(100,100,100,200)
l2a2<-c(200,100,300,400)
pop1<-cbind(l1a1,l1a2, l2a1,l2a2)
## construct population 2
#locus 1
l1a1<-c(11,10,15,20)
l1a2<-c(20,11,30,30)
#locus 2
l2a1<-c(100,101,101,200)
l2a2<-c(200,100,301,400)
pop2<-cbind(l1a1,l1a2, l2a1,l2a2)
## population 1 plus 2
pop12<-rbind(pop1,pop2)
## create suitable data set using loc2rich
p12<-loc2rich(pop12)
a1<-dim(pop1)[1] ; a2<-dim(pop2)[1]
pop1<-p12$loci[1:a1,] ; pop2<-p12$loci[(a1+1):(a1+a2),]
#compare population 1 and population 2
compare2vc_random(pop1=pop1,pop2=pop2,Nrandom=10,verbose=TRUE)

#Another example with real data
data(leirial)
w<-loc2rich(leirial$data, rowlabels=leirial$labels)
##working with the second locus, PP42
a<-w$locus[[2]][which(leirial$labels=="leiria_winter"),-dim(w$locus[[2]])[2]]
b<-w$locus[[2]][which(leirial$labels=="leiria_summer"),-dim(w$locus[[2]])[2]]
out<-comp2cv(pop1=a,pop2=b,nrandom=99,verbose=TRUE)
## observed difference in red
hist(out$rand);abline(v=out$rand[length(out$rand)], col="red")
##end

```

comp2mean

Compares 2 mean values using a randomization test.

Description

Mean values of 2 populations are compared using a randomization procedure. Overlapping populations are allowed.

Usage

```
comp2mean(pop1.vec, pop2.vec, pop3.vec = NULL, nrandom, pr1 = 0.025,
pr2 = 0.975, name.session = "session", verbose = TRUE)
```

Arguments

pop1.vec	A vector with the observed values for population 1.
pop2.vec	A vector with the observed values for population 2.
pop3.vec	A vector with the observed values that are common to population 1 and 2.
nrandom	Number of randomizations to perform.
pr1	Lower probability level for quantile computations (default=0.025).
pr2	Higher probability level for quantile computations (default=0.975).
name.session	A name for the session (optional).
verbose	If TRUE, the function returns the randomized values

Details

Simple randomization tests compares the average values of 2 populations by randomly allocating observed values (manly, 1997). In some cases, populations share some observed values: for example if we compare the mean annual temperature of sites where either species A or B is present and if A and B are sympatric in some localities (see example below). Those shared values are passed to `comp2mean` by the argument `pop3.vec`.

If the mean value for population 1 *latex* mean value for population 2, p is the number of randomizations for which the mean value for population 1 *latex* mean value for population 2 divided by the number of randomizations + 1. If the mean value for population 1 *latex* mean value for population 2, p is the number of randomizations for which the mean value for population 1 *latex* mean value for population 2 divided by the number of randomizations + 1. If *latex* p is not computed ($p=NC$).

Value

res	<p>A data frame showing the outputs of the randomization test:</p> <pre>obs. mv pop1 Observed mean values over samples forming population 1. obs. mv pop2 Observed mean values over samples forming population 2. mv1-mv2 Difference between observed mean values of population 1 and population 2. p . Probability of observing mv1-mv2 (see details above). quantile for pr1 Quantile value for probability level pr1. quantile for pr2 Quantile value for probability level pr2. randomized cv1-cv2 Mean values of randomized and the observed values. nrandom Number of randomizations used in the test.</pre>
rand	<p>A vector of <code>Nrandom+1</code> values corresponding to the <code>nrandom</code> randomized values of <code>cv1-cv2</code> <i>plus</i> the corresponding observed value. <code>rand</code> is available if <code>verbose == TRUE</code>.</p>

Note

The observed difference between populations is included in the numerator and the denominator when computing the probability p . This is justified because if the null hypothesis (there is no difference between populations) is true then the observed difference between populations is just another value for the randomization distribution (Manly, 1997, p. 7).

Author(s)

Jean-Pierre Rossi, <jean-pierre.rossi@supagro.inra.fr>

References

Manly, B.F.J. (1997). Randomization and Monte Carlo methods in biology. Chapman & Hall.

See Also

[comp2mcv](#), [rich](#)

Examples

```
# The example of mandible length of male and female golden jackals from Manly (1997),
# p.4.
males<-c(120, 107, 110, 116, 114, 111, 113, 117, 114, 112)
females<-c(110, 111, 107, 108, 110, 105, 107, 106, 111, 111)
comp2mean(pop1.vec=males,pop2.vec=females,nrandom=99,
  name.session="golden jackals - Manly (1997) p.4")

# Maximum temperature in a set of sites where the beetle Tomicus destruens
# or T. piniperda are present. Both species are present at 4 sites.
data(Tomicus)
comp2mean(pop1.vec=Tomicus$destruens,pop2.vec=Tomicus$piniperda,
  pop3.vec=Tomicus$both, nrandom=99)

###using comp2mean with outputs of rich
a<-matrix(data=rpois(100,2), ncol=10, nrow=10)
b<-matrix(data=rpois(100,0.5), ncol=10, nrow=10)
x<-rich(matrix(data=rpois(30,2), ncol=5, nrow=6),
  nrandom=50,verbose=TRUE)
y<-rich(matrix(data=rpois(30,0.5), ncol=5, nrow=6),
  nrandom=50,verbose=TRUE)
comp2mean(pop1.vec=x$sumrow,pop2.vec=y$sumrow,
  nrandom=100,verbose=FALSE)
```

Description

Shared species or alleles are common to pairs of sites or populations. `compshared` computes the observed shared richness for couples of site or populations. Shared richness is expressed either in absolute value or as the ratio to the observed richness in each site/population. These values are compared to the corresponding expected values under the hypothesis of no difference between sites or populations.

Usage

```
function(lmatrix, nrandom=99, pr1=0.05, pr2=0.10,
name.session="session", verbose=TRUE)
```

Arguments

<code>lmatrix</code>	A list with two components: matrices corresponding to the sites/populations to compare.
<code>nrandom</code>	Number of randomizations to be performed. Default fixed to 99.
<code>pr1</code>	First probability level used to compute the quantile values of the randomized data sets.
<code>pr2</code>	Second probability level used to compute the quantile values of the randomized data sets.
<code>name.session</code>	A string that can be used to describe the analysis.
<code>verbose</code>	If <code>verbose</code> is set to <code>TRUE</code> <code>compshared</code> returns an additional data frame that contains the observed and randomized richnesses.

Value

<code>res</code>	<p>A data frame with the summary statistics for the observed and randomized data:</p> <p><code>obs shared</code> Observed shared richness.</p> <p><code>obs shared first quantile</code> First quantile for randomized shared richness.</p> <p><code>obs shared second quantile</code> Second quantile for randomized shared richness.</p> <p><code>obs S1</code> Richness of population 1.</p> <p><code>obs S2</code> Richness of population 2.</p> <p><code>shared/S1</code> Ratio of shared richness to richness of population 1.</p> <p><code>shared/S1 first quantile</code> First quantile for the ratio of randomized shared richness to richness of population 1.</p> <p><code>shared/S1 second quantile</code> Second quantile for the ratio of randomized shared richness to richness of population 1.</p> <p><code>shared/S2</code> Ratio of shared richness to richness of population 2.</p> <p><code>shared/S2 first quantile</code> First quantile for the ratio of randomized shared richness to richness of population 2.</p> <p><code>shared/S2 second quantile</code> Second quantile for the ratio of randomized shared richness to richness of population 2.</p> <p><code>nrandom</code> Number of randomization.</p>
------------------	---

```

rand      Data frame with the raw outputs from the randomisations (returned only if
          verbose==TRUE):
pop1      Richness of population 1.
pop2      Richness of population 2.
shared     Shared richness between population 1 and 2.
shared_pop1  Ratio of the shared richness to the richness of population 1.
shared_pop2  Ratio of the shared richness to the richness of population 2.

```

Warning

The approach behind the calculations of this function are still in development.

Note

A low shared richness may be simply explained by marked differences in richness between sites/populations. Such differences can be tested using [comp2cv](#). In such a case, the relatives richnesses should be used (see example below).

Author(s)

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See Also

[shared](#), [comp2cv](#)

Examples

```

# simple example
sp1<-c(1,2,3,4,5)
sp2<-c(0,0,0,0,0)
sp3<-c(1,1,0,0,0)
sp4<-c(0,0,0,0,0)
site1<-cbind(sp1, sp2, sp3, sp4)
colnames(site1)<-c("sp1", "sp2", "sp3", "sp4")
sp1<-c(1,2,3)
sp2<-c(1,0,0)
sp3<-c(0,0,0)
sp4<-c(0,0,0)
site2<-cbind(sp1, sp2, sp3, sp4)
colnames(site2)<-c("sp1", "sp2", "sp3", "sp4")
data<-list(site1,site2)
names(data)<-c("site1","site2")
compshared(data, nrandom = 99, verbose = T)

#More realistic data set: sites highly differ by their richness.
data(leiria1)
w<-loc2rich(leiria1$data, rowlabels=leiria1$labels)
##working with the second locus, PP42
a<-w$locus[[2]][which(leiria1$labels=="leiria_winter"),-dim(w$locus[[2]])[2]]

```

```

b<-w$locus[[2]][which(leiria1$labels=="leiria_summer"),-dim(w$locus[[2]])[2]]
data<-list(a,b)
names(data)<-c("leiria_winter","leiria_summer")

#Populations differ by their associated richness:
comp2cv(pop1=a,pop2=b,nrandom=99,verbose=FALSE)

s<-compshared(data, nrandom = 999, verbose = T)

layout(matrix(c(1:3),3,1))
hist(s$rand$shared)
abline(v=s$rand$shared[length(s$rand$shared)], col="red")
abline(v=s$res[2,1], col="blue")
abline(v=s$res[3,1], col="green")

hist(s$rand$shared_pop1)
abline(v=s$rand$shared_pop1[length(s$rand$shared_pop1)], col="red")
abline(v=s$res[7,1], col="blue")
abline(v=s$res[8,1], col="green")

hist(s$rand$shared_pop2)
abline(v=s$rand$shared_pop2[length(s$rand$shared_pop2)], col="red")
abline(v=s$res[10,1], col="blue")
abline(v=s$res[11,1], col="green")
layout(1)
#Pop 1 shares a lower proportion of alleles while Pop 2 shares all its alleles.
# The significant departure from expectations under the null hypothesis of
# no difference between populations observed for population 1 is explained
# by a strong difference in richness. Pop 2 is a impoverished sub-sample
# of population 1.

```

ef

Soil macrofauna in a tropical forest site (Elahe, French Guyana).

Description

The `ef` data set is a data frame describing the species abundance of soil macrofauna in a set of soil samples collected in a secondary forest in French Guyana. These data were collected in the vicinity of the Wayana village of Elahe situated on the Tampoc river.

Usage

```
data(ef)
```

Format

`ef` is a data frame of observation of 121 species (columns) at 30 sampling locations (rows).

Source

J.P. Rossi, L. Celini, P. Mora, J. Mathieu, E. Lapied, J. Nahmani, J.-F. Ponge, P. Lavelle (2010). Decreasing fallow duration in tropical slash-and-burn agriculture alters soil macro-invertebrate diversity: A case study in southern French Guiana. *Agriculture, Ecosystems and Environment* 135, 148-154.

Examples

```
## Estimating species richness using \code{\link{rich}}
data(ef)
rich(matrix=ef)
```

leirial	<i>Microsatellite data for individuals from 2 populations of pine processionary moth <i>Thaumetopoea pityocampa</i></i>
---------	---

Description

`leirial` contains the microsatellite data for individuals sampled within 2 populations of the pine processionary moth *Thaumetopoea pityocampa* at the locus PP07 and PP42. The data consists of a list of 2 items:

`data` A data frame with all locus and alleles. Each locus is represented by 2 juxtaposed columns.
`labels` A vector with the label of each individual (i.e. the name of the population from which each individual originates).

Usage

```
data(leirial)
```

Source

H. Santos, J. Rousselet, E. Magnoux, M.R. Paiva, M. Branco, C. Kerdelhue (2007). Genetic isolation through time: allochronic differentiation of a phenologically atypical population of the pine processionary moth. *Proceedings of the Royal Society of London Series B* 274, 935-941.

Examples

```
data(leirial)
loc2rich(leirial$data, rowlabels=leirial$labels)

#using loc2rich to compare cumulated allelic richness using comp2cv
data(leirial)
w<-loc2rich(leirial$data, rowlabels=leirial$labels)
##working with the second locus, PP42
a<-w$locus[[2]][which(leirial$labels=="leiria_winter"),]
b<-w$locus[[2]][which(leirial$labels=="leiria_summer"),]
comp2cv(pop1=a, pop2=b, nrandom=99)
```

loc2rich	<i>Converts individual by locus data matrix to individual by allele matrix. Suitable for diploid organisms. %% ~~function to do ... ~~</i>
----------	--

Description

loc2rich converts genetic data matrix showing individuals as rows and locus as columns into a simple individuals by alleles data table. The resulting data matrix is suitable for analyses using [rich](#).

Usage

```
loc2rich(matrix, rowlabels=NULL)
```

Arguments

matrix	A data matrix with individuals as rows and locus as columns. Each locus must be described by 2 columns (diploid organisms). <code>rowlabels</code> is an optional vector indicating a label (e.g. population of origin) of each individual (rows).
--------	--

Details

loc2rich creates an output giving a general data matrix with individuals as rows and alleles as columns. Alleles are ordered in function of their occurrence in the input data matrix for each locus. The function also returns a simple data table for each locus corresponding to the individual by allele matrix. loc2rich handles null alleles or missing values. When NA are present in `matrix`, loc2rich removes the corresponding individuals (see below).

Value

A list with the following components:

loci	A $i \times k$ data matrix with individuals i as rows and alleles k as columns (all locus pooled). 1 indicates the presence of allele k in individual i . All individuals displaying NAs are removed.
labels	A vector indicating the names of the locus.
locus	A list of matrices corresponding to each locus. Each element is a matrix indicate whether an allele is present (1) or not (0) for each individual. Individuals displaying NAs for a locus are removed from the output corresponding to that locus but not from matrices corresponding to other locus.
rrows	The number corresponding to the rows corresponding to individuals having at least one NA.

Author(s)

Jean-Pierre Rossi, <jean-pierre.rossi@supagro.inra.fr>

See Also[rich](#)**Examples**

```
#locus 1
l1a1<-c(10,NA,10,20)
l1a2<-c(20,10,30,30)
#locus 2
l2a1<-c(100,100,100,200)
l2a2<-c(200,100,300,400)
#locus 3
l3a1<-c(110,100,111,210)
l3a2<-c(200,100,301,NA)
label<-c("a","b","c","d")
pop<-cbind(l1a1,l1a2, l2a1,l2a2,l3a1,l3a2);pop
loc2rich(pop, rowlabels=label)

#using loc2rich to compare cumulated allelic richness using comp2cv
data(leirial)
w<-loc2rich(leirial$data, rowlabels=leirial$labels)
##working with the second locus, PP42
a<-w$locus[[2]][which(leirial$labels=="leiria_winter"),]
b<-w$locus[[2]][which(leirial$labels=="leiria_summer"),]
comp2cv(pop1=a,pop2=b,nrandom=99)
```

rich-package

*Analyses of species or allelic richness***Description**

Computes cumulated or average richness, shared species/alleles. Compares 2 or more observed data sets by mean of randomization tests.

Details

Package:	rich
Type:	Package
Version:	0.1
Date:	2010-04-16
License:	GPL (>= 2)
LazyLoad:	yes

`rich` allows simple comparisons between data sets by means of randomization tests. Different

functions provide useful statistics on observed richness.

Author(s)

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Examples

```
data(ef)
rich(matrix=ef)
```

rich	<i>Cumulated and average richness over a set of samples and associated confidence interval</i>
------	--

Description

Computes the cumulated and average species richness over a set of samples and the associated bootstrap statistics.

Usage

```
rich(matrix, verbose = FALSE, nrandom = NULL)
```

Arguments

matrix	matrix is a typical species-sample matrix. Rows correspond to samples whereas columns stand for species.
verbose	If verbose=FALSE a simplified output is returned.
nrandom	Number of randomizations if bootstrap estimations are required. Values < 10 are set to 10.

Details

rich can be used to compute basic descriptive statistics from typical species by sample data sets or populations by alleles data table derived from the function [loc2rich](#).

Value

cr	Cumulated richness over samples or populations.
mr	Mean richness over samples or populations.
mrsd	Standard deviation of the richness over samples or populations.
singletons	Species/allele with at most one observation.
doubletons	Species/allele with at most two observations.
uniques	Species (allele) encountered in only one sample (individual).

duplicates	Species (allele) encountered in only two samples (individuals).
bootCR	<p>A data frame showing the outputs of the bootstrap analyses of the <i>cumulated richness</i> (computed if <code>is.null(nrandom) == FALSE</code>):</p> <p><code>cr.obs</code> Observed cumulated richness, equal to <code>cr</code> above.</p> <p><code>cr.boot</code> Mean of the bootstrap values.</p> <p><code>cr.bcorr</code> Mean of the bootstrap values corrected for the bias estimated below.</p> <p><code>cr.bias</code> Bias.</p> <p><code>cr.se</code> Standard error of the cumulated richness estimated by bootstrap. This is estimated as the standard deviation of the bootstrap values.</p> <p><code>cr.lbn</code> Lower bound of the first order normal approximation confidence interval (see boot.ci {boot}).</p> <p><code>cr.ubn</code> Upper bound of the first order normal approximation confidence interval (see boot.ci {boot}).</p>
bootMR	<p>A data frame showing the outputs of the bootstrap analyses of the <i>mean richness</i> (computed if <code>is.null(nrandom) == FALSE</code>):</p> <p><code>mr.obs</code> Observed mean richness, equal to <code>mr</code> above.</p> <p><code>mr.boot</code> Mean of the bootstrap values.</p> <p><code>mr.bcorr</code> Mean of the bootstrap values corrected for the bias estimated below.</p> <p><code>mr.bias</code> Bias.</p> <p><code>mr.se</code> Standard error of the mean richness estimated by bootstrap. This is estimated as the standard deviation of the bootstrap values.</p> <p><code>mr.lbn</code> Lower bound of the first order normal approximation confidence interval (see boot.ci {boot}).</p> <p><code>mr.ubn</code> Upper bound of the first order normal approximation confidence interval (see boot.ci {boot}).</p>
nrandom	Number of randomizations used in the bootstrap.
richvec	A vector indicating the observed richness in each sample or populations. The mean of <code>richvec</code> corresponds to <code>mr</code> (available if <code>verbose == TRUE</code>).
matrix	The data set passed to <code>rich</code> as the <code>matrix</code> argument (available if <code>verbose == TRUE</code>).
matrixbin	Binary (presence/absence) transformation of the data set passed to <code>rich</code> as the <code>matrix</code> argument (available if <code>verbose == TRUE</code>).
sumrow	A vector of the sum of species/allele for each sample/population (available if <code>verbose == TRUE</code>).
sumcol	A vector of the sum of sample/population for each species/allele (available if <code>verbose == TRUE</code>).
zeroes	Number of zeroes in the data set (available if <code>verbose == TRUE</code>).

Author(s)

Jean-Pierre Rossi, <jean-pierre.rossi@supagro.inra.fr>

Examples

```
data(ef)
## No bootstrap statistics
rich(matrix=ef)
## Bootstrap estimation based on 499 randomizations
rich(matrix=ef, nrandom=499)
## Bootstrap estimation based on 499 randomizations, full output
data(mat)
rich(matrix=mat$mat1, nrandom=499, verbose=TRUE)

##Random data matrix
a<-matrix(data=rpois(80,0.45), ncol=8, nrow=10)
colnames(a) <- c("a","b","c","d","e","f","g","h")
rownames(a) <- c("unit01","unit02","unit03","unit04",
"unit05","unit06","unit07","unit08","unit09","unit10")
rich(a, nrandom=499, verbose=TRUE)
```

shared

Computes the number of species/alleles shared between samples/populations and other useful statistics.

Description

shared computes the richness of each group of sample (site) or populations, the number of species/alleles shared between pairs of sites/populations and the total number of species/alleles for each pairs of sites/populations.

Usage

```
shared(lmatrix)
```

Arguments

lmatrix A list which each component is a data matrix representing the species/allele composition of a site/population. All matrices must have the same size.

Details

With allelic data sets, shared can be used on the whole matrix or on the matrices associated to each locus.

Value

A data frame with: on the diagonal the observed richness for each site/population, above the diagonal: the richness common to pairs of sites/populations (shared richness) and below the diagonal: the total richness for pooled pairs of sites.

Author(s)

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See Also

[rich](#), [compshared](#)

Examples

```
sp1<-c(1,2,3,4,5)
sp2<-c(0,0,0,0,0)
sp3<-c(1,1,0,0,0)
sp4<-c(0,0,0,0,0)
site1<-cbind(sp1, sp2, sp3, sp4)
colnames(site1)<-c("sp1", "sp2", "sp3", "sp4")
sp1<-c(1,2,3)
sp2<-c(1,0,0)
sp3<-c(0,0,0)
sp4<-c(0,0,0)
site2<-cbind(sp1, sp2, sp3, sp4)
colnames(site2)<-c("sp1", "sp2", "sp3", "sp4")
sp1<-c(1,2,3,4)
sp2<-c(1,0,0,0)
sp3<-c(1,0,0,0)
sp4<-c(1,0,0,0)
site3<-cbind(sp1, sp2, sp3, sp4)
colnames(site3)<-c("sp1", "sp2", "sp3", "sp4")

data<-list(site1,site2, site3)
names(data)<-c("site1","site2","site3")
shared(data)
```

Tomicus

Maximum temperature at sites hosting 2 species of closely related bark-beetles of genus Tomicus.

Description

The Tomicus data set consists of a list with 3 components:

destruens Maximum temperature at 33 sites where *T. destruens* was observed.

piniperda Maximum temperature at 20 sites where *T. piniperda* was observed.

both Maximum temperature at 4 sites where both *T. destruens* and *T. piniperda* were observed in sympatry.

Usage

```
data(Tomicus)
```

Format

Tomicus is a list of 3 vectors.

Source

A. Horn, J.-P. Rossi, F. Lieutier, C. Kerdelhue (submitted). Climate and host availability affect the respective distributions of two closely related bark-beetles in Europe and the Mediterranean Basin. *Agricultural and Forest Entomology*.

Examples

```
## Comparing mean temperatures at sites where either T. destruens,  
T. piniperda or both are present using comp2mean  
data(Tomicus)  
comp2mean(pop1.vec=Tomicus$destruens, pop2.vec=Tomicus$piniperda,  
pop3.vec=Tomicus$both, nrandom=99)
```


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