Package ‘rich’

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Description Computes rarefaction curves, cumulated and mean species richness. Compares these estimates by means of randomization tests.
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Description

Species richnesses are computed as the cumulative value over all samples. Richnesses are compared by mean of a randomization test without controlling for differences of sampling regime of communities density.

Usage

c2cv(com1,com2,nrandom=99,pr1=0.025,pr2=0.975,verbose=TRUE)

Arguments

- **com1**: A first species-sample matrix (community 1). Rows correspond to samples whereas columns stand for species.
- **com2**: A second species-sample matrix (community 2). Rows correspond to samples whereas columns stand for species.
- **nrandom**: Number of randomizations to be performed. Default fixed to 99.
- **pr1**: Lower probability level for quantile computations. Default fixed to 0.025.
- **pr2**: Higher probability level for quantile computations. Default fixed to 0.975.
- **verbose**: If **verbose** is **TRUE** c2cv returns a vector that contains the observed and randomized differences between richnesses.

Details

If the observed richness for community 1 \( \geq \) observed value for community 2, c2cv returns a probability \( p \) estimated as the number of randomizations for which the observed value for community 1 \( \geq \) observed value for community 2 divided by the number of randomization + 1. Similarly, if the observed value for community 1 \( \leq \) observed value for community 2, \( p \) corresponds to the frequency of such situation in the randomizations.
Value

If verbose==TRUE c2cvm returns a data frame and a vector with the randomized values. Otherwise, only the data frame is returned.

res A data frame with the outputs of the randomization test:
cv1 Observed cumulative richness for community 1.
cv2 Observed cumulative richness for community 2.
cv1-cv2 Difference between observed cumulative richness of community 1 and community 2.
p Probability of encountering such a value for cv1-cv2 (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.
nr random Number of randomizations used in the test.

rand A vector of nr + 1 values corresponding to the observed difference of cv1-cv2 and the randomized values. rand is available if verbose == TRUE.

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)

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References


See Also
c2m, rich

Examples

```r
# Not run:
data(efeb)
c2cv(com1=efeb$ef, com2=efeb$eb, nr random=100, verbose=FALSE)
```

## End(Not run)
**Description**

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

**Usage**

c2m(pop1, pop2, pop3= NULL, nrandom, pr1=0.025, pr2=0.975, verbose=TRUE)

**Arguments**

- **pop1** A vector with the observed values for population 1.
- **pop2** A vector with the observed values for population 2.
- **pop3** A vector with the observed values that are common to population 1 and 2.
- **nrandom** Number of randomizations to perform. Default fixed to 99.
- **pr1** Lower probability level for quantile computations. Default fixed to 0.025.
- **pr2** Higher probability level for quantile computations. Default fixed to 0.975.
- **verbose** If `verbose` is TRUE `c2m` returns a vector that contains the observed and randomized differences between mean richnesses.

**Details**

This randomization test compares the average value of a quantitative variable sampled in 2 populations. Details are available in 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 `c2m` by the argument `pop3`.

If the mean value for population 1 ≥ mean value for population 2, p is the number of randomizations for which the mean value for population 1 ≥ mean value for population 2 divided by the number of randomizations + 1. If the mean value for population 1 ≤ mean value for population 2, p is the number of randomizations for which the mean value for population 1 ≤ mean value for population 2 divided by the number of randomizations + 1. If mv1 = mv2 p in not computed (p=NC).

**Value**

- **res** A data frame showing the outputs of the randomization test:
  - mv1 Observed mean values over samples forming population 1.
  - mv2 Observed mean values over samples forming population 2.
  - mv1-mv2 Difference between observed mean values of population 1 and population 2.
  - p Probability of encountering such a value for mv1-mv2 (see details above).
  - quantile for pr1 Quantile value for probability level pr1.
Quantile for probability level \( pr2 \).

**randomized** \( mv1-mv2 \) 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 observed difference of \( mv1-mv2 \) and the randomized values. \( rand \) is available if \( verbose == TRUE \).

**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**


**See Also**

c2cv, rich

**Examples**

```r
# Not run:
# 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)
males<-c(110, 111, 107, 108, 110, 105, 107, 106, 111, 111)
out <- c2m(pop1=males, pop2=females, nrandom=99)
out$res
hist(out$rand)
abline(v=out$res[3,1], col="red")
abline(v=out$res[5,1], col="blue")
abline(v=out$res[6,1], col="blue")

# Compare simulated datasets
pop1<-rnorm(10)
pop2<-rnorm(10)
out <- c2m(pop1=pop1, pop2=pop2, nrandom=99)
out$res
hist(out$rand)
abline(v=out$res[3,1], col="red")
abline(v=out$res[5,1], col="blue")
abline(v=out$res[6,1], col="blue")
```
# Maximum temperature in a set of sites where the bark beetle *Tomicus destruens* # or *T. piniperda* are present. Both species are present at 4 sites.
data(Tomicus)
out <- c2m(pop1=Tomicus$destruens, pop2=Tomicus$piniperda, pop3=Tomicus$both, nrandom=99)
out$res
hist(out$rand)
abline(v=out$res[3,1], col="red")
abline(v=out$res[5,1], col="blue")
abline(v=out$res[6,1], col="blue")

# using c2m with outputs of rich
data(ef)
o1 <- rich(matrix=ef, nrandom=99, verbose=TRUE)
data(ea)
o2 <- c2m(pop1=o1$sumrow, pop2=o2$sumrow, nrandom=999, verbose=TRUE)
hist(out$rand)
abline(v=out$res[3,1], col="red")
abline(v=out$res[5,1], col="blue")
abline(v=out$res[6,1], col="blue")

## End(Not run)

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**ea**

*Soil macrofauna in a tropical field under traditional slash-and-burn (Elahe, French Guiana)*

---

**Description**

The *ea* data set is a data frame describing the species abundance of soil macrofauna in a set of soil samples collected in a field (aka abattis) in French Guiana. These data were collected in the vicinity of the Wayana village of Elahe situated on the Tampoc river.

**Usage**

data(ea)

**Format**

*ea* is a data frame containing the observations of 45 species (columns) at 30 sampling locations (rows).

**Source**

**Examples**

```r
## Estimating species richness using rich
data(ef)
rich(matrix=ef)
```

---

**ef**  
*Soil macrofauna in a tropical forest site (Elahe, French Guiana)*

**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 Guiana. These data were collected in the vicinity of the Wayana village of Elahe situated on the Tampoc river.

**Usage**

```r
data(ef)
```

**Format**

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

**Source**


**Examples**

```r
## Estimating species richness using rich
data(ef)
rich(matrix=ef)
```
Description

The *efea* data set is a list of two data sets. Each one is a data frame giving the species abundance of soil macrofauna in a set of soil samples. *efeb* corresponds to samples collected in a secondary forest in French Guiana while *efeb* contains data collected in in a field (aka abattis) in French Guiana. These data were collected in the vicinity of the Wayana village of Elahe situated on the Tampoc river.

Usage

data(efea)

Format

*efea* is a list of two data frame containing the observations of 142 species (columns) at 30 sampling locations (rows).

Source


Examples

data(efea)
rich(matrix=efea[[1]])
shared(efea)

Description

The *efeb* data set is a list of two data sets. Each one is a data frame giving the species abundance of soil macrofauna in a set of soil samples. *efeb* corresponds to samples collected in a secondary forest in French Guiana while *efeb* contains data collected in the same site just after the forest has been cut and burnt following the traditional Amerindian slash-and-burn system. These data were collected in the vicinity of the Wayana village of Elahe situated on the Tampoc river.
**rarc**

**Usage**

```r
data(efeb)
```

**Format**

`efeb` is a list of two data frame containing the observations of 134 species (columns) at 30 sampling locations (rows).

**Source**


**Examples**

```r
data(efeb)
rich(matrix=efeb[[1]])
shared(efeb)
```

---

**rarc**  
*Computes rarefaction curves and statistical envelop*

**Description**

`rarc` computes rarefaction curves and returns a data frame with bootstrap estimates of species richness, its statistical envelop and the average number of individuals for a given sample size.

**Usage**

```r
rarc(matrix, samplesize=NULL, nrandom=99, p1=0.975, p2=0.025, save=FALSE)
```

**Arguments**

- `matrix`: matrix is a typical species-sample matrix. Rows correspond to samples whereas columns stand for species.
- `samplesize`: A vector containing the different sample sizes for which the computations are required. If missing or non vector, `samplesize` is replaced by a sequence from 1 to the maximum possible sample size given the size of `matrix`.
- `nrandom`: `nrandom` is the number of a randomizations used in the bootstrap estimation. Values of `nrandom <10` or `NULL` are set to 99.
- `p1`: The probability value used to compute the upper bound of the statistical envelop using `quantile`. Default set to 0.975.
- `p2`: The probability value used to compute the lower bound of the statistical envelop using `quantile`. Default set to 0.025.
- `save`: If TRUE the function returns the raw values used in the estimation of the quantiles.
raref

**Value**

out  A data frame with 5 columns giving the mean species richness, the lower and upper bound of the richness corresponding to the quantile values for p1 and p2, the mean number of individuals and the sample size.

bootstrapped.val  Generated if save=TRUE. A list of length of the number of different sample sizes analyzed containing the raw values used to computed the quantiles. These values can be used for example to compute the standard error as illustrated in the examples below.

**Author(s)**

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

**See Also**

raref, raref2, rich

**Examples**

```r
## Not run:
data(ef)
t <- rarc(ef,samplesize=c(5,10,15,20,25), nrandom=30, p1=0.975, p2=0.025)
head(t)

# Plot the outputs
plot(t$out[,6],t$out[,1], type="b", ylim=range(c(t$out[,2],t$out[,3])),
xlab="number of sampling units", ylab="richness")
points(t$out[,6], t$out[,2], type="1", col="red")
points(t$out[,6], t$out[,3], type="1", col="blue")

## End(Not run)

#See the package vignette for more examples. Type: vignette("rich_introduction").
```

---

**raref**

Estimates the species richness for a given number of sampled individuals on the basis of the corresponding rarefaction curve.

**Description**

raref computes rarefaction curve and interpolates the species richness corresponding to a given density of individuals.

**Usage**

raref(matrix, dens, nrandom=99)
Arguments

matrix

dens

nrandom

Value

raref returns a list with two components.

rar

Sinterp

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References


See Also

rarc, raref2, rich

Examples

## Not run:
data(ef)

raref2(ef, dens=1100, nrandom=100)

## End(Not run)

raref2 Estimates the species richness for a given number of sampled individuals on the basis of the corresponding rarefaction curve

Description

raref2 computes an estimation of the species richness by thinning the data matrix so that the overall corresponding density is comprised in a fixed interval.
Usage

raref2(matrix, dens, tolerance, nrandom=99)

Arguments

matrix matrix is a typical species-sample matrix. Rows correspond to samples whereas columns stand for species.
dens A number corresponding to the density for which a species richness estimation is required. dens must be comprised within the range of the observed density.
tolerance A number used to calculate the range of acceptable values for the density of simulated communities. Let $D$ be largest density (com1 or com2). The acceptable interval is $D \pm tolerance \times D$.
nrandom nrandom is the number of a randomizations used in the bootstrap estimation. Values of nrandom <10 or NULL are set to 99.

Value

raref2 returns a list with two components.

mean.boot The mean value of the bootstrap estimates of the species richness.
sd.boot The standard deviation of the bootstrap estimates.

Author(s)

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

See Also

raref, rich

Examples

## Not run:
data(ef)
raref2(matrix=ef,dens=1100,tolerance=0.01,nrandom=50)

## End(Not run)

rich Species richness, their confidence interval and other useful indices

Description

Computes the cumulative and average species richness over a set of samples, the associated bootstrap statistics and other useful indices.
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 or randomizations if bootstrap estimations are required. Non-null values < 10 are set to 99.

Details

rich computes basic descriptive statistics from typical species by sample data sets.

Value

- **cr**: Cumulated richness over sampling units.
- **mr**: Mean richness over sampling units.
- **mrsd**: Standard deviation of the mean richness.
- **singletons**: Species with at most one observation.
- **doubletons**: Species with at most two observations.
- **uniques**: Species encountered in only one sample.
- **duplicates**: Species encountered in only two samples.

**bootCR**

- **cr.obs**: Observed cumulative richness, equal to cr above.
- **cr.boot**: Mean of the bootstrap values.
- **cr.bcorr**: Mean of the bootstrap values corrected for the bias estimated below.
- **cr.bias**: Bias.
- **cr.se**: Standard error of the cumulative richness estimated by bootstrap. This is estimated as the standard deviation of the bootstrap values.
- **cr.lbn**: Lower bound of the first order normal approximation confidence interval (see boot.ci {boot}).
- **cr.ubn**: Upper bound of the first order normal approximation confidence interval (see boot.ci {boot}).

**bootMR**

- **mr.obs**: Observed mean richness, equal to mr above.
- **mr.boot**: Mean of the bootstrap values.
- **mr.bcorr**: Mean of the bootstrap values corrected for the bias estimated below.
- **mr.bias**: Bias.
- **mr.se**: Standard error of the mean richness estimated by bootstrap. This is estimated as the standard deviation of the bootstrap values.
mr.lbn  Lower bound of the first order normal approximation confidence interval (see boot.ci {boot}).
mr.ubn  Upper bound of the first order normal approximation confidence interval (see boot.ci {boot}).
nrandom  Number of randomizations used in the bootstrap.
richvec  A vector containing the observed richness in each sample or populations. The mean of richvec corresponds to mr (available if verbose == TRUE).
matrix  The data set passed to rich as the matrix argument (available if verbose == TRUE).
matrixbin  Binary (presence/absence) transformation of the data set passed to rich as the matrix argument (available if verbose == TRUE).
sumrow  A vector of the sum of species for each sample (available if verbose == TRUE).
sumcol  A vector of the sum of sample for each species (available if verbose == TRUE).
zeroes  Number of zeroes in the data set (available if verbose == TRUE).

Author(s)
Jean-Pierre Rossi <jean-pierre.rossi@supagro.inra.fr>

References

See Also
rarc, raref2, raref

Examples
data(ef)
# No bootstrap statistics
rich(matrix=ef)

## Not run:
# Bootstrap estimation based on 499 randomizations
rich(matrix=ef, nrandom=499)
## End(Not run)

shared  Computes the number of species shared by groups of sampling units and other useful statistics

Description

shared computes the richness of each group of sample depicting a community, the number of species shared by pairs of communities and the total number of species for each pairs of community.
shared

Usage

shared(lmatrix)

Arguments

lmatrix A list of data matrices representing the species composition of local communities. All matrices must have the same size.

Value

A data frame with: on the diagonal the observed richness for each local community, above the diagonal: the richness common to pairs of communities (shared richness) and below the diagonal: the total richness for pooled pairs of communities.

Author(s)

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

References

Empirical data have been presented in a way very similar to what is returned by shared in the following papers:


See Also

rich

Examples

data(efeb)
shared(efeb)

sp1<-c(1,2,3,4,5)
sp2<-c(0,0,0,0,0)
sp3<-c(1,0,0,0,0)
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)
The `tomicus` data set consists of a list with 3 components:

destroyens 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


Examples

```r
## Comparing mean temperatures at sites where either T. destruens, 
## T. piniperda or both are present using comp2mean
data(tomicus)
c2m(pop1=vector1, pop2=vector2, pop3=vector3, nrandom=99)
```
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