

# Package ‘rich’

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**Type** Package

**Title** Computes and Compares Species Richnesses

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**Depends** R (>= 3.1.0)

**Imports** vegan, boot

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

**License** GPL (>= 2)

**LazyLoad** TRUE

**Suggests** knitr, gplots, rmarkdown

**VignetteBuilder** knitr

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c2cv	<i>Comparison of 2 values of species richness using a randomization procedure</i>
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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` `c2cm` returns a data frame and a vector with the randomized values. Otherwise, only the data frame is returned.

<code>res</code>	A data frame with the outputs of the randomization test: <code>cv1</code> Observed cumulative richness for community 1. <code>cv2</code> Observed cumulative richness for community 2. <code>cv1-cv2</code> Difference between observed cumulative richness of community 1 and community 2. <code>p</code> Probability of encountering such a value for <code>cv1-cv2</code> (see details above). <code>quantile for pr1</code> Quantile value for probability level <code>pr1</code> . <code>quantile for pr2</code> Quantile value for probability level <code>pr2</code> . <code>randomized cv1-cv2</code> Mean values of randomized and the observed values. <code>nrandom</code> Number of randomizations used in the test.
<code>rand</code>	A vector of <code>nrandom+1</code> values corresponding to the observed difference of <code>cv1-cv2</code> and the randomized values. <code>rand</code> is available if <code>verbose == TRUE</code> .

**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**

[c2m](#), [rich](#)

**Examples**

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

## End(Not run)
```

c2m

*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**

```
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  $\geq$  mean value for population 2,  $p$  is the number of randomizations for which the mean value for population 1  $\geq$  mean value for population 2 divided by the number of randomizations + 1. If the mean value for population 1  $\leq$  mean value for population 2,  $p$  is the number of randomizations for which the mean value for population 1  $\leq$  mean value for population 2 divided by the number of randomizations + 1. If  $mv1 = mv2$   $p$  is 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 pr2 Quantile value 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

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

### See Also

[c2cv](#), [rich](#)

### Examples

```
## 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)
females<-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 <- rich(matrix=ea, nrandom=99, verbose=TRUE)
out <- 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)

```

---

ea	<i>Soil macrofauna in a tropical field under traditional slash-and-burn (Elahe, French Guiana)</i>
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---

## 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

Rossi, J.-P., Celini, L., Mora, P., Mathieu, J., Lapied, E., Nahmani, J., Ponge, J.-F., and Lavelle, P. (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 rich
data(ea)
rich(matrix=ea)
```

---

ef	<i>Soil macrofauna in a tropical forest site (Elahe, French Guiana)</i>
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---

## 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

```
data(ef)
```

## Format

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

## Source

Rossi, J.-P., Celini, L., Mora, P., Mathieu, J., Lapied, E., Nahmani, J., Ponge, J.-F., and Lavelle, P. (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 rich
data(ef)
rich(matrix=ef)
```

---

efea	<i>Soil macrofauna in a tropical forest site and cultivated plot (traditional slash-and-burn, Elahe, French Guiana)</i>
------	---

---

### 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\$ef corresponds to samples collected in a secondary forest in French Guiana while efeb\$ea contains data 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(efea)
```

### Format

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

### Source

Rossi, J.-P., Celini, L., Mora, P., Mathieu, J., Lapied, E., Nahmani, J., Ponge, J.-F., and Lavelle, P. (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

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

---

efeb	<i>Soil macrofauna in a tropical forest site before and after deforestation (traditional slash-and-burn, Elahe, French Guiana)</i>
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---

### 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\$ef corresponds to samples collected in a secondary forest in French Guiana while efeb\$eb 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.



**Usage**

```
data(efeb)
```

**Format**

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

**Source**

Rossi, J.-P., Celini, L., Mora, P., Mathieu, J., Lapied, E., Nahmani, J., Ponge, J.-F., and Lavelle, P. (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**

```
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**

```
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.

**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**

```
## 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="l", col="red")
points(t$out[,6] , t$out[,3], type="l", col="blue")

## End(Not run)

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

---

raref	<i>Estimates the species richness for a given number of sampled individuals on the basis of the corresponding rarefaction curve</i>
-------	---

---

**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	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.
nrandom	nrandom is the number of a randomizations used in the bootstrap estimation. Values of nrandom <10 or NULL are set to 99.

**Value**

raref	raref returns a list with two components.
rar	A data frame with three columns giving the observed species richness for different sample size and corresponding density of individuals.
Sinterp	A vector with the term dens and the corresponding interpolated species richness.

**Author(s)**

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

**References**

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

**See Also**

[rarc](#), [raref2](#), [rich](#)

**Examples**

```
## Not run:
data(ef)
raref(ef, dens=1100, nrandom=100)

## End(Not run)
```

---

raref2	<i>Estimates the species richness for a given number of sampled individuals on the basis of the corresponding rarefaction curve</i>
--------	---

---

**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 of 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	A data frame showing the outputs of the bootstrap analyses of the cumulative richness (computed if nrandom != FALSE): 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	A data frame showing the outputs of the bootstrap analyses of the mean richness (computed if nrandom != FALSE): 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.

<code>mr.lbn</code>	Lower bound of the first order normal approximation confidence interval (see <code>boot.ci {boot}</code> ).
<code>mr.ubn</code>	Upper bound of the first order normal approximation confidence interval (see <code>boot.ci {boot}</code> ).
<code>nrandom</code>	Number of randomizations used in the bootstrap.
<code>richvec</code>	A vector containing 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> ).
<code>matrix</code>	The data set passed to <code>rich</code> as the <code>matrix</code> argument (available if <code>verbose == TRUE</code> ).
<code>matrixbin</code>	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> ).
<code>sumrow</code>	A vector of the sum of species for each sample (available if <code>verbose == TRUE</code> ).
<code>sumcol</code>	A vector of the sum of sample for each species (available if <code>verbose == TRUE</code> ).
<code>zeroes</code>	Number of zeroes in the data set (available if <code>verbose == TRUE</code> ).

**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**

[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)
```

---

<code>shared</code>	<i>Computes the number of species shared by groups of sampling units and other useful statistics</i>
---------------------	--

---

**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.

**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:

Rossi, J.-P., Mathieu, J., Cooper, M., and Grimaldi, M. (2006). Soil macrofaunal biodiversity in amazonian pastures: Matching sampling with patterns. *Soil Biology & Biochemistry*, 38, 2178-2187.

Rossi, J.-P., Celini, L., Mora, P., Mathieu, J., Lapied, E., Nahmani, J., Ponge, J.-F., and Lavelle, P. (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.

**See Also**

[rich](#)

**Examples**

```
data(efeb)
shared(efeb)

sp1<-c(1,2,3,4,5)
sp2<-c(0,0,0,0,0)
sp3<-c(1,1,0,0,0)
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	<i>Maximum temperature at sites hosting 2 species of closely related bark-beetles of genus Tomicus</i>
---------	--

---

### 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

Horn, A. (2006) Comparaison des distributions passee et presente de deux especes proches de scolytes, *Tomicus piniperda* et *T. Destruens* (Coleoptera: Scolytinae). These de l'Universite d'Orleans, France 180pp.

### Examples

```

## Comparing mean temperatures at sites where either T. destruens,
## T. piniperda or both are present using comp2mean
data(Tomicus)
c2m(pop1=Tomicus$destruens,pop2=Tomicus$piniperda,
pop3=Tomicus$both, nrandom=99)

```



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