

# Package ‘cati’

May 9, 2018

**Type** Package

**Title** Community Assembly by Traits: Individuals and Beyond

**Version** 0.99.2

**Date** 2018-05-09

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**Depends** R (>= 3.0.2), nlme, ade4, ape,

**Imports** e1071, rasterVis, hypervolume, FD, geometry, vegan

**Suggests** lattice, spacodiR, entropart, fBasics, picante, mice, knitr

**Description** Detect and quantify community assembly processes using trait values of individuals or populations, the T-statistics and other metrics, and dedicated null models.

**License** GPL (>= 2)

**URL** <https://github.com/adrietaudiere/cati>

**RoxygenNote** 6.0.1

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2018-05-09 13:47:37 UTC

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cati-package

*Community Assembly by Traits: Individuals and Beyond*

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## Description

A package to detect and quantify community assembly processes using trait values of individuals or populations, the T-statistics and other metrics, and dedicated null models.

## Details

Package: cati  
 Type: Package  
 Version: 0.99.1  
 Date: 2015-05-28  
 License: GPL (>= 2)  
 Depends: R (>= 3.0.2), nlme, ade4, ape  
 Imports: e1071, mice, rasterVis, hypervolume, FD, geometry, vegan  
 Suggests: lattice, spacodiR, entropart, fBasics, picante

This package provides functions to calculate T-statistics (Tstats function) and other uni-traits metrics (ComIndex function) to test community assembly traits measured on individuals and beyond (e.g. populations, functional groups). Variance partitioning (partvar function) and density plot (plotDistri function) are also available. Finally, this package includes functions to summarize community assembly metrics and functions to plot standardized effect size of index.

Development versions, forum, Darwin finches's dataset, and tutorial are available at <https://github.com/adrientaudiere/cati/>. The reference manual is available at <http://cran.r-project.org/web/packages/cati/cati.pdf> and the tutorial at [https://github.com/adrientaudiere/cati/blob/Package-cati/tutorials/vignette\\_Darwin\\_finches/vignette.pdf](https://github.com/adrientaudiere/cati/blob/Package-cati/tutorials/vignette_Darwin_finches/vignette.pdf).

### Author(s)

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Cyrille Violle

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AbToInd	<i>Internal function. Transform abundance data matrix into individual like matrix.</i>
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### Description

Transform abundance data matrix into individual like matrix to allows the use of ComIndex and ComIndexMulti on populationnal or specific traits values.

### Usage

```
AbToInd(traits, com, type.sp.val = "count")
```

### Arguments

traits	Individual Matrix of traits with traits in columns. "traits" matrix must have row names (e.g. species or populationnal names).
com	Community data matrix with species in rows and sites in column.
type.sp.val	Either "count" or "abundance". Use abundance when all values in the com matrix are not superior to one. Using abundance is EXPERIMENTAL. This function round abundance to fit count data.

### Details

Internal function

### Value

A list of objects:

\$traits	Individual traits matrix
\$sp	Vector of species attributes
\$ind.plot	Vector of sites attributes

### Author(s)

Adrien Taudiere

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as.listofindex      *Transform index results in a list of index*

---

### Description

Transform various results from functions Tstats, ComIndex or ComIndexMulti in a list of index. Useful to use the functions plot.listofindex (S3 method) and ses.listofindex.

### Usage

```
as.listofindex(x, namesindex = NULL)
```

### Arguments

x                    A list of objects of class Tstats, ComIndex or ComIndexMulti  
namesindex          Optional, the names of index in the same order as in x.

### Value

A list of observed values and corresponding "null" values (i.e. produced by null models) in the form "list(index1, null model index1, index2, null model index2 ...)"

### Author(s)

Adrien Taudiere

### See Also

[ses.listofindex](#); [plot.listofindex](#)

### Examples

```
data(finch.ind)

res.finch <- Tstats(traits.finch, ind.plot = ind.plot.finch,
sp = sp.finch, nperm = 9, print = FALSE)

## Not run:
#### Use a different regional pool than the binding of studied communities
#create a random regional pool for the example

reg.p <- rbind(traits.finch, traits.finch[sample(1:2000,300), ])

res.finch2 <- Tstats(traits.finch, ind.plot = ind.plot.finch,
sp = sp.finch, reg.pool=reg.p, nperm = 9, print = FALSE)

plot(as.listofindex(list(res.finch,res.finch2)))
```

```
##### Use a different regional pool for each communities
#create a random regional pool for each communities for the example
list.reg.p <- list(
  traits.finch[sample(1:290,200), ], traits.finch[sample(100:1200,300), ],
  traits.finch[sample(100:1500, 1000), ], traits.finch[sample(300:800,300), ],
  traits.finch[sample(1000:2000, 500), ], traits.finch[sample(100:900, 700), ] )

# Warning: the regional pool need to be larger than the observed communities
table(ind.plot.finch)
# For exemple, the third community need a regional pool of more than 981 individuals

res.finch3 <- Tstats(traits.finch, ind.plot = ind.plot.finch,
  sp = sp.finch, reg.pool=list.reg.p, nperm = 9, print = FALSE)

plot(as.listofindex(list(res.finch, res.finch2, res.finch3)))

## End(Not run)
```

---

Auxiliary functions      *Auxiliary functions*

---

## Description

Auxiliary functions

## Usage

```
funky.col(n)
```

## Arguments

n                      number of color for the funky palette

## Details

funky.col is a clone of the palette funky from the adegenet package.

## Value

A color palette

## Author(s)

Thibault Jombart

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ComIndex	<i>Computing metrics to test and quantify the non-random assembly of communities</i>
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## Description

Computing the moments of the trait distribution and other metrics to test and quantify the non-random assembly of communities.

## Usage

```
ComIndex(traits = NULL, index = NULL, nullmodels = NULL,
ind.plot = NULL, sp = NULL, com = NULL, SE = 0, namesindex = NULL,
reg.pool = NULL, SE.reg.pool = NULL, nperm = 99, printprogress = TRUE,
independantTraits = TRUE, type.sp.val = "count")
```

```
## S3 method for class 'ComIndex'
plot(x, type = "normal",
col.index = c("red", "purple", "olivedrab3"), add.conf = TRUE,
color.cond = TRUE, val.quant = c(0.025, 0.975), ...)
```

```
## S3 method for class 'ComIndex'
print(x, ...)
```

```
## S3 method for class 'ComIndex'
summary(object, ...)
```

## Arguments

traits	Individual Matrix of traits with traits in column (or species matrix when using "com" instead of "ind.plot").
index	A vector of function to apply to traits vectors in the form "mean(x, na.rm = TRUE)" or "range(x)", see examples for more complexe functions.
nullmodels	A vector of names corresponding to null models tu use for each index. <b>local</b> (or 1) corresponds to a randomization of individual values within a given community. <b>regional.ind</b> (or 2) corresponds to randomization of individual values within region, ie within all the dataset. A value of <b>regional.pop</b> (or 2sp) corresponds to randomization of population values (each individual value are replaced by the mean value of it population) within region. Finally a value of <b>regional.pop.prab</b> (or 2sp.prab) mirror null model <b>regional.pop</b> but without taking indo account species abundance. For example, if nullmodels = c("local", "regional.ind"), the first index will be calculated on the null model <b>local</b> and the second index on the null model <b>regional.ind</b> . If only one value is given, all the the null model will be determined by this value.

ind.plot	Factor defining the name of the plot (site or community) in which the individual is.
sp	Factor defining the species which the individual belong to.
com	Community data matrix with species (or populations) in rows and sites in column. Use only if ind.plot = NULL. "traits" matrix and "com" matrix must have the same number of rows.
SE	A single value or vector of standard errors associated with each traits. Especially allow to handle measurement errors. Not used with populational null model.
namesindex	A vector of names for index.
reg.pool	Regional pool data for traits. If not informed, traits is considere as the regional pool. This matrix need to be larger (more rows) than the matrix "traits". Use only for null model <b>regional.ind</b> .
SE.reg.pool	A single value or vector of standard errors associated with each traits in each regional pool. Use only if reg.pool is used. Need to have the same dimension as reg.pool.
nperm	Number of permutations. If NULL, only observed values are returned.
printprogress	Logical value; print progress during the calculation or not.
independantTraits	Logical value (default: TRUE). If independantTraits is true (default), each traits is sample independently in null models, if not, each lines of the matrix are randomized, keeping the relation (and trade-off) among traits.
type.sp.val	Only if ind.plot = NULL. Either "count" or "abundance". Use abundance when one value or more in the com matrix are inferior to one. Using abundance is EXPERIMENTAL. This function round abundance to fit count data.
x	An object of class ComIndex.
object	An object of class ComIndex.
type	Type of plot. Possible type = "simple", "simple_range", "normal", "barplot" and "bytraits".
col.index	Vector of colors for index.
add.conf	Logical value; Add confidence intervals or not.
color.cond	Logical value; If color.cond = TRUE, color points indicate T-statistics values significantly different from the null model and grey points are not different from null model.
val.quant	Numeric vectors of length 2, giving the quantile to calculate confidence interval. By default val.quant = c(0.025,0.975) for a bilateral test with alpha = 5%.
...	Any additional arguments are passed to the plot, print or summary function. See <a href="#">plot.listofindex</a> for more arguments.

## Details

Compute statistics (e.g. mean, range, CVNND and kurtosis) to test community assembly using null models. For each statistic this function returns observed values and the related null distribution. This function implement four null models which keep unchanged the number of individual

per community. Model **local** (1) corresponds to randomization of individual values within community. Model **regional.ind** (2) corresponds to randomization of individual values within region. Model **regional.pop** (2sp) corresponds to randomization of population values within region. Model **regional.pop.prab** (2sp.prab) corresponds to randomization of population values within region but without taking into account for abundance.

In most cases, models **local** and **regional.ind** correspond to index at the individual level and the model **regional.pop** and **regional.pop.prab** to index at the species level (or any other aggregate variable like genus, family or functional group).

S3 method plot for class listofindex:

- Normal type plot means, standard deviations, ranges and confidence intervals of T-statistics.
- Simple\_range type plot means, standard deviations and range of T-statistics
- Simple type plot T-statistics for each site and traits and the mean confidence intervals by traits
- Barplot type plot means, standard deviations and confidence intervals of T-statistics in a barplot fashion
- Bysites type plot each metrics for each sites
- Bytraits type plot each metrics for each traits

## Value

An object of class "ComIndex" corresponding to a list of lists:

<code>\$obs</code>	List of observed values for each trait in each community. Each component of the list corresponds to a matrix containing the result for each custom function.
<code>\$null</code>	List of null values for each trait in each community. Each component of the list corresponds to an array containing the result of the permutations for each custom function.
<code>\$list.index</code>	List of index values and related null models. Internal use in other function. Traits in columns.
<code>\$list.index.t</code>	List of index values and related null models. Internal use in other function. Traits in rows.
<code>\$sites_richness</code>	Number of species per site.
<code>\$namestraits</code>	Names of traits.
<code>\$traits</code>	traits data
<code>\$ind.plot</code>	name of the plot in which the individual is
<code>\$sp</code>	groups (e.g. species) which the individual belong to
<code>\$nullmodels</code>	List of null models used for each indices.
<code>\$call</code>	call of the function Tstats

## Author(s)

Adrien Taudiere



**See Also**

[ComIndexMulti](#); [plot.listofindex](#); [ses](#)

**Examples**

```

data(finch.ind)

## Not run:
#Define the functions that will be calculating
funct<-c("mean(x, na.rm = TRUE)", "kurtosis(x, na.rm = TRUE)",
        "max(x, na.rm = TRUE) - min(x, na.rm = TRUE)" )

#Test against the null model regional.ind
res.finch.sp_regional.ind<-ComIndex(traits = traits.finch, index = funct, sp = sp.finch,
                                   nullmodels = "regional.ind", ind.plot = ind.plot.finch,
                                   nperm = 9, print = FALSE)

#Test against the null model regional.pop
#Individuals values are transformed in populational values
res.finch.sp_regional.pop<-ComIndex(traits = traits.finch, index = funct, sp = sp.finch,
                                   nullmodels = "regional.pop", ind.plot = ind.plot.finch,
                                   nperm = 9, print = FALSE)

#We can calculate index with or without intraspecific variance.

#calculate of means by population (name_sp_site is a name of a population)
#determine the site for each population (sites_bypop)

name_sp_sites = paste(sp.finch, ind.plot.finch, sep = "_")
traits.by.pop<-apply(traits.finch, 2 ,
                    function (x) tapply(x, name_sp_sites, mean, na.rm = TRUE))

sites_bypop<-lapply(strsplit(paste(rownames(traits.by.pop), sep = "_"), split = "_"),
                   function(x) x[3])

#New list of function "funct"

funct.1<-c("tapply(x, ind.plot.finch, function(x) mean(x, na.rm = TRUE))",
          "tapply(x, ind.plot.finch, function(x) kurtosis(x, na.rm = TRUE))",
          "tapply(x, ind.plot.finch, function(x) max(x, na.rm = TRUE)-min(x, na.rm = TRUE))",
          "tapply(x, ind.plot.finch, function(x) CVNND(x, na.rm = TRUE))" )

fact<-unlist(sites_bypop)
funct.2<-c("tapply(x, fact, function(x) mean(x, na.rm = TRUE))",
          "tapply(x, fact, function(x) kurtosis(x, na.rm = TRUE))",
          "tapply(x, fact, function(x) max(x, na.rm = TRUE)-min(x, na.rm = TRUE))",
          "tapply(x, fact, function(x) CVNND(x, na.rm = TRUE))")

res.finch.withIV<-ComIndex(traits = traits.finch, index = funct.1,

```

```

      sp = sp.finch, nullmodels = "regional.ind",
      ind.plot = ind.plot.finch, nperm = 9, print = FALSE)

res.finch.withoutIV<-ComIndex(traits = traits.finch, index = funct.2,
      sp = sp.finch, nullmodels = "regional.pop",
      ind.plot = ind.plot.finch, nperm = 9, print = FALSE)

#ComIndex class are associated to S3 methods plot, print and summary.

res.finch.withIV
summary(res.finch.withIV)
plot(res.finch.withIV)
plot(res.finch.withoutIV)

plot(as.listofindex(list(res.finch.withIV, res.finch.withoutIV)))

## End(Not run)

```

---

ComIndexMulti

*Computing multitraits metrics to test and quantify the non-random assembly of communities*


---

## Description

Computing multitraits metrics to test and quantify the non-random assembly of communities

## Usage

```

ComIndexMulti(traits = NULL, index = NULL, by.factor = NULL,
  nullmodels = NULL, ind.plot = NULL, sp = NULL, com = NULL,
  SE = 0, namesindex = NULL, reg.pool = NULL, SE.reg.pool = NULL,
  nperm = 99, printprogress = TRUE, independantTraits = TRUE,
  type.sp.val = "count")

## S3 method for class 'ComIndexMulti'
plot(x, type = "normal",
  col.index = c("red", "purple", "olivedrab3"), add.conf = TRUE,
  color.cond = TRUE, val.quant = c(0.025, 0.975), ...)

## S3 method for class 'ComIndexMulti'
print(x, ...)

## S3 method for class 'ComIndexMulti'
summary(object, ...)

```

**Arguments**

traits	Individual Matrix of traits with traits in column (or species matrix when using "com" instead of "ind.plot").
index	A vector of functions to apply to traits vectors in the form "mean(x, na.rm = TRUE)" or "range(x)".
by.factor	A factor to split the Matrix of traits and compute index for each subset eg for each site.
nullmodels	A vector of names corresponding to null models to use for each index. <b>local</b> (or 1) corresponds to a randomization of individual values within a given community. <b>regional.ind</b> (or 2) corresponds to randomization of individual values within region, ie within all the dataset. A value of <b>regional.pop</b> (or 2sp) corresponds to randomization of population values (each individual value are replaced by the mean value of it population) within region. Finally a value of <b>regional.pop.prab</b> (or 2sp.prab) mirror null model <b>regional.pop</b> but without taking into account species abundance. For example, if nullmodels = c("local", "regional.ind"), the first index will be calculated on the null model <b>local</b> and the second index on the null model <b>regional.ind</b> . If only one value is given, all the the null model will be determined by this value.
ind.plot	Factor defining the name of the plot (site or community) in which the individual is.
sp	Factor defining the species which the individual belong to.
com	Community data matrix with species (or populations) in rows and sites in column. Use only if ind.plot = NULL. "traits" matrix and "com" matrix must have the same number of rows.
SE	A single value or vector of standard errors associated with each traits. Especially allow to handle measurement errors. Not used with populational null model.
namesindex	A vector of names for metrics.
reg.pool	Regional pool data for traits. If not informed, traits is considere as the regional pool. This matrix need to be larger (more rows) than the matrix "traits". Use only for null model 2.
SE.reg.pool	A single value or vector of standard errors associated with each traits in each regional pool. Use only if reg.pool is used. Need to have the same dimension as reg.pool.
nperm	Number of permutations. If NULL, only observed values are returned.
printprogress	Logical value; print progress during the calculation or not.
independantTraits	Logical value (default: TRUE). If independantTraits is true (default), each traits is sample independently in null models, if not, each lines of the matrix are randomized, keeping the relation (and trade-off) among traits.
type.sp.val	Only if ind.plot = NULL. Either "count" or "abundance". Use abundance when all values in the com matrix are not superior to one.
x	An object of class ComIndexMulti.
object	An object of class ComIndexMulti.

type	Type of plot. Possible type = "simple", "simple_range", "normal", "barplot" and "bytraits".
col.index	Vector of colors for index.
add.conf	Logical value; Add confidence intervals or not.
color.cond	Logical value; If color.cond = TRUE, color points indicate T-statistics values significantly different from the null model and grey points are not different from null model.
val.quant	Numeric vectors of length 2, giving the quantile to calculate confidence interval. By default val.quant = c(0.025,0.975) for a bilateral test with alpha = 5%.
...	Any additional arguments are passed to the plot, print or summary function creating the core of the plot and can be used to adjust the look of resulting graph. See <a href="#">plot.listofindex</a> for more arguments.

### Details

This function implement four null models which keep unchanged the number of individual per community. Model **local** (1) corresponds to randomization of individual values within community. Model **regional.ind** (2) corresponds to randomization of individual values within region. Model **regional.pop** (2sp) corresponds to randomization of population values within region. Model **regional.pop.prab** (2sp.prab) corresponds to randomization of population values within region but whitout taking into account for abundance.

S3 method plot for class listofindex:

- Normal type plot means, standard deviations, ranges and confidence intervals of T-statistics.
- Simple\_range type plot means, standard deviations and range of T-statistics
- Simple type plot T-statistics for each site and traits and the mean confidence intervals by traits
- Barplot type plot means, standard deviations and confidence intervals of T-statistics in a barplot fashion
- Bysites type plot each metrics for each sites
- Bytraits type plot each metrics for each traits

### Value

A list of lists:

\$obs	List of observed values for each trait in each community. Each component of the list correspond to a matrix containing the result for each custom function.
\$null	List of null values for each trait in each community. Each component of the list correspond to an array containing the result of the permutations for each custom function.
\$sites_richness	Number of species per site.
\$namestraits	Names of traits.
\$traits	traits data
\$ind.plot	name of the plot in which the individual is

\$sp	groups (e.g. species) which the individual belong to
\$nullmodels	List of null models used for each indices.
\$call	call of the function Tstats
\$list.index	List of index values and associate null models. Internal use in other function. Traits in columns.
\$list.index.t	List of index values and associate null models. Internal use in other function. Traits in rows.

**Author(s)**

Adrien Taudiere

**See Also**[ComIndex](#); [plot.listofindex](#); [ses](#)**Examples**

```

data(finch.ind)

## Not run:
#For most multivariate functions we need to replace (or exclude) NA values.
#For this example, we use the package mice to complete the data.

comm<-t(table(ind.plot.finch,1:length(ind.plot.finch)))

library(mice)
traits = traits.finch
mice<-mice(traits.finch)
traits.finch.mice<-complete(mice)

#A simple example to illustrate the concept of the function ComIndexMulti

n_sp_plot<-as.factor(paste(sp.finch, ind.plot.finch, sep = "_"))
res.sum.1<-ComIndexMulti(traits.finch,
  index = c("sum(scale(x), na.rm = T)", "sum(x, na.rm = T)"),
  by.factor = n_sp_plot, nullmodels = "regional.ind",
  ind.plot = ind.plot.finch, nperm = 9, sp = sp.finch)
res.sum.1

#A more interesting example using the function hypervolume
library(hypervolume)

hv<-hypervolume(traits.finch.mice,
  reps = 100,bandwidth = 0.2,
  verbose = F, warnings = F)
plot(hv)

```

```

hv.1<-ComIndexMulti(traits.finch.mice,
  index = c("as.numeric(try(hypervolume(na.omit(x), reps = 100,
    bandwidth = 0.2, verbose = F, warnings = F)@Volume))"),
  by.factor = rep(1,length(n_sp_plot)), nullmodels = "regional.ind",
  ind.plot = ind.plot.finch, nperm = 9, sp = sp.finch)

hv.1

## End(Not run)

```

---

decompCTRE

*Variance partitioning for multiple traits*


---

### Description

This function decomposes the variation in community trait composition into three sources: (i) the intraspecific trait variability, (ii) the variability due to species turnover and (iii) their covariation is also separated. This decomposition is computed for the whole variation in the trait values and, The formula specified, across the contribution of various explanatory variables considered in the model. Barplot.decompCTRE allow to plot the result of the decomposition.

### Usage

```

decompCTRE(traits = NULL, formula = ~1, ind.plot = NULL, sp = NULL,
  printprogress = TRUE, ...)

## S3 method for class 'decompCTRE'
barplot(height, resume = TRUE, ...)

```

### Arguments

traits	Matrix of traits with traits in column
height	An object of class decompCTRE obtain by the function decompCTRE.
formula	The formula parameter must be a one-sided formula, i.e. starting with a tilde (~) character. The response variable is specified by the next two arguments, specif.avg and const.avg. By default set to ~1.
ind.plot	Factor defining the name of the plot (site or community) in which the individual is.
sp	Factor defining the species which the individual belong to.
printprogress	Logical value; print progress during the calculation or not.
resume	Logical. If resume = FALSE, plot one graphic by traits.
...	Optional additional arguments

### Value

An object of class "decompCTRE".

**Author(s)**

Adrien Taudiere Jan Leps

**References**

Leps, Jan, Francesco de Bello, Petr Smilauer and Jiri Dolezal. 2011. Community trait response to environment: disentangling species turnover vs intraspecific trait variability effects. *Ecography* 34 (5): 856-863.

**See Also**

[barplot.decompCTRE](#); [traitflex.anova](#)

**Examples**

```
data(finch.ind)

res.decomp <- decompCTRE(traits = traits.finch, sp = sp.finch,
ind.plot = ind.plot.finch, print = FALSE)

barplot.decompCTRE(res.decomp)

par(mfrow = c(2,2))
barplot.decompCTRE(res.decomp, resume = FALSE)
par(mfrow = c(1,1))
```

---

finch.ind

*Finch morphological data*

---

**Description**

Individual morphological data for Darwin's finches. `finch` is the all data.frame. `ind.plot.finch` and `sp.finch` respectively correspond to the Island and the species attribute of each individual. `traits.finch` is the matrix of traits with four traits in rows and 2677 individuals in columns.

**Usage**

```
data(finch.ind)
```

**Format**

A data.frame of 2677 individuals in rows and 14 columns.

**Details**

See <http://bioquest.org/birdd/morph.php> for more information on database.

**Source**

<http://bioquest.org/birdd/morph.php>

**Examples**

```
data(finch.ind)
```

---

Fred	<i>Functional richness, evenness and divergence following Villeger et al. 2008</i>
------	--

---

**Description**

Compute the 3 functional diversity indices (multi-traits) presented in Villeger et al. 2008 (Ecology 89 2290-2301): Functional richness (FRic), Functional evenness (FEve), Functional divergence (FDiv)

**Usage**

```
Fred(traits, ind.plot)
```

**Arguments**

traits	Individual Matrix of traits with traits in columns. NA are not allowed .
ind.plot	Factor defining the name of the plot in which the individual is.

**Details**

For each trait, values are standardized (mean=0 and standard deviation=1) For FRic computation, number of individuals must be higher than number of traits

**Value**

list of 4 vectors with values of indices in each sites

\$nbind	number of individuals
\$FRic	functional richness index
\$FEve	functional evenness index
\$FDiv	functional divergence index

**Author(s)**

Sebastien Villeger sligthy modified by Adrien Taudiere

**See Also**

[ComIndexMulti](#) [ComIndex](#)



**Examples**

```
data(finch.ind)
## Not run:
#For most multivariate functions we need to replace (or exclude) NA values.
#For this example, we use the package mice to complete the data.

comm<-t(table(ind.plot.finch,1:length(ind.plot.finch)))

library(mice)
traits = traits.finch
mice<-mice(traits.finch)
traits.finch.mice<-complete(mice)
fred<-Fred(traits.finch.mice, ind.plot.finch)

## End(Not run)
```

---

IndexByGroups	<i>Apply metrics to groups.</i>
---------------	---------------------------------

---

**Description**

Transforme a list of metrics to apply them to groups, typically to populations.

**Usage**

```
IndexByGroups(metrics, groups)
```

**Arguments**

metrics	A vector of metrics like the argument "index" of function ComIndex
groups	Name of the factor to apply the metrics to groups in the form "pop", e.g. population

**Value**

A vector of transformed metrics

**Author(s)**

Adrien Taudiere

---

MinMaxMST	<i>Ratio of the shortest distance to the longest distance in a minimum spanning tree</i>
-----------	--

---

### Description

Ratio of the shortest distance to the longest distance in a minimum spanning tree.

### Usage

```
MinMaxMST(traits, gower.dist = TRUE, scale.tr = TRUE, method.dist = "euclidian")
```

### Arguments

traits	Traits matrix (traits in column)
gower.dist	Calculate gower distance using the function gowdis from package FD.
scale.tr	Does traits need to be scale before multi-traits metric calculation? Only use when gower.dist = FALSE. Default is yes.
method.dist	Method to calculate the distance in case of multi-traits metric (function dist). Only use when gower.dist = FALSE. Default is euclidian.

### Value

The value of the ratio of the shortest distance to the longest distance in a minimum spanning tree.

### Author(s)

Aiba et al., 2013 modified by Adrien Taudiere

### References

Stubbs, WJ., and Wilson, JB. 2004. Evidence for limiting similarity in a sand dune community. *Journal of Ecology* 92: 557-567. Aiba, M., Katabuchi, M., Takafumi, H., Matsuzaki, S.S., Sasaki, T. & Hiura, T. 2013. Robustness of trait distribution metrics for community assembly studies under the uncertainties of assembly processes. *Ecology*, 94, 2873-2885.

### Examples

```
## Not run:

data(finch.ind)

MinMaxMST(traits.finch[1:10,])
MinMaxMST(traits.finch[1:10,], gower.dist = FALSE)
MinMaxMST(traits.finch[1:10,], gower.dist = FALSE, scale.tr = FALSE)

## End(Not run)
```

---

Neighbourhood distance metrics

*Coefficient of variation, mean, minimum and standard deviation of the nearest neighbourhood distance.*

---

### Description

CVNND : Coefficient of variation of the nearest neighbourhood distance

MNND : Mean of the nearest neighbourhood distance

MinNND : Minimum of the nearest neighbourhood distance

SDNND : Standard deviation of the nearest neighbourhood distance

SDND : Standard deviation of the neighbourhood distance

MND : Mean of the neighbourhood distance

### Usage

```
CVNND(traits, div_range = FALSE, na.rm = FALSE, scale.tr = TRUE,
method.dist = "euclidian")
```

```
MNND(traits, div_range = FALSE, na.rm = FALSE, scale.tr = TRUE,
method.dist = "euclidian")
```

```
MinNND(traits, div_range = FALSE, na.rm = FALSE, scale.tr = TRUE,
method.dist = "euclidian")
```

```
SDNND(traits, div_range = FALSE, na.rm = FALSE, scale.tr = TRUE,
method.dist = "euclidian")
```

```
SDND(trait, div_range = FALSE, na.rm = FALSE)
```

```
MND(trait, div_range = FALSE, na.rm = FALSE)
```

### Arguments

traits	Trait vector (uni-trait metric) or traits matrix (Multi-traits metric), traits in column.
trait	Trait vector
div_range	Does metric need to be divided by the range? Default is no.
na.rm	If div_range=TRUE, a logical value indicating whether NA values should be stripped before the computation proceeds.
scale.tr	Does traits need to be scale before multi-traits metric calculation? Default is yes.
method.dist	Method to calculate the distance in case of multi-traits metric (function dist). Default is euclidian.

**Value**

One value corresponding to the metric value.

**Author(s)**

Adrien Taudiere

**References**

Aiba, M., Katabuchi, M., Takafumi, H., Matsuzaki, S.S., Sasaki, T. & Hiura, T. 2013. Robustness of trait distribution metrics for community assembly studies under the uncertainties of assembly processes. *Ecology*, 94, 2873-2885. Jung, Vincent, Cyrille Violle, Cedric Mondy, Lucien Hoffmann, et Serge Muller. 2010. Intraspecific variability and trait-based community assembly: Intraspecific variability and community assembly. *Journal of Ecology* 98 (5): 1134-1140.

**Examples**

```
data(finch.ind)

CVNND(traits.finch[,1], na.rm = TRUE)
CVNND(traits.finch[,1], div_range = TRUE, na.rm = TRUE)
CVNND(traits.finch, na.rm = TRUE)
CVNND(traits.finch, scale.tr = FALSE, na.rm = TRUE)
SDND(traits.finch[,1], na.rm = TRUE)
```

---

partvar

*Variance partitioning accross nested scales*

---

**Description**

Variance partitioning accross nested scales using a decomposition (varcomp function) of variance on restricted maximum likelihood (REML) method (lme function). See Messier et al. 2010 for more information. barPartvar and piePartvar are associated plotting functions.

**Usage**

```
partvar(traits, factors, printprogress = TRUE)
barPartvar(partvar, col.bar = NA, ...)
piePartvar(partvar, col.pie = NA, ...)
```

**Arguments**

traits	Matrix of traits with traits in column
factors	A matrix of factors with the first column corresponds to the higher level factor, the second row the second higher level factor and so on.
printprogress	Logical value; print progress during the calculation or not.

partvar	The result of the partvar function.
col.bar	Vector of colors of bars
...	Any additional arguments are passed to the pie function.
col.pie	Vector of color for pie.

### Value

An object of class "partvar" corresponding to a matrix of variance values with traits in rows and nested factors in column.

### Author(s)

Adrien Taudiere Julie Messier

### References

Messier, Julie, Brian J. McGill, et Martin J. Lechowicz. 2010. How do traits vary across ecological scales? A case for trait-based ecology: How do traits vary across ecological scales? *Ecology Letters* 13(7): 838-848. doi:10.1111/j.1461-0248.2010.01476.x.

### See Also

[piePartvar](#); [barPartvar](#)

### Examples

```
data(finch.ind)

cond<-seq(1,length(sp.finch)*2, by = 2)
genus <- as.vector(unlist(strsplit(as.vector(sp.finch),"_"))[cond])

res.partvar.finch <- partvar(traits = traits.finch,
  factors = cbind(sites = as.factor(as.vector(ind.plot.finch)),
  species = as.factor(as.vector(sp.finch)), genus = as.factor(genus)))

res.partvar.finch

oldpar<-par()
par(mfrow = c(2,2), mai = c(0.2,0.2,0.2,0.2))
piePartvar(res.partvar.finch)
par(oldpar)

barPartvar(res.partvar.finch)
```

---

plot.listofindex      *Plot community assembly index*

---

### Description

Plot community assembly index and confidence intervals using a list of index. S3 method for class listofindex.

### Usage

```
## S3 method for class 'listofindex'
plot(x, type = "normal",
     col.index = c("red", "purple", "olivedrab3"), add.conf = TRUE,
     color.cond = TRUE, val.quant = c(0.025, 0.975),
     grid.v = TRUE, grid.h = TRUE, xlim = NULL, ylim = NULL,
     cex.text = 0.8, plot.ask = FALSE, srt.text = 90, alpha = 0.4, ...)
```

### Arguments

x	A list of index and related null models obtained from to the as.listofindex function.
type	Type of plot. Possible type = "simple", "simple_range", "normal", "barplot" and "bytraits".
col.index	Vector of colors for index.
add.conf	Logical value; Add confidence intervals or not.
color.cond	Logical value; If color.cond = TRUE, color points indicate T-statistics values significantly different from the null model and grey points are not different from null model.
val.quant	Numeric vectors of length 2, giving the quantile to calculate confidence interval. By default val.quant = c(0.025,0.975) for a bilateral test with alpha = 5%.
grid.v	Logical value; print vertical grid or not
grid.h	Logical value; print horizontal grid or not
xlim	Numeric vectors of length 2, giving the x coordinates range
ylim	Numeric vectors of length 2, giving the y coordinates range
cex.text	Numeric value; the magnification to be used for text relative to the current setting of cex
plot.ask	Logical value; ask for plotting the next plot or not.
srt.text	Degree of rotation for text.
alpha	Degree of transparency for null models aera.
...	Any additional arguments are passed to the plot function creating the core of the plot and can be used to adjust the look of resulting graph.

**Details**

S3 method plot for class listofindex: -Normal type plot means, standard deviations, ranges and confidence intervals of T-statistics. -Simple\_range type plot means, standard deviations and range of T-statistics -Simple type plot T-statistics for each site and traits and the mean confidence intervals by traits -Barplot type plot means, standard deviations and confidence intervals of T-statistics in a barplot fashion -Bysites type plot each metrics for each sites -Bytraits type plot each metrics for each traits

**Value**

None; used for the side-effect of producing a plot.

**Author(s)**

Adrien Taudiere

**See Also**

[as.listofindex](#); [plot.Tstats](#); [ses.listofindex](#)

**Examples**

```
data(finch.ind)

res.finch <- Tstats(traits.finch, ind.plot = ind.plot.finch,
sp = sp.finch, nperm = 9, print = FALSE)

## Not run:
#### Use a different regional pool than the binding of studied communities
#create a random regional pool for the example

reg.p <- rbind(traits.finch, traits.finch[sample(1:2000,300), ])

res.finch2 <- Tstats(traits.finch, ind.plot = ind.plot.finch,
  sp = sp.finch, reg.pool=reg.p, nperm = 9, print = FALSE)

plot(as.listofindex(list(res.finch,res.finch2)))

#### Use a different regional pool for each communities
#create a random regional pool for each communities for the example
list.reg.p <- list(
traits.finch[sample(1:290,200), ], traits.finch[sample(100:1200,300), ],
traits.finch[sample(100:1500, 1000), ], traits.finch[sample(300:800,300), ],
traits.finch[sample(1000:2000, 500), ], traits.finch[sample(100:900, 700), ] )

# Warning: the regional pool need to be larger than the observed communities
table(ind.plot.finch)
# For exemple, the third community need a regional pool of more than 981 individuals
```

```
res.finch3 <- Tstats(traits.finch, ind.plot = ind.plot.finch,
  sp = sp.finch, reg.pool=list.reg.p, nperm = 9, print = FALSE)

plot(as.listofindex(list(res.finch, res.finch2, res.finch3)))

## End(Not run)
```

---

plotCorTstats

*Plot the bivariate relationships between T-statistics*


---

### Description

Plot the bivariate relationships between the three T-statistics namely T\_IP.IC, T\_IC.IR and T\_PC.PR.

### Usage

```
plotCorTstats(tstats = NULL, val.quant = c(0.025, 0.975),
  add.text = FALSE, bysite = FALSE, col.obj = NULL, plot.ask = TRUE,
  multipanel = TRUE, ...)
```

### Arguments

tstats	The list resulting from the function Tstats.
val.quant	Numeric vector of length 2, giving the quantile to calculate confidence interval. By default val.quant = c(0.025,0.975) for a bilateral test with alpha = 5%.
add.text	Logical value; Add text or not.
bysite	Logical value; plot per site or by traits.
col.obj	Vector of colors for object (either traits or sites).
plot.ask	Logical value; Ask for new plot or not.
multipanel	Logical value. If TRUE divides the device to shown several traits graphics in the same device.
...	Any additional arguments are passed to the plot function creating the core of the plot and can be used to adjust the look of resulting graph.

### Value

None; used for the side-effect of producing a plot.

### Author(s)

Adrien Taudiere

### See Also

[Tstats](#); [plot.Tstats](#); [plotSESvar](#)



**Examples**

```

data(finch.ind)
res.finch <- Tstats(traits.finch, ind.plot = ind.plot.finch,
sp = sp.finch, nperm = 9)

plotCorTstats(res.finch, bysite = FALSE)
plotCorTstats(res.finch, bysite = TRUE)

```

---

plotDistri

*Plot function to represent density of trait values*


---

**Description**

Plot function to represent density of trait values

**Usage**

```

plotDistri(traits = NULL, var.1 = NULL, var.2 = NULL, col.dens = NULL,
plot.ask = TRUE, ylim.cex = 1, cex.leg = 0.8, polyg = TRUE,
multipanel = TRUE, leg = TRUE, xlim = NULL, ylim = NULL,
main = "default", ...)

```

**Arguments**

traits	Matrix of traits with traits in column.
var.1	The first variable defines the division of each plots, in most case either a vector of species or name of sites.
var.2	The second variable define the division by color, in most case either a vector of species or name of sites.
col.dens	A vector of colors for the second variable.
plot.ask	Logical value; ask for plotting the next plot or not.
ylim.cex	Numeric value; the magnification to be used for range of y axe
cex.leg	Numeric value; the magnification to be used for legend relative to the current setting of cex
polyg	Logical value; do the mean distribution is full or empty
multipanel	Logical value. If TRUE divides the device to shown several traits graphics in the same device.
leg	Logical value; if TRUE print the legend.
ylim	Numeric vectors of length 2, giving the y coordinates range
xlim	Numeric vectors of length 2, giving the y coordinates range
main	Title for the plot. Default set automatic title using informations in the input dataset.
...	Any additional arguments are passed to the plot function creating the core of the plot and can be used to adjust the look of resulting graph.

**Value**

None; used for the side-effect of producing a plot.

**Author(s)**

Adrien Taudiere

**See Also**

[plotSpPop](#)

**Examples**

```

data(finch.ind)

## Not run:
#Plot the distribution of trait values for populations,
#species, sites and regional scales.

### First, let try the distribution for all populations
#of Darwin finches.

par(mfrow = c(4,4), cex = 0.5)
plotDistri(traits.finch, sp.finch, ind.plot.finch, ylim.cex = 3,
plot.ask = FALSE, multipanel = FALSE, leg = FALSE)

### Then we can inverse the second and the third arguments
#to plot the distribution for all finches species.

par(mfrow = c(4,4), cex = 0.5)
plotDistri(traits.finch, ind.plot.finch, sp.finch, ylim.cex = 8,
plot.ask = FALSE, multipanel = FALSE, leg = FALSE)

### Only one trait to plot using leg = TRUE to plot the legend

par(mfrow=c(2,3))
plotDistri(as.matrix(traits.finch[,1]), ind.plot.finch, sp.finch,
  ylim.cex=8, plot.ask = FALSE, multipanel = FALSE, leg = TRUE, cex.leg=0.5)

### You can also plot trait distribution for all species in the region

par(mfrow = c(1,1), cex = 1)
plotDistri(traits.finch, rep("region", times = dim(traits.finch)[1]),
sp.finch, ylim.cex = 6, plot.ask = FALSE, leg = FALSE)

## End(Not run)

### You can also plot trait distribution for all sites
#without taking into account species identity

```

```
plotDistri(traits.finch, rep("toutes_sp", times = dim(traits.finch)[1]),
ind.plot.finch, ylim.cex = 3, plot.ask = FALSE)
```

---

plotRandtest

*Plot result of observed indices values against null distribution*

---

### Description

Function to plot result of observed indices values against null distribution.

### Usage

```
plotRandtest(x, alternative = "two-sided", ...)
```

### Arguments

x	An object of class listofindex, ComIndex, ComIndexMulti or Tstats.
alternative	Indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter. "greater" corresponds to positive association, "less" to negative association.
...	Any additional arguments are passed to the plot function creating the core of the plot and can be used to adjust the look of resulting graph.

### Value

None; used for the side-effect of producing a plot.

### Author(s)

Adrien Taudiere

### See Also

[ComIndex](#); [ComIndexMulti](#); [Tstats](#); [as.listofindex](#); [plot.listofindex](#)

### Examples

```
data(finch.ind)
## Not run:
res.finch <- Tstats(traits.finch, ind.plot = ind.plot.finch,
sp = sp.finch, nperm = 99, print = FALSE)

par(mfrow = c(4,4))

plotRandtest(res.finch)
plotRandtest(res.finch, alter = "less")

## End(Not run)
```

---

`plotSESvar`*Plot SES values against a variable*

---

**Description**

Plot standardized effect size values against a variable

**Usage**

```
plotSESvar(index.list, variable = NULL, ylab = "variable",
  color.traits = NULL, val.quant = c(0.025, 0.975), resume = FALSE,
  multipanel = TRUE)
```

**Arguments**

<code>index.list</code>	A list of index and the associate null models in the forme: <code>list( index_1 = index_1_observed, index_1_nm = null.model.index_1 ,index_2 = index_2_observed, index_2_nm = null.model.index_2, ...)</code> .
<code>variable</code>	The variable against standardized effect sizes are plotted.
<code>ylab</code>	Label for the variable.
<code>color.traits</code>	A vector of colors corresponding to traits.
<code>val.quant</code>	Numeric vectors of length 2, giving the quantile to calculation confidence interval. By default <code>val.quant = c(0.025,0.975)</code> for a bilateral test with alpha = 5%.
<code>resume</code>	Logical value; <code>resume = FALSE</code> by default; Simplify the plot by plotting the mean and standard error for index value of multiple traits
<code>multipanel</code>	Logical value. If <code>TRUE</code> divides the device to shown several traits graphics in the same device.

**Value**

None; used for the side-effect of producing a plot.

**Author(s)**

Adrien Taudiere

**See Also**

[plot.listofindex](#); [ses](#)

**Examples**

```

data(finch.ind)
res.finch <- Tstats(traits.finch, ind.plot = ind.plot.finch, sp = sp.finch,
nperm = 9)

par(mfrow = c(2,2))
species.richness <- table(ind.plot.finch)
plotSESvar(as.listofindex(list(res.finch)), species.richness,
multipanel = FALSE)

#Same plot with resume = TRUE.

par(mfrow = c(2,2))
plotSESvar(as.listofindex(list(res.finch)), species.richness,
resume = TRUE, multipanel = FALSE)
par(mfrow = c(1,1))

```

---

plotSpPop

*Plot populations values against species values*


---

**Description**

Plot populations values against species values. The objectif is to see the contribution of intra-specific vs inter-specific variation to trait gradient.

**Usage**

```

plotSpPop(traits = NULL, ind.plot = NULL, sp = NULL,
col.ind = rgb(0.5, 0.5, 0.5, 0.5), col.pop = NULL, col.sp = NULL,
col.site = NULL, resume = FALSE, p.val = 0.05, min.ind.signif = 10,
multipanel = TRUE, col.nonsignif.lm = rgb(0, 0, 0, 0.5),
col.signif.lm = rgb(1, 0.1, 0.1, 0.8), silent = FALSE)

```

**Arguments**

traits	Individual Matrix of traits with traits in columns.
ind.plot	Factor defining the name of the plot in which the individual is.
sp	Factor defining the species which the individual belong to.
col.ind	Color for individual values.
col.pop	Color for populational mean values.
col.sp	Color for species mean values.
col.site	Color for sites mean values.
resume	Logical, if TRUE plot a simple form of the plot.
p.val	Chosen p.value to print significant linear relationship using linear model. Argument past to the lm funtion internally.

min.ind.signif Minimum individual to print significant linear relationship.  
 multipanel Logical value. If TRUE divides the device to shown several traits graphics in the same device.  
 col.nonsignif.lm Color for non significant linear relationship.  
 col.signif.lm Color for significant linear relationship.  
 silent Logical value, if resume = FALSE do not print warning argument.

### Details

Example of utilisation: Cornwell, W.K., Ackerly, D.D., 2009. Community assembly and shifts in plant trait distributions across an environmental gradient in coastal California. *Ecological Monographs* 79, 109-126.

### Value

None; used for the side-effect of producing a plot.

### Author(s)

Adrien Taudiere

### See Also

[plotDistri](#)

### Examples

```
data(finch.ind)
plotSpPop(traits.finch, ind.plot.finch, sp.finch, silent = TRUE)

#If we change the value of the threshold
#(alpha = 10% instead of 5%
#and the minimum individual to represent significativity
#fixed to 3 instead of 10 by default)
#we can see some significant relationships.

plotSpPop(traits.finch, ind.plot.finch, sp.finch, p.val = 0.1,
min.ind.signif = 3, silent = TRUE)

#For a more simple figure, add the option resume = TRUE.
#Again if we change the value of the threshold
#(alpha = 10% instead of 5%
#and the minimum individual to represent significativity
# fixed to 3 instead of 10 by default)
#we can see some significant relationships.

plotSpPop(traits.finch, ind.plot.finch, sp.finch, silent = TRUE,
resume = TRUE, col.pop = "grey")
```

```
plotSpPop(traits.finch, ind.plot.finch, sp.finch, silent = TRUE,
resume = TRUE, col.pop = "grey", col.sp = "black")
```

```
plotSpPop(traits.finch, ind.plot.finch, sp.finch, silent = TRUE,
resume = TRUE, col.pop = "grey", col.sp = "black",
p.val = 0.1, min.ind.signif = 3)
```

plotSpVar

*Plot populations values against species values***Description**

Plot populations values against species values. The objectif is to see the contribution of intra-specific vs inter-specific variation to trait gradient.

**Usage**

```
plotSpVar(traits = NULL, ind.plot = NULL, sp = NULL, variable = NULL,
col.ind = rgb(0.5, 0.5, 0.5, 0.5), col.pop = NULL, col.sp = NULL,
col.site = NULL, resume = FALSE, p.val = 0.05, min.ind.signif = 10,
multipanel = TRUE, col.nonsignif.lm = rgb(0, 0, 0, 0.5),
col.signif.lm = rgb(1, 0.1, 0.1, 0.8), silent = FALSE)
```

**Arguments**

traits	Individual Matrix of traits with traits in columns.
ind.plot	Factor defining the name of the plot in which the individual is.
sp	Factor defining the species which the individual belong to.
variable	A matrix of variables corresponding to each site (in rows) and each trait (in columns). If you want to plot all traits against one variable, variable can be a vector of numerical values.
col.ind	Color for individual values.
col.pop	Color for populational mean values.
col.sp	Color for species mean values.
col.site	Color for sites mean values.
resume	Logical, if TRUE plot a simple form of the plot.
p.val	Chosen p.value to print significant linear relationship using linear model. Argument past to the lm funtion internally.
min.ind.signif	Minimum individual to print significant linear relationship.
multipanel	Logical value. If TRUE divides the device to shown several traits graphics in the same device.
col.nonsignif.lm	Color for non significant linear relationship.
col.signif.lm	Color for significant linear relationship.
silent	Logical value, if resume = FALSE do not print warning argument.

**Value**

None; used for the side-effect of producing a plot.

**Author(s)**

Adrien Taudiere

**See Also**

[plotDistri](#)

**Examples**

```
data(finch.ind)

#Random variable for this example
variable <- c(1,5,15,6,3,25)

plotSpVar(traits.finch, ind.plot.finch, sp.finch, variable,
silent = TRUE)

#If we change the value of the threshold
#(alpha = 10% instead of 5%
#and the minimum individual to represent significativity
#fixed to 3 instead of 10 by default)
#we can see some significant relationships.

plotSpVar(traits.finch, ind.plot.finch, sp.finch, variable,
p.val = 0.1, min.ind.signif = 3, silent = TRUE)

#For a more simple figure, add the option resume = TRUE.
#Again if we change the value of the threshold
#(alpha = 10% instead of 5%
#and the minimum individual to represent significativity
# fixed to 3 instead of 10 by default)
#we can see some significant relationships.

plotSpVar(traits.finch, ind.plot.finch, sp.finch, variable,
silent = TRUE, resume = TRUE, col.pop = "grey")

plotSpVar(traits.finch, ind.plot.finch, sp.finch, variable,
silent = TRUE, resume = TRUE, col.pop = "grey", col.sp = "black")

plotSpVar(traits.finch, ind.plot.finch, sp.finch, variable,
silent = TRUE, resume = TRUE, col.pop = "grey", col.sp = "black",
p.val = 0.1, min.ind.signif = 3)
```



---

Pval	<i>Calcul of p-value for object of class Tstats, ComIndex, ComIndexMulti and listofindex</i>
------	--

---

**Description**

Calcul of p-value for object of class Tstats, ComIndex, ComIndexMulti and listofindex. This test equates to finding the quantile in exp in which obs would be found (under a one-tailed test).

**Usage**

```
Pval(x, na.rm = TRUE)
```

**Arguments**

x	An object of class Tstats, ComIndex, ComIndexMulti or listofindex.
na.rm	A logical value indicating whether NA values should be stripped before the computation proceeds.

**Value**

A list of p-value for each metrics, traits and grouping if needed (e.g. sites)

**Author(s)**

Adrien Taudiere

**Examples**

```
data(finch.ind)
res.finch <- Tstats(traits.finch, ind.plot = ind.plot.finch,
sp = sp.finch, nperm = 9, print = FALSE)

Pval(res.finch)
```

---

RandCom	<i>Toy model to simulate internal and/or external filtering</i>
---------	---

---

**Description**

Toy model to simulate internal and/or external filtering

**Usage**

```
RandCom(Ncom = 10, Nsp = 20, Nind.com = 100, sdlog = 1.5,
min_value_traits = 80, max_value_traits = 200,
cv_intra_sp = 1.5, cv_intra_com = 1.5,
Int_Filter_Strength = 50, Ext_Filter_Strength = 50, Filter="None")
```

**Arguments**

Ncom	Number of communities (or sites).
Nsp	Number of species at the regional scale.
Nind.com	Number of individuals by communities.
sdlog	Parameter of the log normal distribution for species abundances distribution within communities.
min_value_traits	Minimum mean value for traits distributions.
max_value_traits	Maximum mean value for traits distributions.
cv_intra_sp	Coefficient of variation for intra-specific distributions. The more the value is high the less there is internal filtering. Used only for the trait 1 (normally distributed).
cv_intra_com	Coefficient of variation for intra-community distributions. The more the value is high the less there is external filtering. Used only for the trait 1 (normally distributed)
Int_Filter_Strength	Strength of internal filtering in percentage. Use in addition to cv_intra_sp by distributing mean species trait more or less evenly. In the most extreme case (if Int_Filter_Strength==100), species have equally distributed mean values along the trait gradient.
Ext_Filter_Strength	Strength of external filtering in percentage. Use in addition to cv_intra_com by distributing mean communities trait more or less evenly. In the most extreme case (if Ext_Filter_Strength==100), communities have equally distributed mean values along the trait gradient.
Filter	The type of filter to simulate. Either "None", "Internal", "External" or "Both"

**Details**

In this version of the function, the trait 1 follows a normal distribution whereas the trait 2 follows a uniform distribution.

**Value**

\$data\$com	Vector of simulated communities for each individual.
\$data\$sp	Vector of simulated species for each individual.
\$data\$trait1	Vector of simulated value for the trait 1: normally distributed.
\$data\$trait2	Vector of simulated value for the trait 2: normally distributed.
\$call	call of the function Tstats

**Author(s)**

Cecile Albert and Adrien Taudiere

**Examples**

```
res <- RandCom()
```

---

RaoRel	<i>Alpha, gamma and beta-components for taxonomic, functional and phylogenetic diversity</i>
--------	--

---

**Description**

The Rao function computes alpha, gamma and beta-components for taxonomic, functional and phylogenetic diversity with the Rao index. The script integrates two functions: "Qdecomp", by Villeger et Mouillot (J Ecol, 2008) modified by Wilfried Thuiller, and "disc", by S. Pavoine, in the package ade4. For a regional assemblage of C local communities  $\gamma = \text{mean}(\alpha) + \beta$ , where: gamma is the diversity of the regional pool, alpha is the diversity of the local community and beta is the turn over between local communities diversity is estimated with the Rao quadratic entropy index (Rao 1982)

**Usage**

```
RaoRel(sample, dfunc, dphyl, weight = FALSE, Jost = FALSE,
        structure = NULL)
```

**Arguments**

sample	Community matrix of abundance (c x s) of the s species for the c local communities.
dfunc	matrix (s x s) or dist object with pairwise functional trait distances between the s species
dphyl	As dfunc but for phylogenetic distances
weight	Defining if the correction by Villeger & Mouillot (J Ecol, 2008) is applied or not
Jost	Defining if the Jost correction is applied (Jost 2007)
structure	A data frame containing the name of the group to which samples belong see de Bello et al, 2011 for more details.

**Details**

NA are automatically replaced by 0 in "sample". This function use the function "Qdecomp" by Sebastien Villeger & David Mouillot (J Ecol, 2008) modified by Wilfried Thuiller and the function disc originally proposed by Sandrine Pavoine.

**Value**

The results are organized for Taxonomic diversity (\$TD), Functional diversity (\$FD) and phylogenetical diversity (\$PD). Beta and gamma diversities are calculated for the whole data set and for each pair of samples ("Pairwise\_samples"):

\$Richness\_per\_plot(number of species per sample)

\$Relative\_abundance (species relative abundances per plot)

\$Pi (species regional relative abundance)

\$Wc (weighting factor),

\$Mean\_Alpha (mean alpha diversity; for taxonomic diversity the Simpson index is calculated)

\$Alpha (alpha diversity for each sample; for taxonomic diversity the Simpson index is calculated)

\$Gamma (gamma diversity; for taxonomic diversity the Simpson index is calculated)

\$Beta\_add (Gamma-Mean\_Alpha)

\$Beta\_prop (Beta\_add\*100/Gamma)

\$Pairwise\_samples\$Alpha (mean alpha for each pair of samples)

\$Pairwise\_samples\$Gamma (gamma for each pair of samples)

\$Pairwise\_samples\$Beta\_add (beta for each pair of samples as Gamma-Mean\_Alpha)

\$Pairwise\_samples\$Beta\_prop (beta for each pair of samples as Beta\_add\*100/Gamma)

**Author(s)**

Francesco De Bello et al., 2011 modified by Adrien Taudiere

**References**

De Bello, Francesco, Sandra Lavorel, Cecile H. Albert, Wilfried Thuiller, Karl Grigulis, Jiri Dolezal, stepan Janecek, et Jan Leps. 2011. Quantifying the relevance of intraspecific trait variability for functional diversity: Intraspecific variability in functional diversity. *Methods in Ecology and Evolution* 2: 163-174.

**Examples**

```
data(finch.ind)

## Not run:
comm <- t(table(ind.plot.finch,1:length(ind.plot.finch)))
comm.sp <- table(sp.finch, ind.plot.finch)
class(comm.sp) <- "matrix"

traits.finch.sp <- apply( apply(traits.finch, 2, scale ), 2,
function(x) tapply(x, sp.finch, mean, na.rm = TRUE))

mat.dist <- (as.matrix(dist(traits.finch.sp))^2)/2

res.rao <- RaoRel(sample = as.matrix(comm.sp), dfunc = mat.dist, dphyl = NULL,
weight = FALSE, Jost = FALSE, structure = NULL)
```

```

function(x) tapply(x, sp.finch, mean, na.rm=TRUE))

mat.dist <- as.matrix(dist(traits.finch.sp))^2

res.rao <- RaoRel(sample=as.matrix(comm.sp), dfunc=mat.dist, dphyl=NULL,
weight=FALSE, Jost=FALSE, structure=NULL)

witRao <- res.rao$FD$Mean_Alpha #overall within species variance
betRao <- res.rao$FD$Beta_add #between species variance
totRao <- res.rao$FD$Gamma #the total variance

witRao+betRao
totRao

#Now let's take the abundance to calculate Rao diversity.

res.rao.w <- RaoRel(sample = as.matrix(comm.sp), dfunc = mat.dist, dphyl = NULL,
weight = TRUE, Jost = FALSE, structure = NULL)

witRao.w <- res.rao.w$FD$Mean_Alpha #overall within species variance
betRao.w <- res.rao.w$FD$Beta_add #between species variance
totRao.w <- res.rao.w$FD$Gamma #the total variance

witRao.w
betRao.w

#Plot the results

barplot(cbind(c(witRao.w, betRao.w), c(witRao, betRao)),
names.arg = c("abundance", "presence"),
legend.text = c("within species", "between species"),
ylab = "Rao", ylim = c(0,10))

#We can do this analysis for each trait separately.
#First we need to replace (or exclude) NA values.
#For this example, we use the package mice to complete the data.

comm <- t(table(ind.plot.finch,1:length(ind.plot.finch)))

library(mice)

traits = traits.finch

mice <- mice(traits.finch)
traits.finch.mice <- complete(mice)

traits.finch.mice.sp <- apply(apply(traits.finch.mice, 2, scale ), 2,

```

```

function(x) tapply(x, sp.finch, mean, na.rm = TRUE))

trait.rao.w <- list()
witRao.w.bytrait <- c()
betRao.w.bytrait <- c()

for (t in 1 : 4){
  trait.rao.w[[t]] <- RaoRel(sample = as.matrix(comm.sp),
    dfunc = (dist(traits.finch.mice.sp[,t])^2)/2, dphyl = NULL, weight = TRUE,
    Jost = FALSE, structure = NULL)

  witRao.w.bytrait <- c(witRao.w.bytrait, trait.rao.w[[t]]$FD$Mean_Alpha)
  betRao.w.bytrait <- c(betRao.w.bytrait, trait.rao.w[[t]]$FD$Beta_add)
}

#Plot the results by traits.

barplot(t(cbind( witRao.w.bytrait, betRao.w.bytrait)),
  names.arg = colnames(traits.finch),
  legend.text = c("within species", "between species"),
  ylab = "Rao", ylim = c(0,1.5))

## End(Not run)

```

---

samplingSubsetData      *Sampling subset of data.*

---

## Description

Sampling subset of data.

## Usage

```

samplingSubsetData(d = NULL, sampUnit = NULL, nperm = 9,
  type = "proportion", prop = seq(10, 100, by = 10), MinSample = 1,
  Size = NULL)

```

## Arguments

d	Dataframe of data to sample. Each line is an individual.
sampUnit	A Factor defining the sampling unit to impoverish. For example it can be the species or the plot attributes of each individual.
nperm	Number of permutations.
type	Type of sampling. Either <b>proportion</b> , <b>count</b> , <b>propBySize</b> or <b>factorBySize</b> . See details.
prop	Integer between 1 and 100. Categorical proportions to sample in percentage.
MinSample	Minimum number of individual to sample by sample unit. Default is one.

**Size** A vector of value for each individual (type **propBySize** and **factorBySize**) or for each level of factor (**factorBySize** only). Determine the rank of individual/factor when using the sampling schemes **propBySize** and **factorBySize**.

### Details

Sampling scheme **count** sample a number of individuals whereas **proportion** sample a proportion of individuals by sample unit. Sampling scheme **propBySize** sample in each sampling unit (sampUnit) a proportion of the individual ranked using the argument **Size**. Consequently, the biggest individuals (higher **Size**) will be sample before the smaller one. **factorBySize** sample a proportion of sampling unit (sampUnit) ranked using the argument **Size**. For example you can sample only the individuals of the 20% of the more abundant species.

### Value

Return a list list of sample dataframe. The first level of the list depicts the permutation and the second level depicts the different proportion/number of individual sampled by factor.

### Author(s)

Adrien Taudiere

---

ses *Standardized effect size and confidence interval for a matrix of statistics*

---

### Description

calculation standardized effect size and confidence interval for a matrix of statistics and the related null model expressed as a list or as an array. Internal function use by other functions of the package. You can transpose the observed matrix to represent either the SES by traits or by plots.

### Usage

```
ses(obs = NULL, nullmodel = NULL, val.quant = c(0.025, 0.975))
```

### Arguments

**obs** Observed matrix or vector of values.

**nullmodel** Either a list or an array of three (two for a vector of observed values) dimensions corresponding to the null model permutations.

**val.quant** Numeric vectors of length 2, giving the quantile to calculation confidence interval. By default `val.quant = c(0.025,0.975)` for a bilateral test with alpha = 5%.

**Details**

Warning: to detect automatically the correspondence between dimension of observed matrix and null model list or array, observed matrix needs to have different numbers of rows and columns. In the case of same row and column number, please verify manually the correspondance between the rows of the observed matrix and the null model array.

**Value**

A list of three components:

\$ses	Observed value of standardized effect size.
\$ses.inf	Lower limit of the confidence interval.
\$ses.sup	Upper limit of the confidence interval.

**Author(s)**

Adrien Taudiere

**See Also**

[plot.listofindex](#); [plotSESvar](#); [ses.listofindex](#)

**Examples**

```
data(finch.ind)

res.finch <- Tstats(traits.finch, ind.plot = ind.plot.finch,
sp = sp.finch, nperm = 9)

ses(res.finch$Tstats$T_IP.IC, res.finch$Tstats$T_IP.IC_nm)
```

---

ses.listofindex	<i>Standardized effect size for a list of index.</i>
-----------------	--

---

**Description**

Standardized effect size and confidence interval for a list of index.

**Usage**

```
ses.listofindex(index.list = NULL, val.quant = c(0.025, 0.975))
```

**Arguments**

index.list	A list of index obtain using the function as.listofindex.
val.quant	Numeric vectors of length 2, giving the quantile to calculation confidence interval. By default val.quant = c(0.025,0.975) for a bilateral test with alpha = 5%.



**Value**

A list which each component correspond to the result of the ses function for an index. Further, each component is a list of three components:

\$ses                    Observed value of standardized effect size.  
 \$ses.inf                Lower limit of the confidence interval.  
 \$ses.sup                Upper limit of the confidence interval.

**Author(s)**

Adrien Taudiere

**See Also**

[as.listofindex](#); [ses](#)

---

SumBL	<i>Sum of branch length of a classification dendrogram (Petchey and Gaston, 2002)</i>
-------	---

---

**Description**

Sum of branch length of a classification dendrogram (Petchey and Gaston, 2002)

**Usage**

```
SumBL(traits, gower.dist = TRUE, method.hclust = "average",
scale.tr = TRUE, method.dist = "euclidian")
```

**Arguments**

traits                    Traits matrix (traits in column)  
 gower.dist                Calculate gower distance using the function gowdis from package FD.  
 method.hclust            Define the method for the hclust function (default is "average" i.e. UPGMA).  
 scale.tr                    Does traits need to be scale before multi-traits metric calculation? Only use  
 when gower.dist = FALSE. Default is yes.  
 method.dist                Method to calculate the distance in case of multi-traits metric (function dist).  
 Only use when gower.dist = FALSE. Default is euclidian.

**Value**

The value of the sum of branch length from a classification dendrogram of traits.

**Author(s)**

Adrien Taudiere

## References

Petchey, OL., and Gaston, KJ. 2002. Functional diversity (FD), species richness and community composition. *Ecology Letters* 5:402-411

## Examples

```
## Not run:

data(finch.ind)
SumBL(traits.finch)
SumBL(traits.finch, gower.dist = FALSE)

## End(Not run)
```

---

traitflex.anova	<i>Variance decomposition for a given trait used in decompCTRE</i>
-----------------	--

---

## Description

This function decomposes variation of trait values within a community into three sources: (i) the intraspecific trait variability, (ii) the variability due to species turnover and (iii) their covariation is also separated. This decomposition is computed for the whole variation in the trait values and, The formula specified, across the contribution of various explanatory variables considered in the model. S3 method plot summarizes graphically the decomposition of trait variation, obtained with the traitflex.anova function. Print is an other S3 method for object of class traitflex.

## Usage

```
traitflex.anova(formula, specif.avg, const.avg, ...)
## S3 method for class 'traitflex'
plot(x, plot.total = FALSE, use.percentage = TRUE,
plot.covar = FALSE, cumul = FALSE,
legend.pos = if (plot.total) "topleft" else "topright",
plot.res = TRUE, ...)

## S3 method for class 'traitflex'
print(x, ...)
```

## Arguments

formula	The formula parameter must be a one-sided formula, i.e. starting with a tilde character. The response variable is specified by the next two arguments, specif.avg and const.avg.
---------	--

<code>specif.avg</code>	Vector with community trait composition values for a single trait. It is calculated from trait values specific to each community (i.e. trait values for individual species are 'specific' to each plot, or habitat, where the species is found)
<code>const.avg</code>	Vector with community trait composition values for a single trait. It is calculated from average (fixed) trait values of individual species (i.e. fixed trait value for individual species used for all habitats where the species is found)
<code>x</code>	An object of class <code>traitflex</code> .
<code>plot.total</code>	Logical value; if TRUE plot not only the individual components of variation, but also the total variation. This is useful particularly when the decomposition was done with non-trivial formula (i.e. with explanatory variables)
<code>use.percentage</code>	Logical value; if TRUE the individual plotted sources of trait variation are shown as percentages of the total variation, on 0-100 scale.
<code>plot.covar</code>	Logical value; if TRUE the covariance between within-species trait variability and the variability due to species composition turnover is plotted as yet another category within the stacked bars. The <code>plot.covar</code> argument is entirely ignored when plotting <code>traitflex</code> object fitted with a formula without any predictor variables.
<code>cumul</code>	Logical value; if TRUE values are shown in a cumulative way.
<code>legend.pos</code>	This argument allows you to specify the position of graph legend. Thus argument is entirely ignored when plotting <code>traitflex</code> object created with a formula without predictors
<code>plot.res</code>	Logical value; if <code>resume = FALSE</code> plot is not shown but the table of values used to print the plot is return.
<code>...</code>	Optional additional arguments.

### Details

The formula parameter must be a one-sided formula, i.e. starting with a tilde character. The response variable is specified by the next two arguments, `specif.avg` and `const.avg`.

### Value

An object of class `traitflex`. There are print and plot methods available for it. The object contains decomposition of sum of squares into intraspecific variation component, compositional variation component, their covariation and total in a `SumSq` element. This is a data frame with multiple rows if predictors were specified in formula argument. The `RelSumSq` element contains the same table relativized to unit row totals. Finally, the `anova.turnover`, `anova.total`, and `anova.diff` elements contain the three aov objects used to decompose the variation.

### Author(s)

Jan Leps et al., 2011 modified by Adrien Taudiere

### References

Leps, Jan, Francesco de Bello, Petr Smilauer and Jiri Dolezal. 2011. Community trait response to environment: disentangling species turnover vs intraspecific trait variability effects. *Ecography* 34 (5): 856-863.

**See Also**

[print.traitflex](#); [plot.traitflex](#); [decompCTRE](#)

---

Tstats

---

*Computing observed T-statistics (T for Traits) and null expectations.*


---

**Description**

Computing observed T-statistics (T for Traits) as three ratios of variance, namely T\_IP.IC, T\_IC.IR and T\_PC.PR. This function can also return the distribution of this three statistics under null models.

**Usage**

```
Tstats(traits, ind.plot, sp, SE = 0, reg.pool = NULL,
SE.reg.pool = NULL, nperm = 99, printprogress = TRUE,
independantTraits = TRUE)

sum_Tstats(x, val.quant = c(0.025, 0.975), type = "all")

ses.Tstats(x, val.quant = c(0.025, 0.975))

## S3 method for class 'Tstats'
barplot(height, val.quant = c(0.025, 0.975),
col.index = c("red", "purple", "olivedrab3", "white"), ylim = NULL, ...)

## S3 method for class 'Tstats'
plot(x, type = "normal", col.index = c("red", "purple", "olivedrab3"),
add.conf = TRUE, color.cond = TRUE, val.quant = c(0.025, 0.975), ...)

## S3 method for class 'Tstats'
print(x, ...)

## S3 method for class 'Tstats'
summary(object, ...)
```

**Arguments**

traits	Individual Matrix of traits with traits in columns. For one trait, use <code>as.matrix()</code> .
ind.plot	Factor defining the name of the plot in which the individual is.
sp	Factor defining the species which the individual belong to.
SE	A single value or vector of standard errors associated with each traits. Especially allow to handle measurement errors. Not used with populational null model.
reg.pool	Regional pool data for traits. If not informed, 'traits' is considered as the regional pool. This matrix need to be larger (more rows) than the matrix "traits". Use only for null model 2 (regional.ind).

SE.reg.pool	A single value or vector of standard errors associated with each traits in each regional pool. Use only if reg.pool is used. Need to have the same dimension as reg.pool.
nperm	Number of permutations. If NULL, only observed values are returned;
printprogress	Logical value; print progress during the calculation or not.
independantTraits	Logical value (default: TRUE). If independantTraits is true (default), each traits is sample independently in null models, if not, each lines of the matrix are randomized, keeping the relation (and trade-off) among traits.
x	An object of class Tstats.
height	An object of class Tstats.
object	An object of class Tstats.
val.quant	Numeric vectors of length 2, giving the quantile to calculation confidence interval. By default val.quant = c(0.025,0.975) for a bilateral test with alpha = 5%.
ylim	Numeric vectors of length 2, giving the y coordinates range
col.index	A vector of three color correspond to the three T-statistics.
color.cond	Logical value; If color.cond = TRUE, color points indicate T-statistics values significantly different from the null model and grey points are not different from null model.
type	For the plot function, type of plot. Possible type = "simple", "simple_range", "normal", "barplot" and "bytraits". For the summary function, type of summary statistics. Either "binary", "percent", "p.value", "site" or "all".
add.conf	Logical value; Add confidence intervals or not.
...	Any additional arguments are passed to the plot function creating the core of the plot and can be used to adjust the look of resulting graph. See <a href="#">plot.listofindex</a> for more arguments.

## Details

### S3 method plot:

-*Normal* type plot means, standard deviations, ranges and confidence intervals of T-statistics.

-*Simple\_range* type plot means, standard deviations and range of T-statistics

-*Simple* type plot T-statistics for each site and traits and the mean confidence intervals by traits

-*Barplot* type plot means, standard deviations and confidence intervals of T-statistics in a barplot fashion

-*Bysites* type plot each metrics for each sites

-*Bytraits* type plot each metrics for each traits

**S3 method print:** print the structure if the object of class Tstats

**S3 method summary:** print the summary statistics of the three T-statistics

**Method summary sum\_Tstats:**

-*Binary* type only test if a T-statistics is significantly different from the null expectation for each trait.

-*Percent* type determine the percentage of sites were the T-statistics is significantly different from the null expectation for each trait. Asterix shows global significance of the test.

-*P-value* type determine the p-value (two unilateral tests) of the T-statistics for each trait and sites.

-*Site* type allows to know in which sites T-statistics deviate from the null expectation.

-*All* type do all the precedent type of summary.

## Value

A list of statistics:

Tstats\$T\_IP.IC Observed ratio between variance of individuals in populations and individuals in communities

Tstats\$T\_IC.IR Observed ratio between variance of individuals in communities and individuals in the region

Tstats\$T\_PC.PR Observed ratio between variance of populations in communities and populations in the region

\$Tstats\$T\_IP.IC\_nm

If nperm is numeric; Result of simulation for T\_IP.IC

\$Tstats\$T\_IC.IR\_nm

If nperm is numeric; Result of simulation for T\_IC.IR

\$Tstats\$T\_PC.PR\_nm

If nperm is numeric; Result of simulation for T\_PC.PR

\$variances\$var\_IP

variance of individuals within populations

\$variances\$var\_PC

variance of populations within communities

\$variances\$var\_CR

variance of communities within the region

\$variances\$var\_IC

variance of individuals within communities

\$variances\$var\_PR

variance of populations within the region

\$variances\$var\_IR

variance of individuals within the region

\$variances\$var\_IP\_nm1

variance of individuals within populations in null model 1

\$variances\$var\_PC\_nm2sp

variance of populations within communities in null model 2sp

\$variances\$var\_IC\_nm1

variance of communities within the region in null model 1

\$variances\$var\_IC\_nm2

variance of individuals within communities in null model 2

```

$variances$var_PR_nm2sp
    variance of populations within the region in null model 2sp
$variances$var_IR_nm2
    variance of individuals within the region in null model 2
$traits
    traits data
$ind.plot
    name of the plot in which the individual is
$sp
    groups (e.g. species) which the individual belong to
$call
    call of the function Tstats

```

**Author(s)**

Adrien Taudiere and Cyrille Violle

**References**

Violle, Cyrille, Brian J. Enquist, Brian J. McGill, Lin Jiang, Cecile H. Albert, Catherine Hulshof, Vincent Jung, et Julie Messier. 2012. The return of the variance: intraspecific variability in community ecology. *Trends in Ecology & Evolution* 27 (4): 244-252. doi:10.1016/j.tree.2011.11.014.

**See Also**

[ComIndex](#); [ComIndexMulti](#); [plotCorTstats](#); [plotSESvar](#); [plot.listofindex](#)

**Examples**

```

data(finch.ind)

res.finch <- Tstats(traits.finch, ind.plot = ind.plot.finch,
sp = sp.finch, nperm = 9, print = FALSE)

res.finch

#Tstats class is associated to S3 methods plot, barplot and summary

plot(res.finch)

## Not run:
plot(res.finch, type = "simple")
plot(res.finch, type = "simple_range")
plot(res.finch, type = "barplot")
plot(res.finch, type = "bysites")
plot(res.finch, type = "bytraits")

## End(Not run)

attributes(sum_Tstats(res.finch))
head(sum_Tstats(res.finch)$p.value, 10)

sum_Tstats(res.finch, type = "binary")
sum_Tstats(res.finch, type = "percent")

```

```

sum_Tstats(res.finch, type = "site")
sum_Tstats(res.finch, type = "p.value")
sum_Tstats(res.finch, type = "all")

barplot(res.finch)

attributes(sum_Tstats(res.finch))
head(sum_Tstats(res.finch)$p.value, 10)

#### An other way to see "ses values" of T-statistics

# Custom theme (from rasterVis package)
require(rasterVis)

my.theme <- BuRdTheme()
# Customize the colorkey
my.ckey <- list(col = my.theme$regions$col)

levelplot(t(ses(res.finch$Tstats$T_IP.IC, res.finch$Tstats$T_IP.IC_nm)$ses),
colorkey = my.ckey, par.settings = my.theme, border = "black")

## Not run:
#### Use a different regional pool than the binding of studied communities
#create a random regional pool for the example

reg.p <- rbind(traits.finch, traits.finch[sample(1:2000,300), ])

res.finch2 <- Tstats(traits.finch, ind.plot = ind.plot.finch,
  sp = sp.finch, reg.pool=reg.p, nperm = 9, print = FALSE)

  plot(as.listofindex(list(res.finch, res.finch2)))

  #### Use a different regional pool for each communities
#create a random regional pool for each communities for the example
list.reg.p <- list(
traits.finch[sample(1:290,200), ], traits.finch[sample(100:1200,300), ],
traits.finch[sample(100:1500, 1000), ], traits.finch[sample(300:800,300), ],
traits.finch[sample(1000:2000, 500), ], traits.finch[sample(100:900, 700), ] )

# Warning: the regional pool need to be larger than the observed communities
table(ind.plot.finch)
# For exemple, the third community need a regional pool of more than 981 individuals

res.finch3 <- Tstats(traits.finch, ind.plot = ind.plot.finch,
  sp = sp.finch, reg.pool=list.reg.p, nperm = 9, print = FALSE)

  plot(as.listofindex(list(res.finch, res.finch2, res.finch3)))

## End(Not run)

#### Use the standard errors of measure in the analysis (argument SE)

```



```
## Not run:  
res.finch.SE0 <- Tstats(traits.finch, ind.plot = ind.plot.finch,  
sp = sp.finch, SE = 0, print = FALSE)  
  
res.finch.SE5 <- Tstats(traits.finch, ind.plot = ind.plot.finch,  
sp = sp.finch, SE = 5, print = FALSE)  
  
plot(as.listofindex(list(res.finch.SE0, res.finch.SE5)))  
  
## End(Not run)
```

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