

Illustrating package cati (Community Assembly by Traits: Individuals and beyond) using Darwin finches data

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Abstract

1) The description of species by functional traits and the subsequent quantification of the functional structure of ecological communities have recently stimulated the field of community ecology. Patterns of trait distribution within communities are increasingly reliable indicator of community assembly processes. Myriad functional diversity indices and analytical tools – including the implementation of null models of community assembly – have been developed to detect and quantify different assembly process. With increased methodological complexities, such as the incorporation of intraspecific trait variation, the construction of a unified R package to test community assembly using functional traits, and its scale-dependency, is imperative and timely particularly to take into account the role of intraspecific variation in community ecology.

2) We introduce the R package cati, available on CRAN, specifically dedicated to community assembly analyses using functional traits. The package includes: (i) the use of single-trait and multi-trait indices to characterize the functional structure of communities; (ii) the partitioning of functional trait variation across spatial scales and organizational levels, noticeably to account for individual differences and their implications for community assembly and the maintenance of species coexistence; (iii) the implementation of flexible null models to detect and quantify environmental filters.

3) cati offers a comprehensive tool to detect and quantify assembly processes and can be applied to any kind of community (plant, animal, fungi...). Moreover, the possibility to import any type of ecological distances (notably phylogenetic and genetic distances) in cati allows a test of the response of different facets of biodiversity to assembly processes.

Key words: Functional space, functional structure, community assembly, ecological niche, environmental filter, individual differences, intraspecific variation, null model, trait, variance decomposition

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1 Introduction

This vignette present the `cati` package for R (Community Assembly by Traits: Individuals and beyond) using Darwin finches data.

2 Getting started

2.1 Installing the package `cati`

Before going further, we shall make sure that `cati` is well installed on the computer. The current version of the package is 0.93. Make sure you have a recent version of R ($\geq 3.0.2$) by typing:

```
R.version.string  
## [1] "R version 3.1.1 (2014-07-10)"
```

Then, install `cati` with dependencies using:

```
install.packages("cati")  
  
## Installing package into 'C:/Users/taudiere/Documents/R/win-library/3.1'  
## (as 'lib' is unspecified)  
## Error: trying to use CRAN without setting a mirror  
  
library("cati")  
  
## Loading required package: nlme  
## Loading required package: ade4  
## Loading required package: ape
```

We can now load the package alongside other useful packages:

```
library("mice")  
  
## Loading required package: Rcpp  
## Loading required package: lattice  
## mice 2.22 2014-06-10  
  
library("hypervolume")  
  
## Loading required package: rgl
```

You can make sure that the right version of the package is installed using:

```
packageDescription("cati", fields = "Version")  
## [1] "0.93"
```

`cati` version should read 0.93.

2.2 Getting help

To get help for a given function, use `?foo` where `foo` is the function of interest. For instance:

```
?Tstats
```

will open up the manpage of T-statistics function (`Tstats`). An 'example' section will shows how to use a function at the end of the manpage.

Note that you can also browse help pages as html pages, using:

```
help.start()
```

To go to the `cati` man page on Rstudio, click 'packages' in the lower right windows, then clik 'cati', and 'cati-package'.

2.3 Data presentation: Darwin finches in Galapagos Island

First we need to load the data.

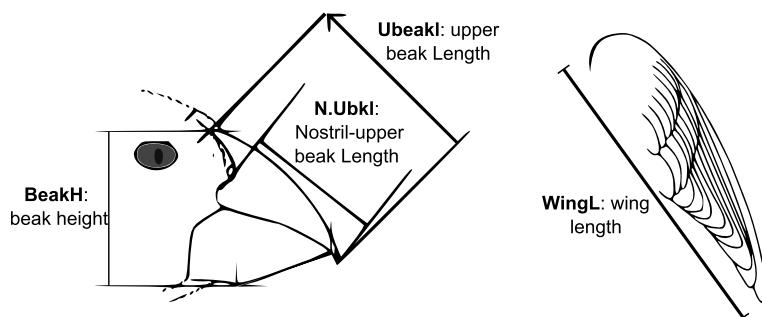
```
data(finch.ind)

#Save default parameters
old.par<-par(no.readonly = TRUE)
```

Now we can see 3 objects: a traits matrix `traits.finch`, a vector of species names `sp.finch` and a vector of sites names `ind.plot`.

```
dim(traits.finch)
#the trait matrix contains 2513 individuals values for 4 traits
table(sp.finch)
#the species names vector contains
#2513 individuals belonging to 12 species
table(ind.plot.finch)
#the sites names vector contains
#2513 individuals belonging to 6 sites (Here 6 Island)
```

The four traits correspond to three beak traits and one wing trait.

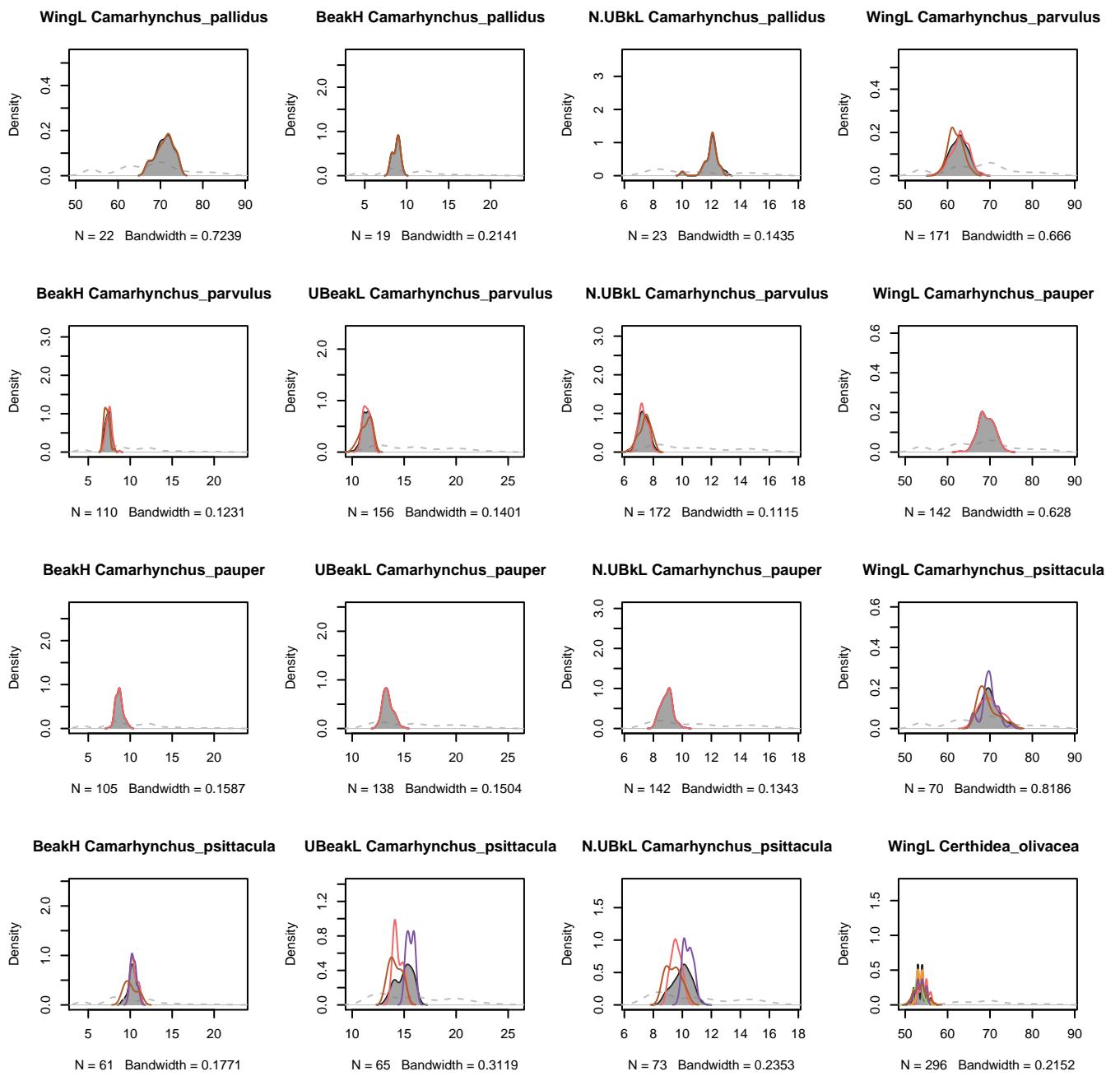


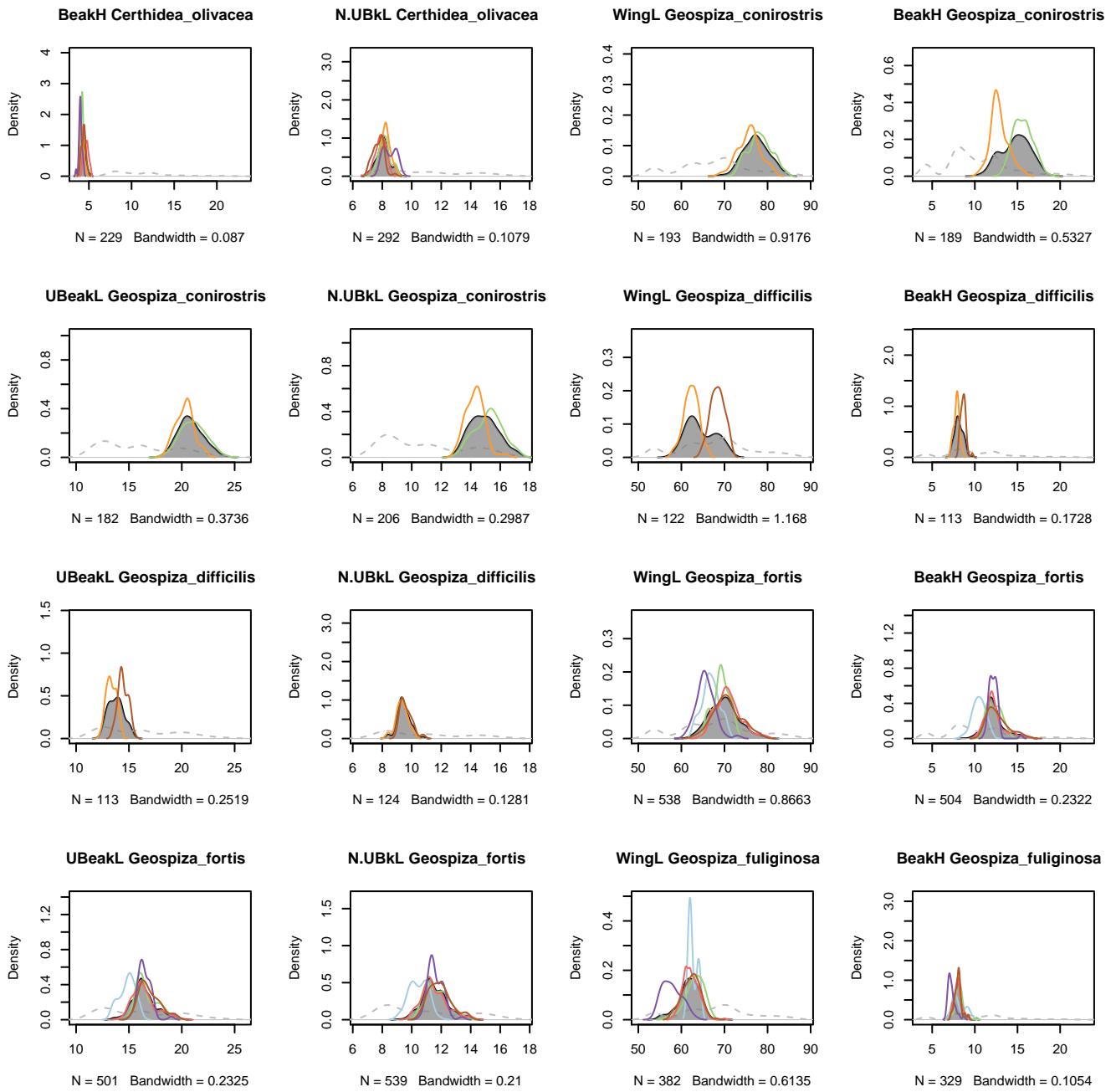
3 Description of traits distributions

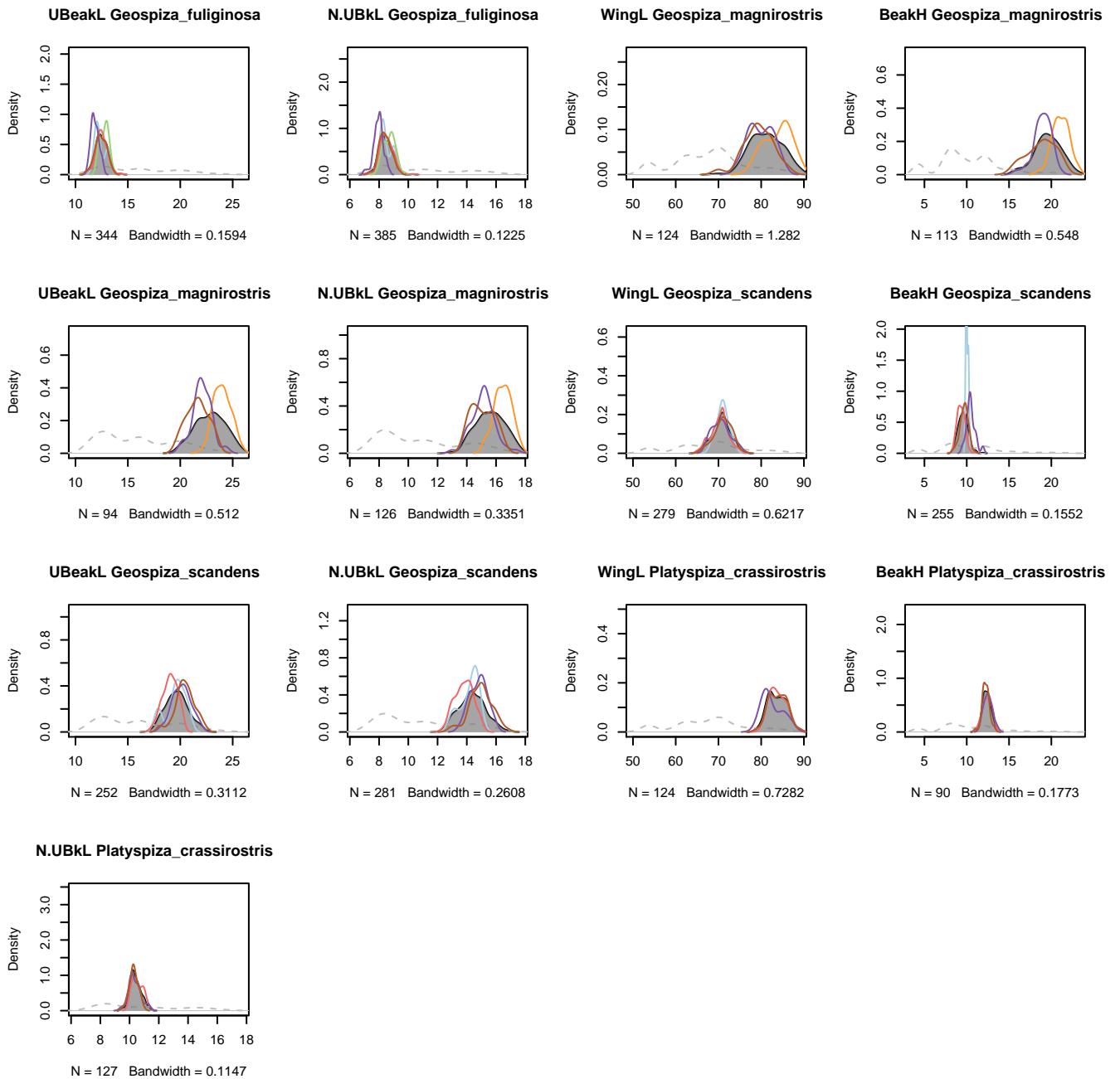
3.1 Plot the kernel density of traits

Plot the distribution of traits values for populations, species, sites and regional scales. First, let try the distribution for all populations of Darwin finches. In R, FALSE and TRUE can be written respectively F and T.

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



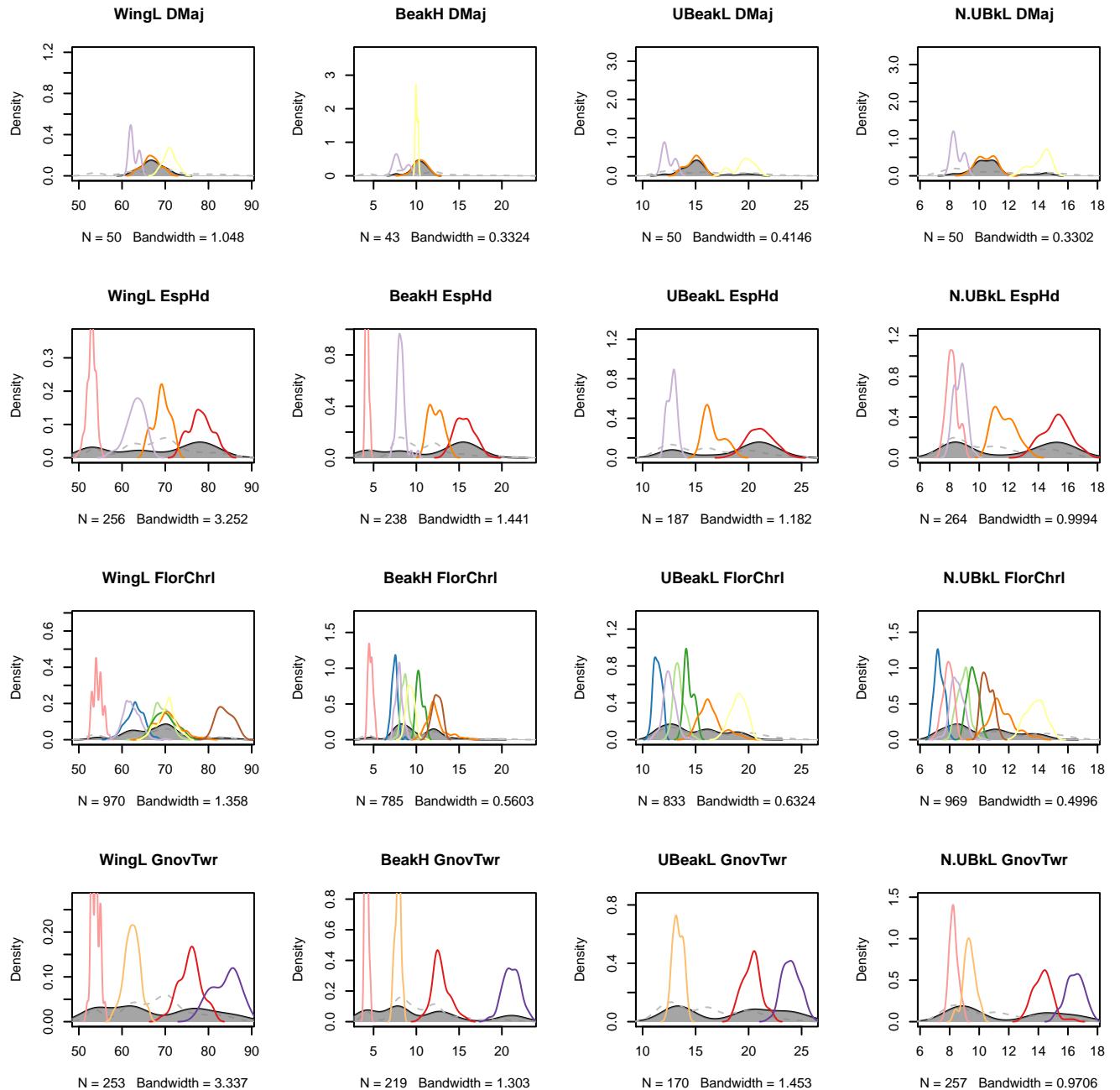


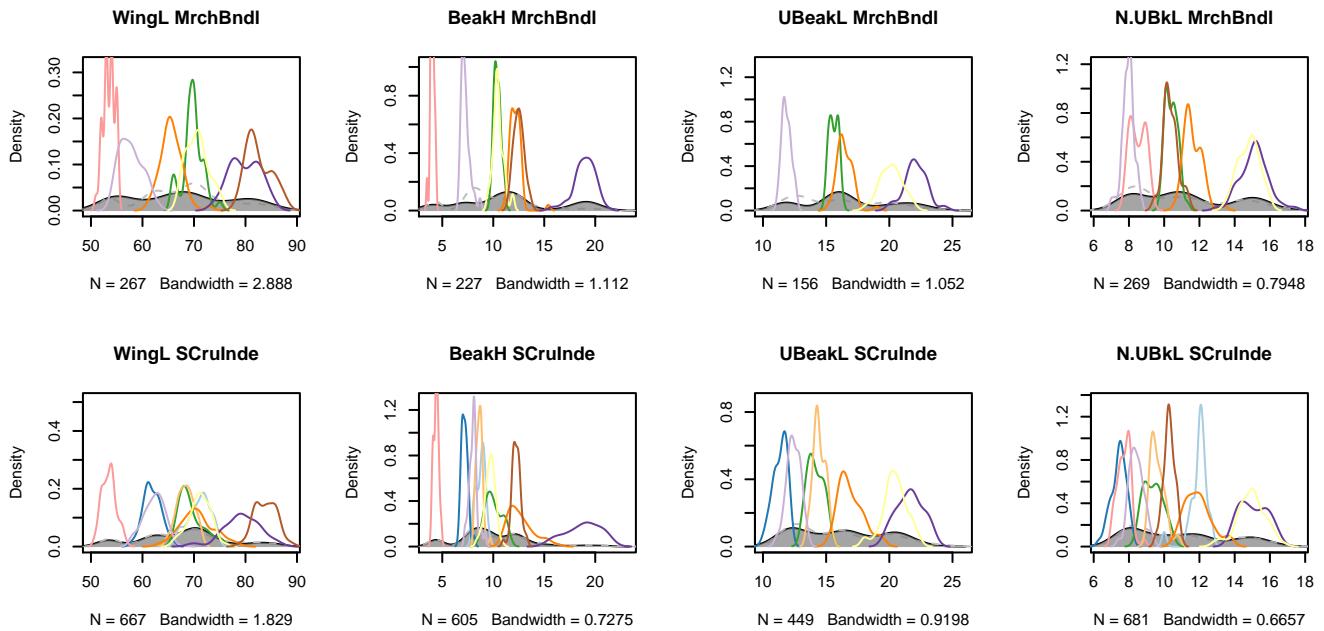


The argument `ylim.cex` define the magnification to be used for range of y axe. To understand the other argument, type `?plotDistri`.

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

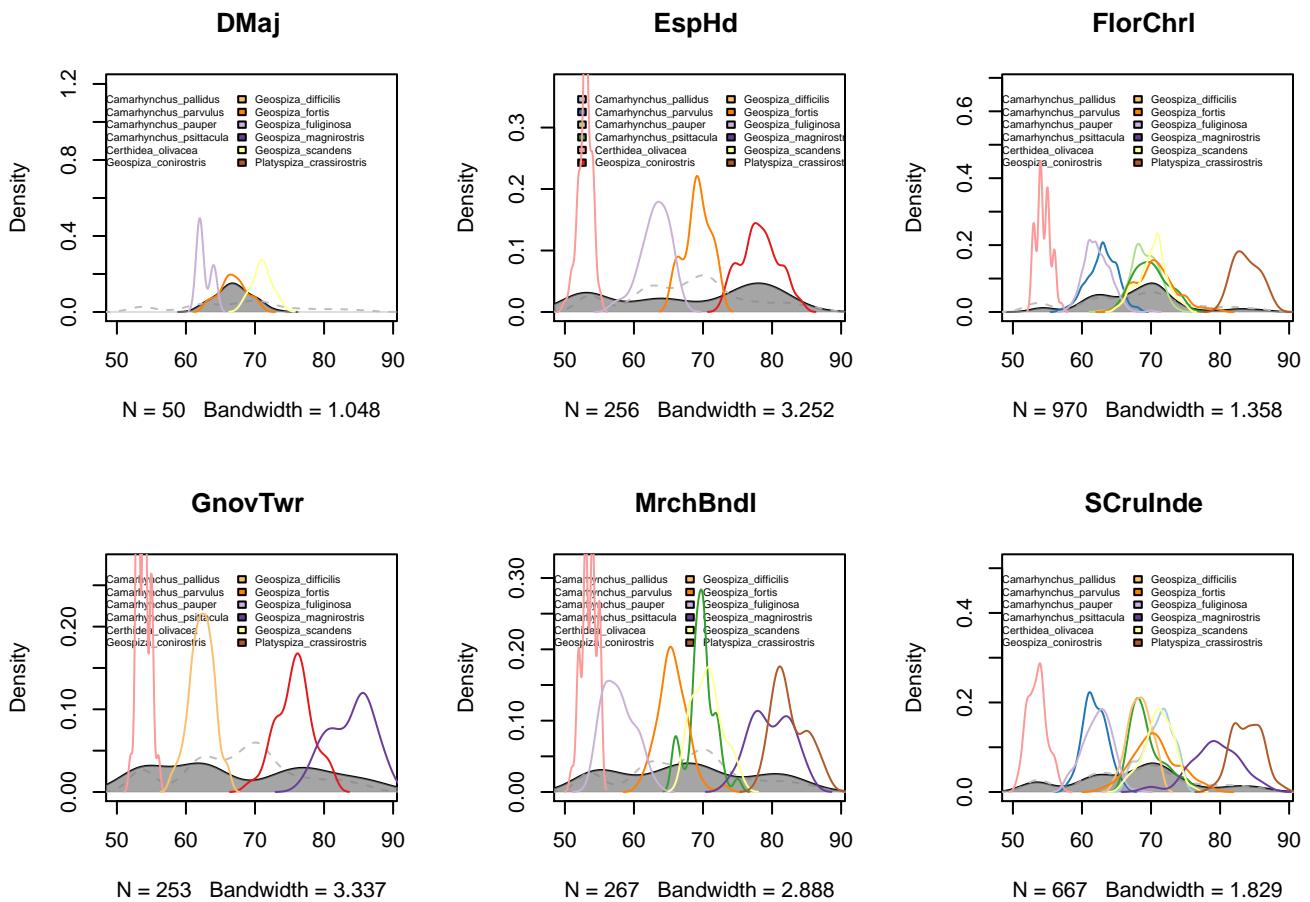
```
par(mfrow = c(4,4), cex = 0.5)
plotDistri(traits.finch, ind.plot.finch, sp.finch,
           ylim.cex = 8, plot.ask = F, multipanel = F, leg = F)
```





Now, see the result for only one trait with the legend (`leg = TRUE`). `cex.leg` specify the magnification of legend.

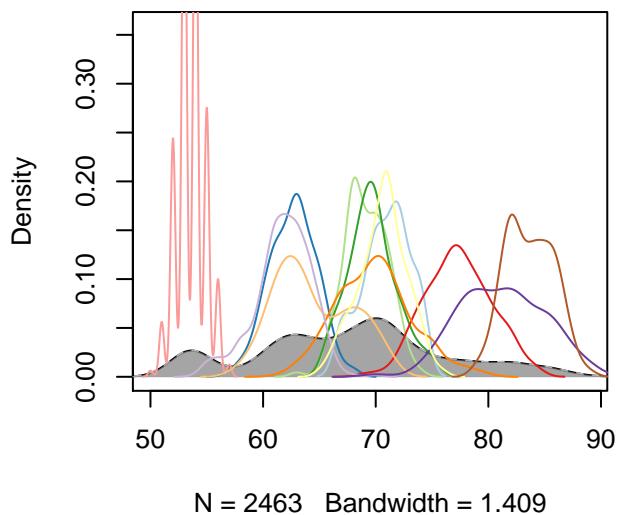
```
par(mfrow = c(2,3))
plotDistri(as.matrix(traits.finch[,1]), ind.plot.finch, sp.finch,
          ylim.cex = 8, plot.ask = F, multipanel = F, leg = T, cex.leg = 0.5)
```



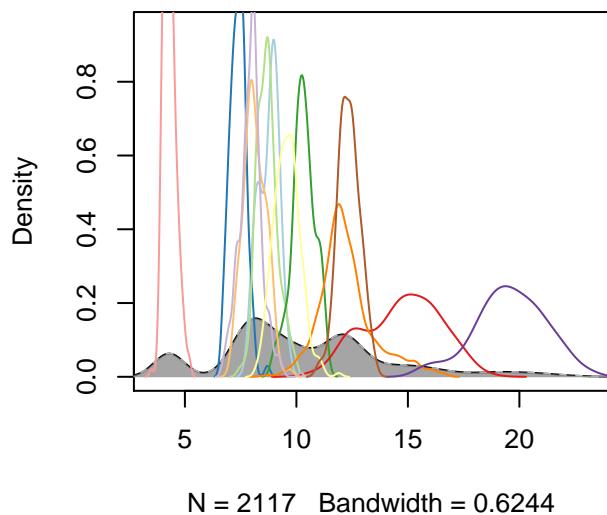
If we want to plot all the sites (regional distribution) or all the species: we can use the following code:

```
par(mfrow = c(4,4), cex = 0.5)
plotDistri(traits.finch, rep("region", times = dim(traits.finch)[1]),
           sp.finch, ylim.cex = 6, plot.ask = F, leg = F)
```

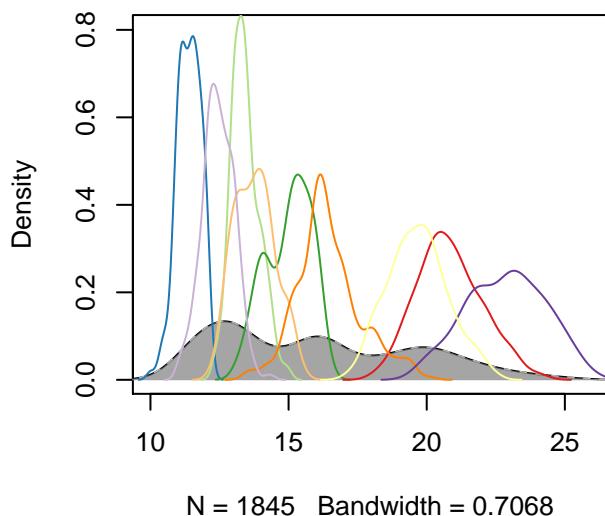
WingL region



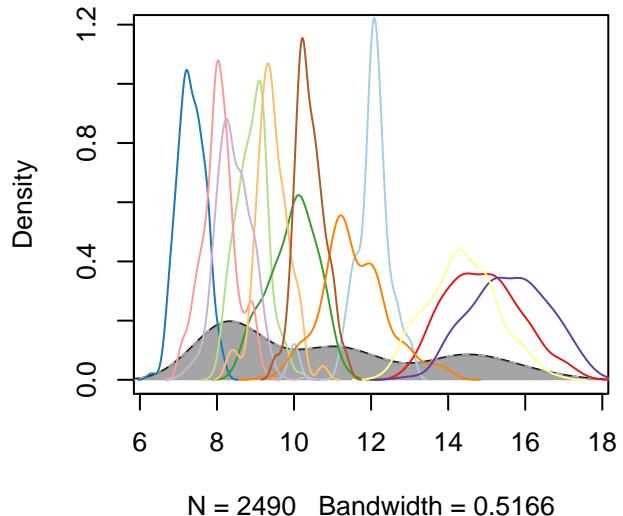
BeakH region



UBeakL region

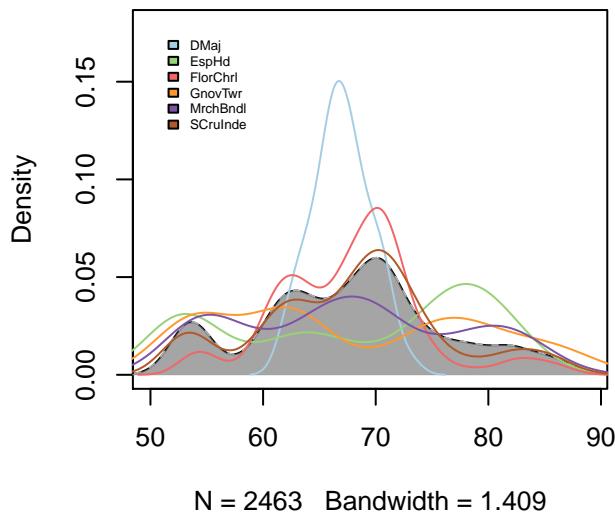


N.UBkL region

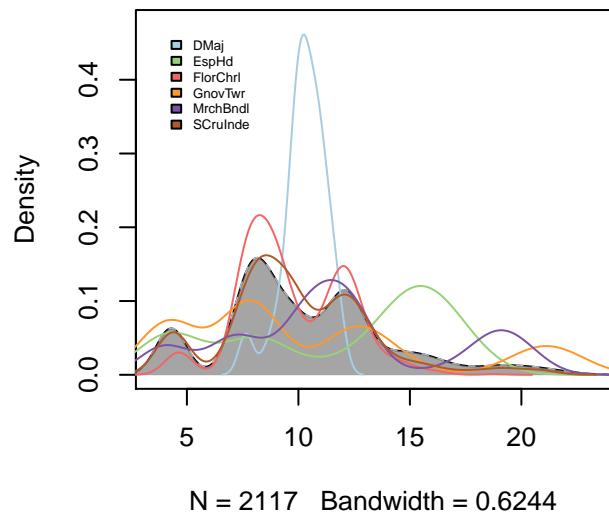


```
plotDistri(traits.finch, rep("toutes_sp", times = dim(traits.finch)[1]),
           ind.plot.finch, ylim.cex = 3, plot.ask = F, cex.leg = 0.5)
```

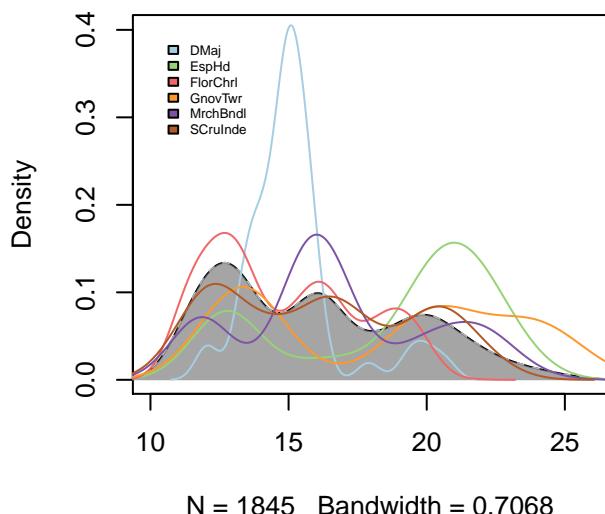
WingL toutes_sp



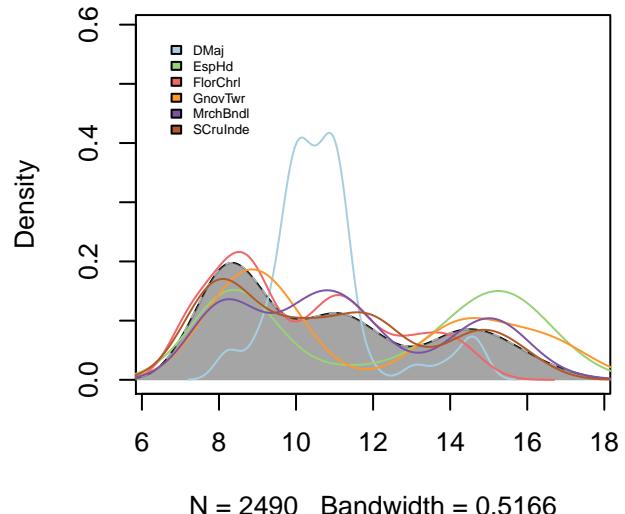
BeakH toutes_sp



UBeakL toutes_sp



N.UBkL toutes_sp



Now we can reset the default graphical parameter:

```
par(old.par)
```

4 Decomposition of variances

4.1 Decomposition of within/among species variances using rao diversity

The Rao function computes , and -components for taxonomic, functional and/or phylogenetic diversity with:

$$\gamma = \text{mean}\alpha + \beta$$

Where: γ is the diversity of the regional pool, α is the diversity of the local community and β is the turnover between

Reference: de Bello, F., Lavorel, S., Albert, C.H., Thuiller, W., Grigulis, K., Dolezal, J., Janecek, S. and Leps, J. (2011) Quantifying the relevance of intraspecific trait variability for functional diversity. Methods in Ecology and Evolution, 2, 163-174.

4.1.1 Multitraits analysis

First, rao diversity can be calculated on the functional space (i.e. considering all traits together).

```
#create individuals community matrix
comm<-t(table(ind.plot.finch,1:length(ind.plot.finch)))
#create species community matrix
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 = T))

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

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

#Check that the total variance is equal
#to between species + within species variances
witRao+betRao

## [1] 8.37

totRao

## [1] 8.37
```

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

```

res.rao.w<-RaoRel(sample = as.matrix(comm.sp),
  dfunc = mat.dist, dphyll = NULL,
  weight = T, Jost = F, 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

## [1] 7.551

betRao.w

## [1] 0.3458

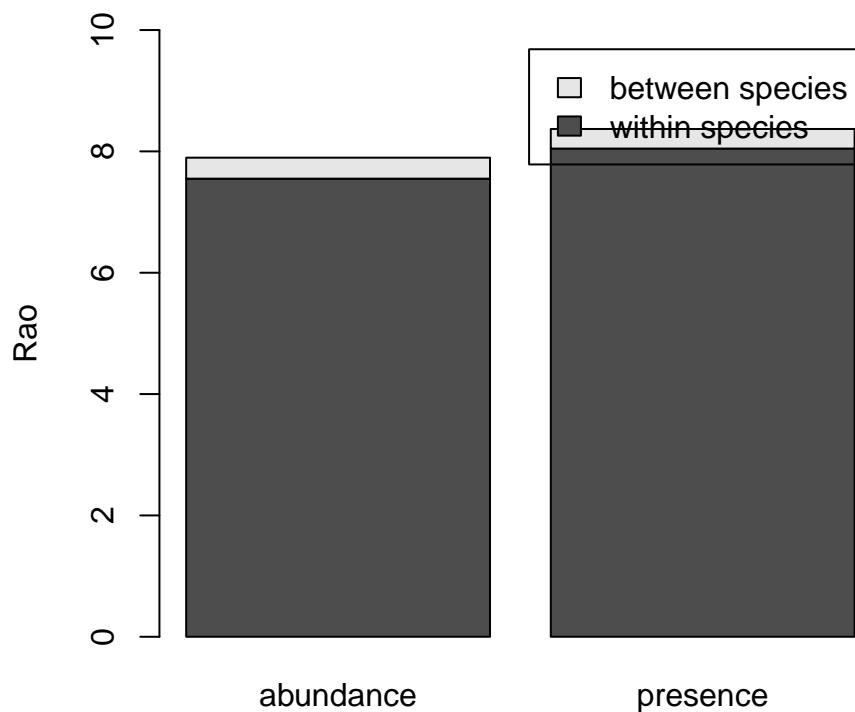
```

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))

```



4.1.2 Unitraits analysis

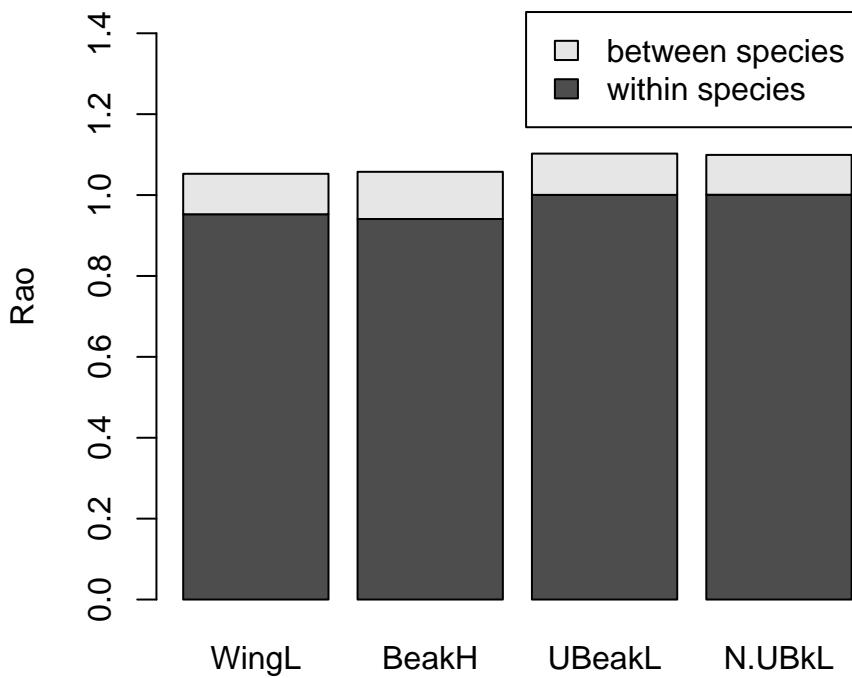
We can also do this analysis for each trait separately. We need to replace (or exclude) NA values. For this example, we use the package `mice` to complete the data.

```
comm<-t(table(ind.plot.finch,1:length(ind.plot.finch)))  
  
require(mice)  
traits = traits.finch  
mice<-mice(traits.finch)  
traits.finch.mice<-complete(mice)
```

```
#Calculate the mean traits value by population using the mice dataset  
traits.finch.mice.sp<-apply(apply(traits.finch.mice, 2, scale ), 2,  
                           function(x) tapply(x, sp.finch, mean, na.rm = T))  
  
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]),  
                            dphyll = NULL, weight = T, Jost = F, 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))
```

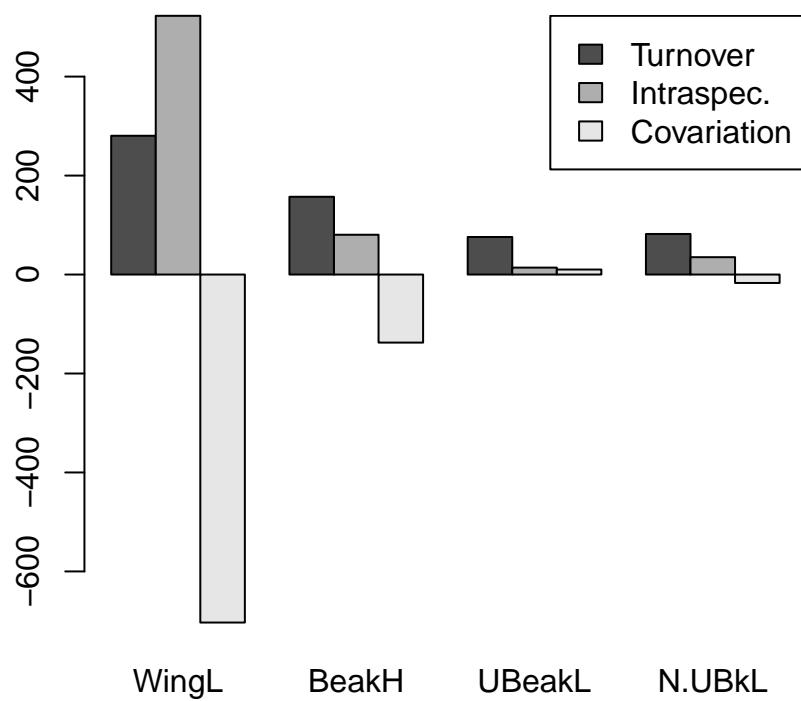


4.2 Decomposition of community trait response to environment into intraspecific trait variability, variability due to species turnover and their covariation.

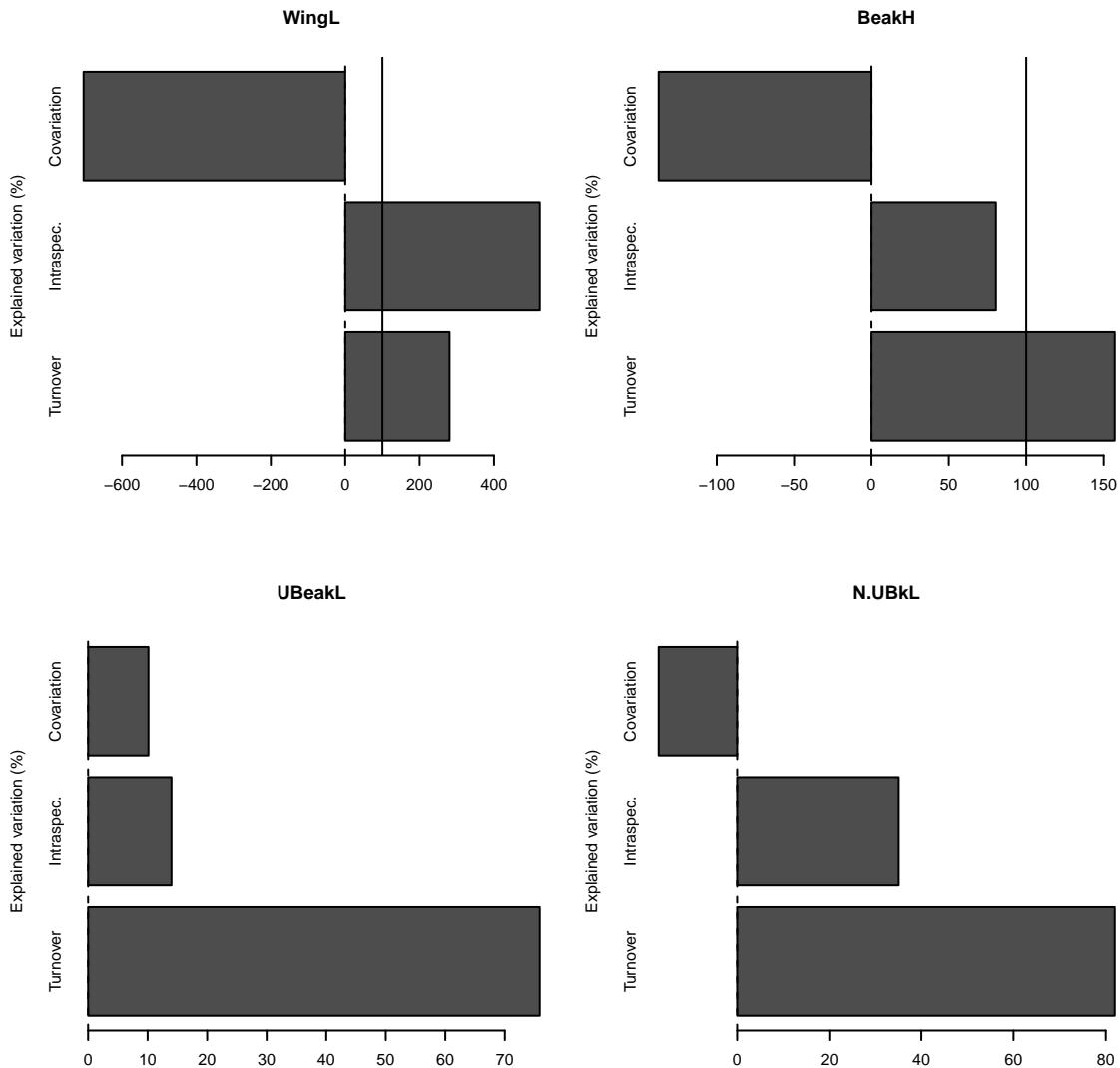
Reference: Leps, J., de Bello, F., Smilauer, P. and Dolezal, J. (2011) Community trait response to environment: disentangling species turnover vs intraspecific trait variability effects. *Ecography*, 34, 856-863.

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

barplot(res.decomp)
```



```
par(mfrow = c(2,2))
barplot(res.decomp, resume = F)
```



```
par(mfrow = c(1,1))
```

4.3 Decomposition of traits variances using nested factors

Variance partitioning across nested scales using the decomposition of variance on restricted maximum likelihood (REML) method (lme function).

Reference: Messier, J., McGill, B. and Lechowicz, M. (2010) How do traits vary across ecological scales? A case for trait-based ecology. Ecology Letters, 13, 838-848.

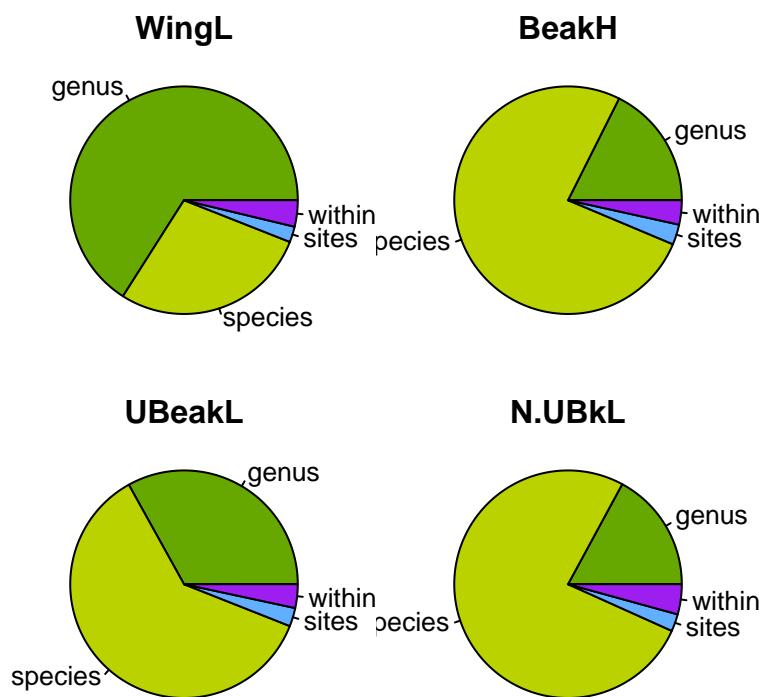
```
vec<- seq(1,length(sp.finch)*2, by = 2)
genus<-as.vector(unlist(strsplit(as.vector(sp.finch), "_"))[vec])
fact<-cbind(genus = as.factor(genus),
            species = as.factor(as.vector(sp.finch)),
            sites = as.factor(as.vector(ind.plot.finch)))

res.partvar.finch<-partvar(traits = traits.finch, factors = fact)

res.partvar.finch
```

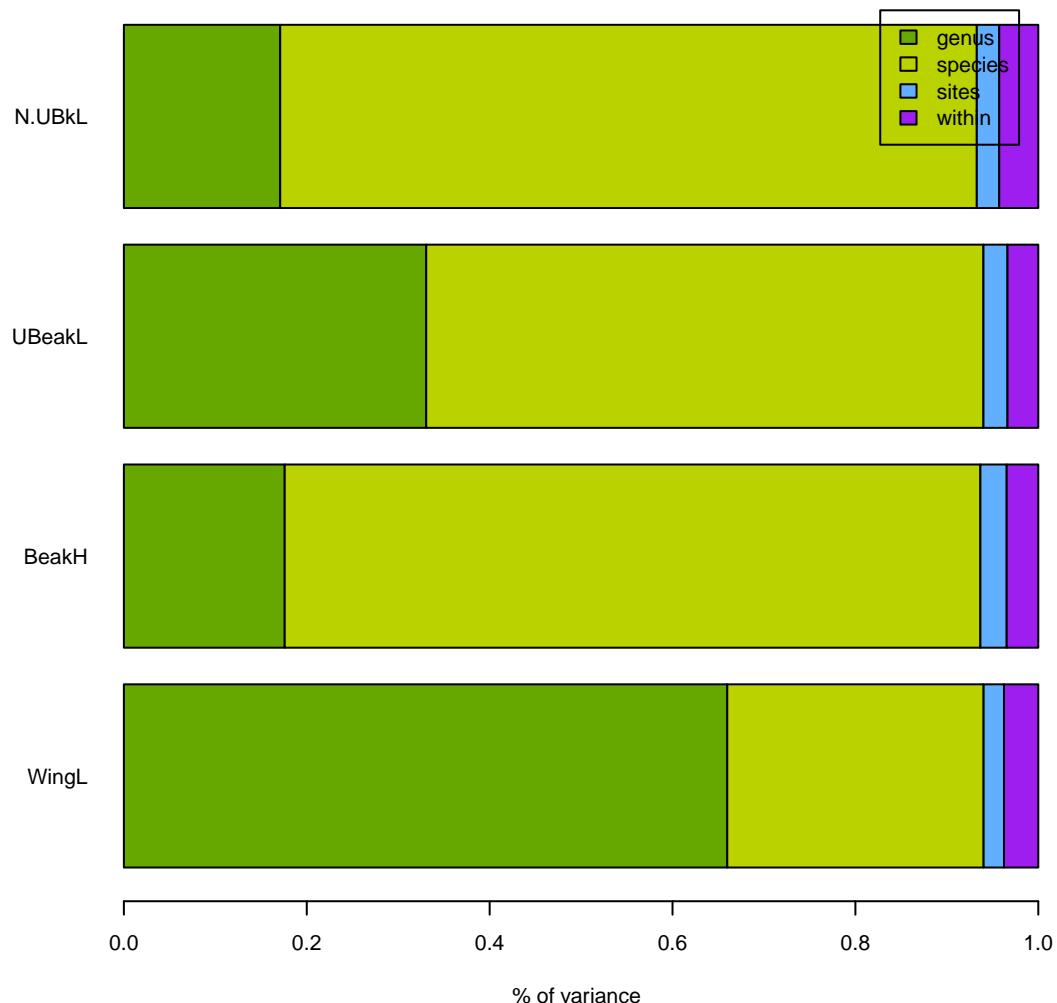
```
par(mfrow = c(2,2), mai = c(0.2,0.2,0.2,0.2)) #save graphical parameters
colors<-c(rgb(102,167,0, maxColorValue = 255),
          rgb(185,210,0, maxColorValue = 255),
          rgb(98,174,255, maxColorValue = 255),
          rgb(158,30,240, maxColorValue = 255))

piePartvar(res.partvar.finch, col = colors)
```



```
par(old.par) #reset old graphical parameters
```

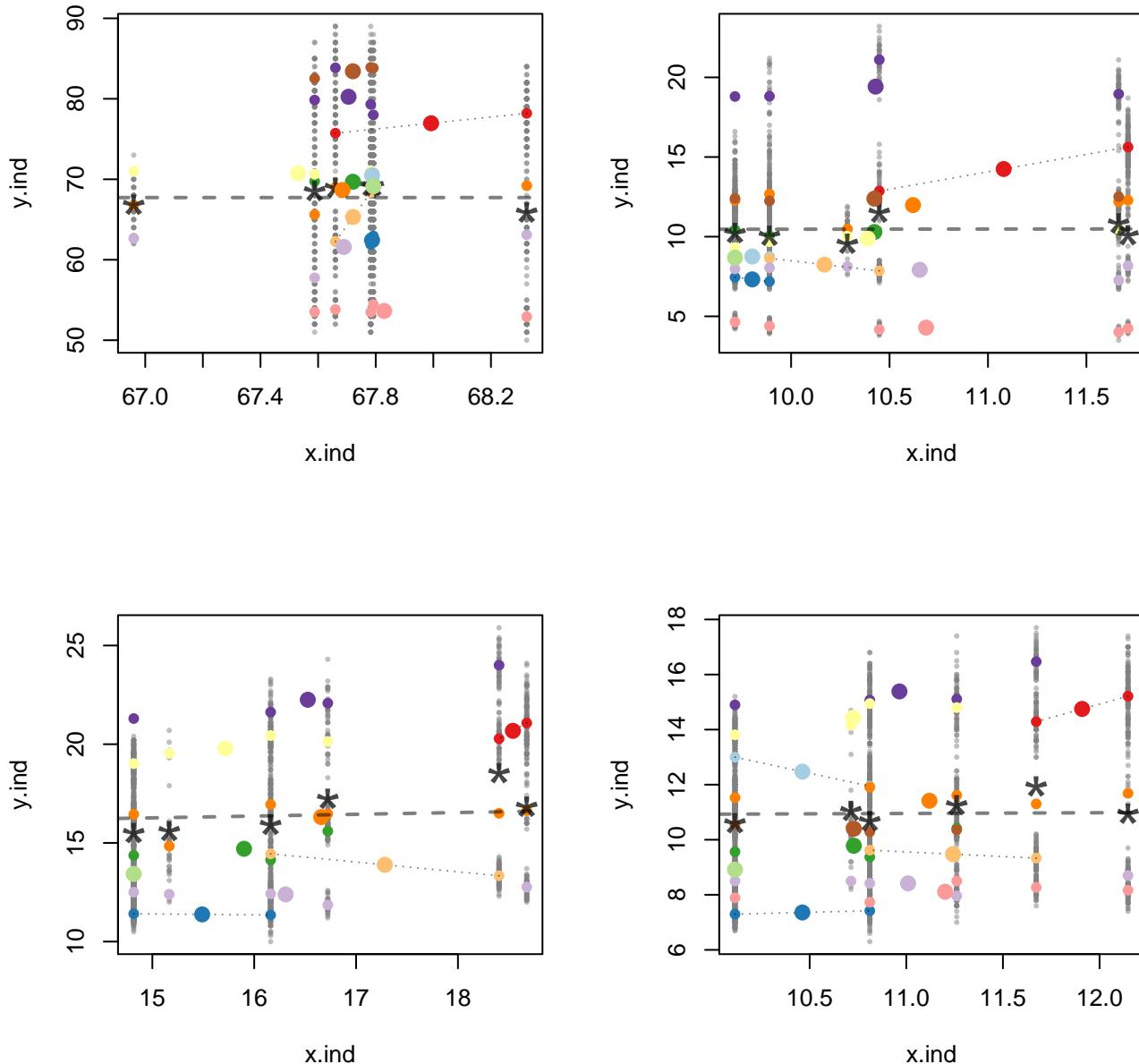
```
barPartvar(res.partvar.finch, col = colors, leg = TRUE)
```



4.4 Plot the relation between populational trait means and sites traits means.

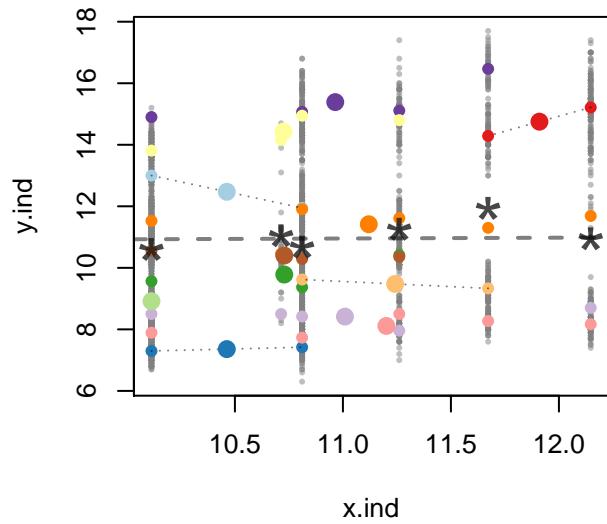
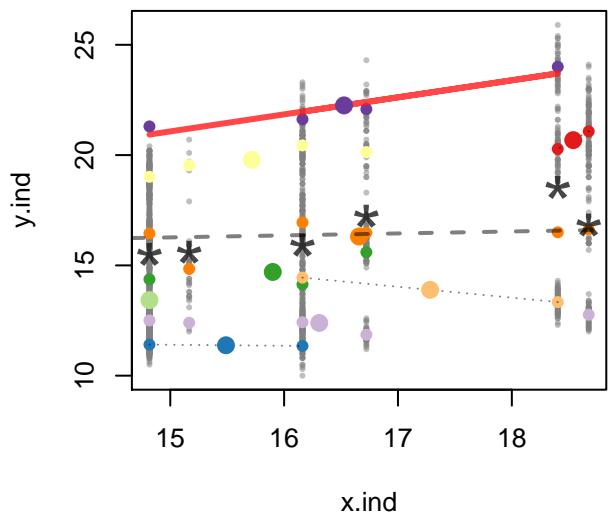
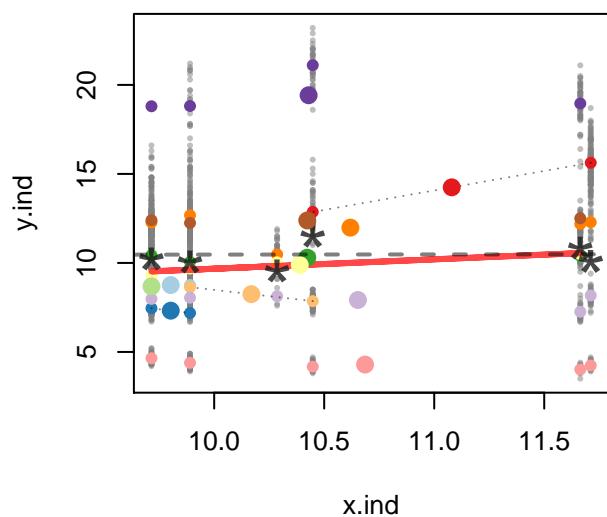
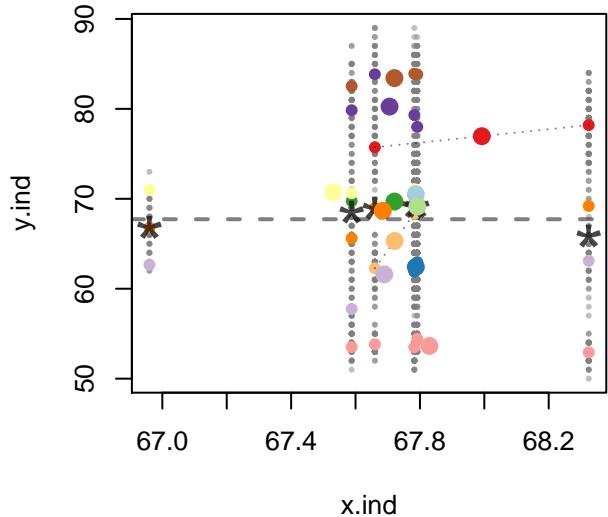
For an example of utilisation see: Cornwell, W.K. and Ackerly, D.D., 2009. Community assembly and shifts in plant trait distributions across an environmental gradient in coastal California. Ecological Monographs, 79, 109-126.

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



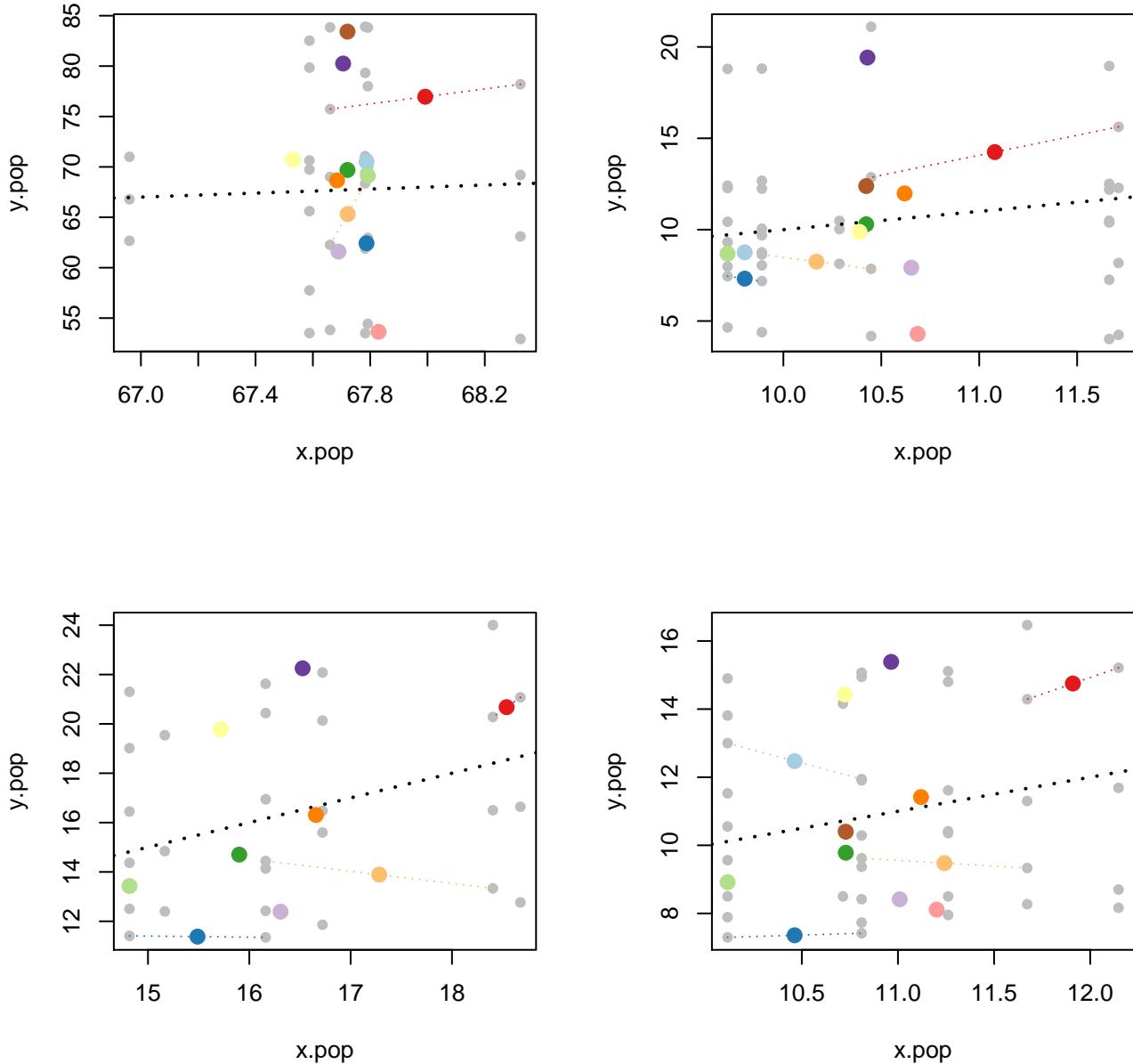
If we change the value of two arguments we can see some significant relationships. Here let's try a more permissive threshold: `alpha = 10%` instead of `5%` (`p.val`) and define a lower minimum of values to represent significance fixed to `3` instead of `10` by default (`min.ind.signif`).

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



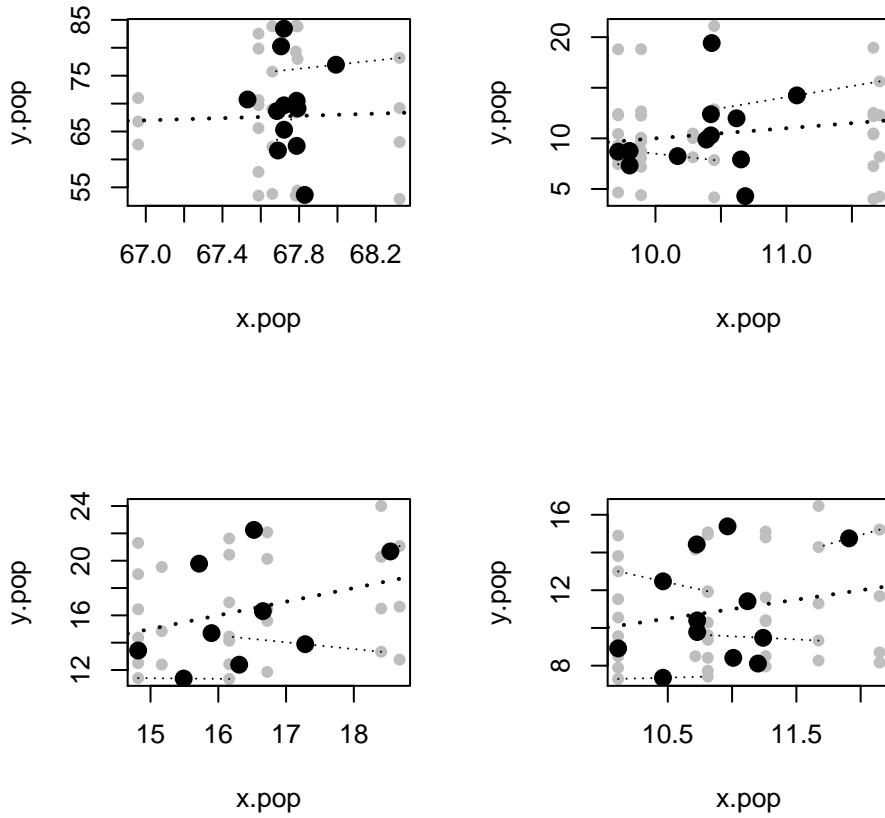
For a more simple figure, add the option resume = TRUE.

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



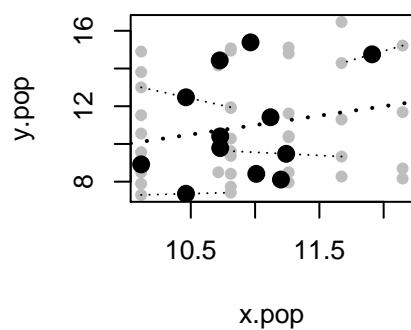
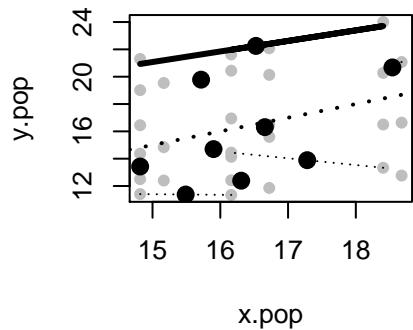
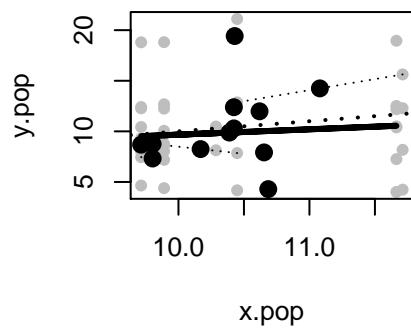
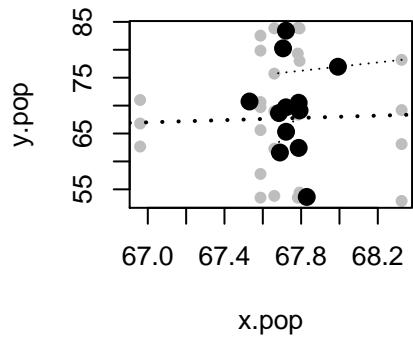
If you are fed up with colors, try this:

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



Again if we change the value of the threshold (`p.val = 0.1` and `min.ind.signif = 3`) we can see some significant relationships.

```
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)
```



5 Test of community assembly

5.1 Ratio of variances: T-statistics

The function `Tstat` computes observed T-statistics (T for Traits; Violle et al (2012)) as three ratios of variance, namely T_{IP}/IC , T_{IC}/IR and T_{PC}/PR . This function can also return the distribution of these three statistics under the three associated null models (respectively `local`, `regional.ind` and `regional.pop`).

Reference: Violle, C., Enquist, B.J., McGill, B.J., Jiang, L., Albert, C., Hulshof, C., Jung, V. and Messier, J. (2012) The return of the variance: intraspecific variability in community ecology. Trends in Ecology and Evolution, 27, 244-252.

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

## #####
## # T-statistiques #
## #####
## class: Tstats
## $call: Tstats(traits = traits.finch, ind.plot = ind.plot.finch, sp = sp.finch,
##               nperm = 9, printprogress = FALSE)
##
## #####
## $Tstats: list of observed and null T-statistics
##
## Observed values
## $T_IP.IC: ratio of within-population variance to total within-community variance
## $T_IC.IR: community-wide variance relative to the total variance in the regional pool
## $T_PC.PR: inter-community variance relative to the total variance in the regional pool
##
## Null values, number of permutation: 9
## $T_IP.IC_nm: distribution of T_IP.IC value under the null model local
## $T_IC.IR_nm: distribution of T_IC.IR value under the null model regional.ind
## $T_PC.PR_nm: distribution of T_PC.PR value under the null model regional.pop
##
## #####
## $variances: list of observed and null variances
##
## #####
## data used
##   data      class      dim
## 1 $traits  data.frame 2513,4
## 2 $ind.plot factor    2513
## 3 $sp      factor    2513
##   content
## 1 traits data
## 2 name of the plot in which the individual is
```

```

## 3 groups (e.g. species) which the individual belong to
##
## #####
## others
## $namestraits: 4 traits
## [1] "WingL"   "BeakH"   "UBeakL"  "N.UBkL"
##
## $sites_richness:
## ind.plot
##      DMaj      EspHd FlorChrl  GnovTwr MrchBndl SCruInde
##      50       267      981      258      270      687

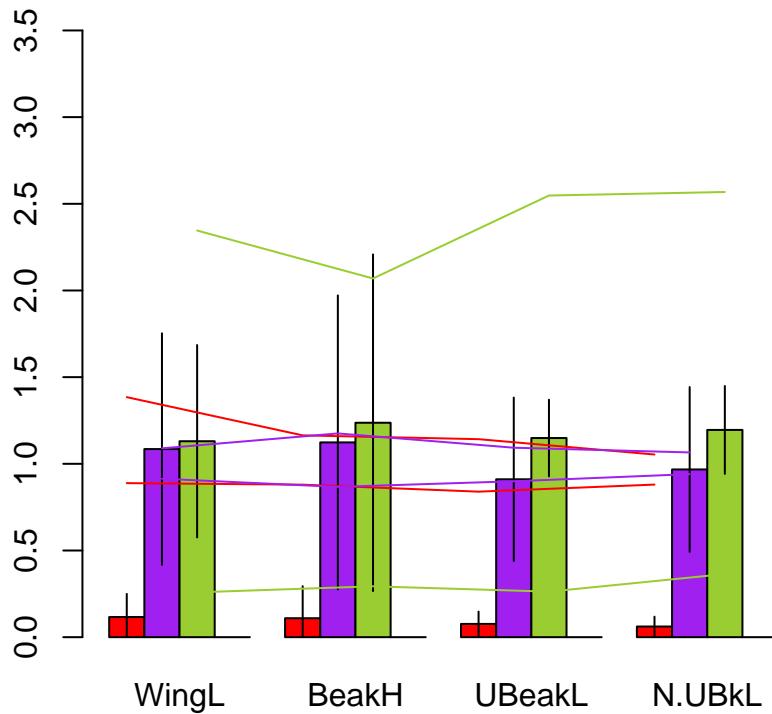
```

5.1.1 S3 methods for class Tstats

Tstats class is associated to S3 methods plot, barplot, print and summary. We have already used the print function in the above script line. Now, how to plot the result of the function Tstats?

We can represent observed values thanks to the `barplot` function.

```
barplot(res.finch, ylim = c(0,3.5))
```

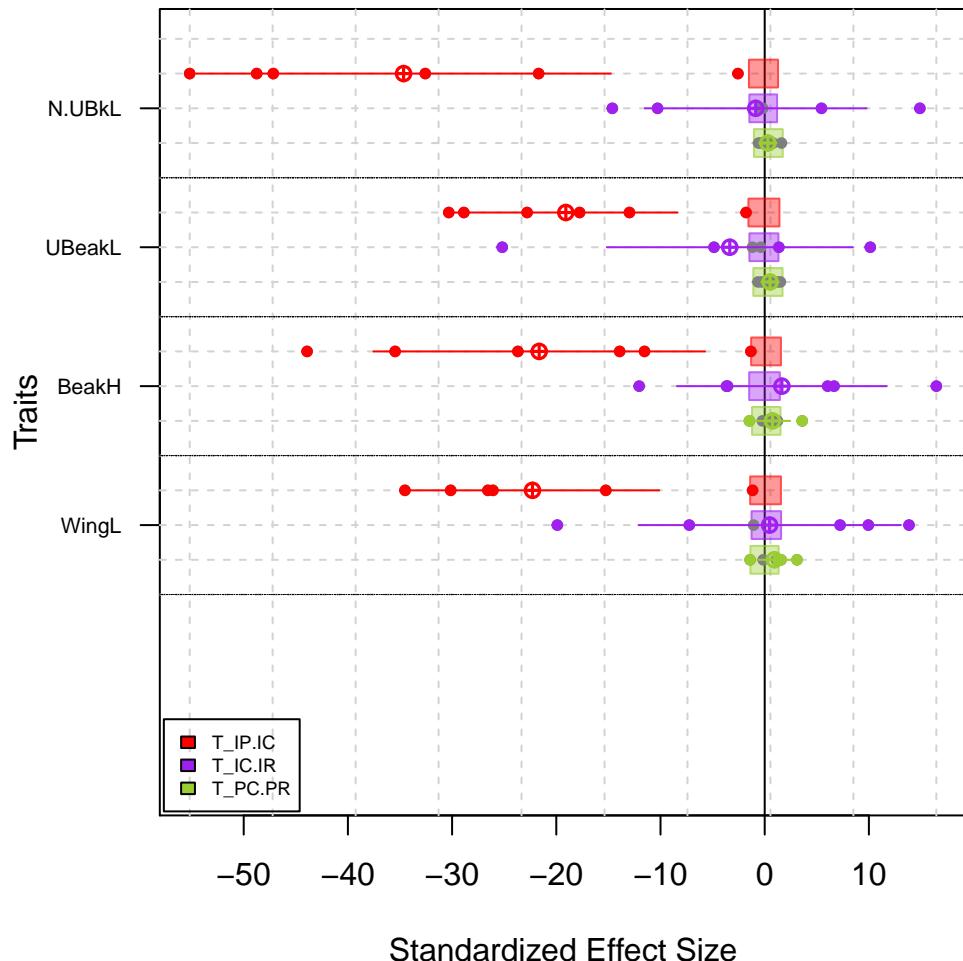


One can be more interested in the significance and the effect size available thanks to null model. In that case, the standardized effect size can be easily plot. Note that the function `ses` can be use directly to calculate standardized effect size without plotting. The Standardized Effect Size (ses) is define as :

$$SES = (I_{obs} - I_{sim}) / \delta_{sim}$$

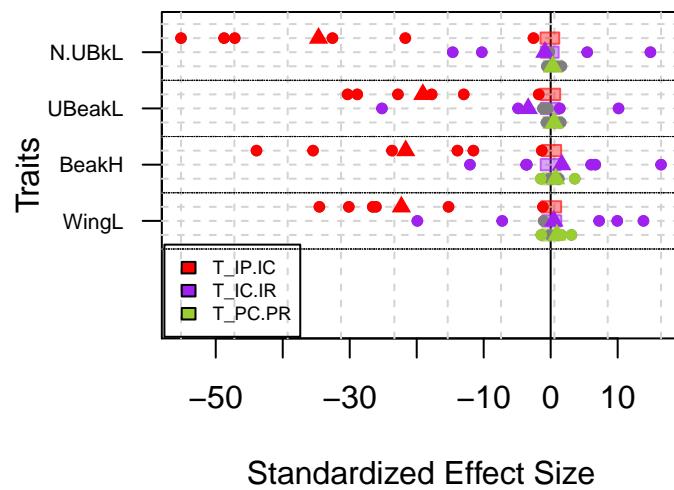
where I_{obs} is the observed value, I_{sim} the mean of values calculated from the null model and δ_{sim} the standard deviation of these simulated values.

```
plot(res.finch)
```

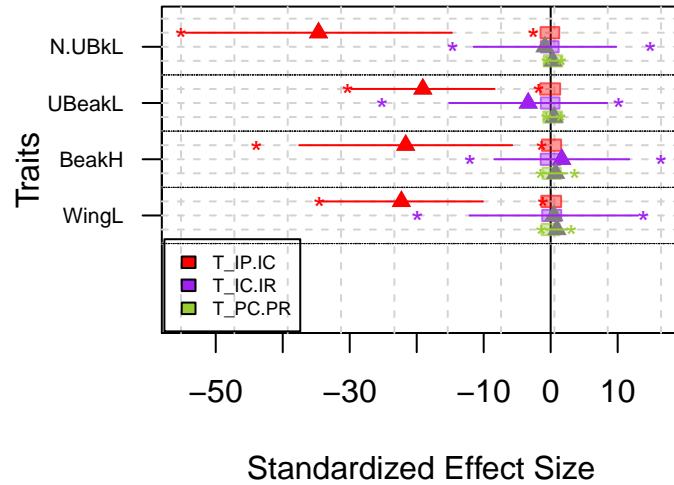


There is multiple kind of representation available.

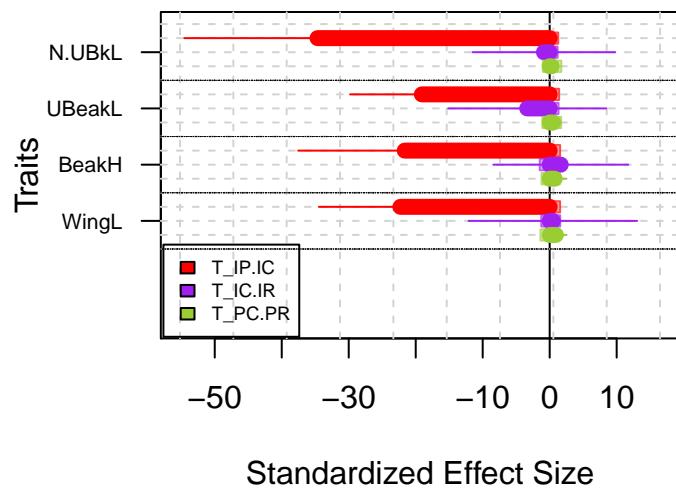
```
plot(res.finch, type = "simple")
```



```
plot(res.finch, type = "simple_range")
```



```
plot(res.finch, type = "barplot")
```

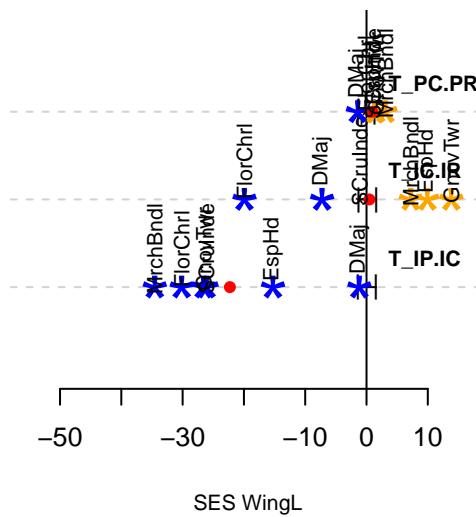


If you want to specifically look at traits or sites statistics, use the argument `type = "bytraits"` or `"bysites"`.

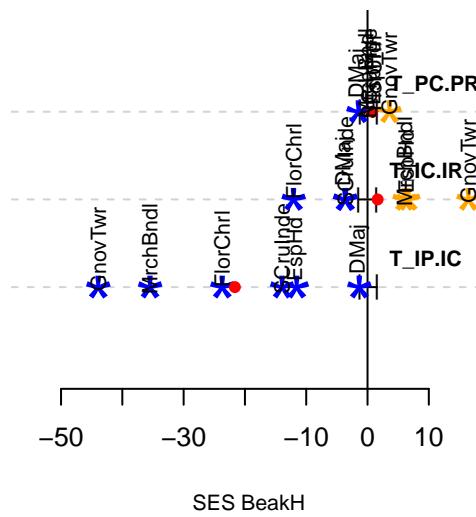
```
par(mfrow=c(2,2))

plot(res.finch, type = "bytraits")
```

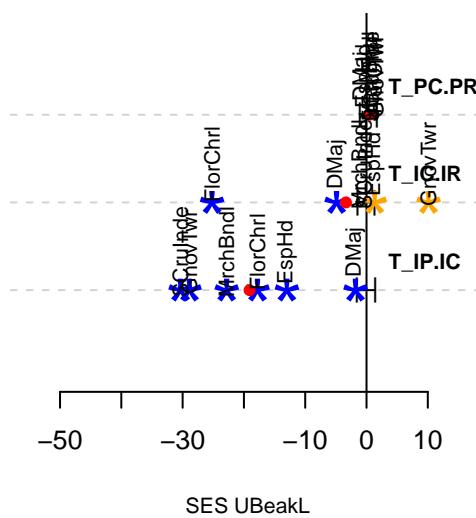
(1:nindex)[i]



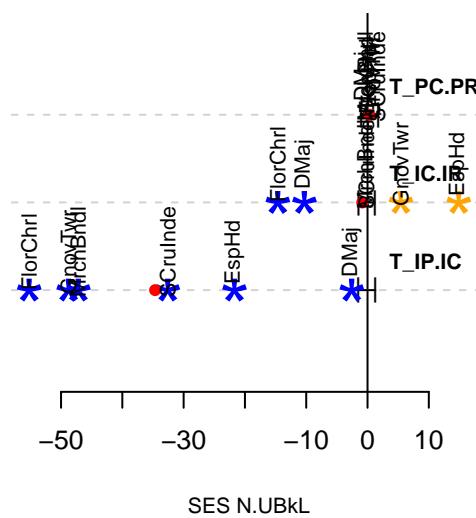
(1:nindex)[i]



(1:nindex)[i]

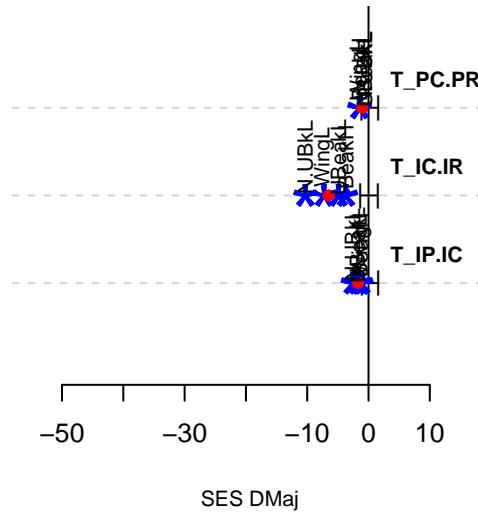


(1:nindex)[i]

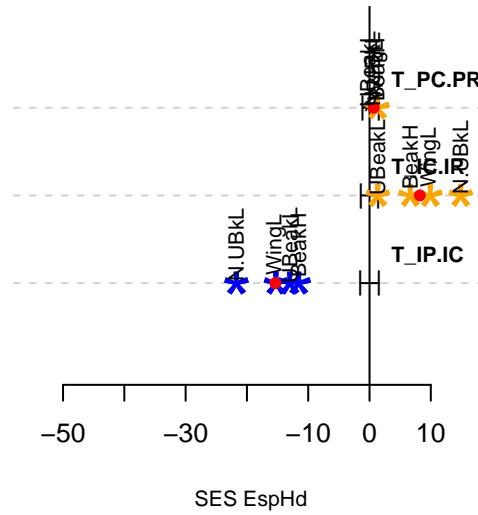


```
plot(res.finches, type = "bysites")
```

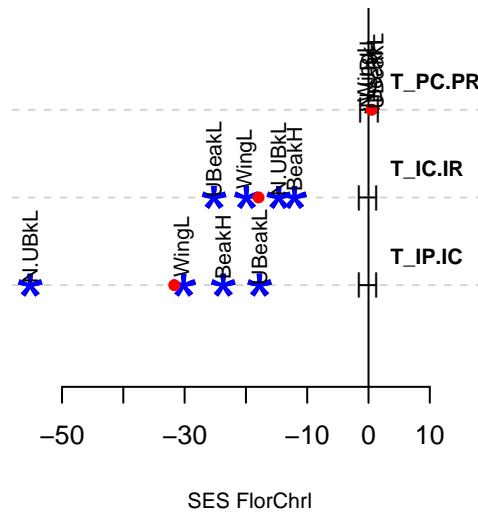
(1:nindex)[1]



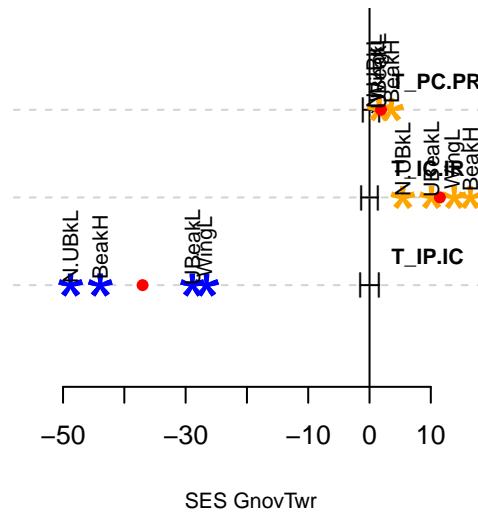
(1:nindex)[1]



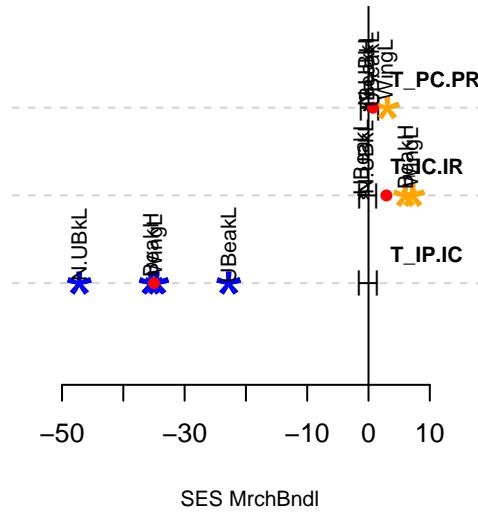
(1:nindex)[1]



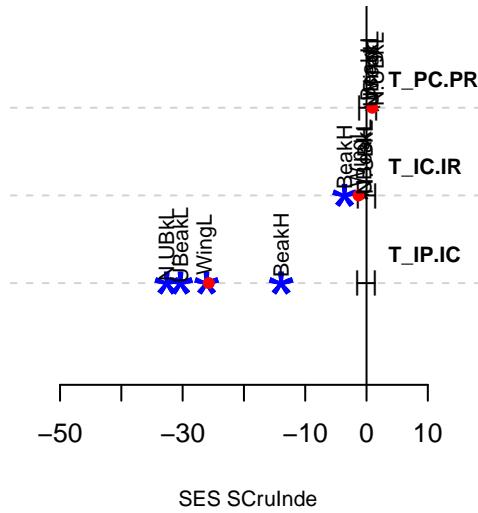
(1:nindex)[1]



(1:nindex)[1]



(1:nindex)[1]



```
par(old.par) # reset default graphical parameters
```

```

summary(res.finches) #S3 summary method for class Tstats

## [1] "Observed values"
## $T_IP.IC
##      WingL        BeakH        UBeakL       N.UBkL
##  Min.   :0.0343   Min.   :0.0153   Min.   :0.0267   Min.   :0.0238
##  1st Qu.:0.0436  1st Qu.:0.0191  1st Qu.:0.0417  1st Qu.:0.0367
##  Median :0.0645  Median :0.0400  Median :0.0544  Median :0.0403
##  Mean   :0.1161  Mean   :0.1094  Mean   :0.0764  Mean   :0.0615
##  3rd Qu.:0.1012 3rd Qu.:0.0580  3rd Qu.:0.0629  3rd Qu.:0.0494
##  Max.   :0.3831  Max.   :0.4852  Max.   :0.2196  Max.   :0.1764
##
## $T_IC.IR
##      WingL        BeakH        UBeakL       N.UBkL
##  Min.   :0.0925   Min.   :0.0632   Min.   :0.246   Min.   :0.257
##  1st Qu.:0.6739  1st Qu.:0.4913  1st Qu.:0.668  1st Qu.:0.724
##  Median :1.1707  Median :1.1831  Median :0.944  Median :0.980
##  Mean   :1.0852  Mean   :1.1236  Mean   :0.911  Mean   :0.968
##  3rd Qu.:1.6257 3rd Qu.:1.6242  3rd Qu.:1.080  3rd Qu.:1.314
##  Max.   :1.7916  Max.   :2.2802  Max.   :1.629  Max.   :1.525
##
## $T_PC.PR
##      WingL        BeakH        UBeakL       N.UBkL
##  Min.   :0.226    Min.   :0.0868   Min.   :0.933   Min.   :0.936
##  1st Qu.:0.898    1st Qu.:0.8625  1st Qu.:0.983  1st Qu.:1.039
##  Median :1.223    Median :1.0589  Median :1.125  Median :1.099
##  Mean   :1.130    Mean   :1.2370  Mean   :1.149  Mean   :1.196
##  3rd Qu.:1.474    3rd Qu.:1.3286  3rd Qu.:1.215  3rd Qu.:1.351
##  Max.   :1.762    Max.   :3.0016  Max.   :1.530  Max.   :1.585
##
## [1] "null values"
## $T_IP.IC_nm
##      Min. 1st Qu. Median     Mean 3rd Qu.     Max.
##      0.422  0.961  0.992    1.000  1.020    3.230
##
## $T_IC.IR_nm
##      Min. 1st Qu. Median     Mean 3rd Qu.     Max.
##      0.678  0.962  1.000    1.000  1.040    1.520
##
## $T_PC.PR_nm
##      Min. 1st Qu. Median     Mean 3rd Qu.     Max.    NA's
##      0.003  0.438  0.838    1.160  1.390    7.460     2

```

```

attributes(sum_Tstats(res.finches)) #Another mean to summarize Tstatistics

## $names
## [1] "p.value" "percent" "sites"    "binary"

```

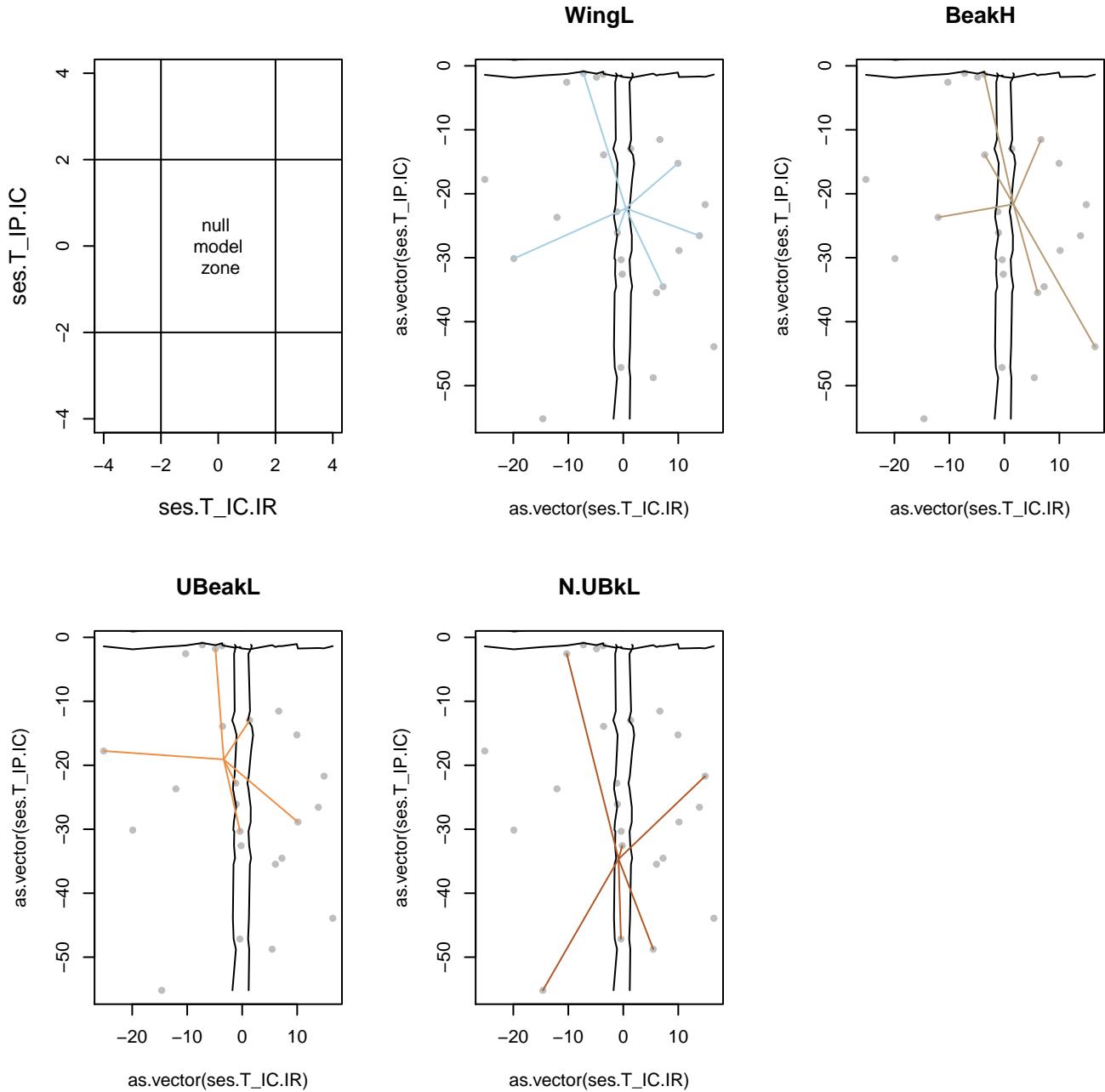
```
head(sum_Tstats(res.finches)$p.value, 10)

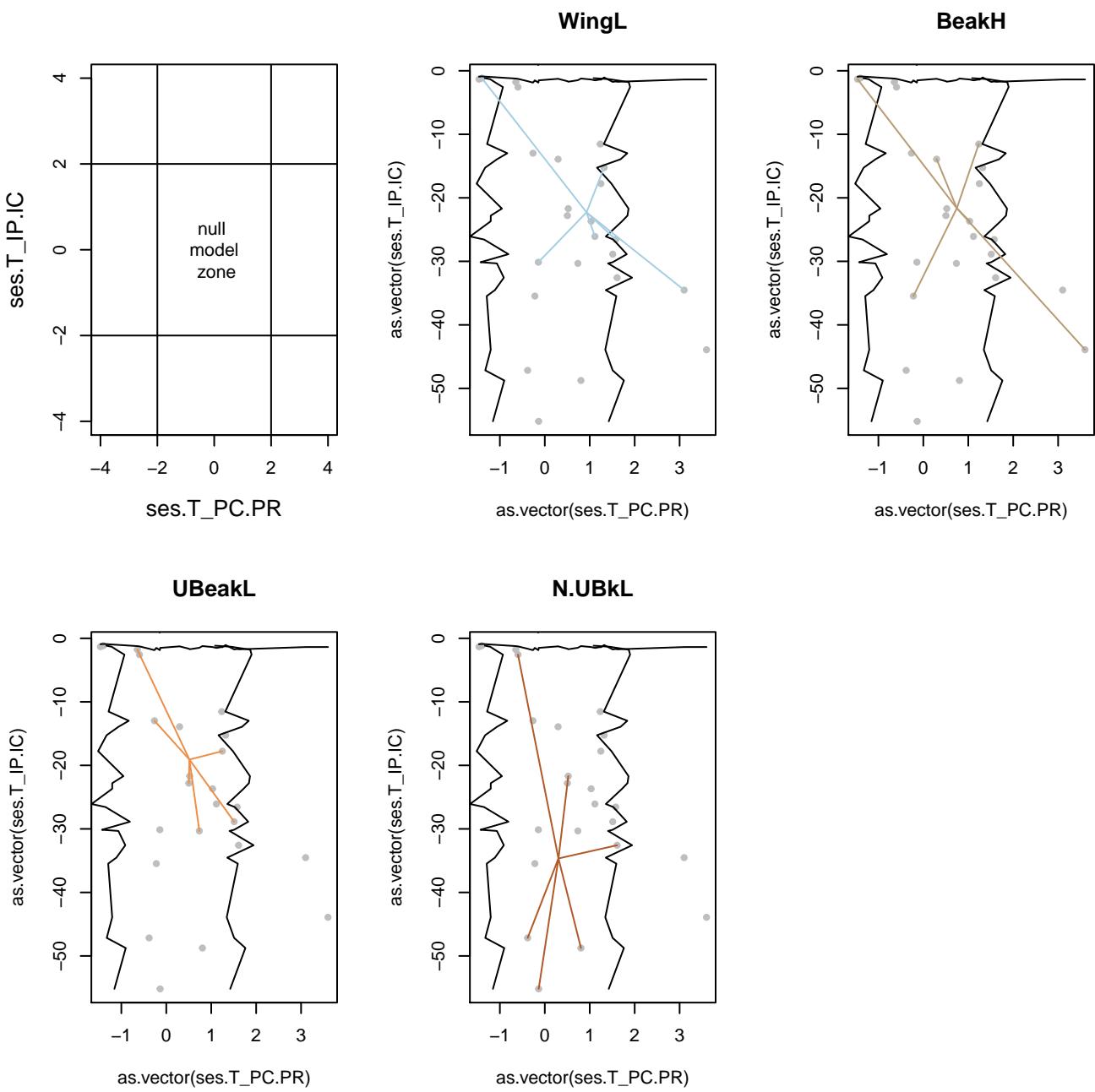
##          WingL  BeakH UBeakL N.UBkL
## T_IP.IC.inf   0.1   0.1   0.1   0.1
## T_IP.IC.sup  1.0   1.0   1.0   1.0
```

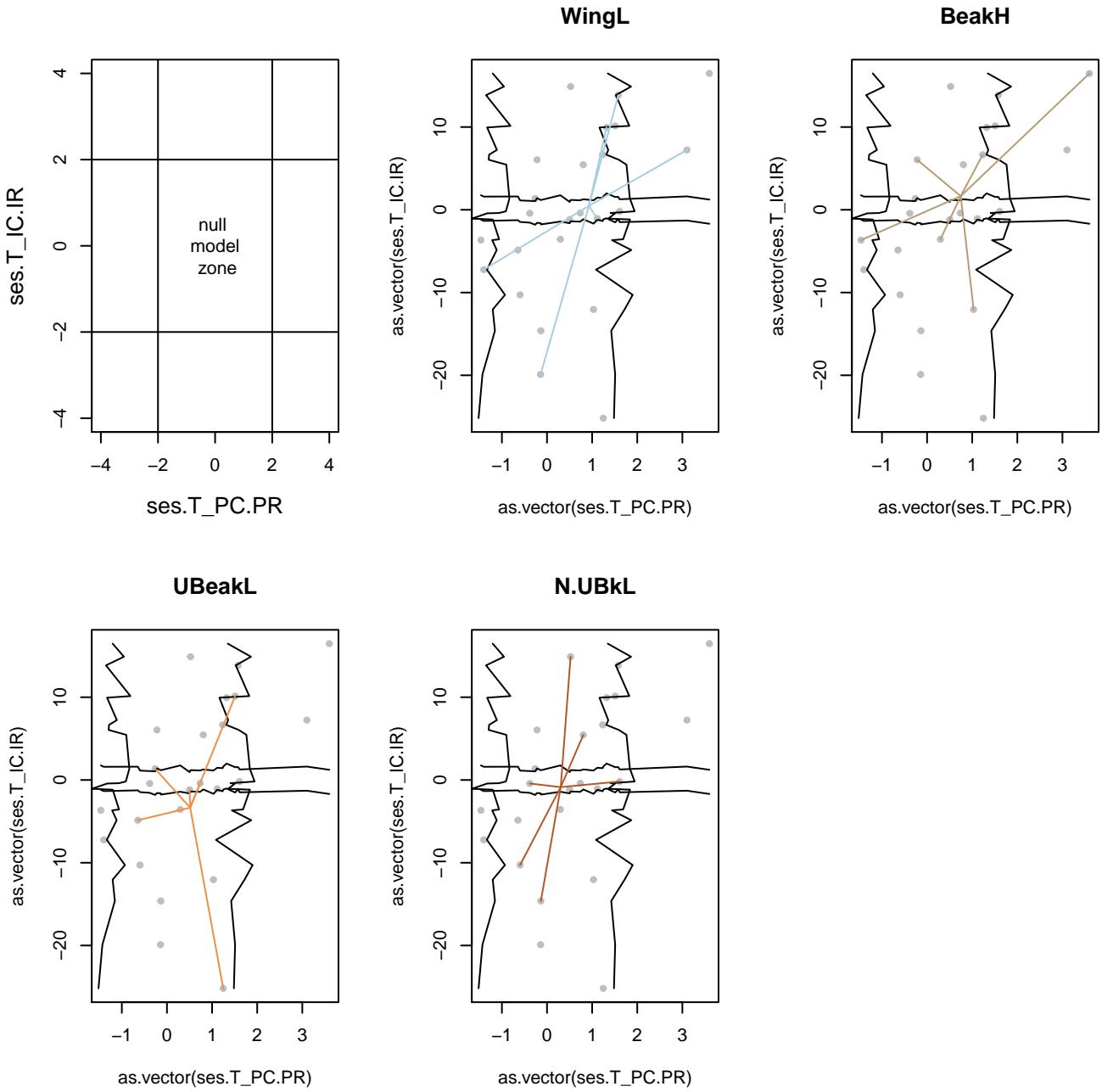
5.1.2 Plot T-statistics correlations

We can also see T-statistics correlations and theirs correlation with others variables (e.g. a gradient variable, or the species richness).

```
par(mfrow = c(2,3))
plotCorTstats(res.finch, plot.ask = FALSE, multipanel = F)
```

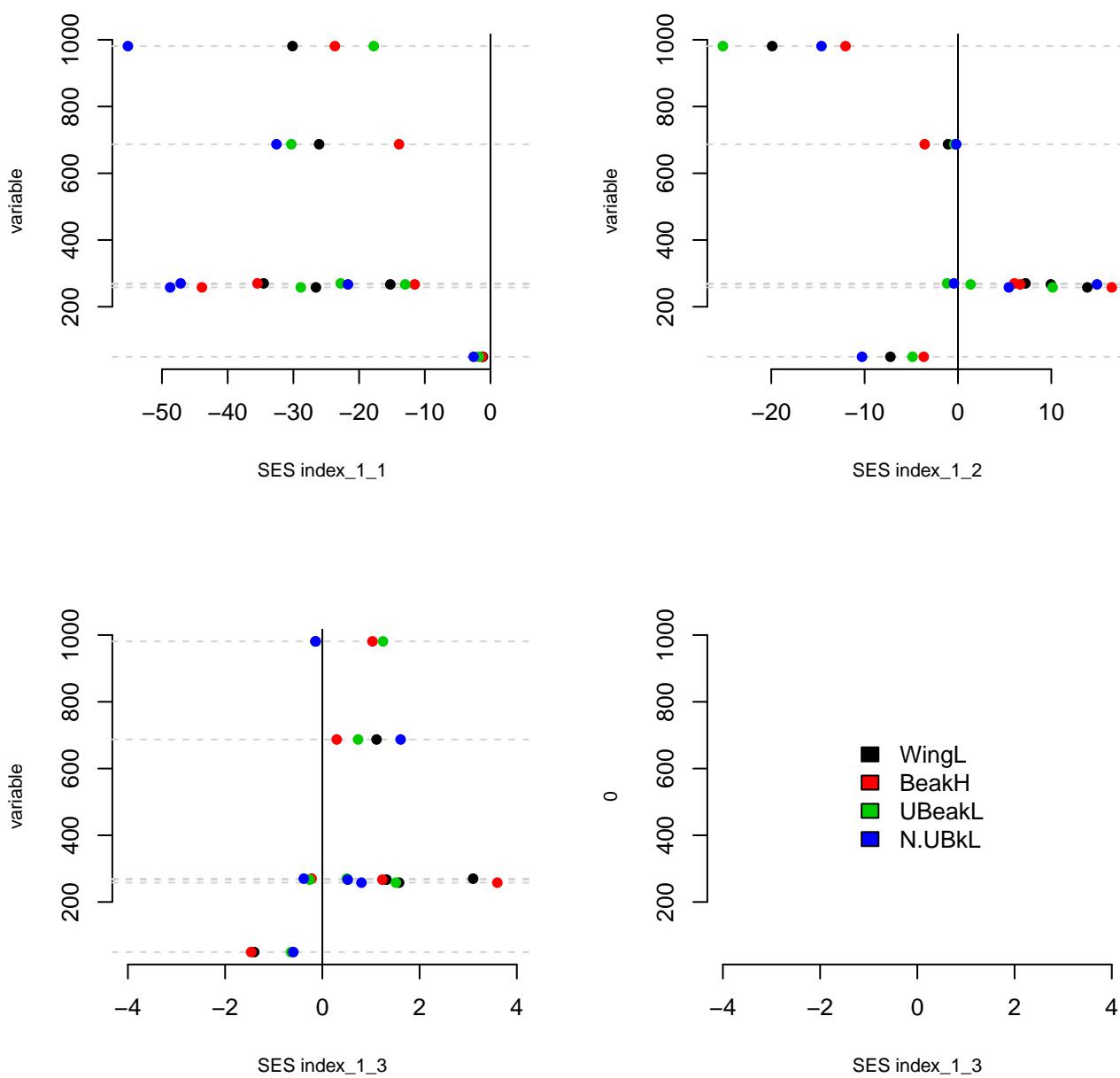






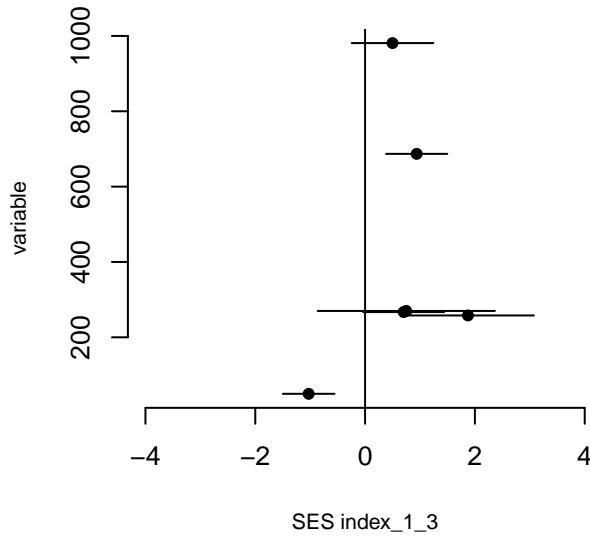
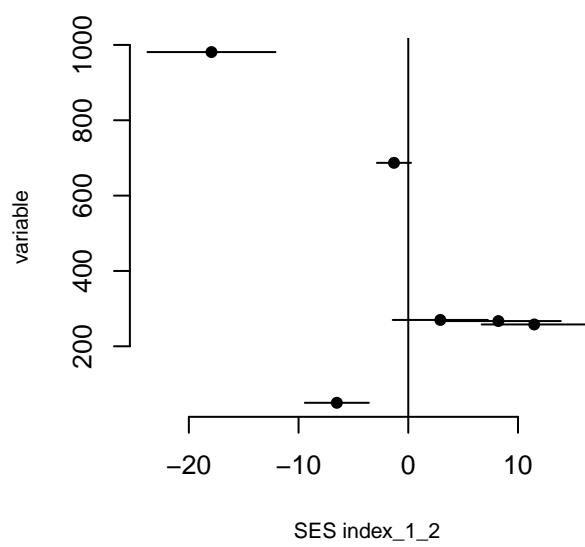
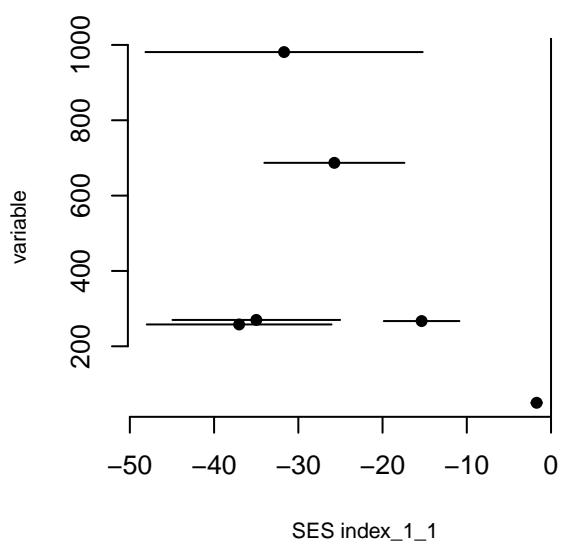
Here we plot T-statistics (in the standardized effect size SES form) in function of species richness by sites.

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



Same plot with `resume = TRUE`.

```
par(mfrow = c(2,2))
plotSESvar(as.listofindex(list(res.finch)), species.richness,
          resume = T, multipanel = F)
```



```
par(mfrow = c(1,1))
```

5.2 Others univariates or multivariates metrics: function ComIndex and ComIndexMulti

The function `ComIndex` allow choosing your own function (like mean, range, variance, ...) to calculate customize metrics. Here `CVNND` refers to the Coefficient of Variation of the Nearest Neighborhood Distance. `ComIndexMulti` do the same things for multivariate metrics.

```
#Define the functions to calculate
funct<-c("mean(x, na.rm = T)", "kurtosis(x, na.rm = T)",
        "max(x, na.rm = T) - min(x, na.rm = T)", "CVNND(x)" )

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

These two functions allows to calculate index by sites for example using "`tapply(x, sites, mean)`".

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

##Null model local is trivial for these functions
##because randomization is within community only

res.finch.ind_mn1<-ComIndex(traits = traits.finch, index = funct, sp = sp.finch,
                             nullmodels = "local", ind.plot = ind.plot.finch,
                             nperm = 9, print = FALSE)
res.finch.ind_mn2<-ComIndex(traits = traits.finch, index = funct, sp = sp.finch,
                             nullmodels = "regional.ind", 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 = T))

sites_bypop<-lapply(strsplit(paste(rownames(traits.by.pop), sep = "_"), split = "_"),
```

```

function(x) x[3])

#We use the precedent list of function "funct"
funct.withIV<-funct

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

```

Now calculate index with or without intraspecific variance thanks to function ComIndex.

```

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

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

```

5.2.1 S3 methods for class ComIndex and ComIndexMulti

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

```

res.finch.withIV

## #####
## # Community metrics calculation #
## #####
## class: ComIndex
## $call: ComIndex(traits = traits.finch, index = funct.withIV, nullmodels = "regional.ind",
##                 ind.plot = ind.plot.finch, sp = sp.finch, nperm = 9, printprogress = FALSE)
##
## #####
## $obs: list of observed values
## $tapply(x, ind.plot.finch, function(x) mean(x, na.rm = T))
## $tapply(x, ind.plot.finch, function(x) kurtosis(x, na.rm = T))
## $tapply(x, ind.plot.finch, function(x) max(x, na.rm = T)-min(x, na.rm = T))
## $tapply(x, ind.plot.finch, function(x) CVNND(x))
##
## #####
## $null: list of null values, number of permutation: 9
## $tapply(x, ind.plot.finch, function(x) mean(x, na.rm = T))_nm ... null model = regional.ind
## $tapply(x, ind.plot.finch, function(x) kurtosis(x, na.rm = T))_nm ... null model = regional.pop
## $tapply(x, ind.plot.finch, function(x) max(x, na.rm = T)-min(x, na.rm = T))_nm ... null model = regional.pop
## $tapply(x, ind.plot.finch, function(x) CVNND(x))_nm ... null model = regional.ind
##

```

```

## #####
## data used
##   data      class      dim
## 1 $traits   data.frame 2513,4
## 2 $ind.plot factor     2513
## 3 $sp       factor     2513
##   content
## 1 traits data
## 2 name of the plot in which the individual is
## 3 groups (e.g. species) which the individual belong to
##
## #####
## others
## $namestraits: 4 traits
## [1] "WingL"   "BeakH"    "UBeakL"   "N.UBkL"
##
## $sites_richness:
##   DMaj     EspHd FlorChrl GnovTwr MrchBndl SCruInde
##   50       267     981     258      270      687

summary(res.finch.withIV)

## [1] "Observed values"
## `$tapply(x, ind.plot.finch, function(x) mean(x, na.rm = T))` 
##   WingL        BeakH        UBeakL        N.UBkL
##   Min. :67.0   Min. : 9.71   Min. :14.8   Min. :10.1
##   1st Qu.:67.6 1st Qu.: 9.99  1st Qu.:15.4  1st Qu.:10.7
##   Median :67.7 Median :10.37  Median :16.4   Median :11.0
##   Mean   :67.7 Mean   :10.62  Mean   :16.7   Mean   :11.1
##   3rd Qu.:67.8 3rd Qu.:11.36 3rd Qu.:18.0  3rd Qu.:11.6
##   Max.   :68.3  Max.   :11.71  Max.   :18.7   Max.   :12.1
##
## `$tapply(x, ind.plot.finch, function(x) kurtosis(x, na.rm = T))` 
##   WingL        BeakH        UBeakL        N.UBkL
##   Min. :-1.466  Min. :-1.360  Min. :-1.600  Min. :-1.752
##   1st Qu.:-1.252 1st Qu.:-0.642 1st Qu.:-1.185 1st Qu.:-1.449
##   Median :-0.821  Median :-0.297  Median :-1.089  Median :-1.083
##   Mean   :-0.622  Mean   :-0.110  Mean   :-0.564  Mean   :-0.740
##   3rd Qu.:-0.274 3rd Qu.: 0.646 3rd Qu.:-0.876 3rd Qu.:-0.946
##   Max.   : 0.865  Max.   : 1.087  Max.   : 2.414  Max.   : 1.950
##
## `$tapply(x, ind.plot.finch, function(x) max(x, na.rm = T)-min(x, na.rm = T))` 
##   WingL        BeakH        UBeakL        N.UBkL
##   Min. :11.0   Min. : 4.3   Min. : 8.7   Min. : 6.50
##   1st Qu.:34.2 1st Qu.:14.6  1st Qu.:11.1  1st Qu.: 8.88
##   Median :35.5  Median :16.1   Median :12.6   Median :10.05
##   Mean   :31.8  Mean   :14.7   Mean   :11.9   Mean   : 9.33
##   3rd Qu.:36.8 3rd Qu.:17.5  3rd Qu.:13.2  3rd Qu.:10.32
##   Max.   :38.0  Max.   :19.4   Max.   :13.6   Max.   :10.50

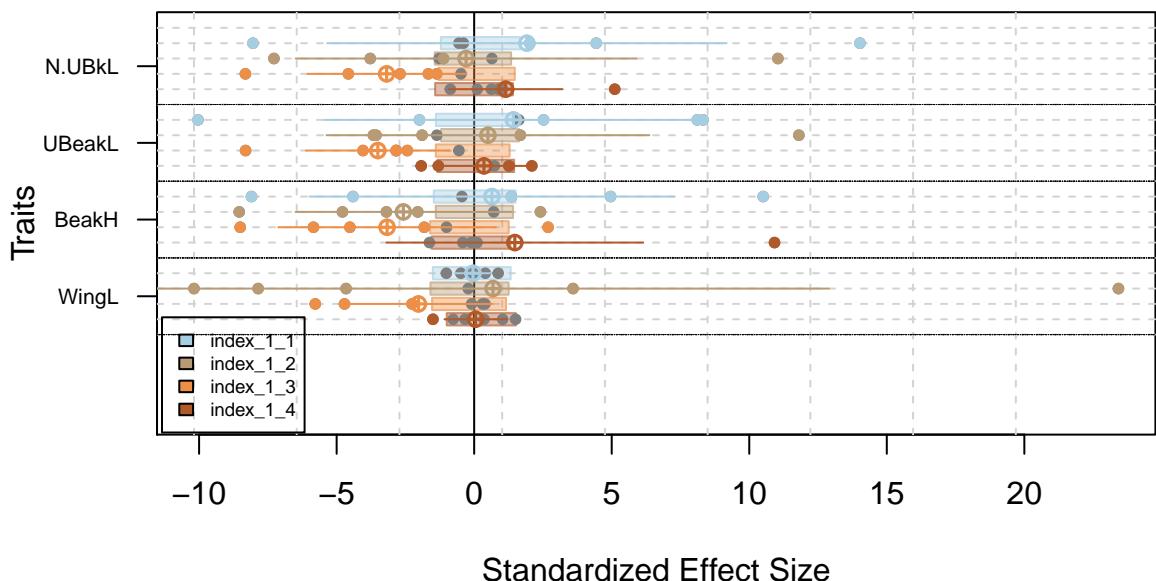
```

```

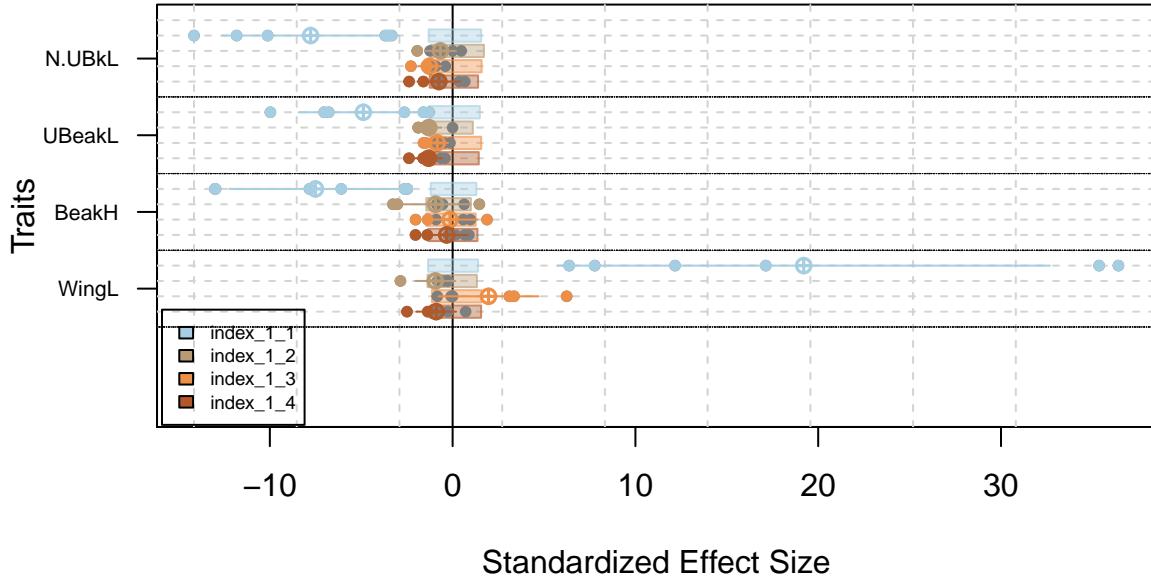
##`tapply(x, ind.plot.finch, function(x) CVNND(x))`#
##      WingL          BeakH          UBeakL        N.UBkL
##  Min.   :0.0000  Min.   :0.268  Min.   :0.139  Min.   :0.0321
##  1st Qu.:0.0000  1st Qu.:0.613  1st Qu.:0.278  1st Qu.:0.2086
##  Median :0.0000  Median :0.651  Median :0.553  Median :0.3482
##  Mean   :0.0374  Mean   :0.602  Mean   :0.666  Mean   :0.4112
##  3rd Qu.:0.0643  3rd Qu.:0.695  3rd Qu.:1.112  3rd Qu.:0.5505
##  Max.   :0.1386  Max.   :0.732  Max.   :1.267  Max.   :0.9588
##
## [1] "null values"
##`tapply(x, ind.plot.finch, function(x) mean(x, na.rm = T))`#
##      Min. 1st Qu. Median  Mean 3rd Qu.    Max.
##      9.66 10.60 13.30 26.20 29.20 70.30
##
##`tapply(x, ind.plot.finch, function(x) kurtosis(x, na.rm = T))`#
##      Min. 1st Qu. Median  Mean 3rd Qu.    Max.
##     -1.360 -0.951 -0.653 -0.445 -0.176  1.590
##
##`tapply(x, ind.plot.finch, function(x) max(x, na.rm = T)-min(x, na.rm = T))`#
##      Min. 1st Qu. Median  Mean 3rd Qu.    Max.
##      8.7   11.4   15.9   19.8  20.8   39.0
##
##`tapply(x, ind.plot.finch, function(x) CVNND(x))`#
##      Min. 1st Qu. Median  Mean 3rd Qu.    Max.
##      0.000 0.097 0.272 0.382 0.613 1.790

plot(res.finch.withIV)

```



```
plot(res.finch.withoutIV)
```



5.2.2 Plot Tstats and other uni/multivariates metrics together

The class `listofindex` permits to stock different metrics computed using `Tstats`, `ComIndex` and `ComIndexMulti` and compared to different null model. To do that we can use the Standardized Effect Size (`ses`) define as :

$$SES = (I_{obs} - I_{sim}) / \delta_{sim}$$

where I_{obs} is the observed value, I_{sim} the mean of values calculated from the null model and δ_{sim} the standard deviation of these simulated values.

```
list.ind1<-list(res.finch.withIV, res.finch.withoutIV)
index.list1<-as.listofindex(list.ind1)

plot(index.list1)
```

```
list.ind<-list(res.finch.withIV, res.finch.withoutIV, res.finch)
namesindex.i.11 = c("mean", "kurtosis", "range", "CVNND",
"mean.pop", "kurtosis.pop", "range.pop", "CVNND.pop",
"T_IP.IC", "T_IC.IR", "T_PC.PR")

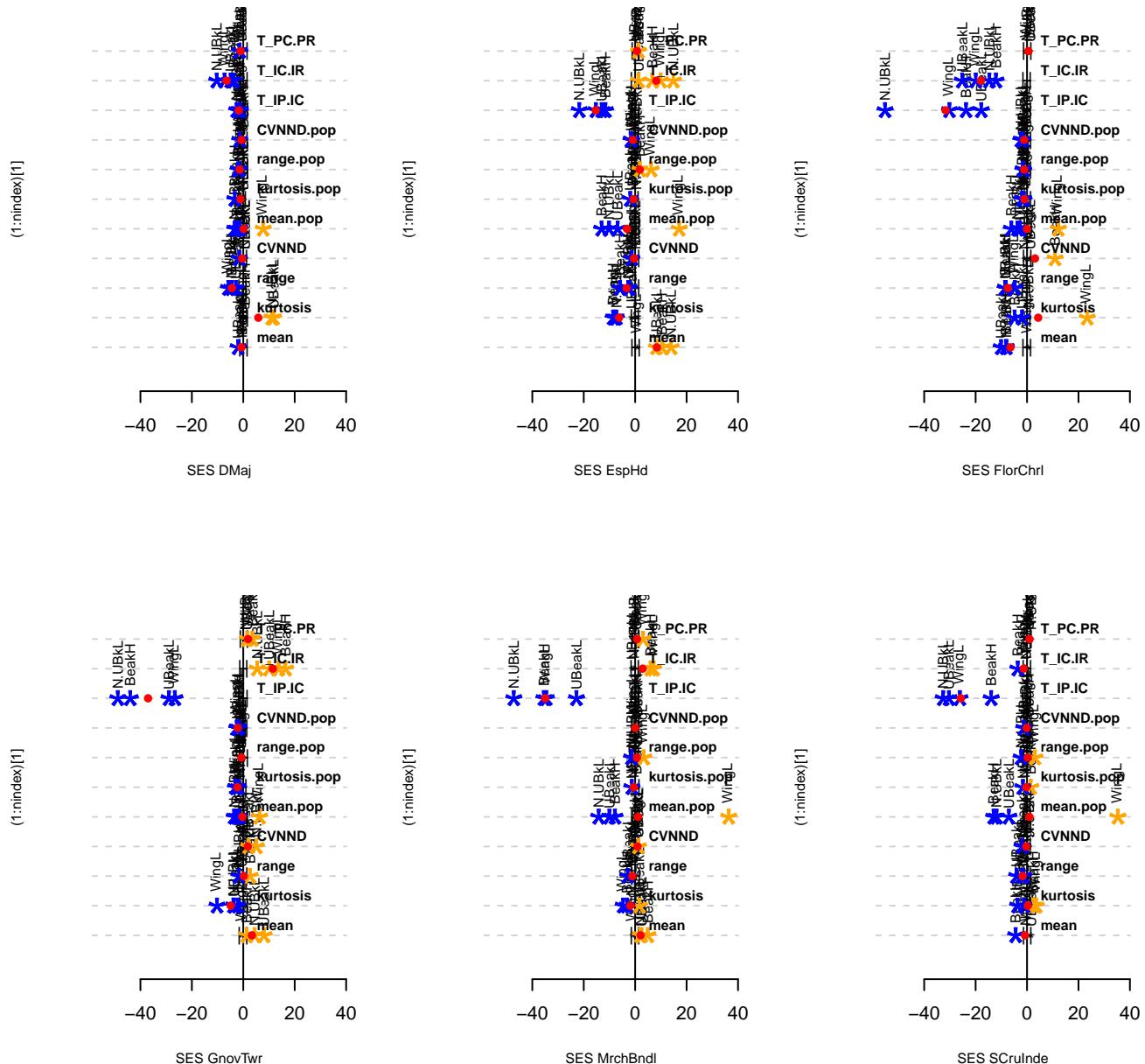
i.11<-as.listofindex(list.ind, namesindex = namesindex.i.11)

class(i.11)

## [1] "listofindex"
```

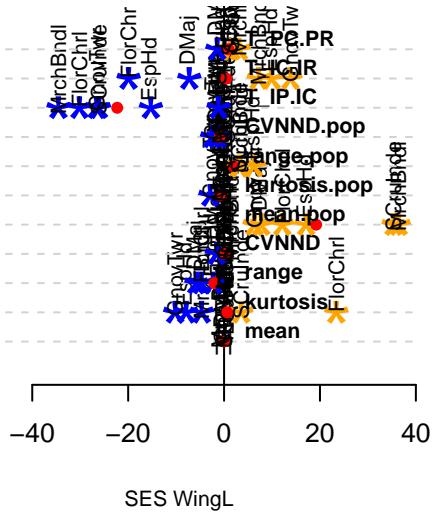
The plot type `bytraits` allows plotting all SES traits values for all sites or all traits

```
par(mfrow = c(2,3))
plot(i.11,type = "bysites")
```

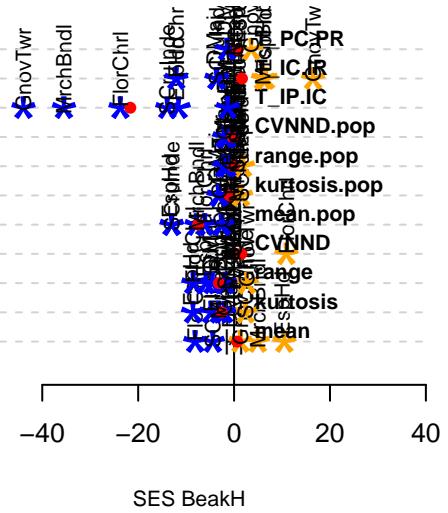


```
par(mfrow = c(2,2))
plot(i.11,type = "bytraits")
```

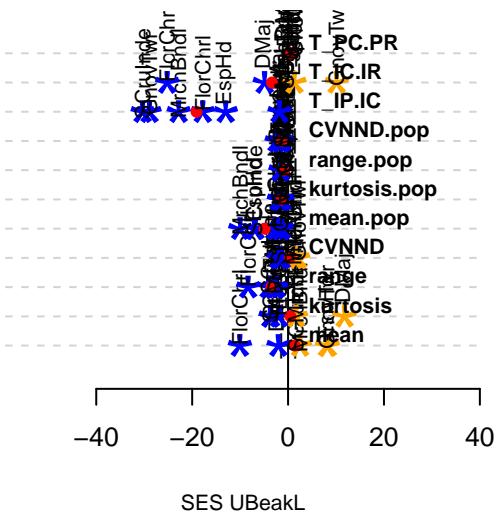
(1:nindex)[i]



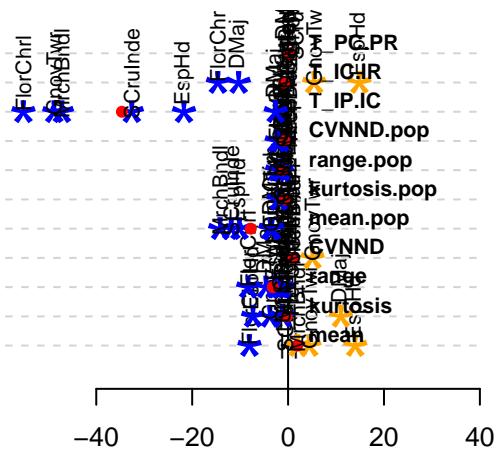
(1:nindex)[i]



(1:nindex)[i]



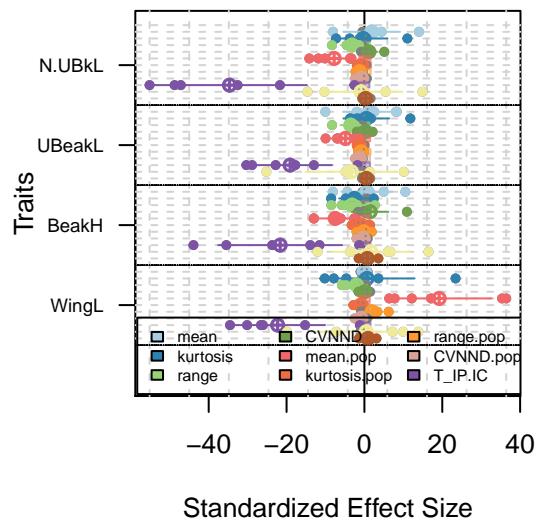
(1:nindex)[i]



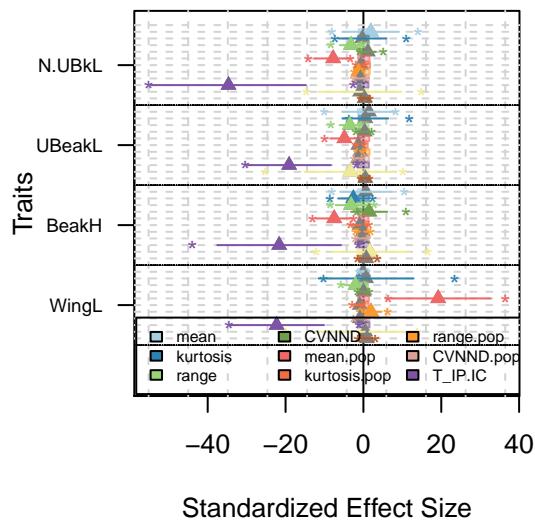
```
par(mfrow = c(1,1))
```

The other plot types are the same as plot.Tstats.

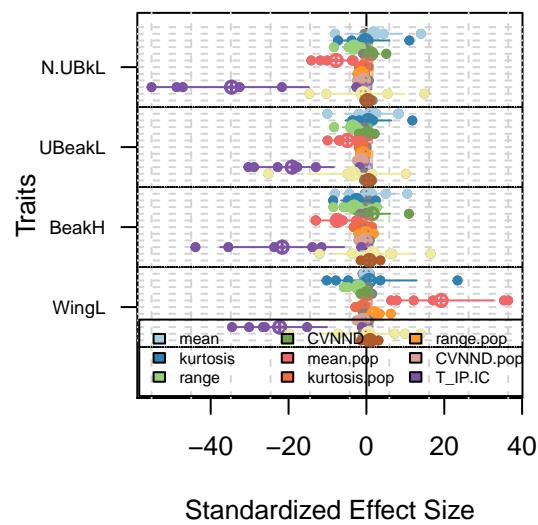
```
par(mfrow = c(2,2))
plot(i.11)
```



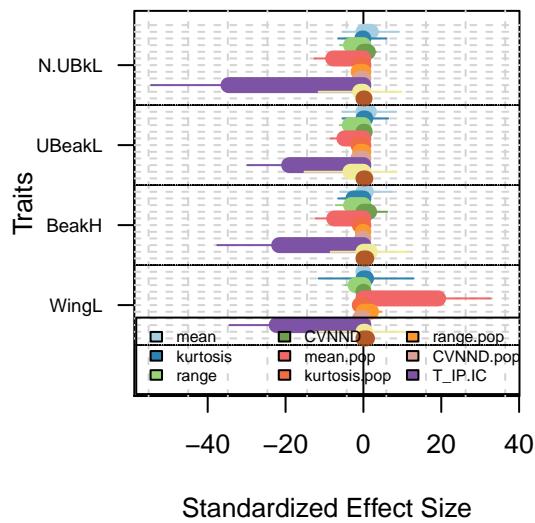
```
plot(i.l1,type = "simple_range")
```



```
plot(i.l1,type = "normal")
```



```
plot(i.l1,type = "barplot")
```



```
par(mfrow = c(1,1))
```

5.3 More information ond multivariates index

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)))  
  
require(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)  
  
## [1] "creating null models"  
## [1] "regional.ind 25 %"  
## [1] "regional.ind 50 %"  
## [1] "regional.ind 75 %"  
## [1] "regional.ind 100 %"  
## [1] "calculation of null values using null models"  
## [1] "sum(scale(x), na.rm = T) 50 %"  
## [1] "sum(x, na.rm = T) 100 %"  
## [1] "calculation of observed values"  
## [1] "50 %"  
## [1] "100 %"  
  
res.sum.1  
  
## #####  
## # Community metrics calculation #  
## #####  
## class: ComIndexMulti  
## $call: ComIndexMulti(traits = 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, sp = sp.finch, nperm = 9)  
##  
## #####  
## $obs: list of observed values  
##   $sum(scale(x), na.rm = T)  
##   $sum(x, na.rm = T)  
##  
## #####  
## $null: list of null values, number of permutation: NA  
##   $sum(scale(x), na.rm = T)_nm ... null model = regional.ind
```

```

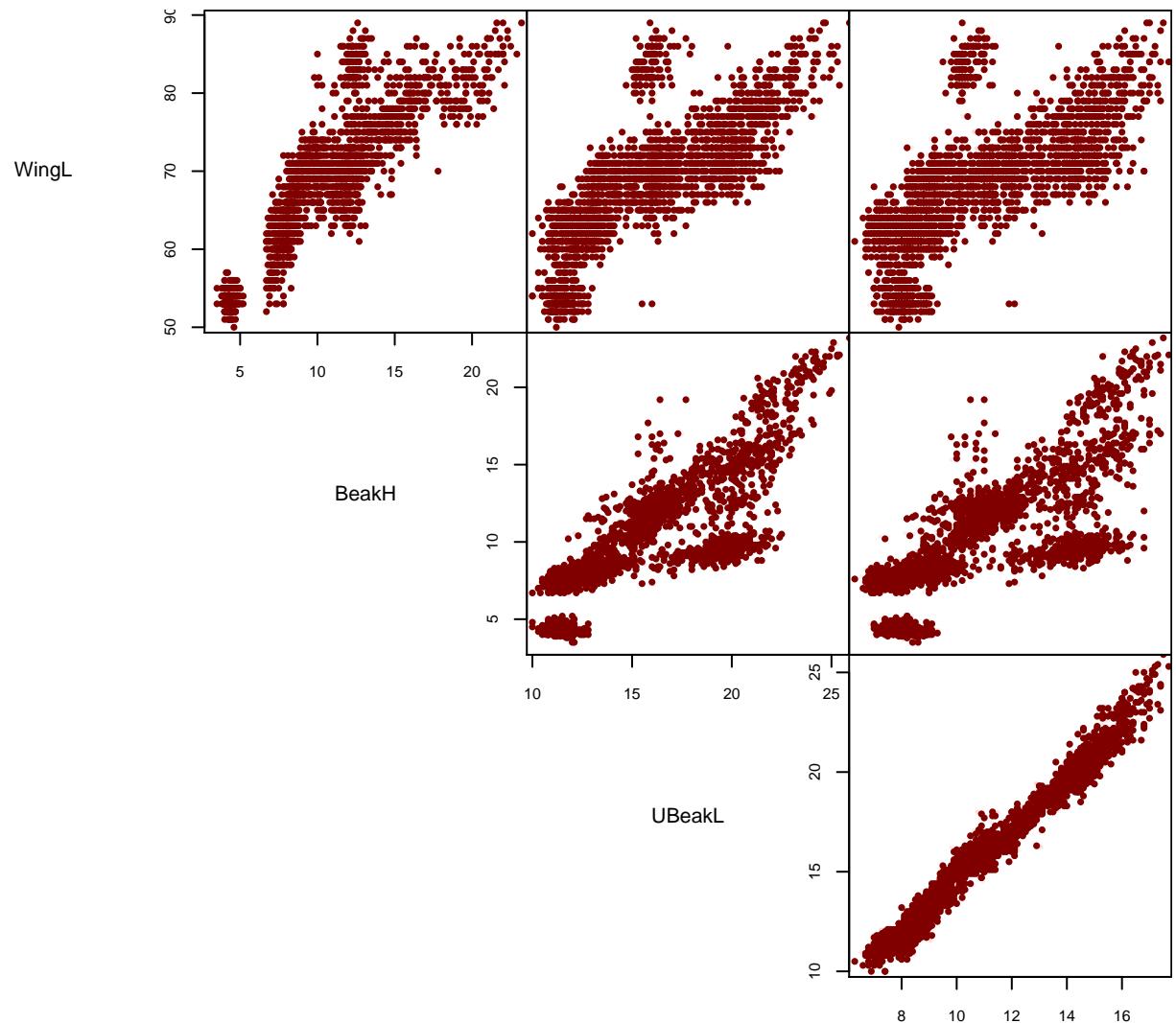
## $sum(x, na.rm = T)_nm ... null model = regional.ind
##
## #####
## data used
##   data      class      dim
## 1 $traits    data.frame 2513,4
## 2 $ind.plot  factor     2513
## 3 $sp        factor     2513
##   content
## 1 traits data
## 2 name of the plot in which the individual is
## 3 groups (e.g. species) which the individual belong to
##
## #####
## others
## $namestraits: 4 traits
## [1] "WingL"   "BeakH"   "UBeakL"  "N.UBkL"
##
## $sites_richness:
##       DMaj     EspHd FlorChrl  GnovTwr MrchBndl SCruInde
##       50       267      981      258      270      687

```

A more interesting example using the function `hypervolume` from the package ... `hypervolume` (Blonder et al., 2014). We show here several results which differed in there factor that delimit the group to calculate different hypervolume (argument `byfactor`).

First, let's try the `hypervolume` function one finch data.

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



Now, we can do the same analysis for each species.

```

hv.list<-new("HypervolumeList")
hv.list2<-list()

for(i in 1: length(table(sp.finch))) {
  hv.list2[[i]]<-hypervolume(traits.finch.mice[sp.finch == levels(sp.finch)[i], ],
    reps = 1000, bandwidth = 0.2,
    verbose = F, warnings = F)
}

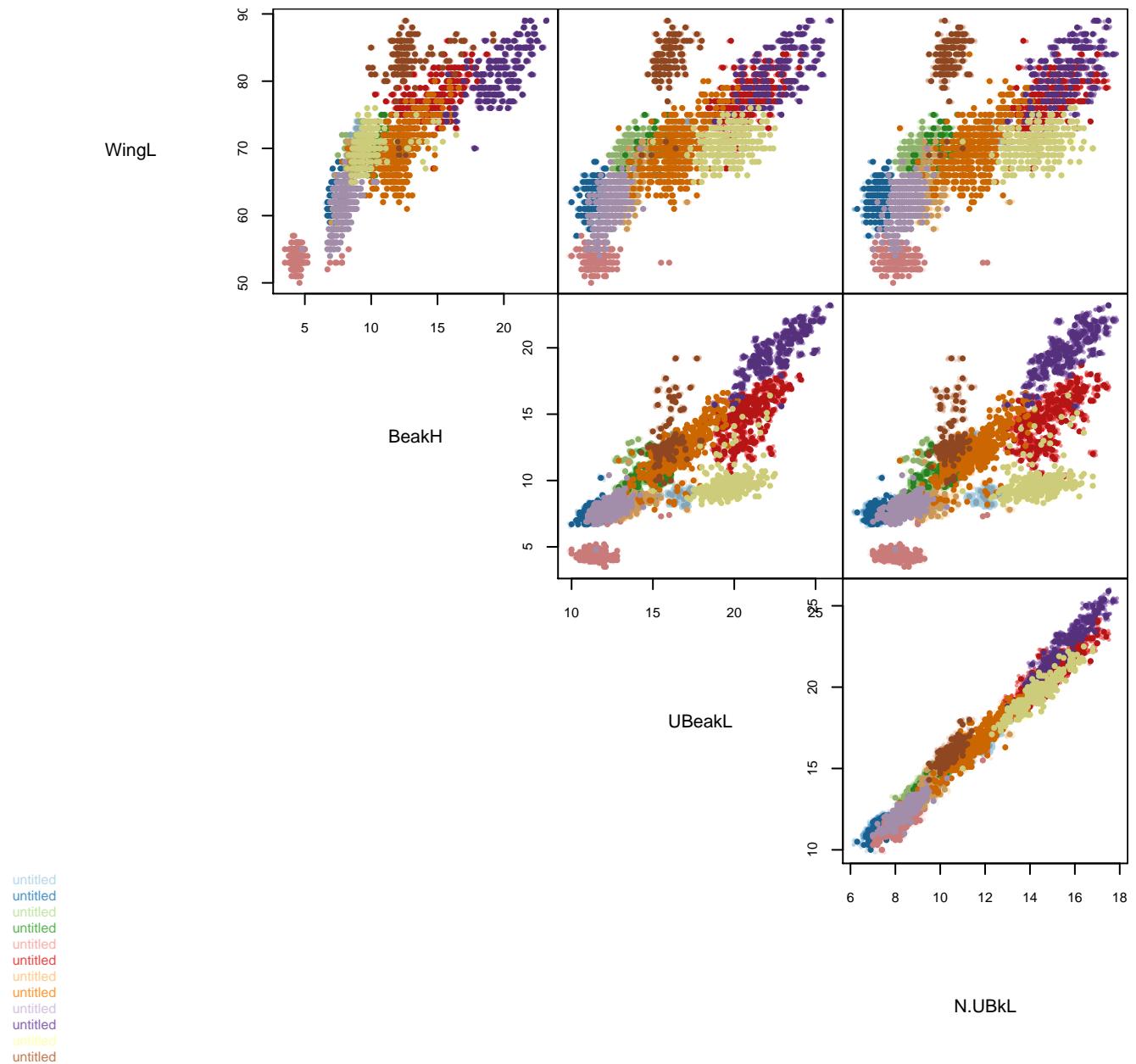
hv.list@HVList<-hv.list2
require(adegenet)

## Loading required package: adegenet
## =====
## adegenet 1.4-2 is loaded
## =====
##
## - to start, type '?adegenet'
## - to browse adegenet website, type 'adegenetWeb()'
## - to post questions/comments: adegenet-forum@lists.r-forge.r-project.org

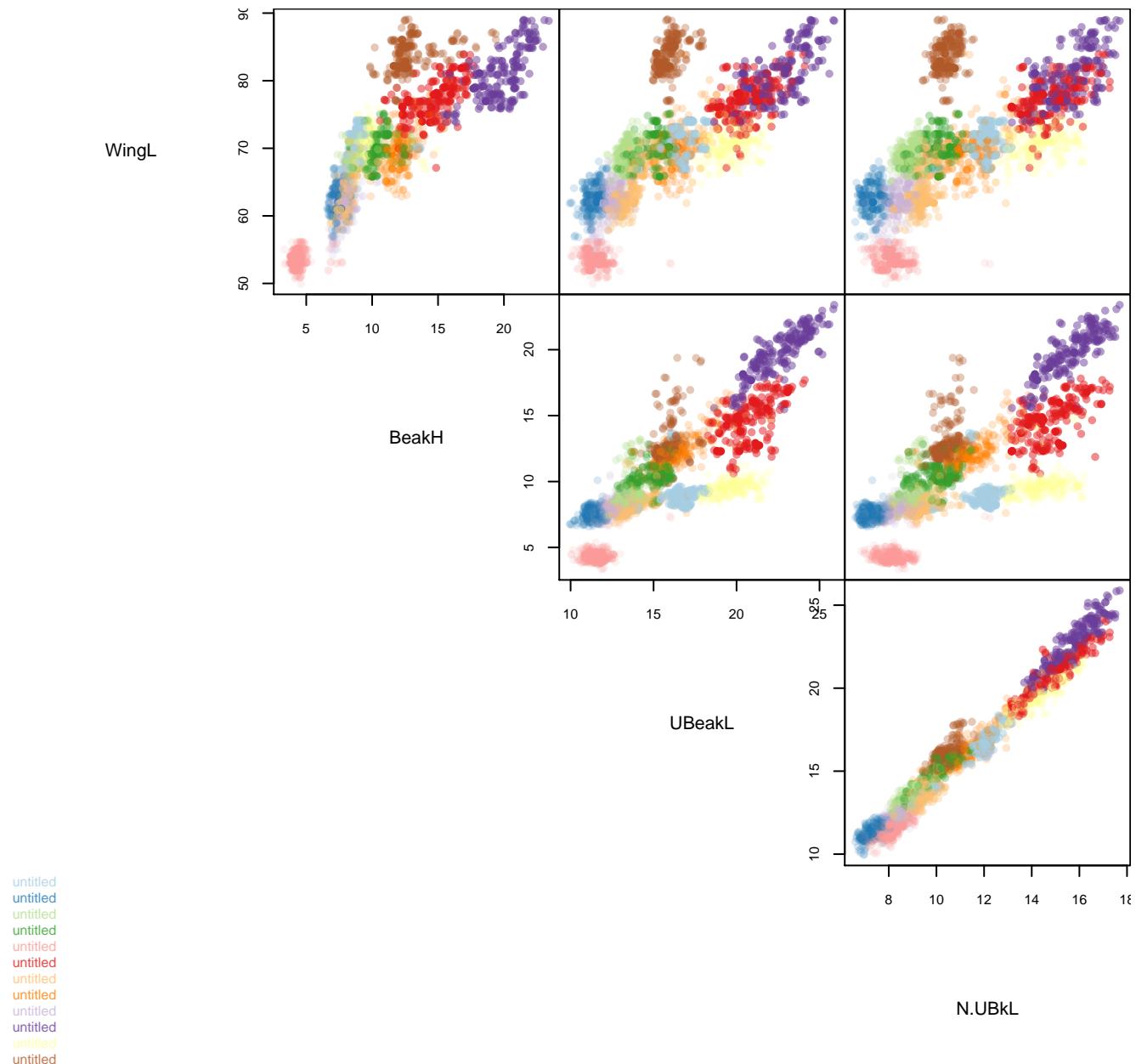
colorhv<-transp(funky(nlevels(sp.finch)), alpha = 0.8)

plot(hv.list, colors = colorhv, darkfactor = 0.8)

```



```
plot(hv.list, colors = colorhv, darkfactor = 0.8, showdata = F, npmax = 200, cex.random = 1)
```



```
summary(hv.list)
```

The standard example of the `hypervolume` package also use finch data but at the species level.

```
doHypervolumeFinchDemo=TRUE
demo('finch', package = 'hypervolume')

##
##
##  demo(finch)
##  -----
## > if (exists('doHypervolumeFinchDemo')==TRUE)
```

```

## +
## +   data(finch)
## +
## +   species_list = unique(finch$Species)
## +   num_species = length(species_list)
## +
## +   hv_finches_list = new("HypervolumeList")
## +   hv_finches_list@HVList = vector(mode="list",length=num_species)
## +
## +   # compute hypervolumes for each species
## +   for (i in 1:num_species)
## +   {
## +     this_species = subset(finch, Species==species_list[i])
## +     # keep the trait data
## +     this_species_log <- log10(this_species[,2:ncol(this_species)])
## +     # make a hypervolume using auto-bandwidth
## +     hv_finches_list@HVList[[i]] <- hypervolume(this_species_log, bandwidth=estimate_bandwidth(
## +                                         this_species_log, min=0.01, max=100, n=100),
## +                                         reps=10000, quantile=0, name=as.character(species_list[i]))
## +   }
## +
## +   # compute all pairwise overlaps
## +   overlap = matrix(NA, nrow=num_species, ncol=num_species)
## +   dimnames(overlap)=list(species_list, species_list)
## +   for (i in 1:num_species)
## +   {
## +     for (j in i:num_species)
## +     {
## +       if (i!=j)
## +       {
## +         # compute set operations on each pair
## +         this_set = hypervolume_set(hv_finches_list@HVList[[i]], hv_finches_list@HVList[[j]])
## +         # calculate a Sorenson overlap index (2 x shared volume / sum of |hv1| + |hv2|)
## +         overlap[i,j] = 2 * this_set@HVList$Intersection@Volume / (hv_finches_list@HVList[[i]]@HVList$Volume + hv_finches_list@HVList[[j]]@HVList$Volume)
## +       }
## +     }
## +   }
## +
## +
## +
## +   # show all hypervolumes
## +   plot(hv_finches_list,npmax=500,darkfactor=0.5,cex.legend=0.25,cex.names=0.75)
## +
## +   # show pairwise overlaps - note that actually very few species overlap in nine dimensions
## +   op <- par(mar=c(10,10,1,1))
## +   image(x=1:nrow(overlap), y=1:nrow(overlap), z=overlap,axes=F,xlab='',ylab='',col=rainbow(10))
## +   box()
## +   axis(side=1, at=1:(length(dimnames(overlap)[[1]])),dimnames(overlap)[[1]],las=2,cex.axis=0.75)
## +   axis(side=2, at=1:(length(dimnames(overlap)[[2]])),dimnames(overlap)[[2]],las=1,cex.axis=0.75)

```

```

## +  par(op)
## +
## +  rm(doHypervolumeFinchDemo)
## + } else
## +
## +  message('Demo does not run by default to meet CRAN runtime requirements.')
## +  message('This demo requires approximately 3 minutes to run.')
## +  message('To run the demo, type')
## +  message('\tdoHypervolumeFinchDemo=TRUE')
## +  message('\tdemo(finch)')
## +  message('at the R command line prompt.')
## +
## Evaluating probability density...
## Building tree... done.
## Querying tree... 5.26316e-006  0.0526368  0.105268  0.1579  0.210532  0.263163  0.315795
## Finished evaluating probability density.
## Beginning volume calculation... done.
## Quantile requested: 0.00  obtained: 0.00
## Evaluating probability density...
## Building tree... done.
## Querying tree... 7.69231e-006  0.0769308  0.153854  0.230777  0.3077  0.384623  0.461546
## Finished evaluating probability density.
## Beginning volume calculation... done.
## Quantile requested: 0.00  obtained: 0.00
## Evaluating probability density...
## Building tree... done.
## Querying tree... 1.23457e-006  0.0123469  0.0246926  0.0370383  0.049384  0.0617296  0.074
## Finished evaluating probability density.
## Beginning volume calculation... done.
## Quantile requested: 0.00  obtained: 0.00
## Evaluating probability density...
## Building tree... done.
## Querying tree... 4.54545e-006  0.0454591  0.0909136  0.136368  0.181823  0.227277  0.27273
## Finished evaluating probability density.
## Beginning volume calculation... done.
## Quantile requested: 0.00  obtained: 0.00
## Evaluating probability density...
## Building tree... done.
## Querying tree... 9.09091e-006  0.0909182  0.181827  0.272736  0.363645  0.454555  0.545464
## Finished evaluating probability density.
## Beginning volume calculation... done.
## Quantile requested: 0.00  obtained: 0.00
## Retaining 30621 points in hv1 and 39557 points in hv2.
## Beginning ball queries...
## Building tree... done.
## Querying tree... 2.528e-005  0.252825  0.505625  0.758425  done.
## Building tree... done.
## Querying tree... 3.26573e-005  0.326606  0.653179  0.979752  done.

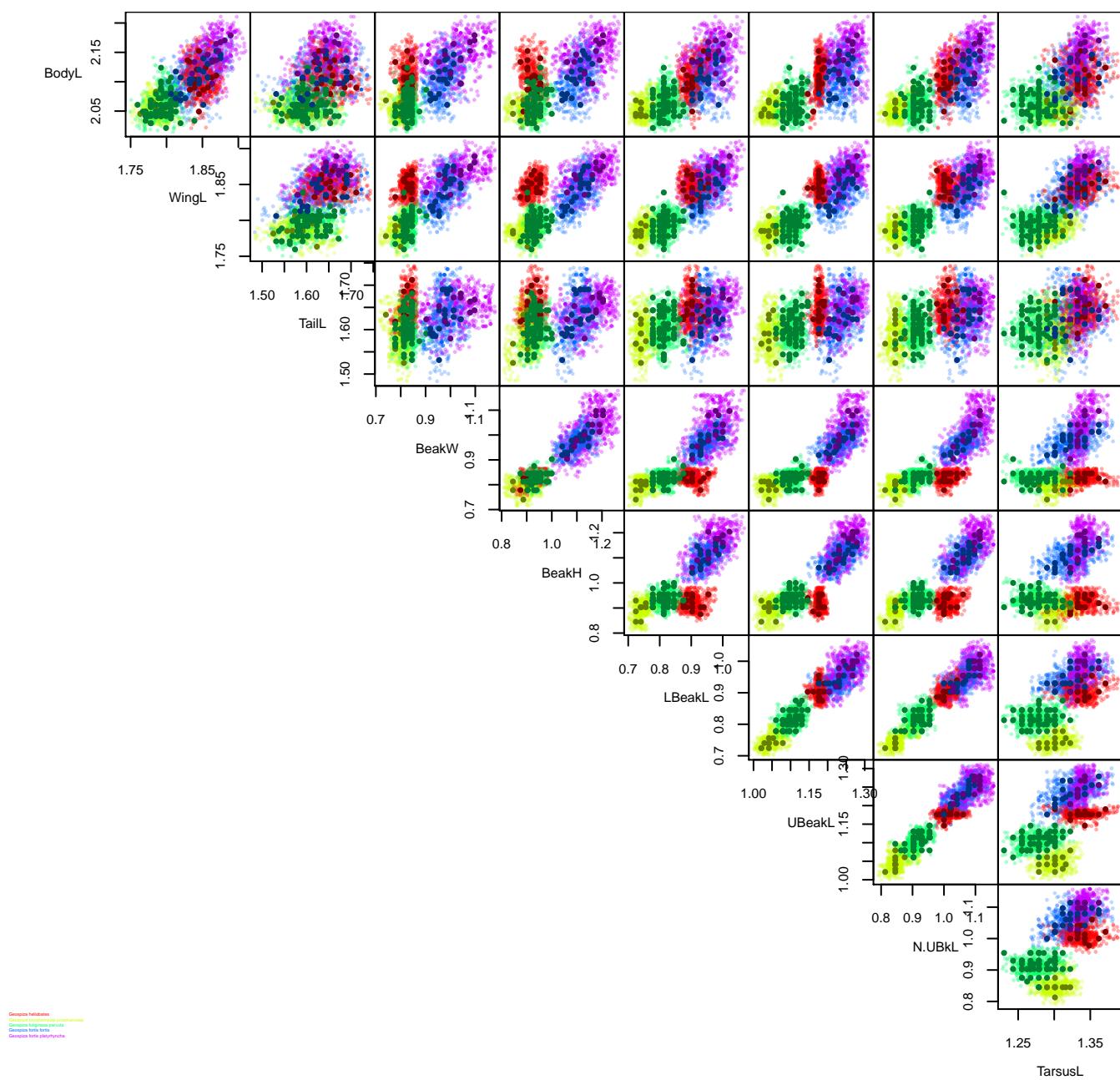
```

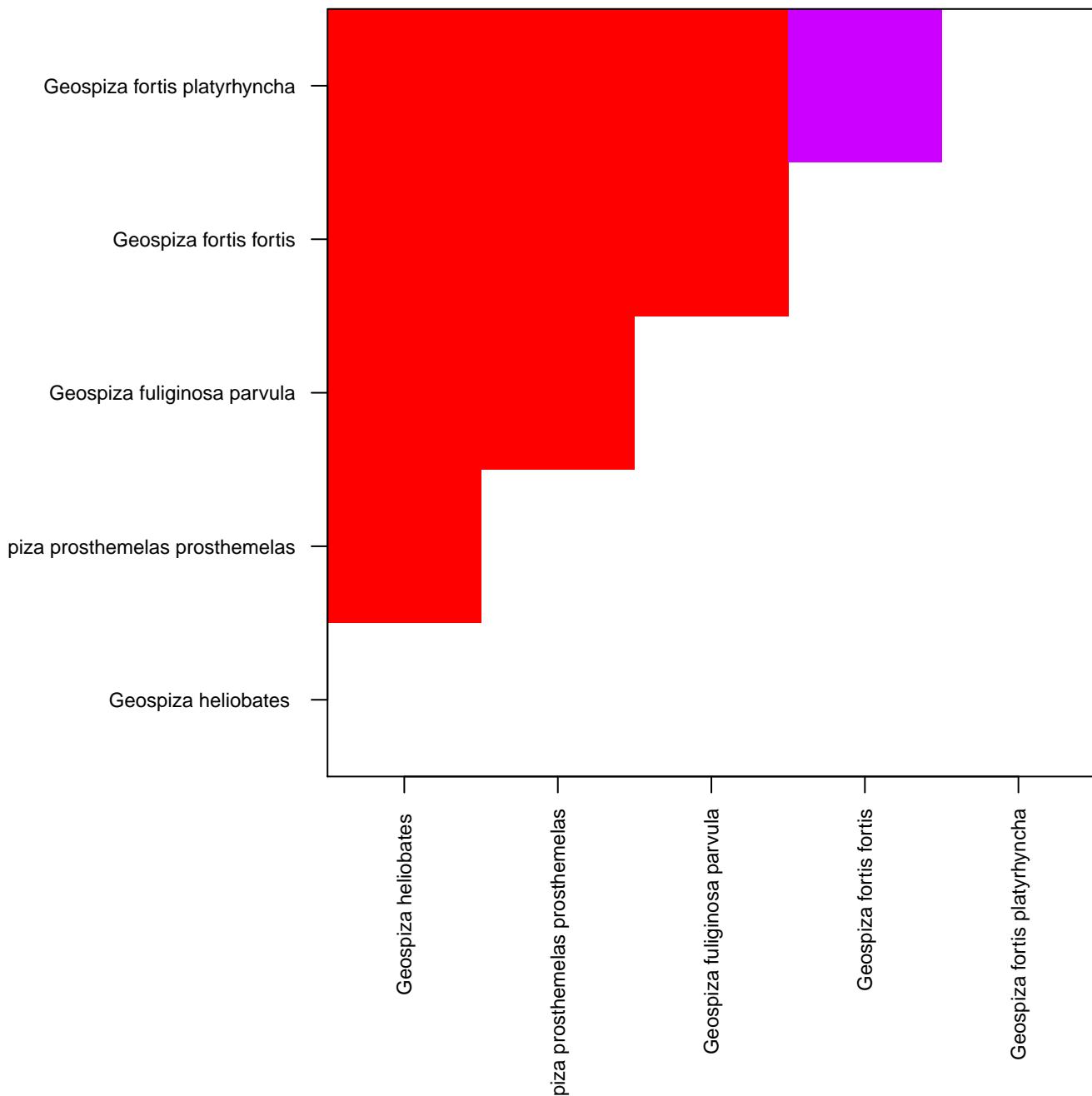
```

## Finished ball queries.
## Retaining 57690 points in hv1 and 56159 points in hv2.
## Beginning ball queries...
## Building tree... done.
## Querying tree... 1.78066e-005  0.178084  0.35615   0.534215  0.712281  0.890347  done.
## Building tree... done.
## Querying tree... 1.7334e-005   0.173358  0.346698  0.520038  0.693378  0.866719  done.
## Finished ball queries.
## Retaining 1265 points in hv1 and 61559 points in hv2.
## Beginning ball queries...
## Building tree... done.
## Querying tree... 1.62446e-005  0.162462  0.324908  0.487354  0.649799  0.812245  0.974691
## Building tree... done.
## Querying tree... 0.000790514  done.
## Finished ball queries.
## Retaining 428 points in hv1 and 31493 points in hv2.
## Beginning ball queries...
## Building tree... done.
## Querying tree... 3.17531e-005  0.317563  0.635094  0.952624  done.
## Building tree... done.
## Querying tree... 0.00233645  done.
## Finished ball queries.
## Retaining 39557 points in hv1 and 29809 points in hv2.
## Beginning ball queries...
## Building tree... done.
## Querying tree... 3.35469e-005  0.335503  0.670972  done.
## Building tree... done.
## Querying tree... 2.528e-005   0.252825  0.505625  0.758425  done.
## Finished ball queries.
## Retaining 1634 points in hv1 and 61559 points in hv2.
## Beginning ball queries...
## Building tree... done.
## Querying tree... 1.62446e-005  0.162462  0.324908  0.487354  0.649799  0.812245  0.974691
## Building tree... done.
## Querying tree... 0.000611995  done.
## Finished ball queries.
## Retaining 553 points in hv1 and 31493 points in hv2.
## Beginning ball queries...
## Building tree... done.
## Querying tree... 3.17531e-005  0.317563  0.635094  0.952624  done.
## Building tree... done.
## Querying tree... 0.00180832  done.
## Finished ball queries.
## Retaining 1231 points in hv1 and 61559 points in hv2.
## Beginning ball queries...
## Building tree... done.
## Querying tree... 1.62446e-005  0.162462  0.324908  0.487354  0.649799  0.812245  0.974691
## Building tree... done.

```

```
## Querying tree... 0.000812348 done.  
## Finished ball queries.  
## Retaining 417 points in hv1 and 31493 points in hv2.  
## Beginning ball queries...  
## Building tree... done.  
## Querying tree... 3.17531e-005 0.317563 0.635094 0.952624 done.  
## Building tree... done.  
## Querying tree... 0.00239808 done.  
## Finished ball queries.  
## Retaining 20847 points in hv1 and 31493 points in hv2.  
## Beginning ball queries...  
## Building tree... done.  
## Querying tree... 3.17531e-005 0.317563 0.635094 0.952624 done.  
## Building tree... done.  
## Querying tree... 4.79685e-005 0.479733 0.959419 done.  
## Finished ball queries.
```





`ComIndexMulti` takes the same arguments as `ComIndex` and an argument by.factor to apply the index on different factors.

```
#all individual are put in the same group: calculate the hypervolume without by.factor
hv.1<-ComIndexMulti(traits.finches,
                      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.finches, nperm = 9, sp = sp.finches)

## [1] "creating null models"
## [1] "regional.ind 25 %"
## [1] "regional.ind 50 %"
## [1] "regional.ind 75 %"
```

```

## [1] "regional.ind 100 %"
## [1] "calculation of null values using null models"
## [1] "as.numeric(try(hypervolume(na.omit(x), reps = 100, \n                                bandwidth = 0.2, verbose = F, warnings = F)@Volume))",
## [1] "calculation of observed values"
## [1] "100 %"

hv.2<-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 = n_sp_plot, nullmodels = "regional.ind",
                      ind.plot = ind.plot.finch, nperm = 9, sp = sp.finch)

## [1] "creating null models"
## [1] "regional.ind 25 %"
## [1] "regional.ind 50 %"
## [1] "regional.ind 75 %"
## [1] "regional.ind 100 %"
## [1] "calculation of null values using null models"
## [1] "as.numeric(try(hypervolume(na.omit(x), reps = 100, \n                                bandwidth = 0.2, verbose = F, warnings = F)@Volume))",
## [1] "calculation of observed values"
## [1] "100 %"

hv.3<-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 = ind.plot.finch, nullmodels ="regional.ind",
                      ind.plot = ind.plot.finch, nperm = 9, sp = sp.finch)

## [1] "creating null models"
## [1] "regional.ind 25 %"
## [1] "regional.ind 50 %"
## [1] "regional.ind 75 %"
## [1] "regional.ind 100 %"
## [1] "calculation of null values using null models"
## [1] "as.numeric(try(hypervolume(na.omit(x), reps = 100, \n                                bandwidth = 0.2, verbose = F, warnings = F)@Volume))",
## [1] "calculation of observed values"
## [1] "100 %"

hv.4<-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 = sp.finch, nullmodels = "regional.ind",
                      ind.plot = ind.plot.finch, nperm = 9, sp = sp.finch)

## [1] "creating null models"
## [1] "regional.ind 25 %"
## [1] "regional.ind 50 %"
## [1] "regional.ind 75 %"
## [1] "regional.ind 100 %"

```

```

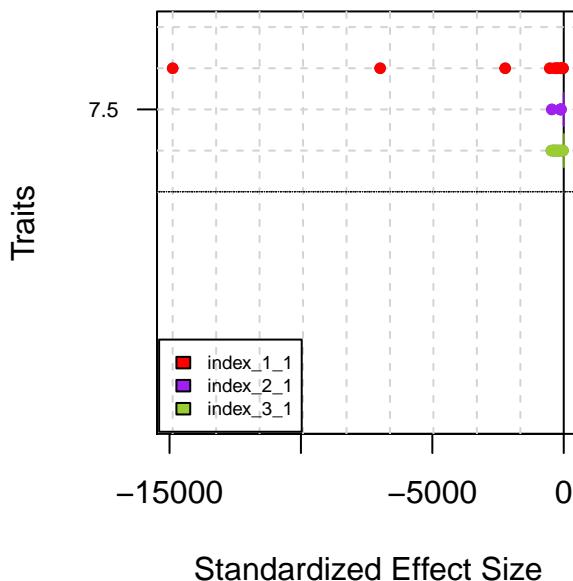
## [1] "calculation of null values using null models"
## [1] "as.numeric(try(hypervolume(na.omit(x), reps = 100, \n                                bandwidth = 0.2
## [1] "calculation of observed values"
## [1] "100 %"

list.ind.multi<-as.listofindex(list(hv.2, hv.3, hv.4))

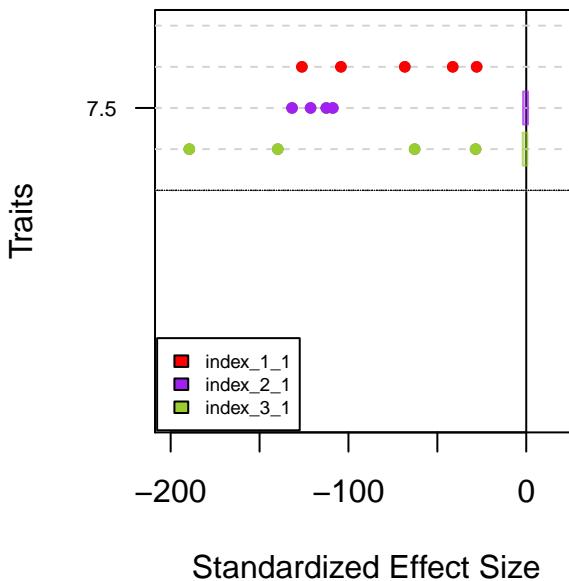
ses.list.multi<-ses.listofindex(list.ind.multi)

plot(list.ind.multi)

```



```
plot(list.ind.multi, xlim = c(-200,20))
```



Compare hypervolume to Villéger's metrics convex hull.

```

require("geometry")

## Loading required package: geometry
## Loading required package: magic
## Loading required package: abind

FA<-as.character("FA")
funct<-c("round(convhulln(x,FA)$vol,6)")

##Null model local is trivial for this function
##because randomization is within community only
Fdis.finch<-ComIndexMulti(traits.finch.mice,
                           index = funct,
                           by.factor = ind.plot.finч, nullmodels = "local",
                           ind.plot = ind.plot.finch, nperm = 9, sp = sp.finch)

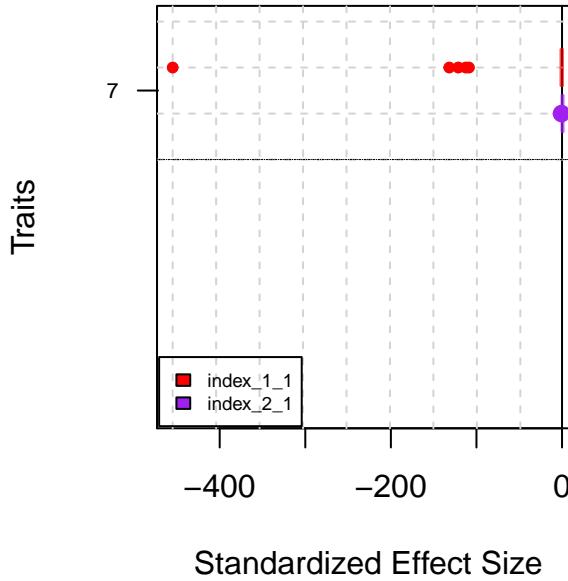
## [1] "creating null models"
## [1] "local 25 %"
## [1] "local 50 %"
## [1] "local 75 %"
## [1] "local 100 %"
## [1] "calculation of null values using null models"
## [1] "round(convhulln(x,FA)$vol,6) 100 %"
## [1] "calculation of observed values"
## [1] "100 %"

list.ind.multi2<-as.listofindex(list(hv.3, Fdis.finch))

ses.list.multi2<-ses.listofindex(list.ind.multi2)

```

```
plot(list.ind.multi2)
```



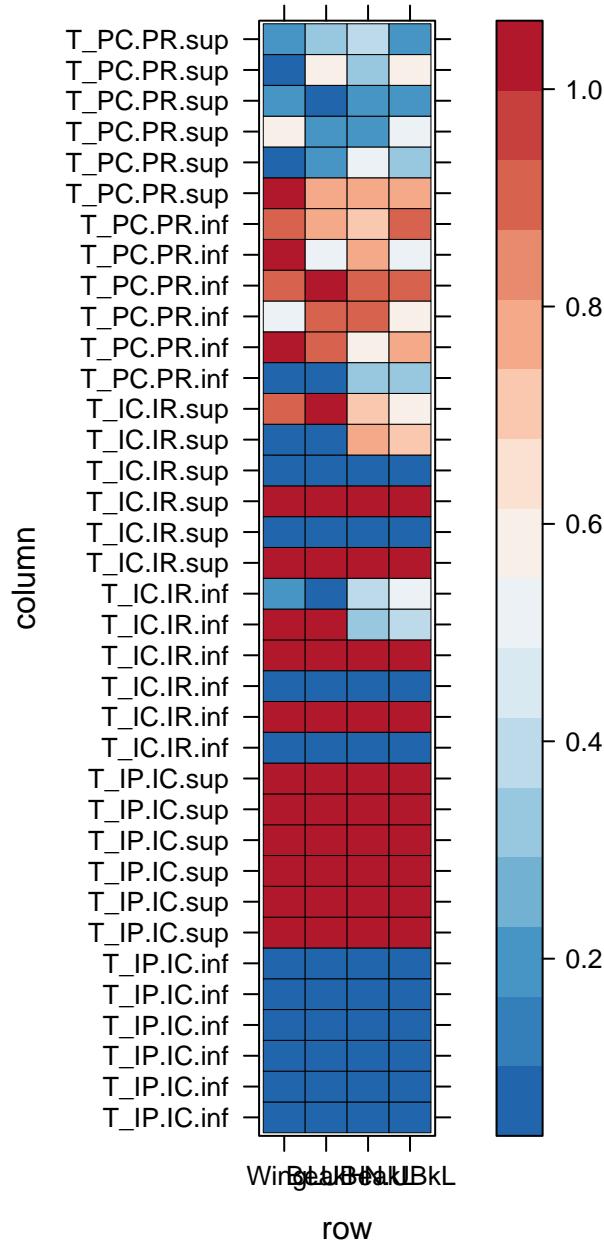
6 Others graphics functions

Use rasterVis to obtain more color schemes.

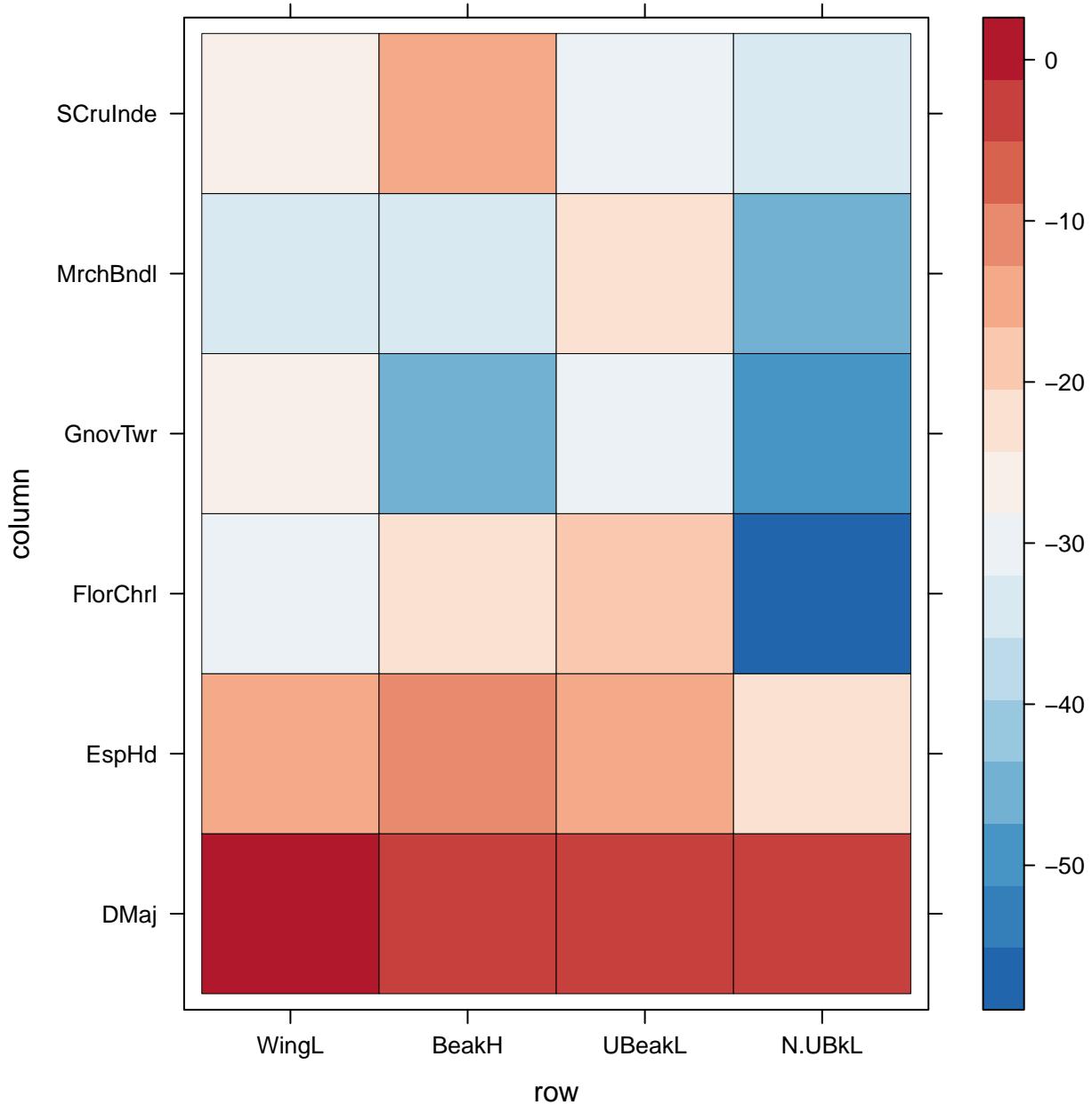
```
## Loading required package: rasterVis
## Loading required package: raster
## Loading required package: sp
##
## Attaching package: 'raster'
##
## The following object is masked from 'package:magic':
##
##     shift
##
## The following objects are masked from 'package:ape':
##
##     rotate, zoom
##
## The following object is masked from 'package:nlme':
##
##     getData
##
## Loading required package: latticeExtra
## Loading required package: RColorBrewer
## Loading required package: hexbin
```

Plot the p-value or the ses values using the function `levelplot`.

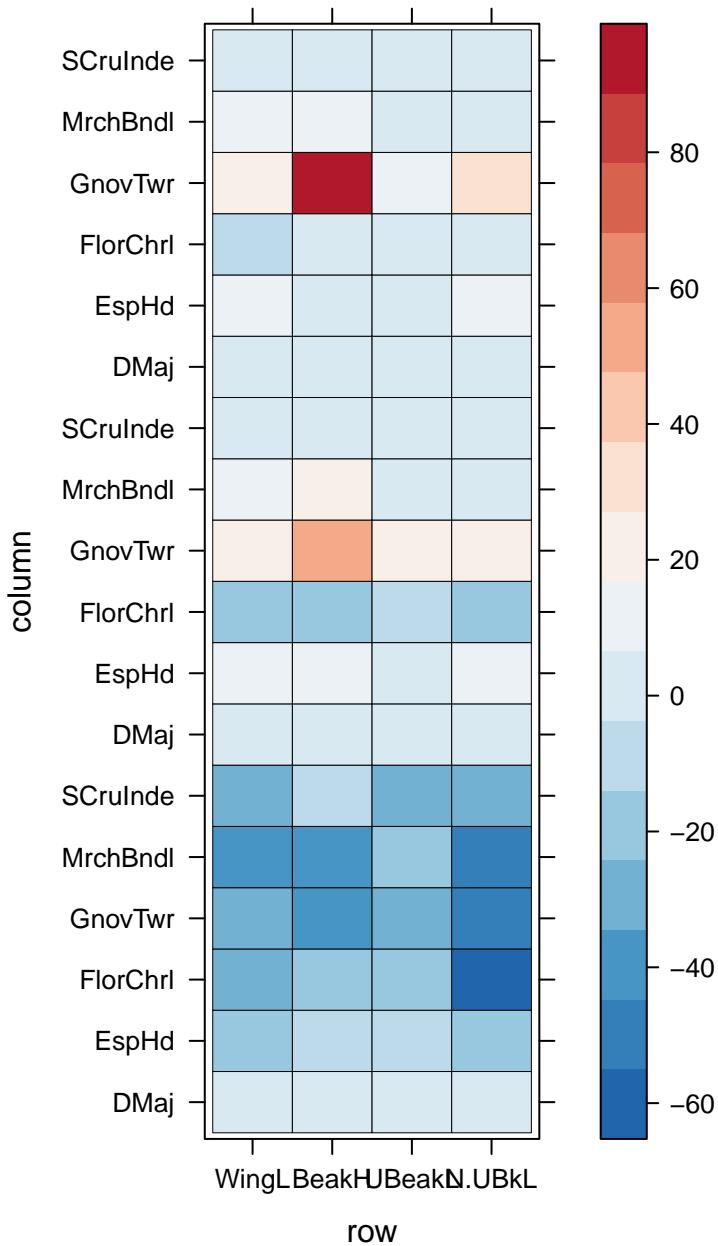
```
levelplot(t(sum_Tstats(res.finch)$p.value),  
colorkey = my.ckey, par.settings = my.theme, border = "black")
```



```
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")
```



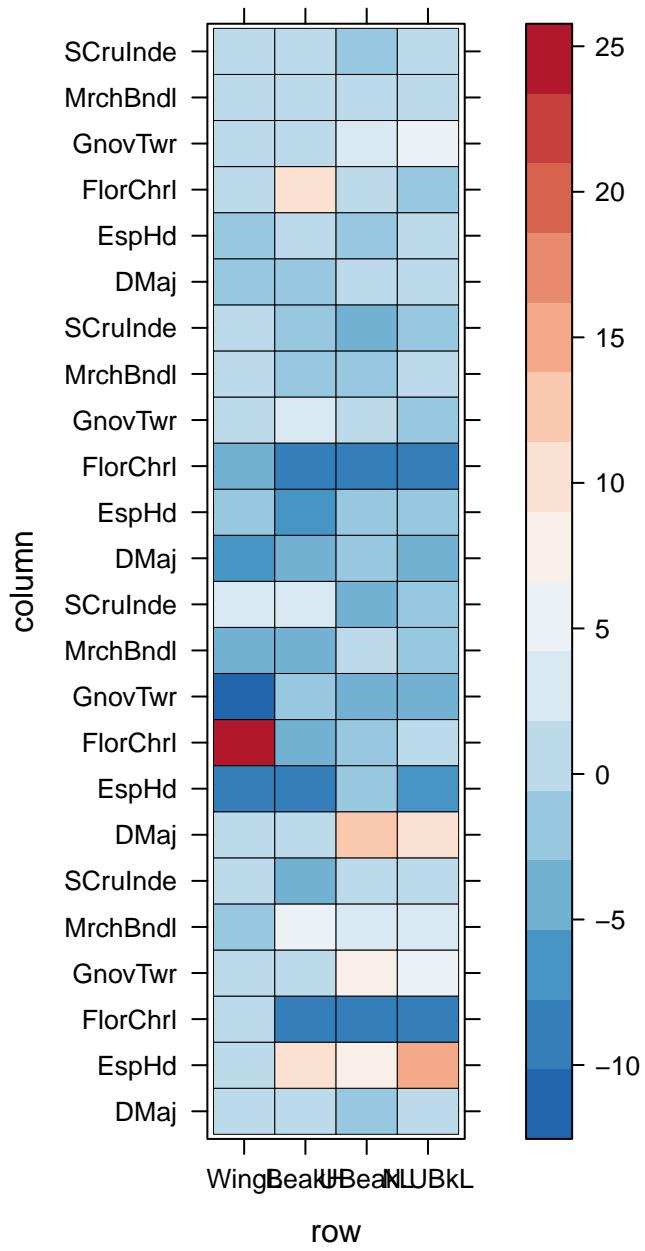
```
levelplot(cbind(t ses(res.finches$Tstats$T_IP.IC, res.finches$Tstats$T_IP.IC_nm)$ses),
          t ses(res.finches$Tstats$T_IC.IR, res.finches$Tstats$T_IP.IC_nm)$ses),
          t ses(res.finches$Tstats$T_PC.PR, res.finches$Tstats$T_IP.IC_nm)$ses))
, colorkey = my.ckey, par.settings = my.theme, border = "black")
```



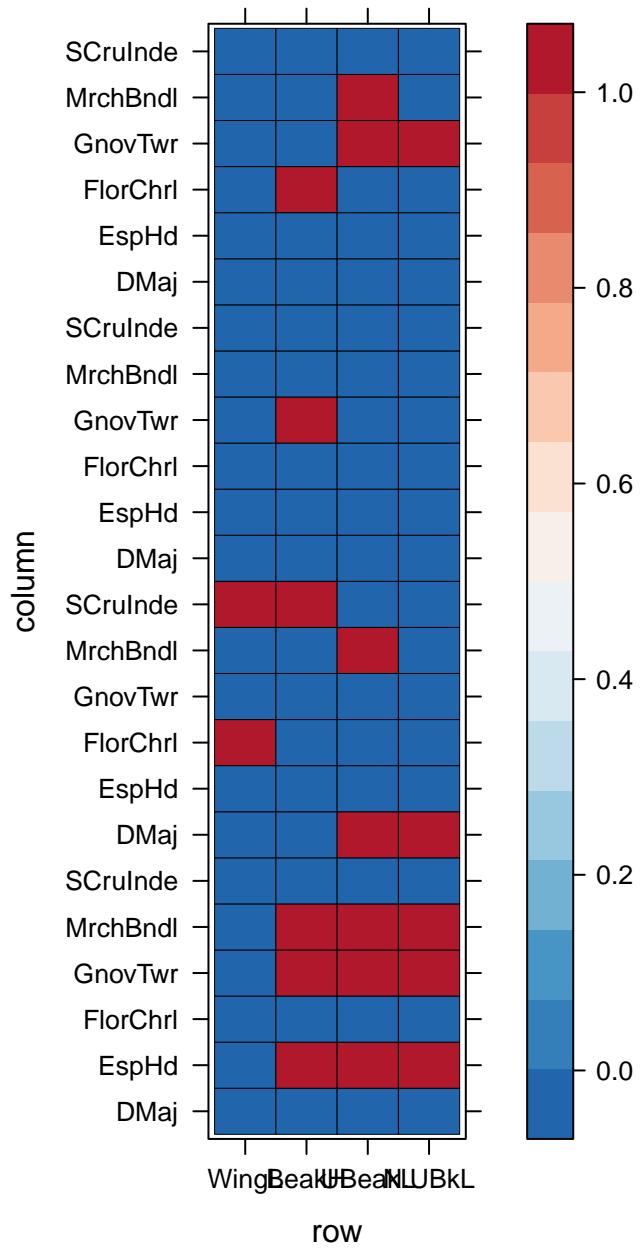
Another example using `ses.listofindex`. The first plot represent "ses" values and the second one the result of a test with H0: observed index value are greater than what we can expect using the null model (alpha = 2.5%).

```
ses.list<-ses.listofindex(i.11)

levelplot(t(rbind(ses.list[[1]]$ses, ses.list[[2]]$ses,
                  ses.list[[3]]$ses, ses.list[[4]]$ses)),
          colorkey = my.ckey, par.settings = my.theme, border = "black")
```



```
levelplot(t(rbind(ses.list[[1]]$ses>ses.list[[1]]$ses.sup,
                  ses.list[[2]]$ses>ses.list[[2]]$ses.sup,
                  ses.list[[3]]$ses>ses.list[[3]]$ses.sup,
                  ses.list[[4]]$ses>ses.list[[4]]$ses.sup)),
          colorkey = my.ckey, par.settings = my.theme, border = "black")
```



Compare metrics calculate on individual against metrics calculate after populationnal meaning

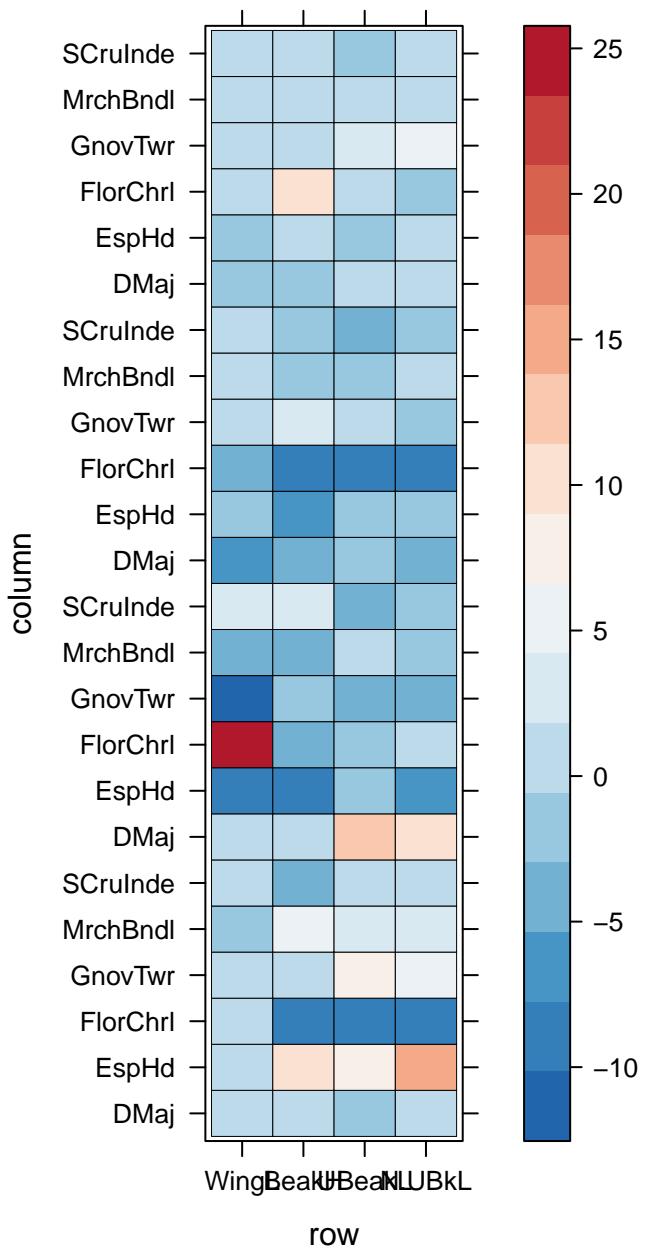
```

ses.ind<-t(rbind(ses.list[[1]]$ses,
  ses.list[[2]]$ses,
  ses.list[[3]]$ses,
  ses.list[[4]]$ses))

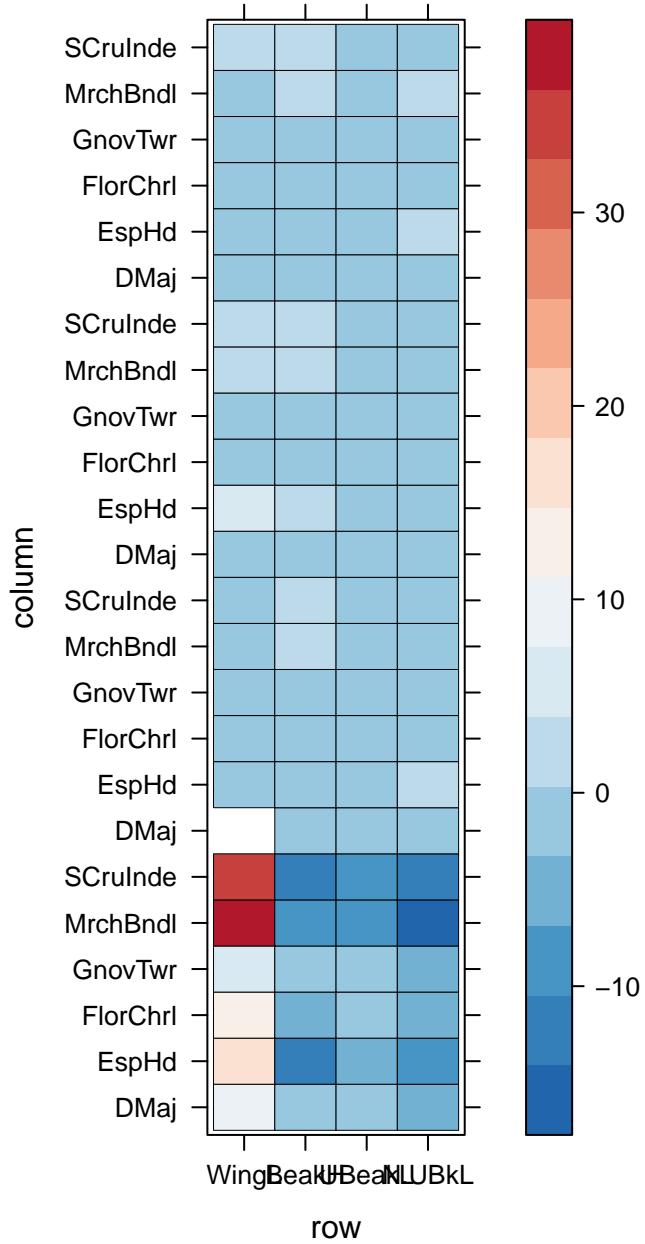
ses.sp<-t(rbind(ses.list[[5]]$ses,
  ses.list[[6]]$ses,
  ses.list[[7]]$ses,
  ses.list[[8]]$ses))

levelplot(ses.ind, colorkey = my.ckey,
  par.settings = my.theme, border = "black")

```



```
levelplot(ses.sp, colorkey = my.ckey,  
         par.settings = my.theme, border = "black")
```



7 Conclusion

To finish, we can do a multivariate analysis of the metrics obtain during this tutorial. Analysis dudi 1 puts together all traits by meaning the SES values for each metrics in each sites whereas analysis dudi 2 analyses all combination of traits / sites / metrics.

```
library(ade4)

matfordudi<-matrix(nrow = length(colMeans(ses.list[[1]]$ses)), ncol = length(names(ses.list))
for(i in 1: length(names(ses.list))){  
  matfordudi[,i]<-colMeans(ses.list[[i]]$ses)
}
```

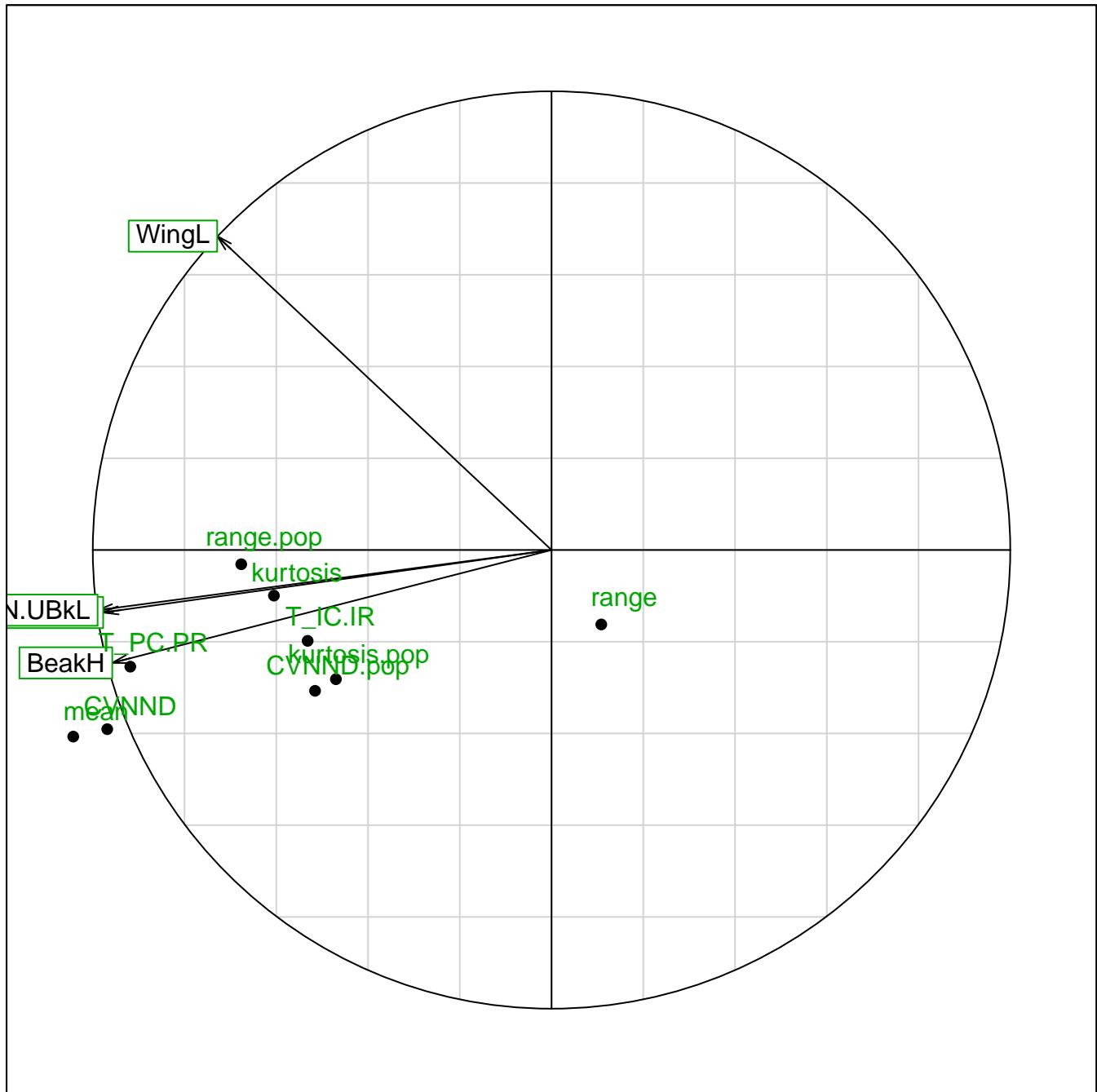
```
colnames(matfordudi)<-names(ses.list)
rownames(matfordudi)<-colnames(traits.finch)

matfordudi2<-matrix(nrow = length(as.vector(ses.list[[1]]$ses)), ncol = length(names(ses.list)))
for(i in 1: length(names(ses.list))){  
  matfordudi2[,i]<-as.vector(ses.list[[i]]$ses)
}
colnames(matfordudi2)<-names(ses.list)
```

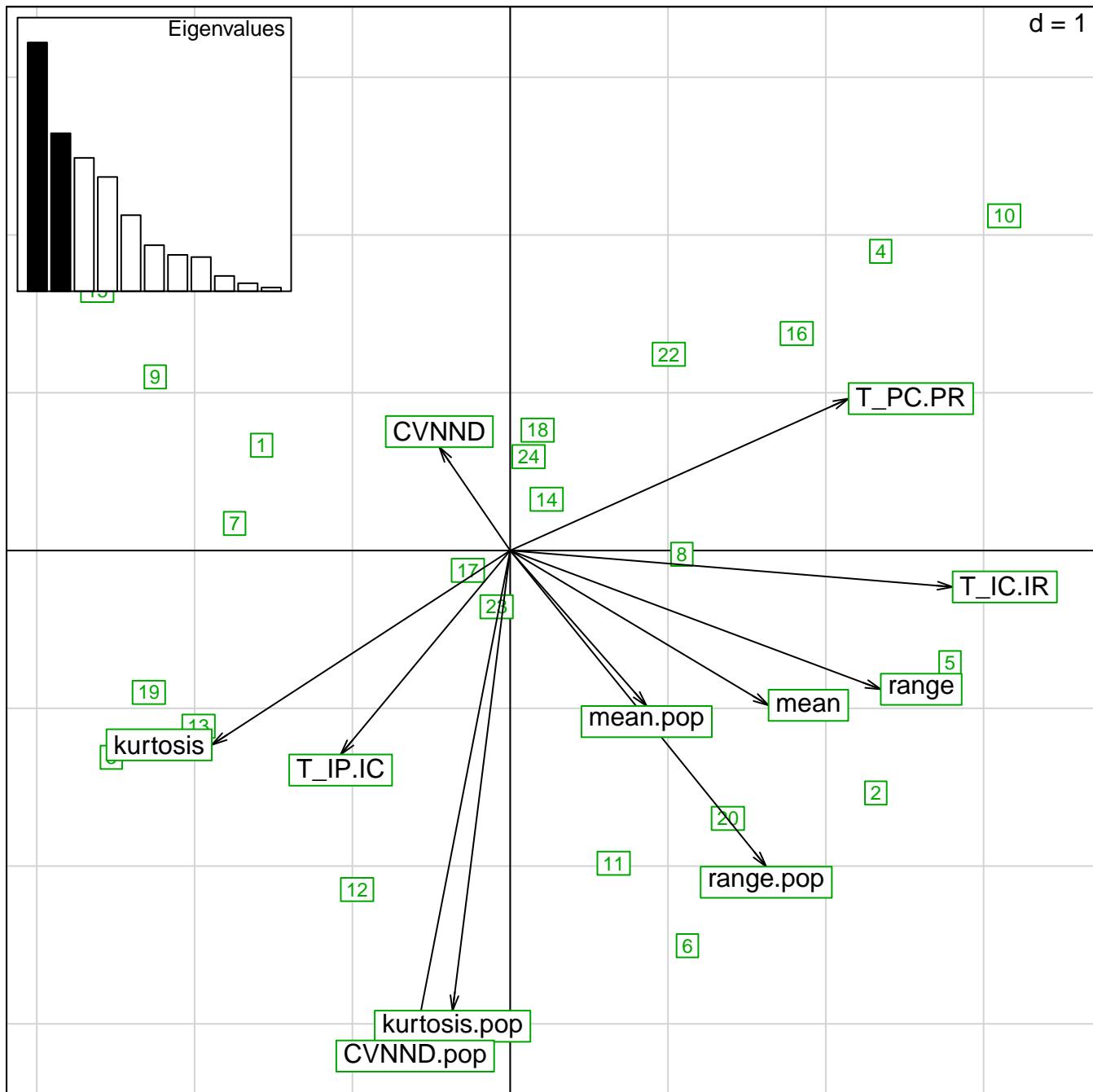
#Use mice for the purpose of this example

```
matfordudi<-complete(mice(matfordudi))
matfordudi2<-complete(mice(matfordudi2))
```

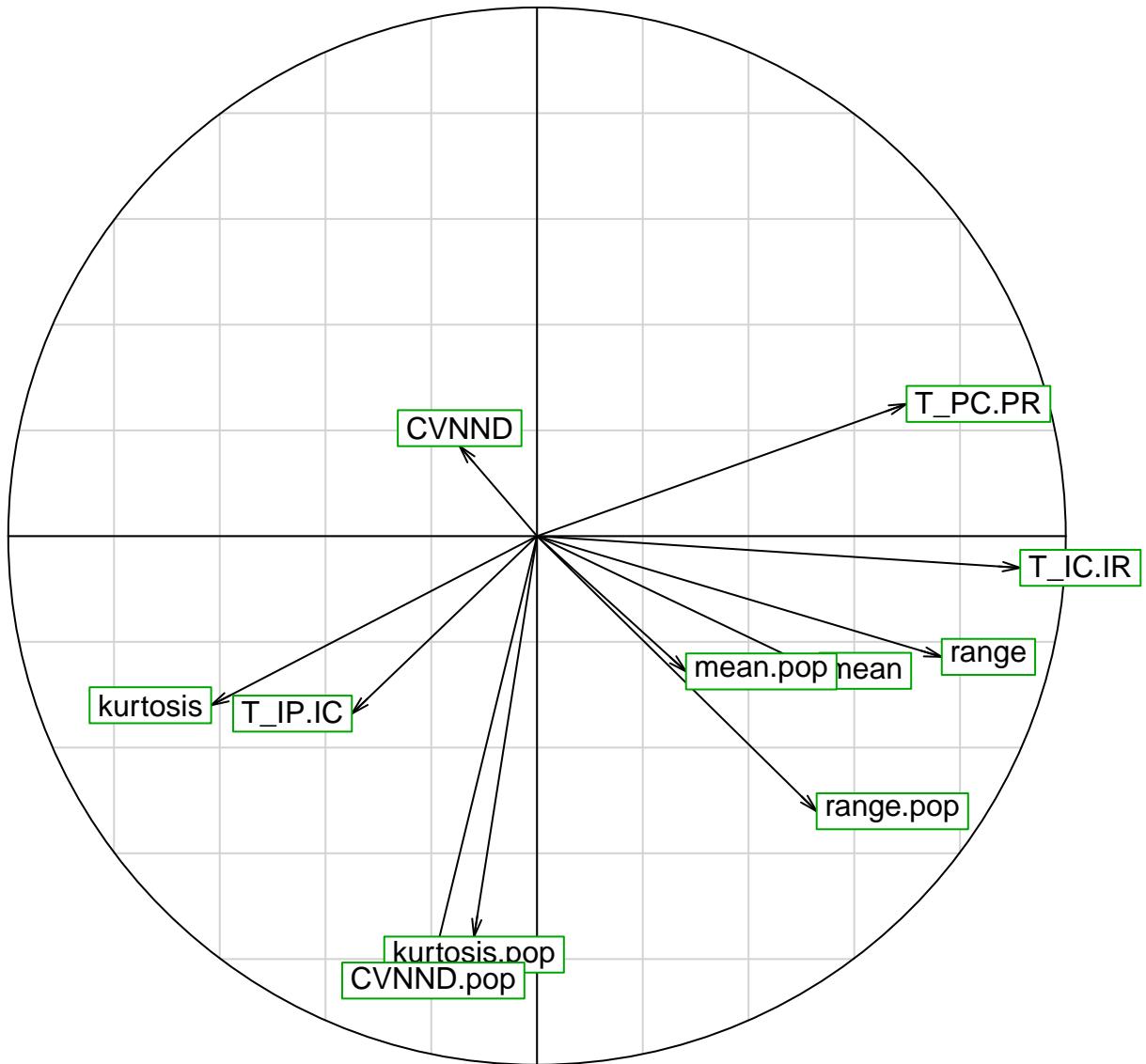
```
res.dudi<-dudi.pca(t(matfordudi), scan = F, nf = 2)
s.corcircle(res.dudi$co)
s.label(res.dudi$li, add.plot = T, clabel = 0, pch = 16)
s.label(res.dudi$li+0.05, add.plot = T, boxes = F)
```



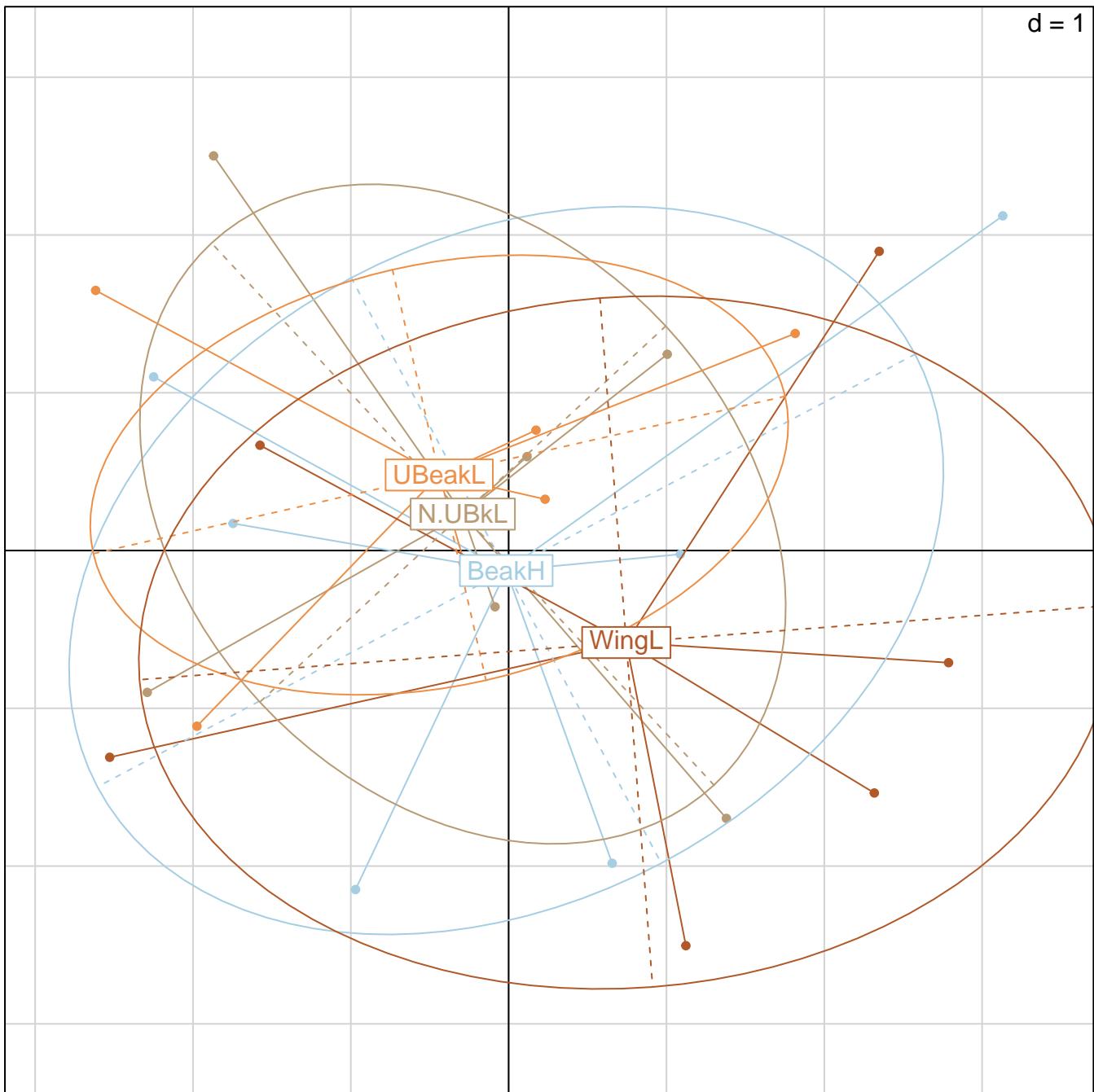
```
res.dudi2<-dudi.pca(matfordudi2, scan = F, nf = 2)
scatter(res.dudi2)
```



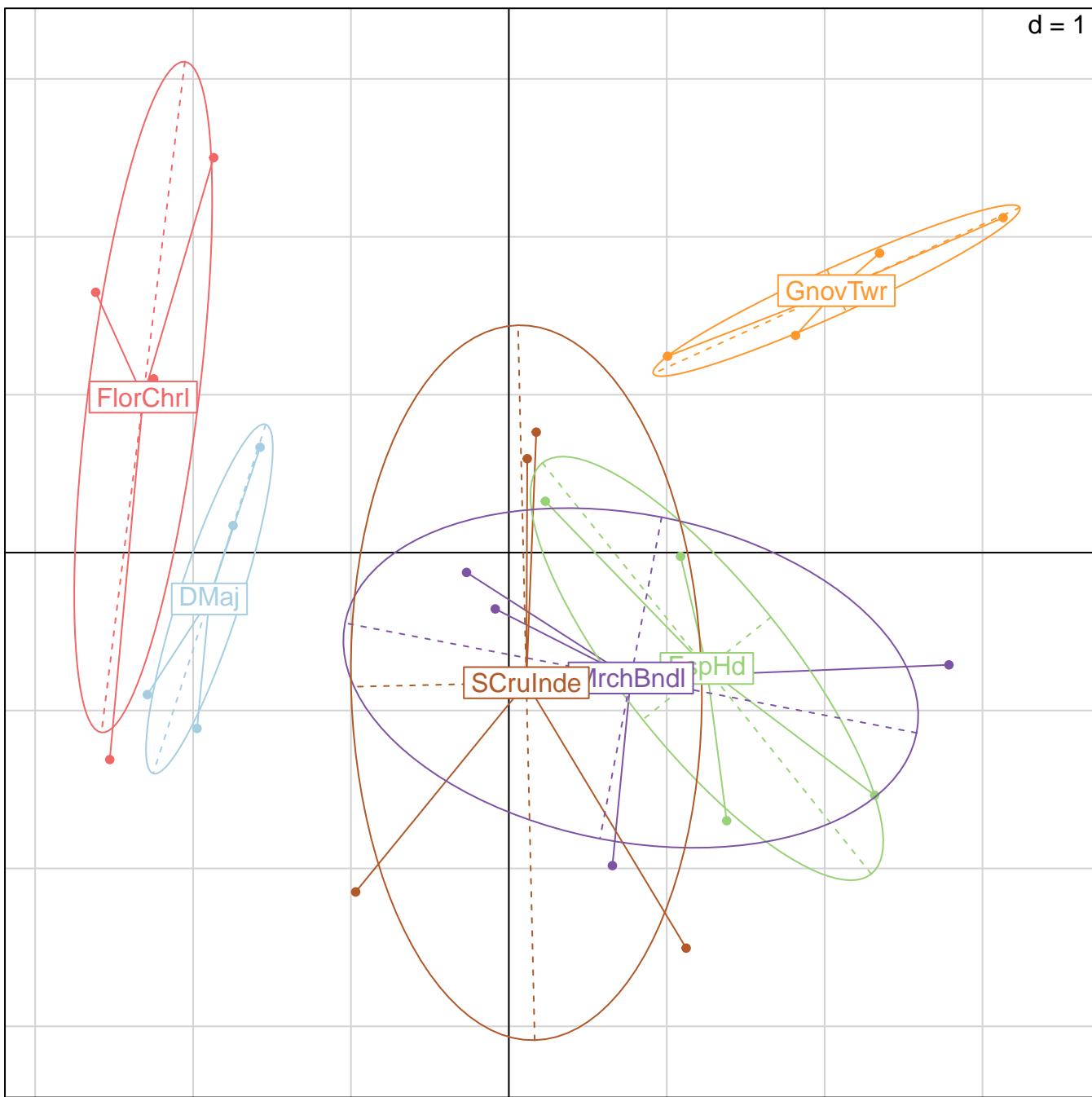
```
s.corcircle(res.dudi2$co)
```



```
s.class(res.dudi2$li, as.factor(c(rep("WingL",6), rep("BeakH",6), rep("UBeakL",6), rep("N.UBk",6)))
```



```
s.class(res.dudi2$li, as.factor(rep(c("DMaj", "EspHd", "FlorChrl", "GnovTwr", "MrchBndl", "SCruInd", "SectCov", "SectLnd", "SectRgn", "SectWld", "SpGrnLnd", "SpGrnRgn", "SpGrnWld", "SpLndRgn", "SpRgnWld", "SpWldRgn", "TwnCov", "TwnLnd", "TwnRgn", "TwnWld", "VegCov", "VegLnd", "VegRgn", "VegWld", "WldCov", "WldLnd", "WldRgn", "WldWld"), 10)))
```



8 Conclusion

9 Acknowledgment