

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

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Abstract

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

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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 0.92. 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", dep=TRUE)  
install.packages("C:/Users/taudiere/Desktop/cati/pkg/cati_0.91.zip", repos=NULL)  
  
## Error: zip file 'C:/Users/taudiere/Desktop/cati/pkg/cati_0.91.zip' not found  
  
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] "0.92"
```

cati version should read 0.92.

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* page, click ‘packages’, ‘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.

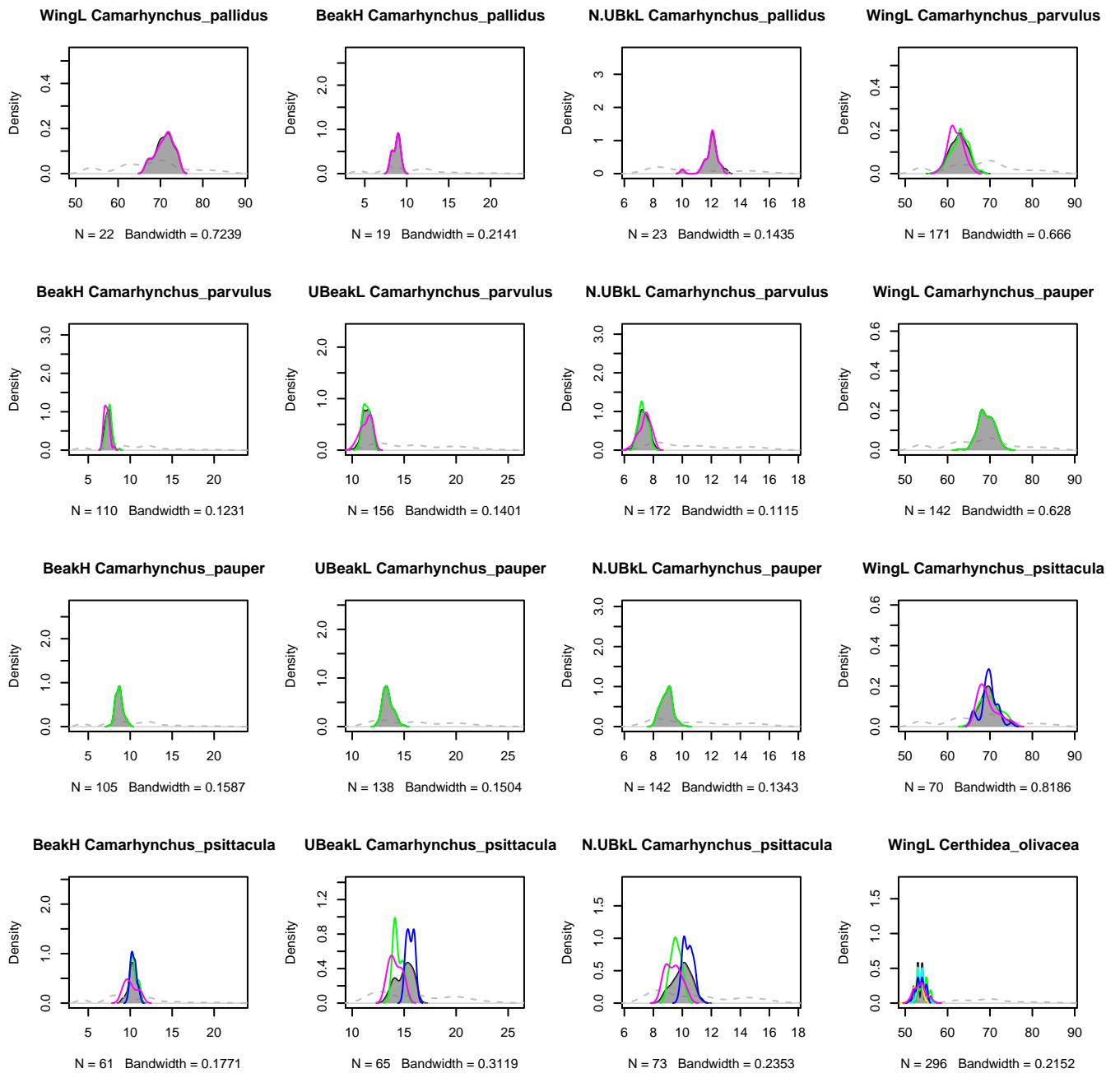
figs/darwinfinch.pdf

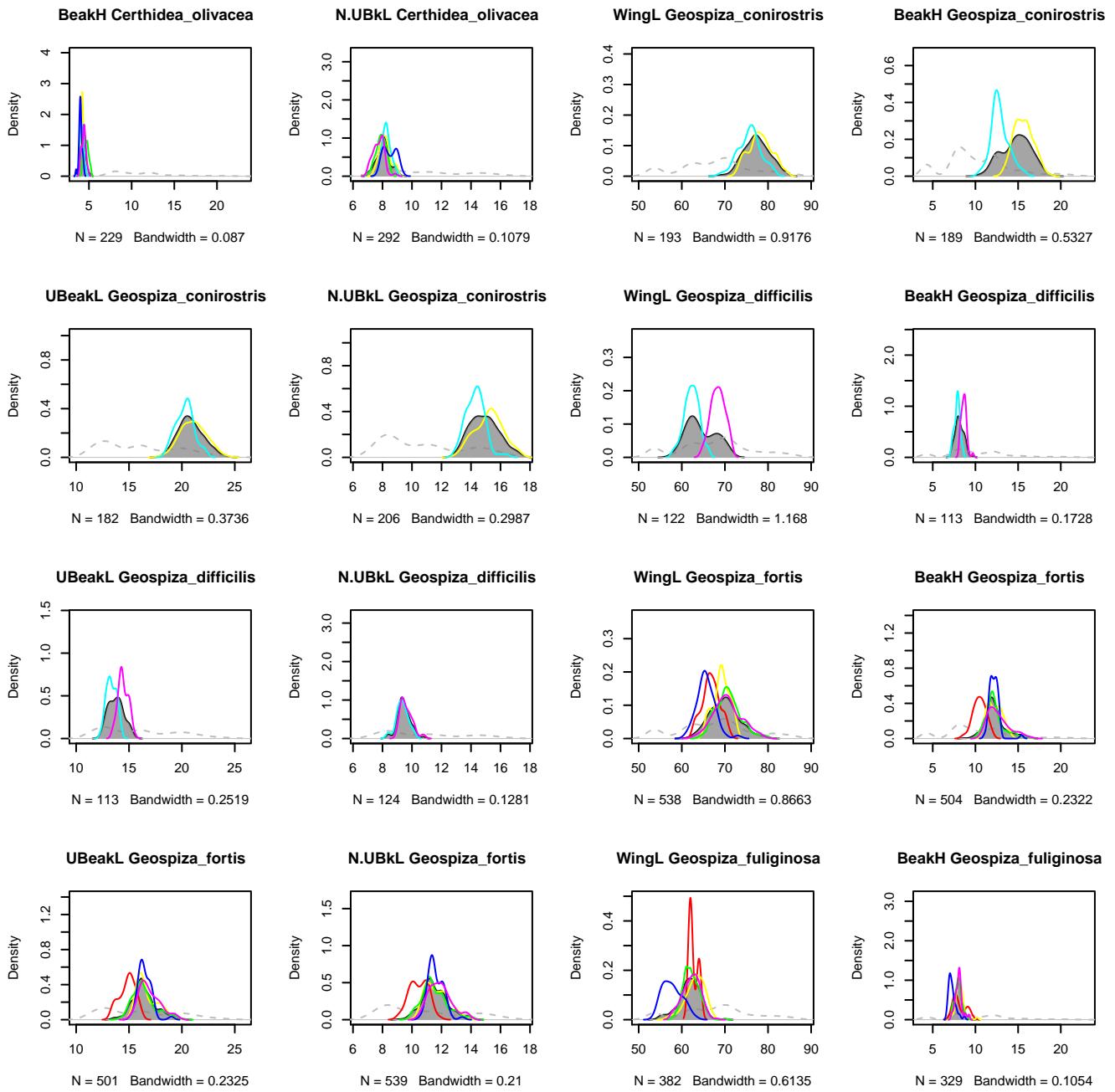
3 Description of traits distributions

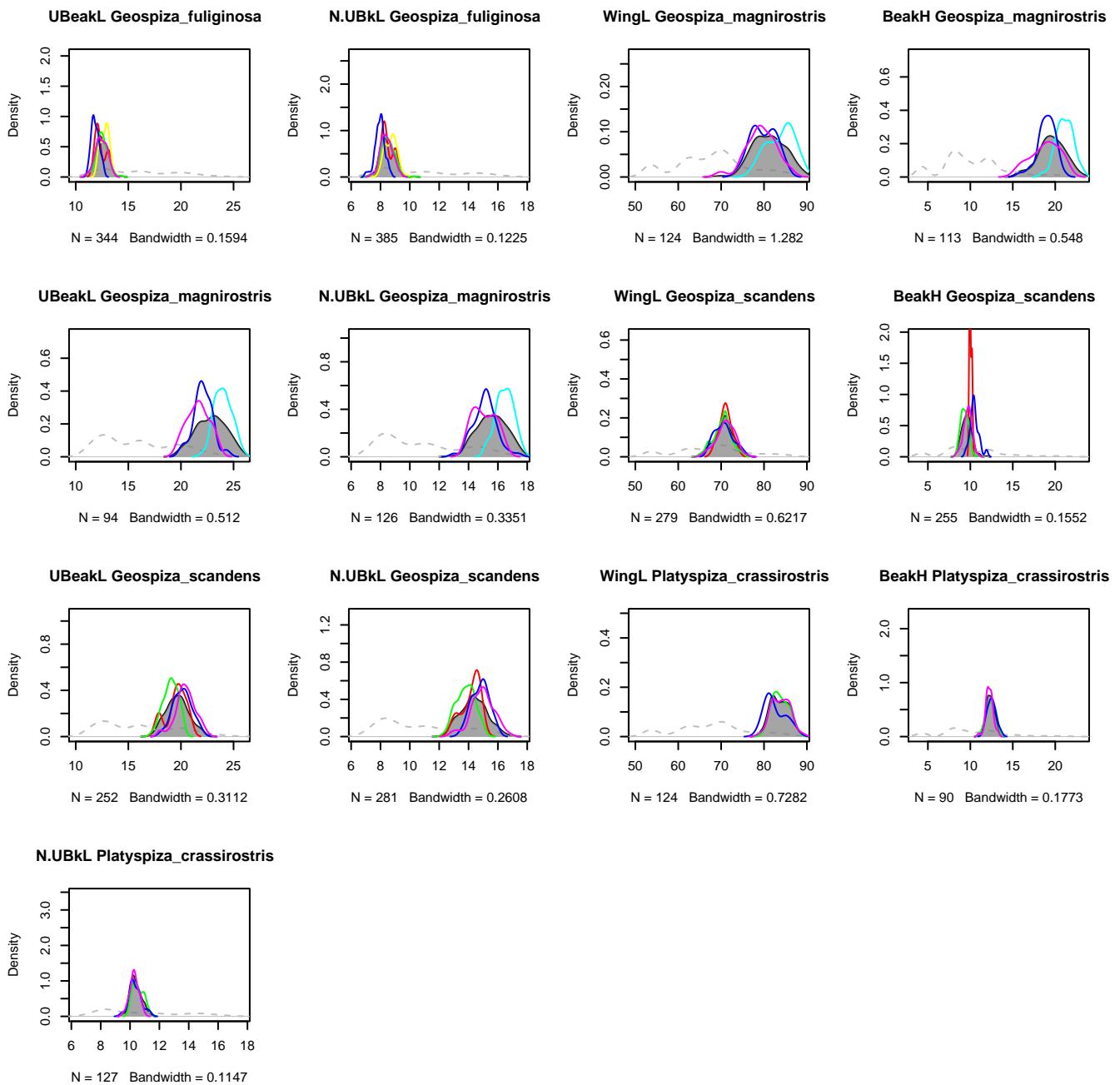
3.1 Plot the kernel density of traits

Plot the distribution of traits values for populations, species, sites and regional scales. First, let try the distribution for all populations of Darwin finches.

```
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)
```

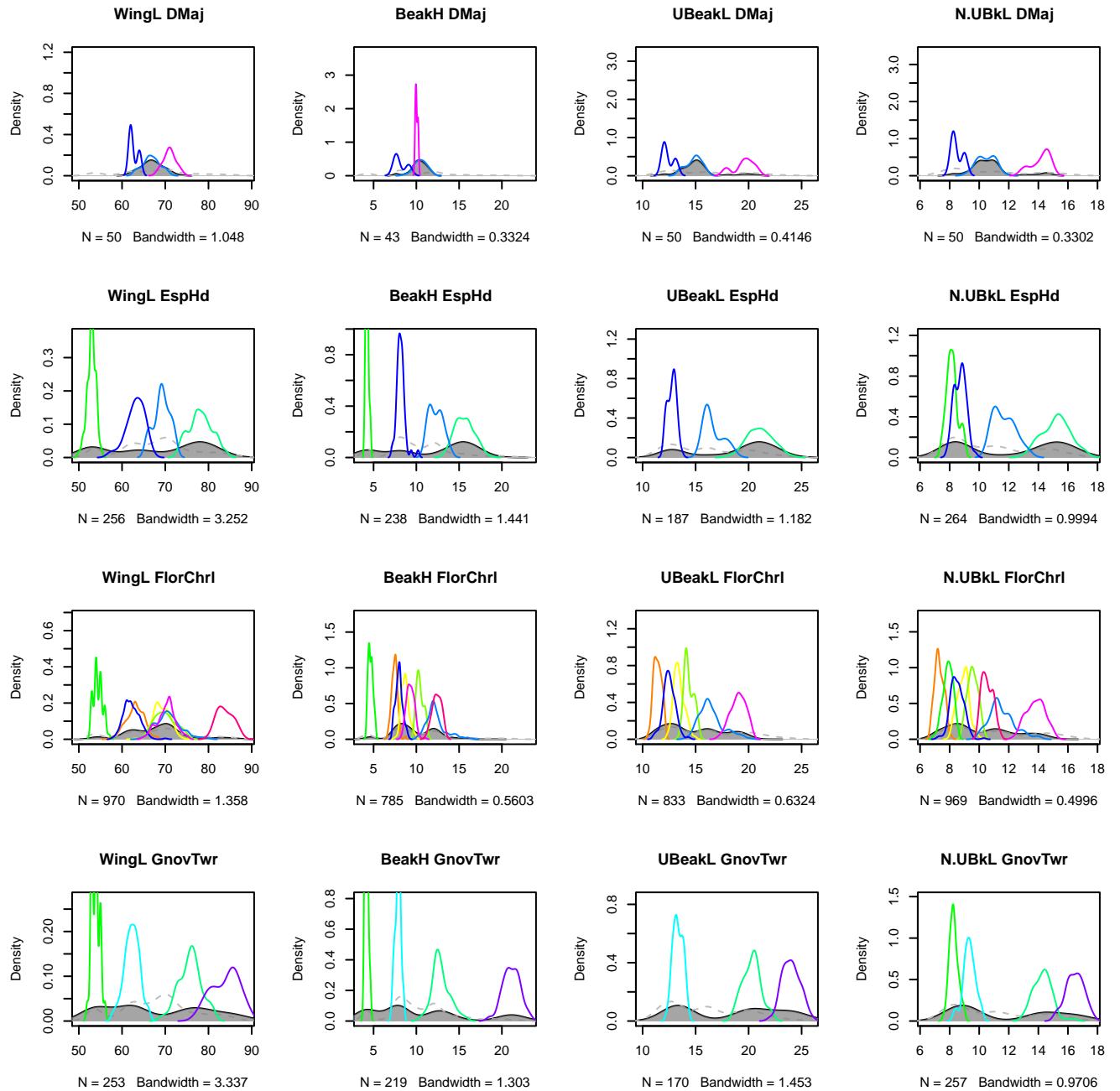


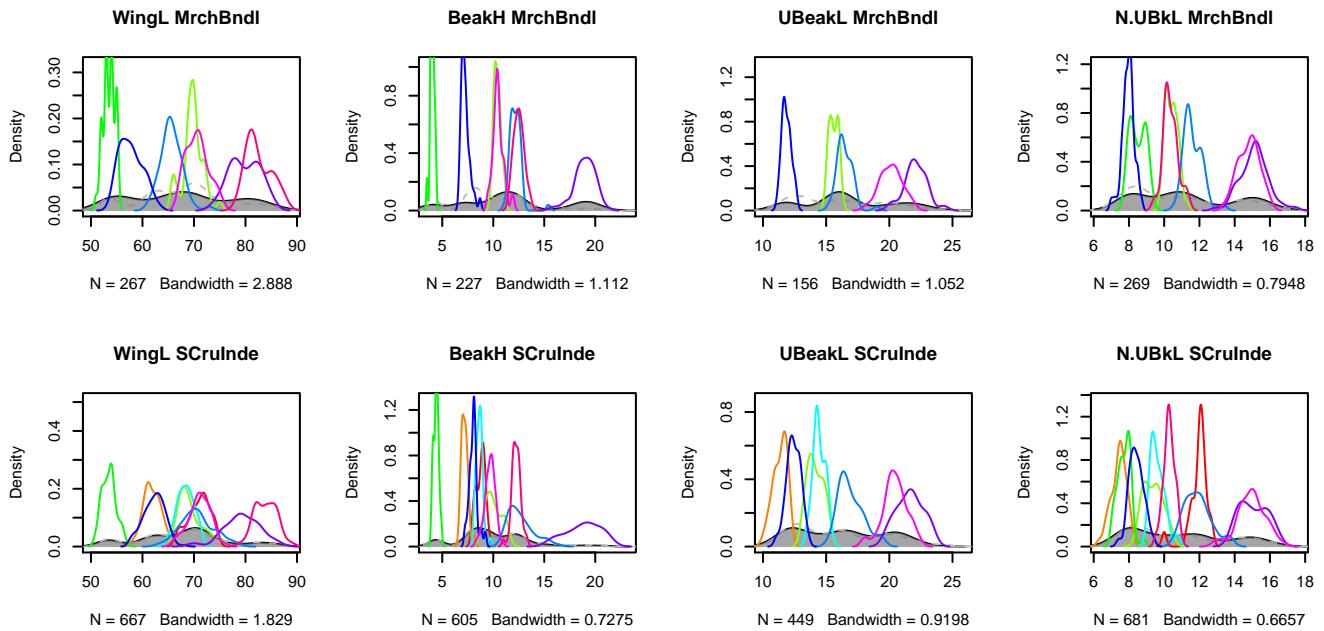




Then we can inverse the second and the third arguments to plot the distribution for all finches species.

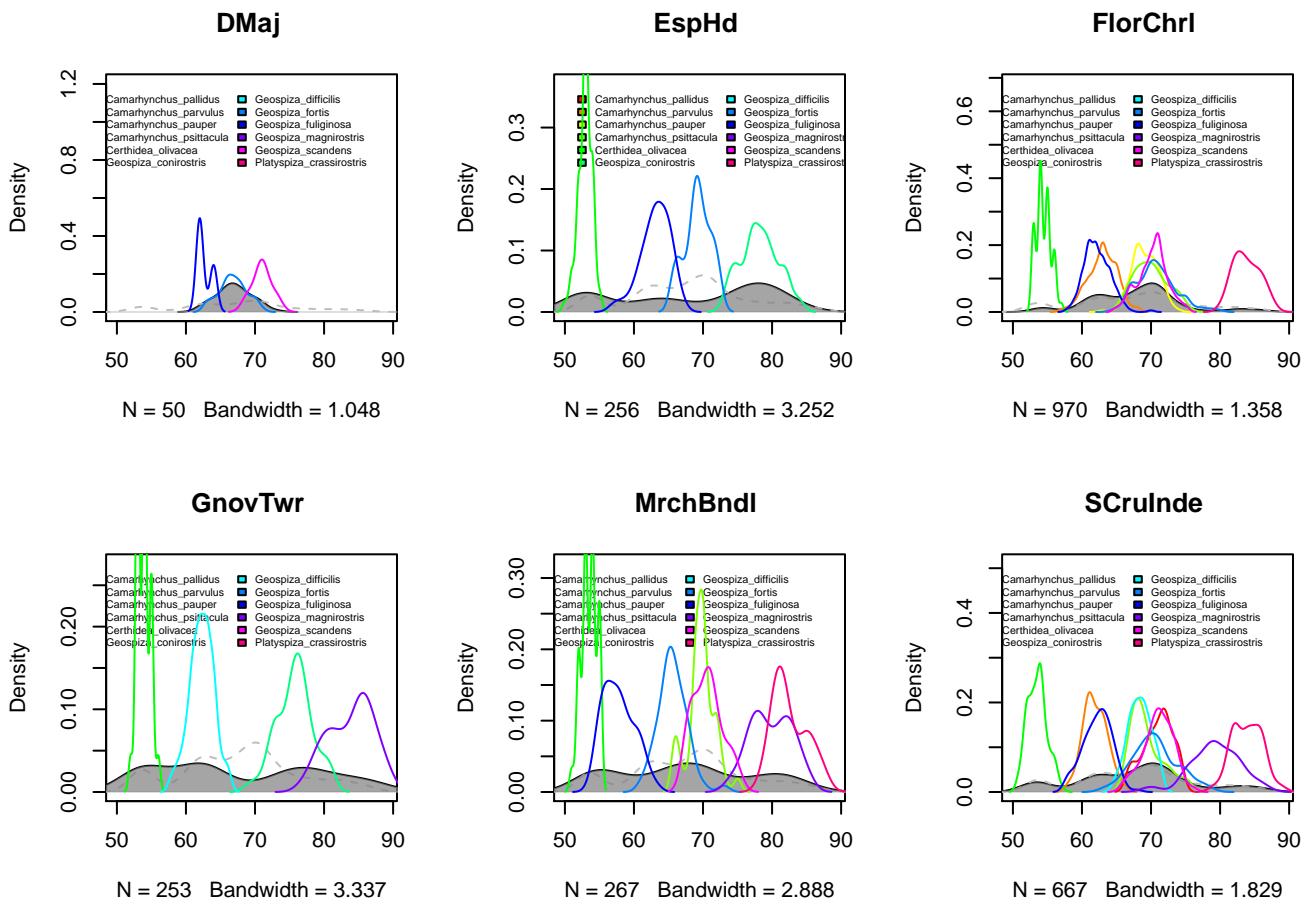
```
par(mfrow=c(4,4), cex=0.5)
plotDistri(traits.finch, ind.plot.finch, sp.finch,
           ylim.cex=8, plot.ask=F, multipanel=F, leg=F)
```





Only one trait to plot using `leg=T` to plot the legend.

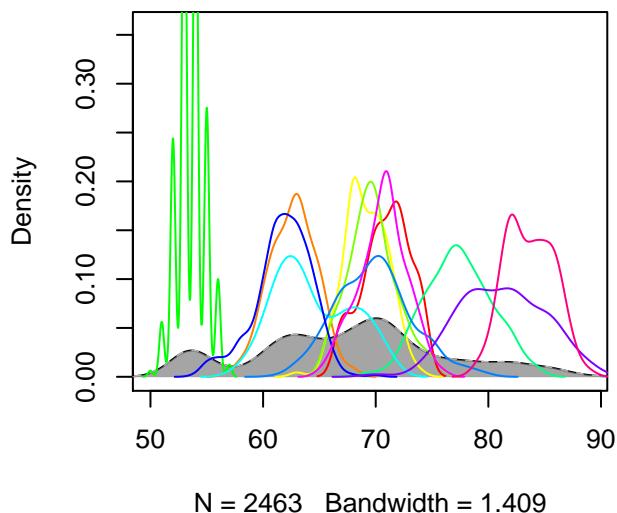
```
par(mfrow=c(2,3))
plotDistri(as.matrix(traits.finch[,1]), ind.plot.finch, sp.finch,
          ylim.cex=8, plot.ask=F, multipanel=F, leg=T, cex.leg=0.5)
```



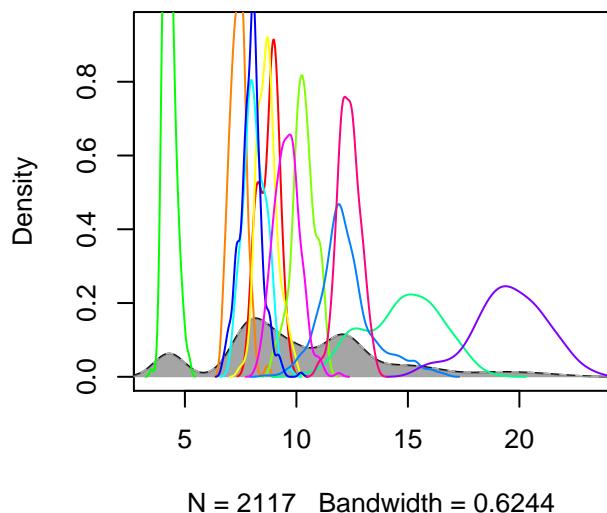
If we want to plot all the sites (regional distribution) or all the species: we can use the following code:

```
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)
```

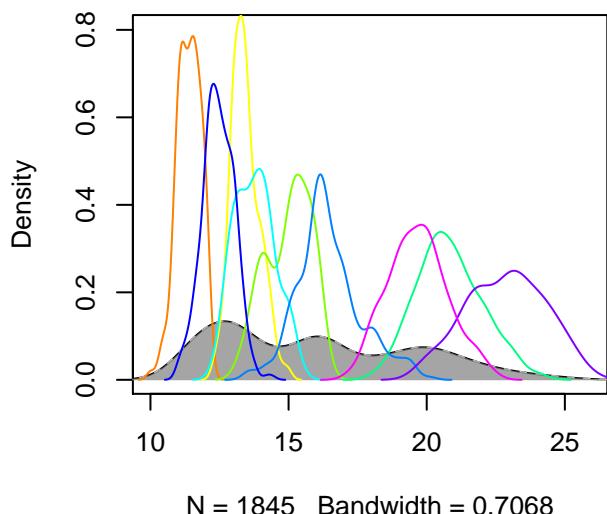
WingL region



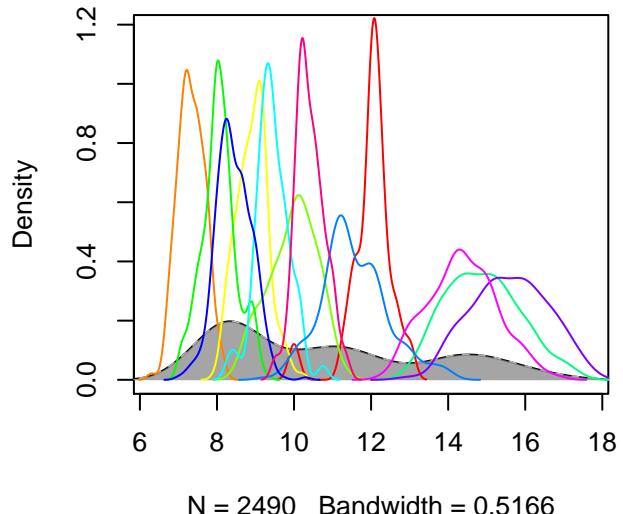
BeakH region



UBeakL region

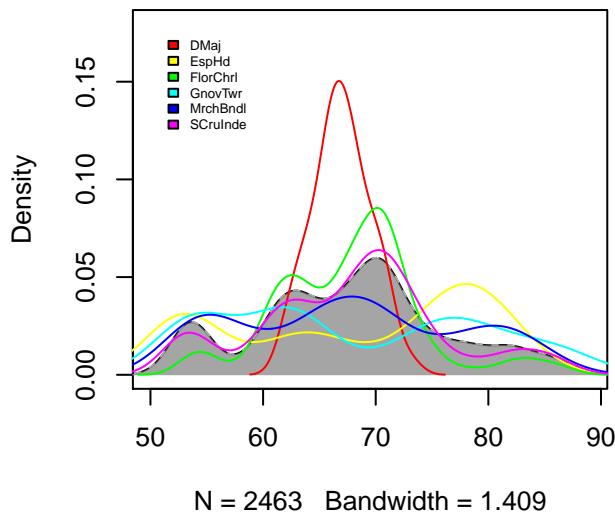


N.UBkL region

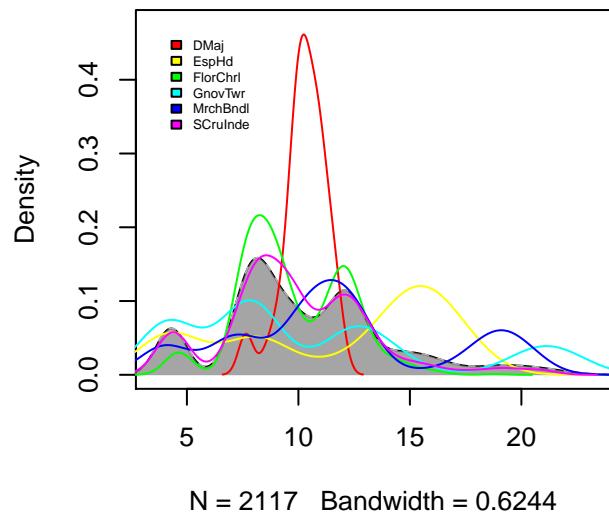


```
plotDistri(traits.finch, rep("toutes_sp", times=dim(traits.finch)[1]),
           ind.plot.finch, ylim.cex=3, plot.ask=F, cex.leg=0.5)
```

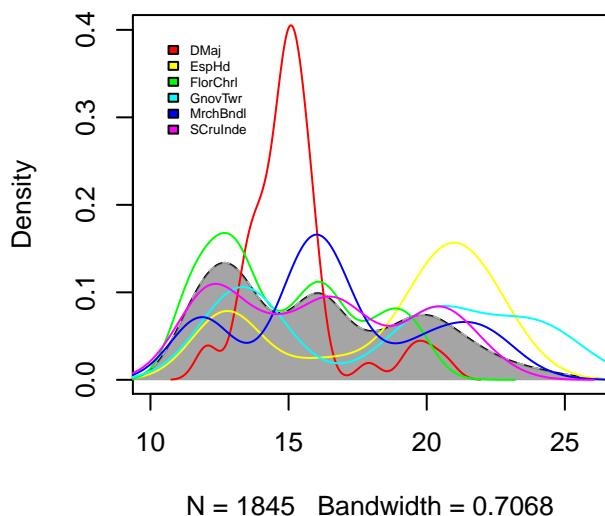
WingL toutes_sp



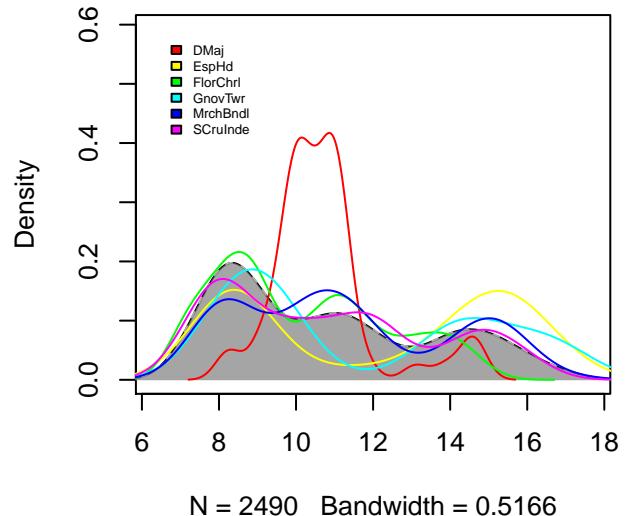
BeakH toutes_sp



UBeakL toutes_sp



N.UBkL toutes_sp



Reset the default 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 functionnal 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, dphyll=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

witRao+betRao

## [1] 8.37

totRao

## [1] 8.37
```

Now let's take the abundance 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

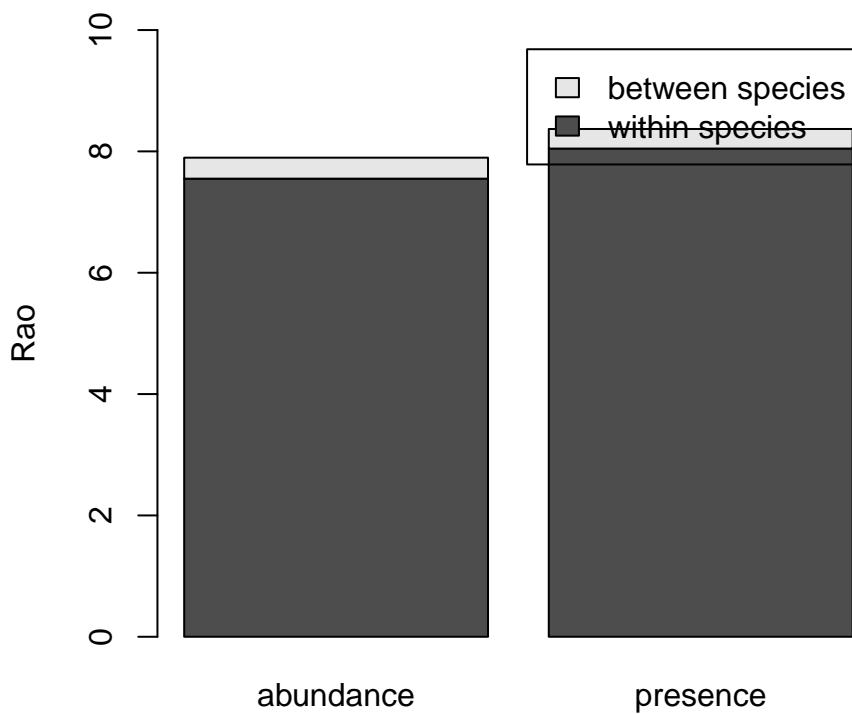
```

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)))

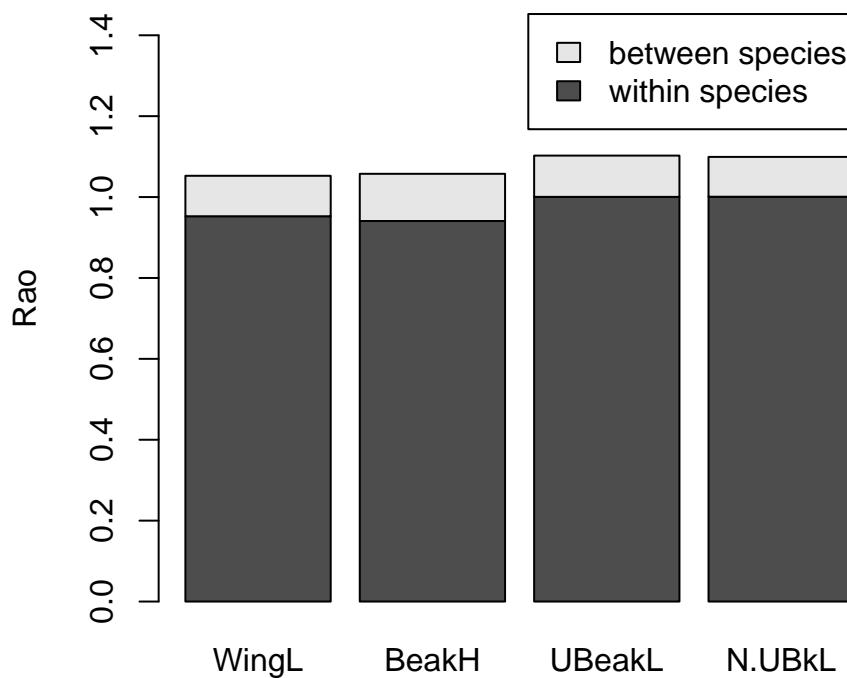
require(mice)
traits=traits.finch
mice<-mice(traits.finch)
traits.finch.mice<-complete(mice)

#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.finches, 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))
```

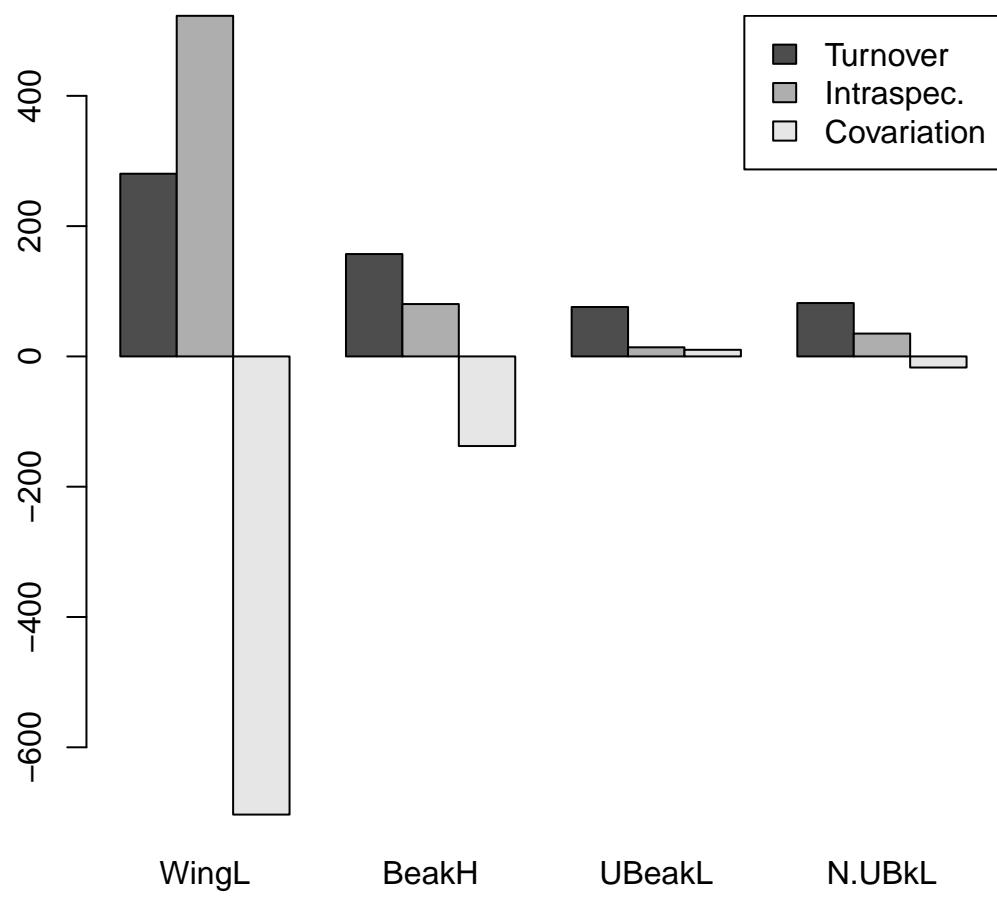


4.2 Decomposition of community trait response to environment into intraspecific trait variability, variability due to species turnover and their covariation.

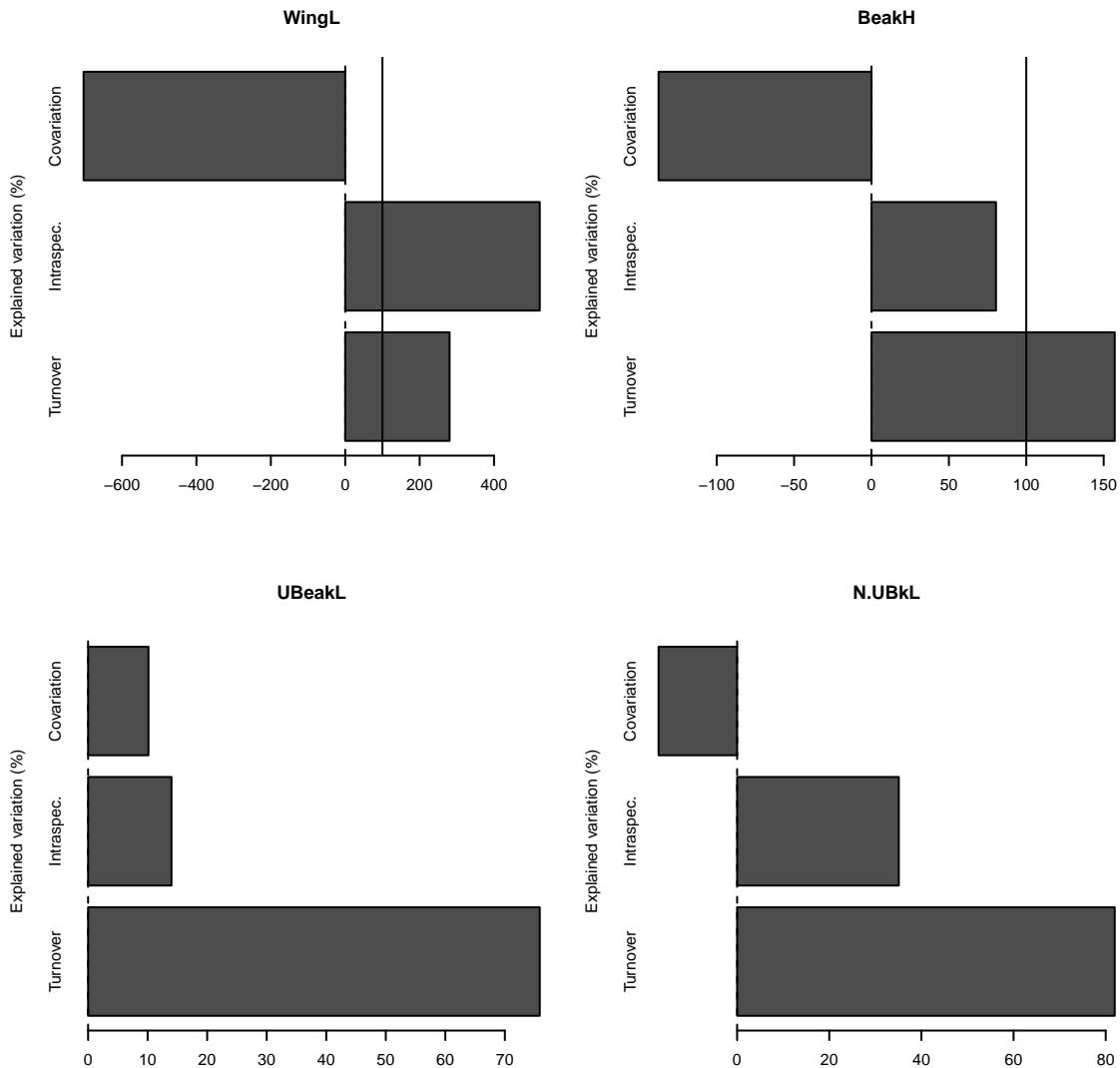
Reference: Leps, J., de Bello, F., Smilauer, P. and Dolezal, J. (2011) Community trait response to environment: disentangling species turnover vs intraspecific trait variability effects. *Ecography*, 34, 856-863.

```
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.

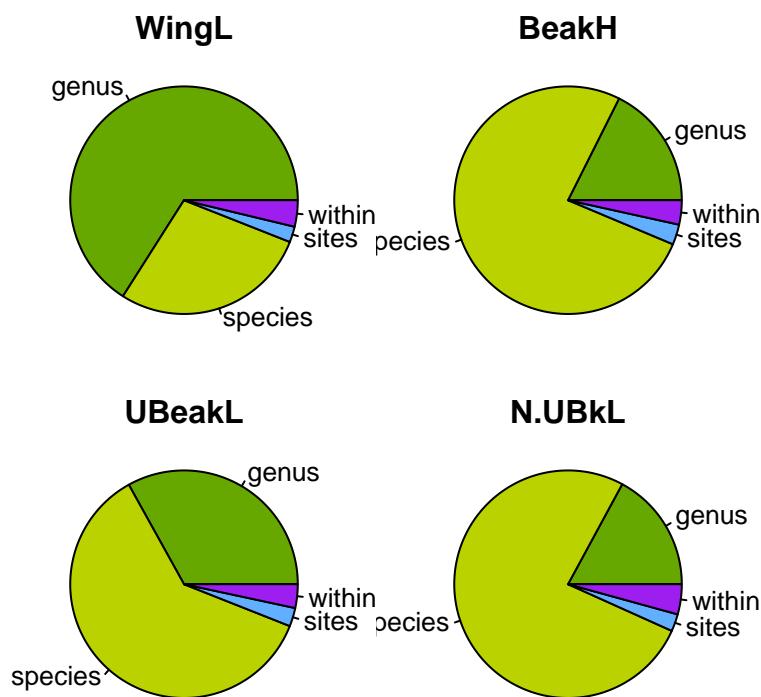
```
vec<- seq(1,length(sp.finch)*2, by=2)
genus<-as.vector(unlist(strsplit(as.vector(sp.finch), "_"))[vec])
fact<-cbind(genus=as.factor(genus),
            species=as.factor(as.vector(sp.finch)),
            sites=as.factor(as.vector(ind.plot.finch)))

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

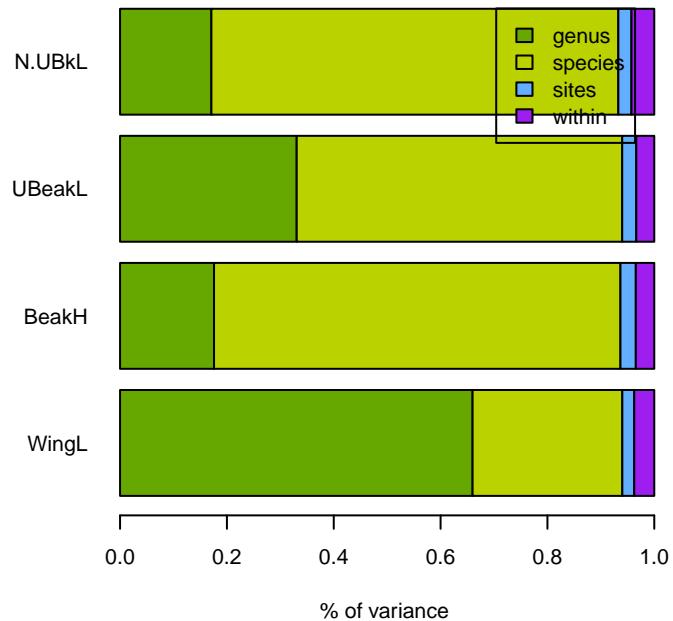
res.partvar.finch
```

```
par(mfrow=c(2,2), mai=c(0.2,0.2,0.2,0.2))
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)
```



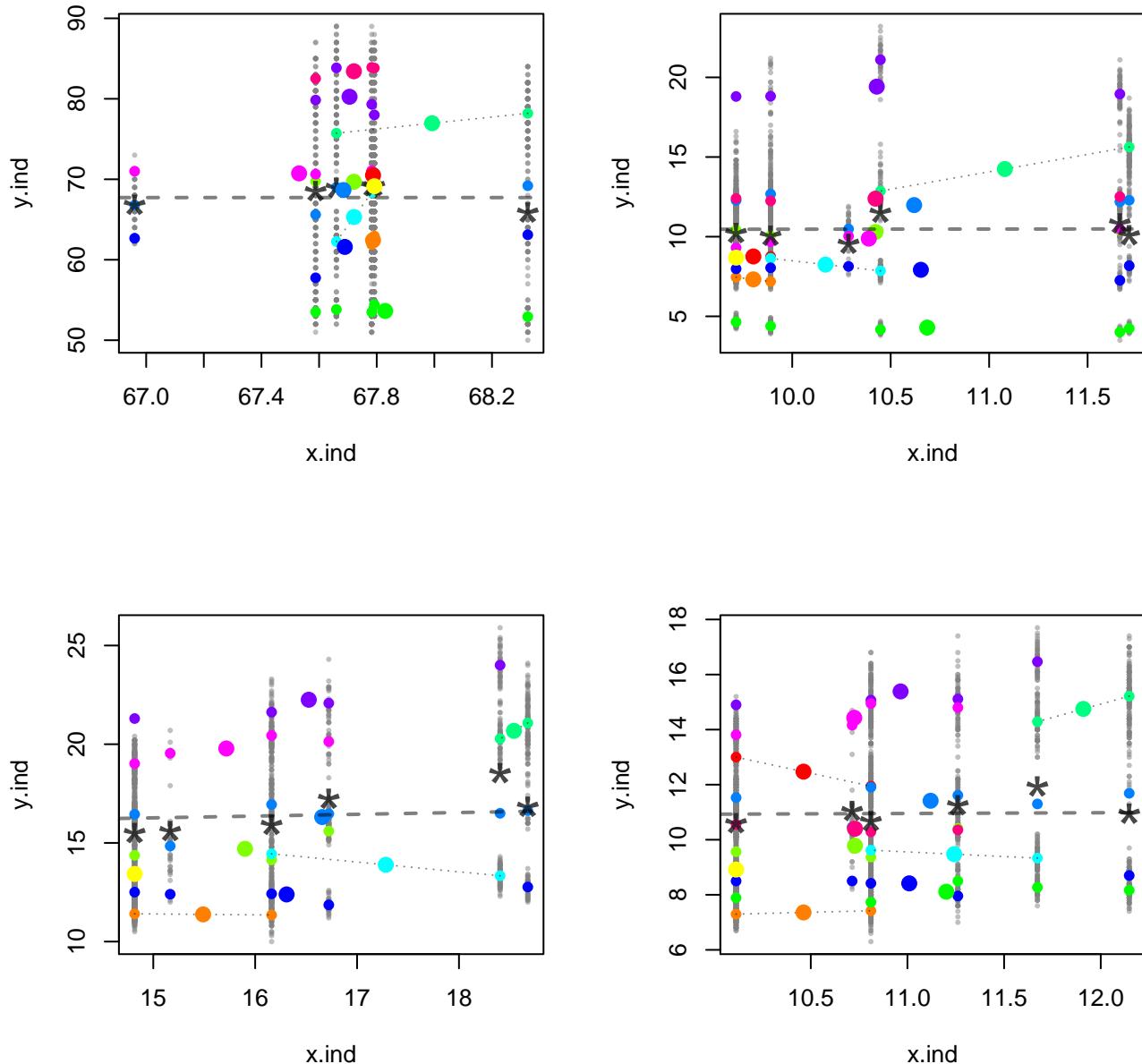
```
par(old.par)
barPartvar(res.partvar.finch, col=colors,
           leg=TRUE)
```



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

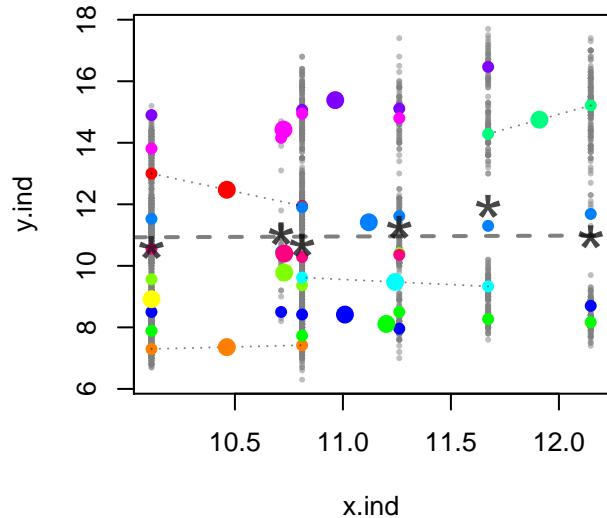
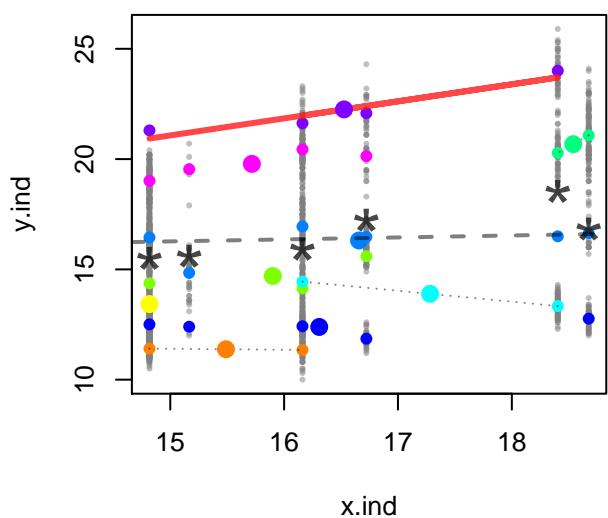
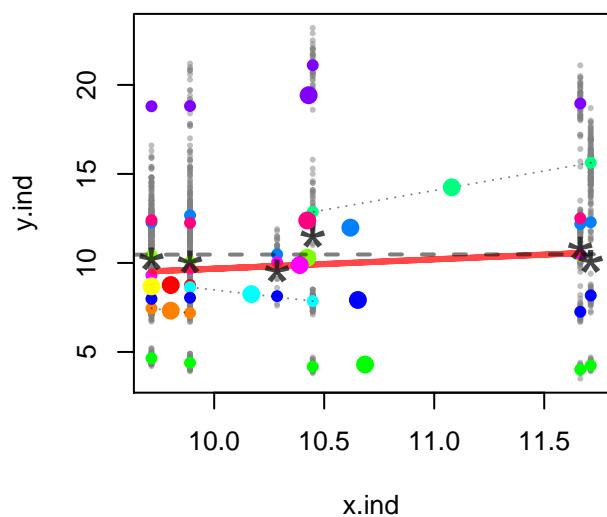
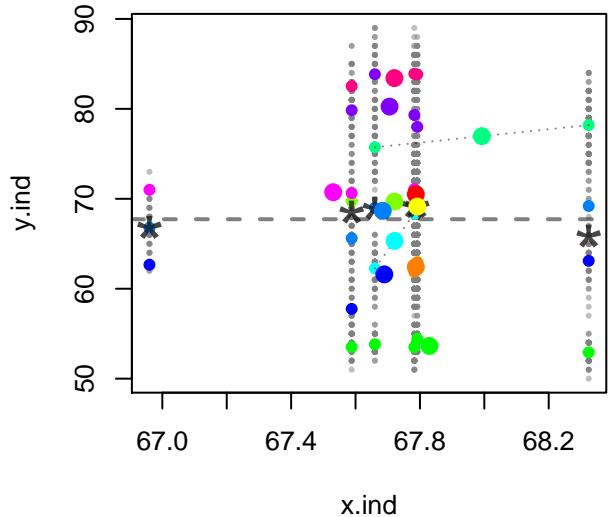
For an example of utilisation see: Cornwell, W.K. and Ackerly, D.D., 2009. Community assembly and shifts in plant trait distributions across an environmental gradient in coastal California. Ecological Monographs 79, 109-126.

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



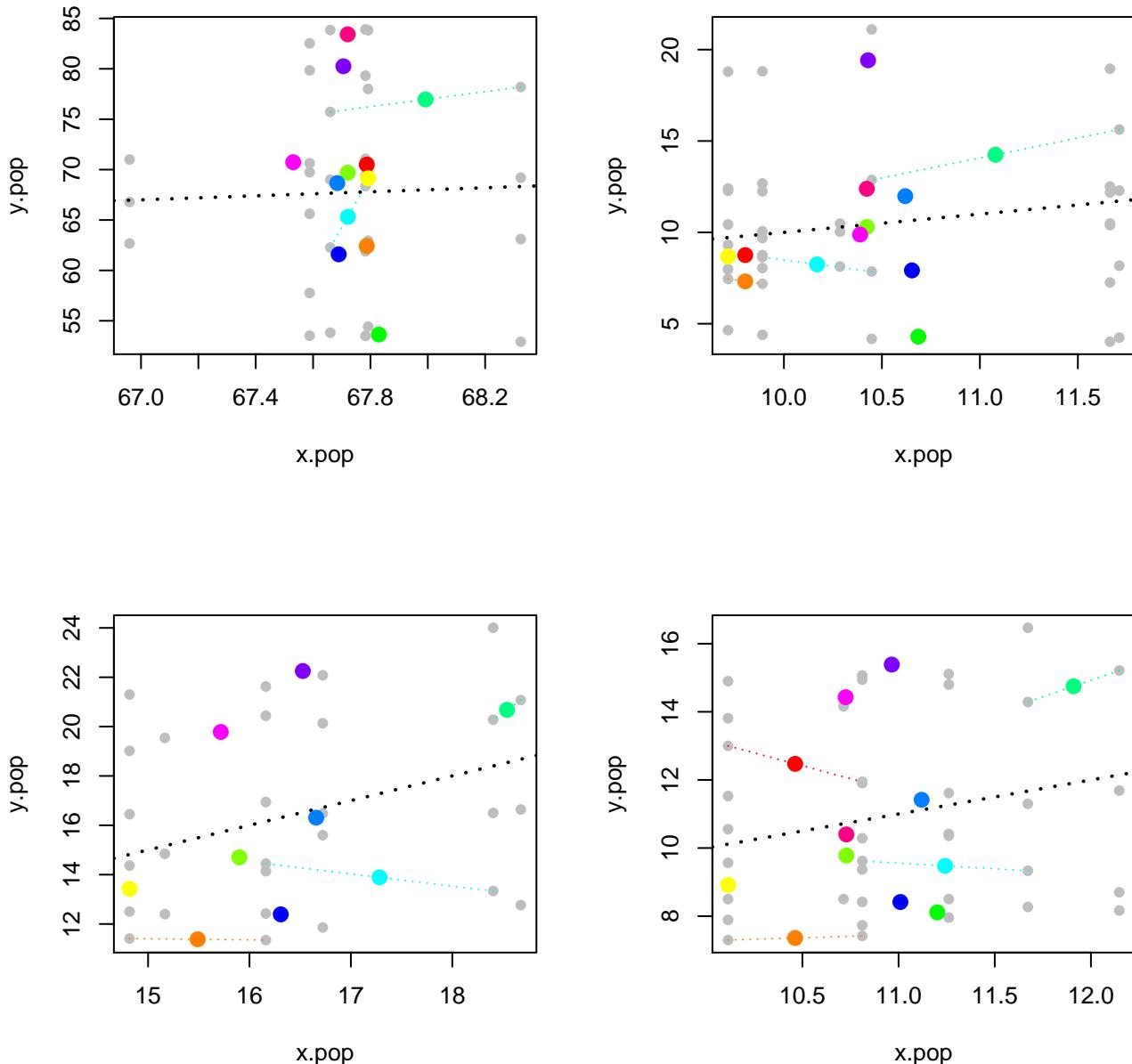
If we change the value of the threshold ($\alpha=10\%$ instead of 5% and the minimum individual to represent singificativity fixed to 3 instead of 10 by default) we can see some significant relationships.

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

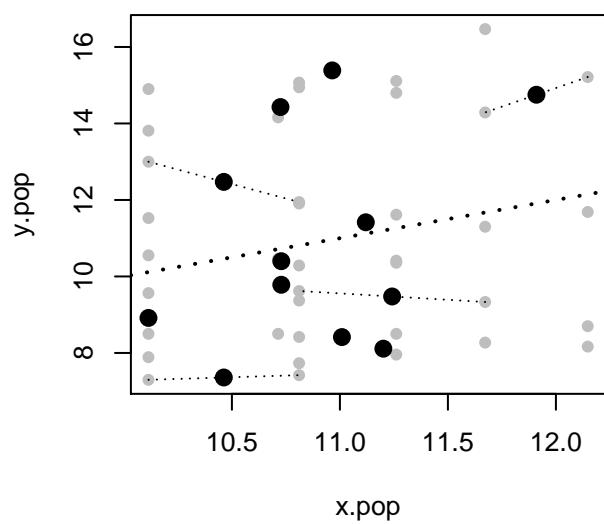
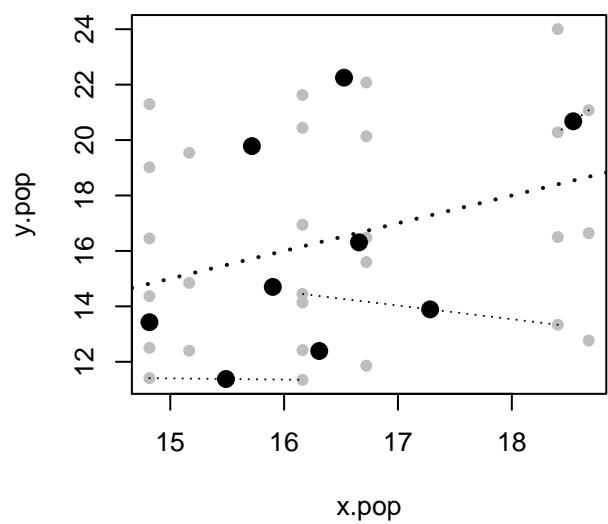
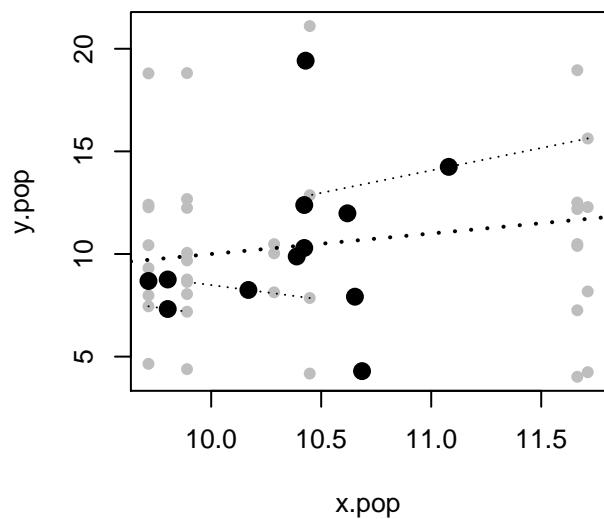
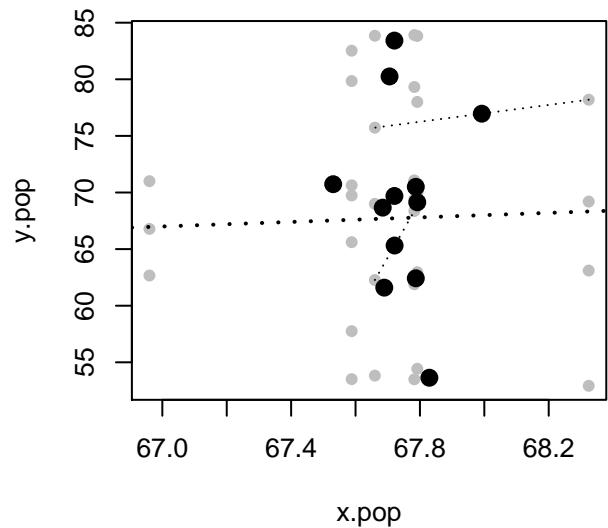


For a more simple figure, add the option `resume=TRUE`. Again if we change the value of the threshold (`alpha=10%` instead of `5%` and the minimum individual to represent singificativity fixed to `3` instead of `10` by default) we can see some significant relationships.

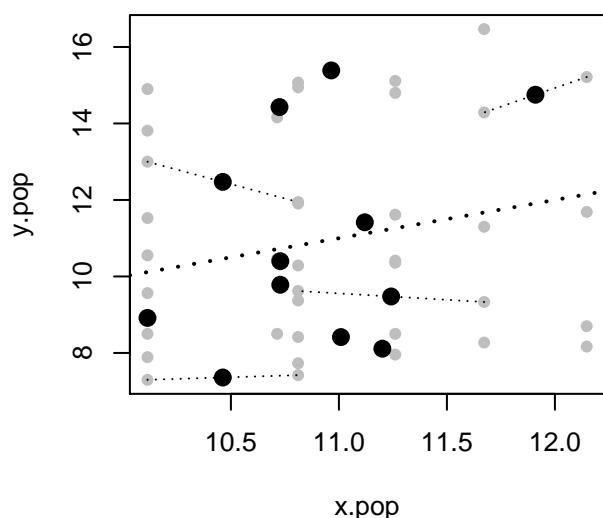
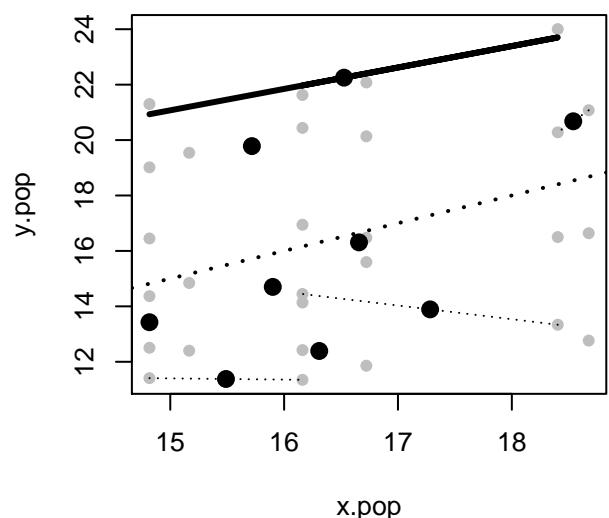
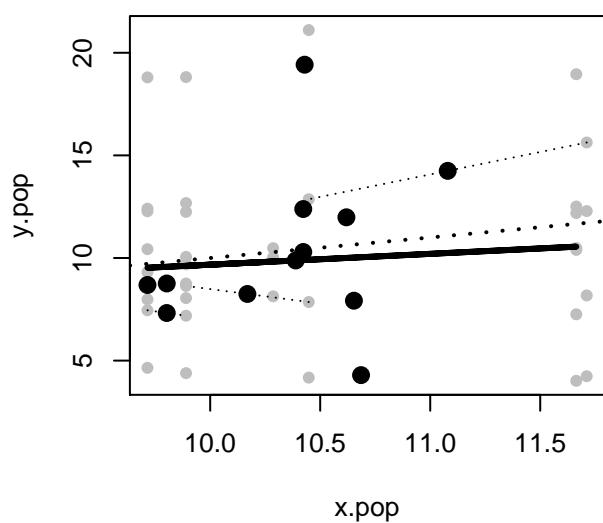
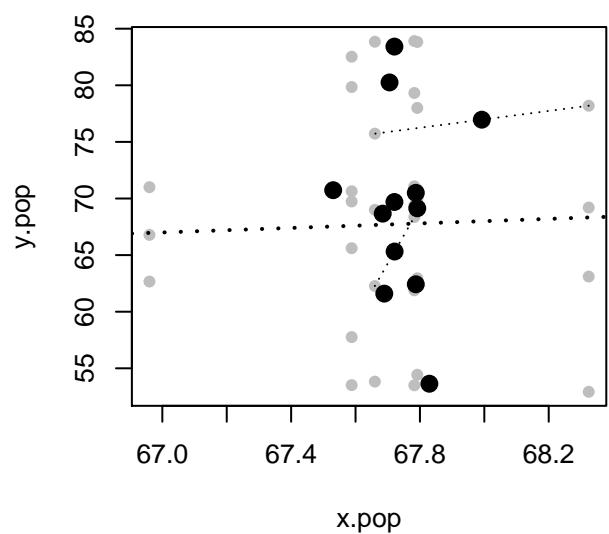
```
plotSpPop(traits.finch, ind.plot.finch, sp.finch,
          silent=TRUE, resume=TRUE, col.pop="grey")
```



```
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)
```



5 Test of community assembly

5.1 Ratio of variances: T-statistics

The function `Tstats` 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 null models.

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
## $T_IC.IR_nm: distribution of T_IC.IR value under the null model
## $T_PC.PR_nm: distribution of T_PC.PR value under the null model
##
## #####
## $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

attributes(res.finch)

## $names
## [1] "Tstats"          "variances"        "traits"           "ind.plot"
## [5] "sp"               "sites_richness"  "namestraits"     "call"
## 
## $class
## [1] "Tstats"

str(res.finch)

## List of 8
## $ Tstats      :List of 6
##   ..$ T_IP.IC   : num [1:6, 1:4] 0.3831 0.0343 0.1084 0.0417 0.0496 ...
##   ... - attr(*, "dimnames")=List of 2
##     ... .$. : chr [1:6] "DMaj" "EspHd" "FlorChrl" "GnovTwr" ...
##     ... .$. : chr [1:4] "WingL" "BeakH" "UBeakL" "N.UBkL"
##   ..$ T_IC.IR   : num [1:6, 1:4] 0.0925 1.7103 0.5752 1.7916 1.3718 ...
##   ... - attr(*, "dimnames")=List of 2
##     ... .$. : chr [1:6] "DMaj" "EspHd" "FlorChrl" "GnovTwr" ...
##     ... .$. : chr [1:4] "WingL" "BeakH" "UBeakL" "N.UBkL"
##   ..$ T_PC.PR   : num [1:6, 1:4] 0.226 1.468 0.871 1.762 1.476 ...
##   ... - attr(*, "dimnames")=List of 2
##     ... .$. : chr [1:6] "DMaj" "EspHd" "FlorChrl" "GnovTwr" ...
##     ... .$. : chr [1:4] "WingL" "BeakH" "UBeakL" "N.UBkL"
##   ..$ T_IP.IC_nm: num [1:9, 1:4, 1:6] 0.948 1 3.226 2.291 2.216 ...
##   ... - attr(*, "dimnames")=List of 3
##     ... .$. : NULL
##     ... .$. : chr [1:4] "WingL" "BeakH" "UBeakL" "N.UBkL"
##     ... .$. : NULL
##   ..$ T_IC.IR_nm: num [1:9, 1:4, 1:6] 0.948 1.183 0.875 1.067 1.067 ...
##   ... - attr(*, "dimnames")=List of 3
##     ... .$. : NULL
##     ... .$. : chr [1:4] "WingL" "BeakH" "UBeakL" "N.UBkL"
##     ... .$. : NULL
##   ..$ T_PC.PR_nm: num [1:9, 1:4, 1:6] 0.707 0.357 5.311 7.249 4.839 ...
##   ... - attr(*, "dimnames")=List of 3
##     ... .$. : NULL

```

```

## ... .$. : chr [1:4] "WingL" "BeakH" "UBeakL" "N.UBkL"
## ... .$. : NULL
## $ variances      :List of 12
##   ..$ var_IP      : num [1:39, 1:4] NA 4.6 4.5 2.94 3.54 ...
##   ..$ var_PC      : num [1:6, 1:4] 17.4 112.8 66.9 135.3 113.3 ...
##   ..$ var_CR      : num [1:4] 1.941 0.473 1.376 0.235
##   ..$ var_IC      : num [1:6, 1:4] 6.49 120.02 40.37 125.72 96.26 ...
##   ..$ var_PR      : num [1:4] 76.8 17.89 13.97 7.36
##   ..$ var_IR      : num [1:4] 70.17 14.01 12.49 7.52
##   ..$ var_IP_nm1  : num [1:9, 1:4, 1:39] NA NA NA NA NA NA NA NA NA ...
##   ..$ var_PC_nm2sp: num [1:9, 1:4, 1:6] 58.7 32.8 557.5 896.8 334.2 ...
##   ..$ var_IC_nm1  : num [1:9, 1:4, 1:6] 6.49 125.4 43.19 25.3 22.78 ...
##   ..$ var_IC_nm2  : num [1:9, 1:4, 1:6] 67.1 81.6 61.8 77.4 76.5 ...
##   ..$ var_PR_nm2sp: num [1:9, 1:4] 83.1 91.9 105 123.7 69.1 ...
##   ..$ var_IR_nm2  : num [1:9, 1:4] 70.8 69 70.6 72.5 71.8 ...
## $ traits          :'data.frame': 2513 obs. of 4 variables:
##   ..$ WingL : int [1:2513] 69 65 65 68 66 68 67 69 67 68 ...
##   ..$ BeakH : num [1:2513] 10.8 10.3 10 9.5 11 10.4 11.3 10.6 10.8 10.3 ...
##   ..$ UBeakL: num [1:2513] 15.2 14.2 13.6 13.5 15 15 15.7 15.3 15.5 15.2 ...
##   ..$ N.UBkL: num [1:2513] 10.6 9.8 9.9 9.9 10.7 10.2 11.2 11.3 11.2 10.2 ...
## $ ind.plot        : Factor w/ 6 levels "DMaj", "EspHd", ... : 1 1 1 1 1 1 1 1 1 ...
## $ sp              : Factor w/ 12 levels "Camarhynchus_pallidus", ... : 8 8 8 8 8 8 8 8 8 ...
## $ sites_richness: 'table' int [1:6(id)] 50 267 981 258 270 687
## -- attr(*, "dimnames")=List of 1
## ... .$. ind.plot: chr [1:6] "DMaj" "EspHd" "FlorChrl" "GnovTwr" ...
## $ namestraits    : chr [1:4] "WingL" "BeakH" "UBeakL" "N.UBkL"
## $ call           : language Tstats(traits = traits.finch, ind.plot = ind.plot.finck, sp =
## - attr(*, "class")= chr "Tstats"

```

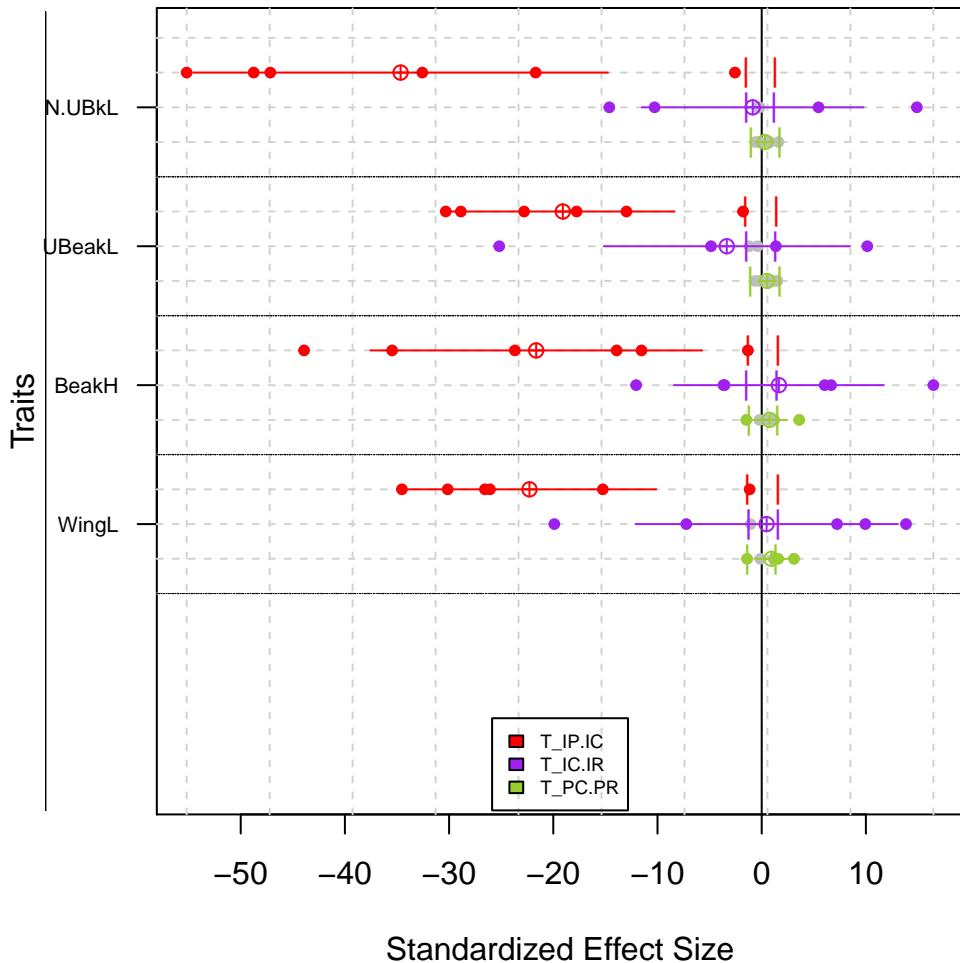
5.1.1 S3 methods for class Tstats

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

```

plot(res.finck)
abline(v=0)

```



There is multiple kind of representation available

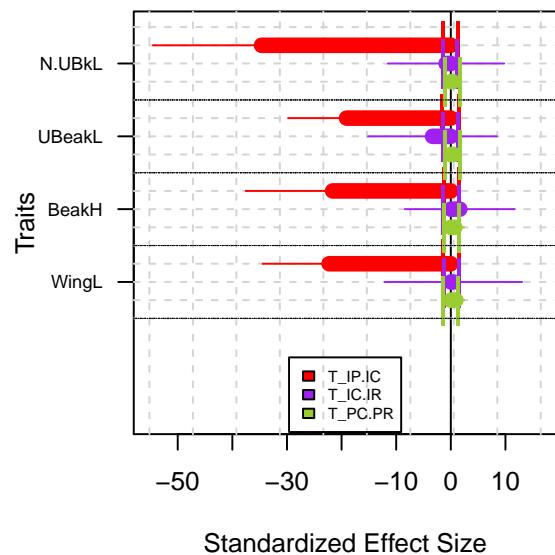
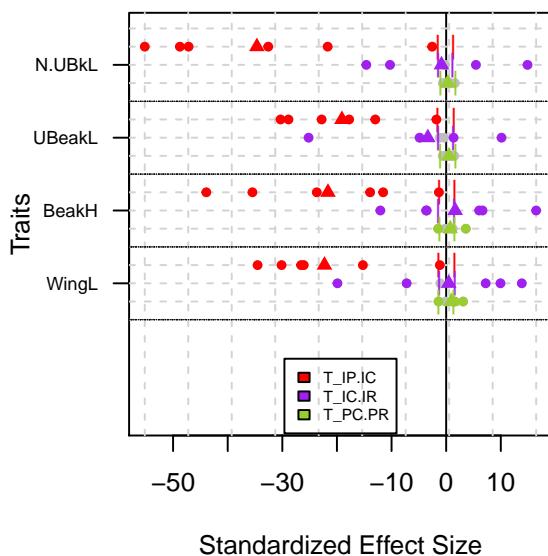
```
par(mfrow=c(2,2))
plot(res.finch, type="color_cond")

## [1] "Error: color_cond is not a valid type of plot"

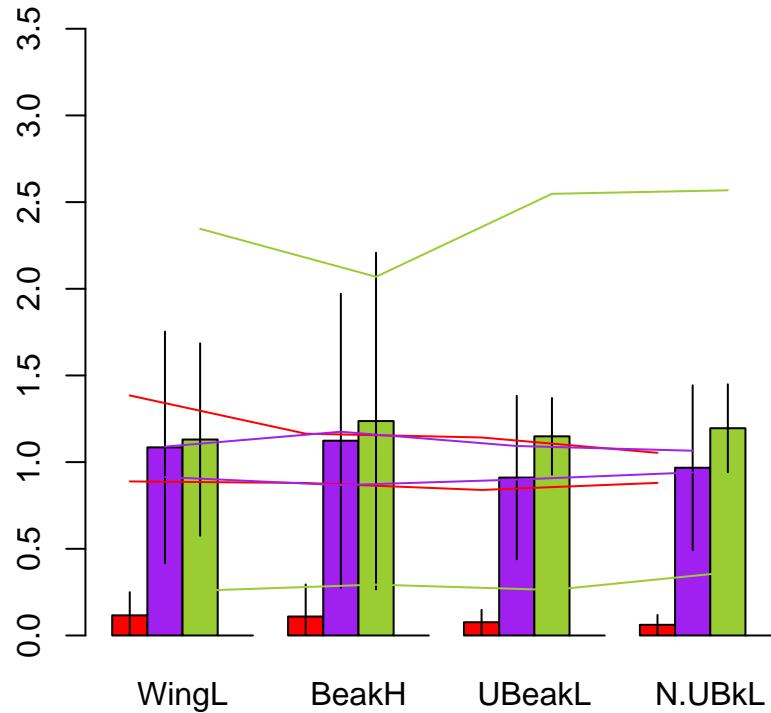
plot(res.finch, type="simple")
plot(res.finch, type="simple_sd")

## [1] "Error: simple_sd is not a valid type of plot"

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



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



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

```
## [1] "Observed values"  
## $T_IC.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.finch)) #An other mean to summarize Tstatistics

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

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

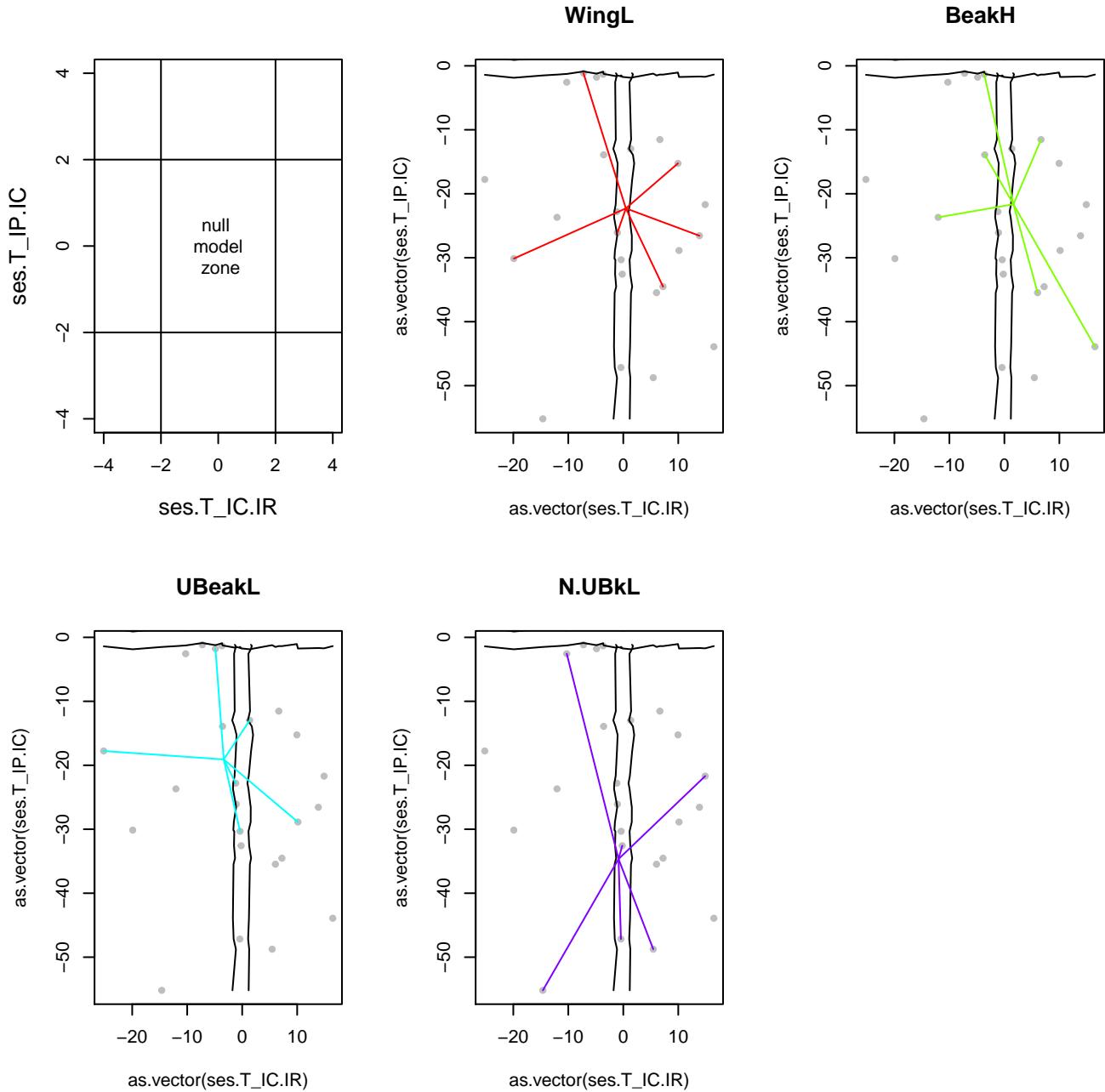
##      WingL BeakH UBeakL N.UBkL
## T_IP.IC.inf 0.1   0.1   0.1   0.1
## T_IP.IC.sup 1.0   1.0   1.0   1.0

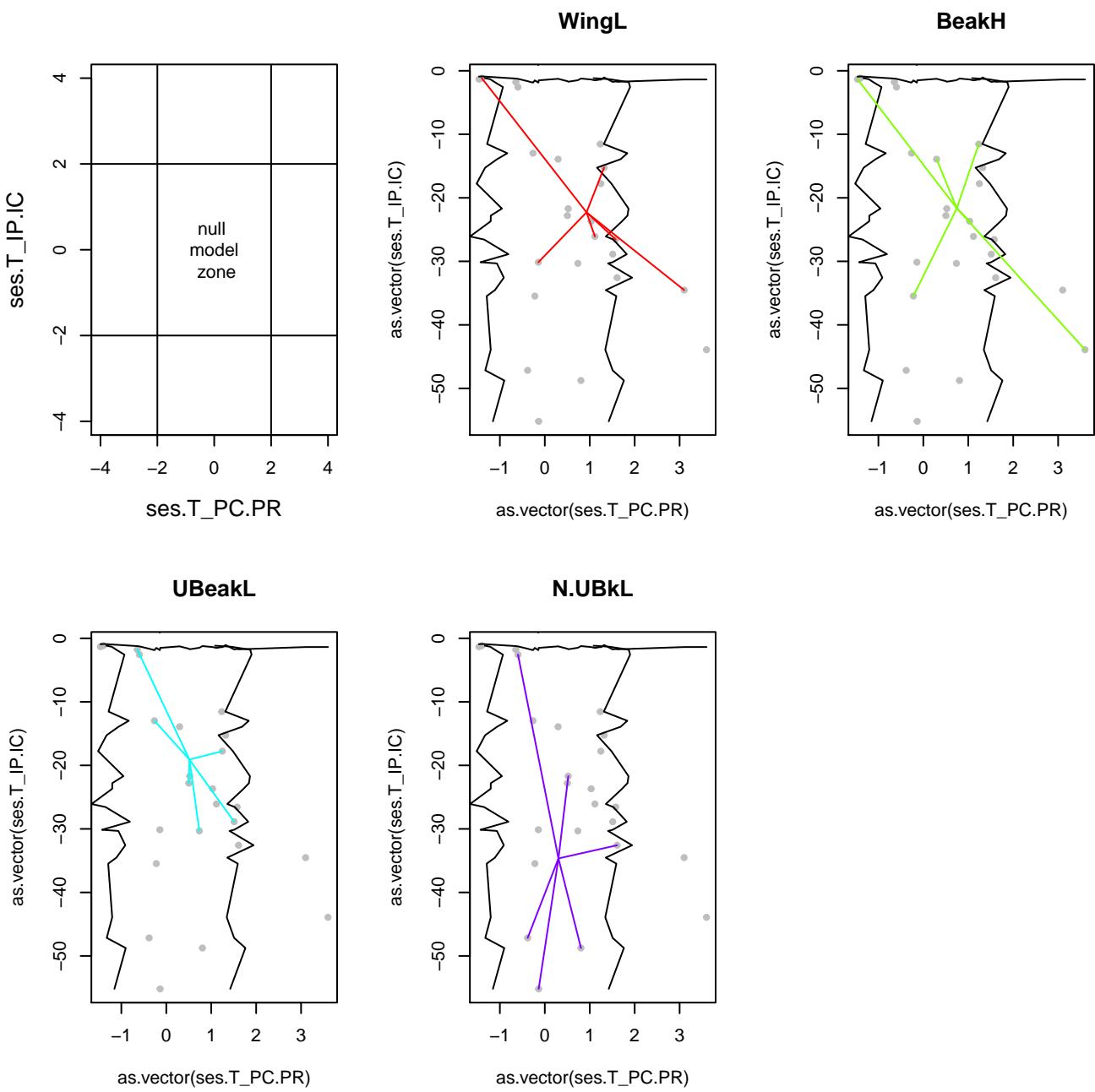
```

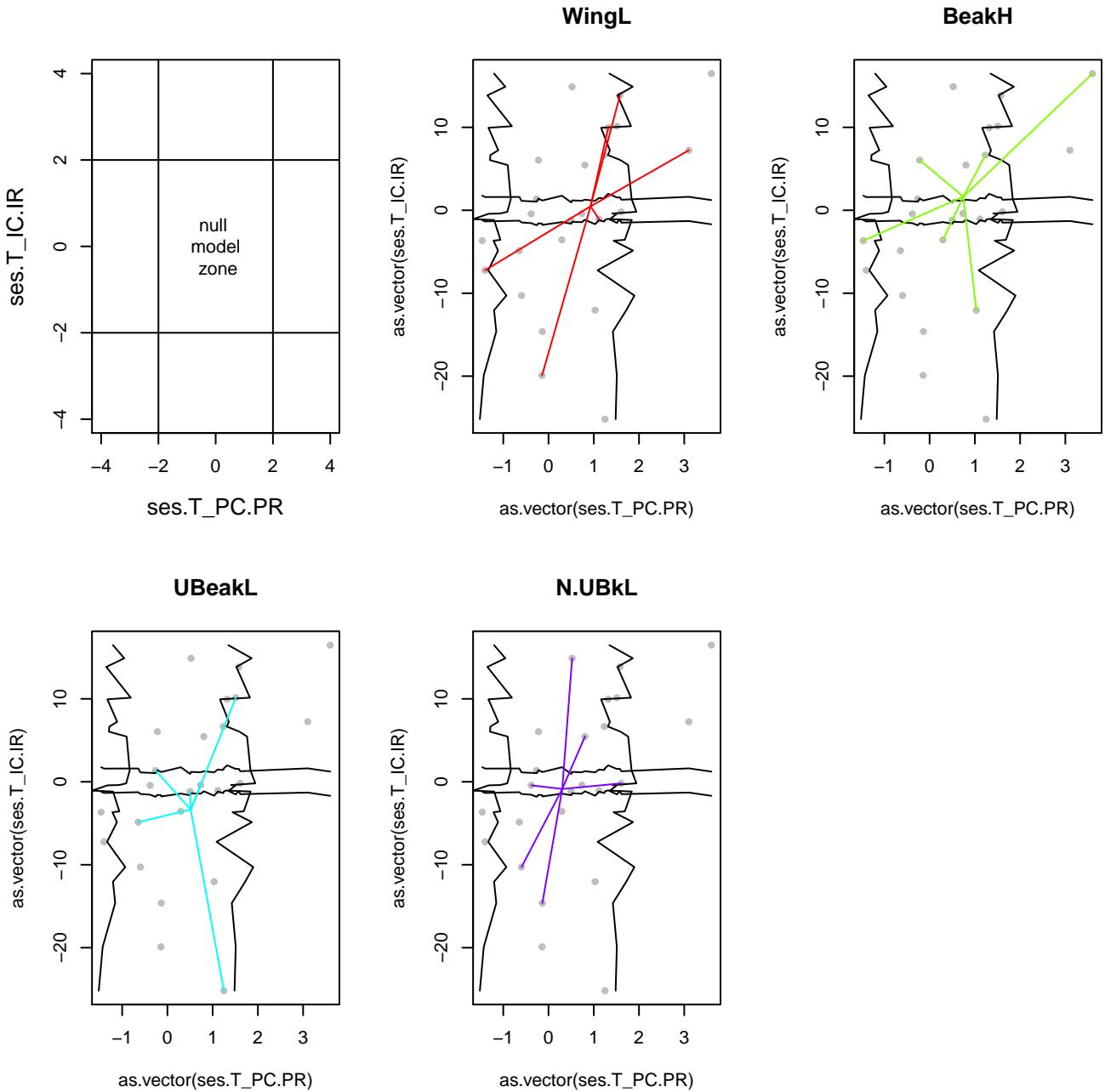
5.1.2 Plot T-statistics correlations

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)
```

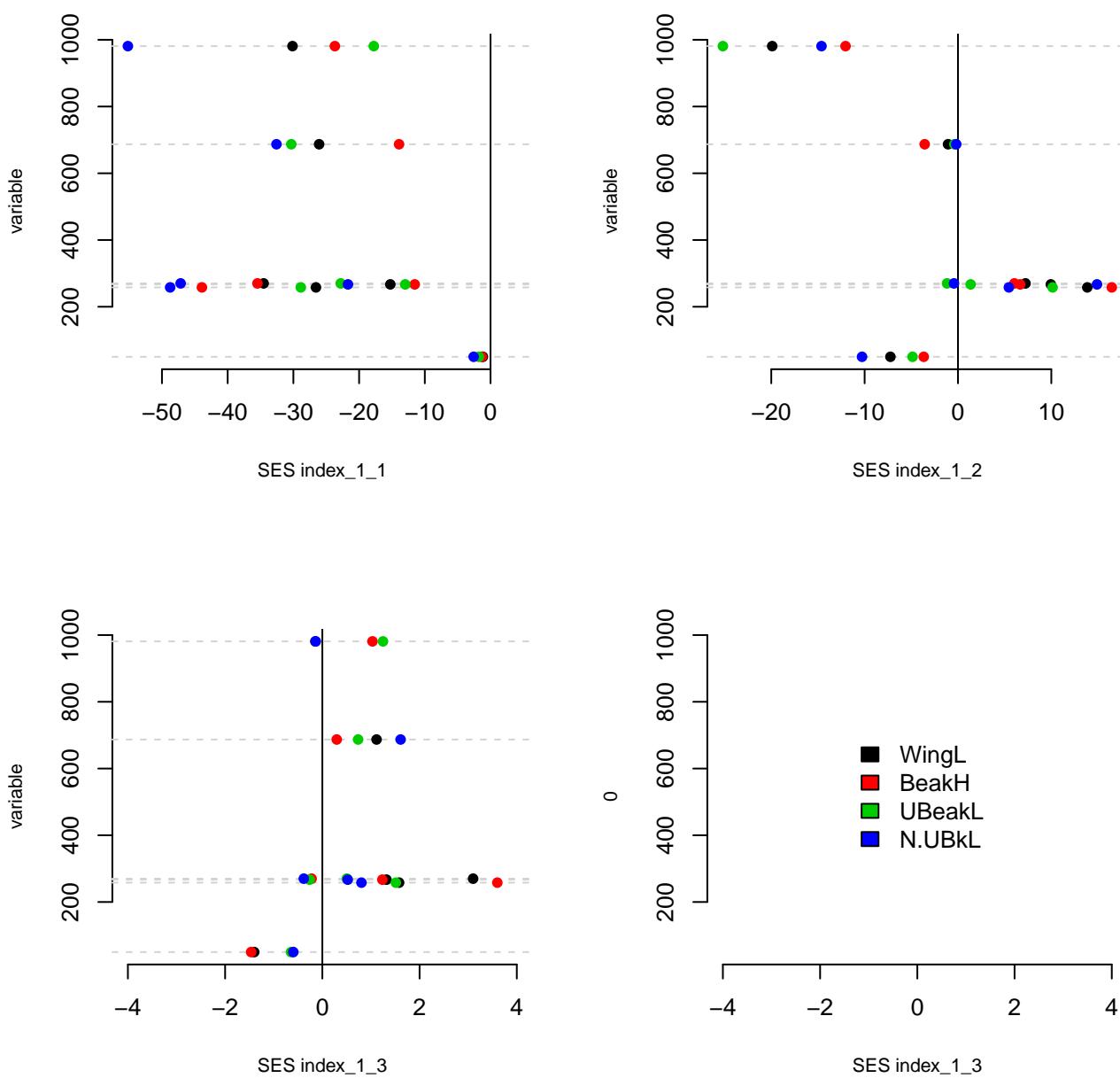






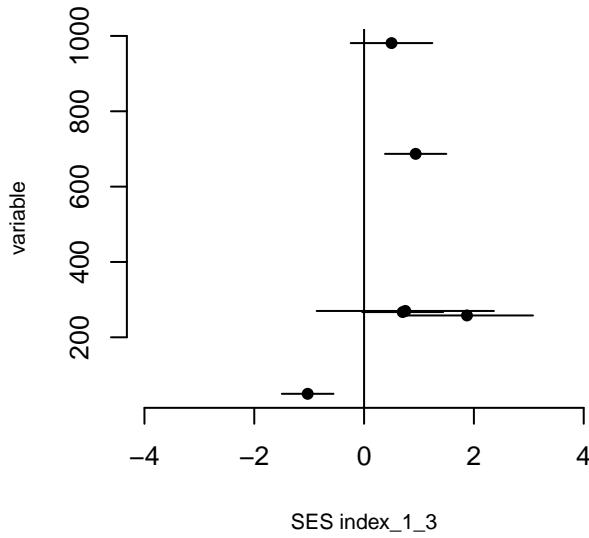
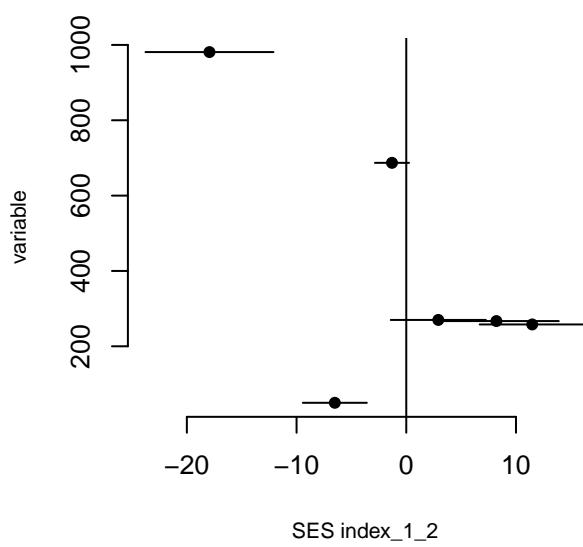
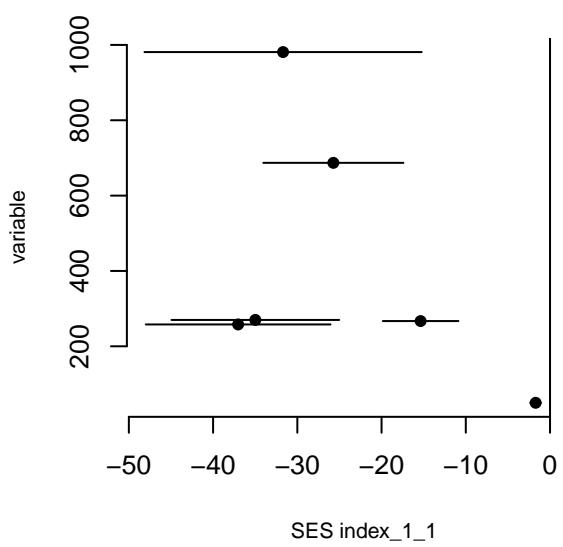
Here we plot T-statistics (in the standardized effect size SES form) in function of species richness by sites.

```
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 metrics: function ComIndex and ComIndexMulti

The function ComIndex allow to choose 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 2
res.finch.sp_mn2<-ComIndex(traits=traits.finch, index=funct, sp=sp.finch,
                            nullmodels=c(2,2,2,2), ind.plot=ind.plot.finch,
                            nperm=9, print=FALSE)

#Test against the null model 2sp
res.finch.sp_mn2sp<-ComIndex(traits=traits.finch, index=funct, sp=sp.finch,
                               nullmodels=rep("2sp",4), ind.plot=ind.plot.finch,
                               nperm=9, print=FALSE)
```

These two functions allows to calcul 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 1 is trivial for this function
##because randomisation is within community only

res.finch.ind_mn1<-ComIndex(traits=traits.finch, index=funct, sp=sp.finch,
                            nullmodels=c(1,1,1,1), ind.plot=ind.plot.finch,
                            nperm=9, print=FALSE)
res.finch.ind_mn2<-ComIndex(traits=traits.finch, index=funct, sp=sp.finch,
                            nullmodels=c(2,2,2,2), ind.plot=ind.plot.finch,
                            nperm=9, print=FALSE)
```

We can calcul index with or without intraspecific variance.

```
#Calcul of means by population (name_sp_site is a name of a population)
#like in the function ComIndex and 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))")

res.finch.withIV<-ComIndex(traits=traits.finch, index=funct.withIV,
                           sp=sp.finch, nullmodels=c(2,2,2,2),
                           ind.plot=ind.plot.finch, nperm=9, print=FALSE)

res.finch.withoutIV<-ComIndex(traits=traits.finch, index=funct.withoutIV,
                               sp=sp.finch, nullmodels=rep("2sp",4),
                               ind.plot=ind.plot.finch, nperm=9, print=FALSE)

```

5.2.1 S3 methods for class ComIndex and ComIndexMulti

Tstats class is 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 = c(2,
##   2, 2, 2), 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
## $tapply(x, ind.plot.finch, function(x) kurtosis(x, na.rm=T))_nm
## $tapply(x, ind.plot.finch, function(x) max(x, na.rm=T)-min(x, na.rm=T))_nm
## $tapply(x, ind.plot.finch, function(x) CVNND(x))_nm
## 
```

```

## #####
## 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

summary(res.finch.withoutIV)

## [1] "Observed values"
## $`tapply(x, fact, function(x) mean(x, na.rm=T))` 
##   WingL           BeakH           UBeakL          N.UBkL
##   Min. :65.9    Min. : 9.55   Min. :15.5    Min. :10.6
##   1st Qu.:67.2   1st Qu.:10.06  1st Qu.:15.7   1st Qu.:10.7
##   Median :68.7   Median :10.15  Median :16.4   Median :11.0
##   Mean   :68.1   Mean   :10.37  Mean   :16.6   Mean   :11.1
##   3rd Qu.:69.1   3rd Qu.:10.68 3rd Qu.:17.1   3rd Qu.:11.2
##   Max.   :69.2   Max.   :11.50  Max.   :18.5   Max.   :11.9
## 
## $`tapply(x, fact, function(x) kurtosis(x, na.rm=T))` 
##   WingL           BeakH           UBeakL          N.UBkL
##   Min. :-2.333   Min. :-2.3333  Min. :-2.33   Min. :-2.33
##   1st Qu.:-1.954 1st Qu.:-2.0761 1st Qu.:-2.27  1st Qu.:-2.04
##   Median :-1.760  Median :-1.4834  Median :-1.98  Median :-1.87
##   Mean   :-1.559  Mean   :-1.2609  Mean   :-1.99  Mean   :-1.84
##   3rd Qu.:-1.033 3rd Qu.:-0.4232 3rd Qu.:-1.77  3rd Qu.:-1.60
##   Max.   :-0.693  Max.   : 0.0779  Max.   :-1.60  Max.   :-1.37
## 
## $`tapply(x, fact, function(x) max(x, na.rm=T)-min(x, na.rm=T))` 

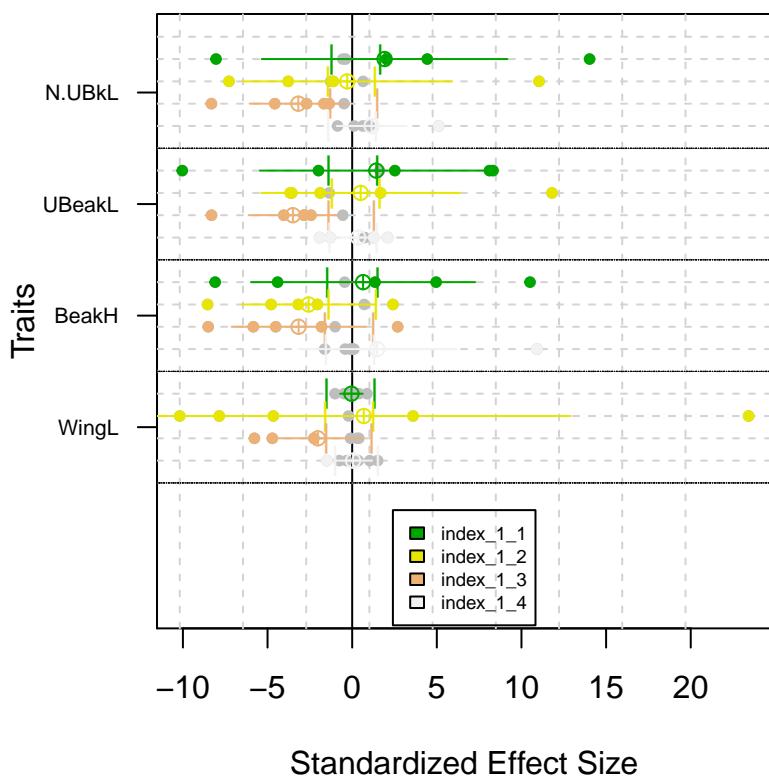
```

```

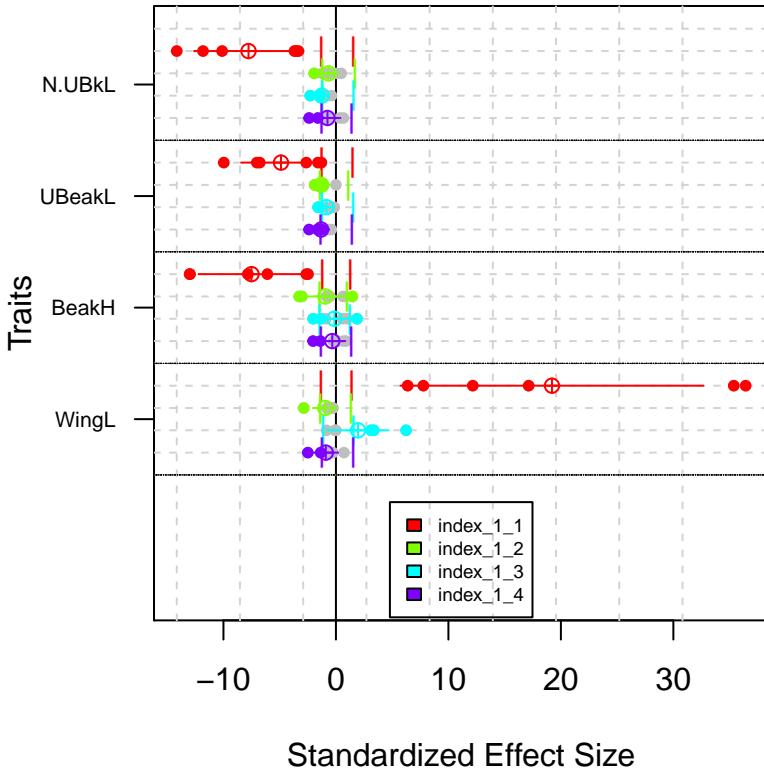
##      WingL        BeakH        UBeakL       N.UBkL
## Min.   : 8.33   Min.   : 2.35   Min.   : 7.14   Min.   :5.66
## 1st Qu.:26.21  1st Qu.:12.08  1st Qu.: 8.71  1st Qu.:7.07
## Median :29.21  Median :14.29  Median :10.06  Median :7.38
## Mean   :25.41  Mean   :12.36  Mean   : 9.42  Mean   :7.22
## 3rd Qu.:29.87  3rd Qu.:14.81  3rd Qu.:10.26  3rd Qu.:7.64
## Max.   :30.41  Max.   :16.93  Max.   :10.67  Max.   :8.20
##
## $`tapply(x, fact, function(x) CVNND(x))` 
##      WingL        BeakH        UBeakL       N.UBkL
## Min.   :0.0132   Min.   :0.0944   Min.   :0.0797   Min.   :0.323
## 1st Qu.:0.1538  1st Qu.:0.5381  1st Qu.:0.1723  1st Qu.:0.356
## Median :0.3944  Median :1.0743  Median :0.4270  Median :0.611
## Mean   :0.5963  Mean   :0.9382  Mean   :0.3873  Mean   :0.606
## 3rd Qu.:1.1147  3rd Qu.:1.3756  3rd Qu.:0.5791  3rd Qu.:0.835
## Max.   :1.3475  Max.   :1.5508  Max.   :0.6732  Max.   :0.913
##
## [1] "null values"
## $`tapply(x, fact, function(x) mean(x, na.rm=T))` 
##      Min. 1st Qu. Median   Mean 3rd Qu.   Max.
##     15.6    24.7   26.7    27.0   28.6    40.3
##
## $`tapply(x, fact, function(x) kurtosis(x, na.rm=T))` 
##      Min. 1st Qu. Median   Mean 3rd Qu.   Max.
##     -2.380  -2.000  -1.420  -1.200  -0.856  3.270
##
## $`tapply(x, fact, function(x) max(x, na.rm=T)-min(x, na.rm=T))` 
##      Min. 1st Qu. Median   Mean 3rd Qu.   Max.
##     1.98   10.00  14.10   18.90  21.40   75.30
##
## $`tapply(x, fact, function(x) CVNND(x))` 
##      Min. 1st Qu. Median   Mean 3rd Qu.   Max.
##     0.0163  0.6800  1.0500  1.0900  1.4300  2.6300

plot(res.finch.withIV)

```



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



5.2.2 Plot Tstats and other uni/multivariates metrics together

The class `listofindex` permit to stock differents 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)
```

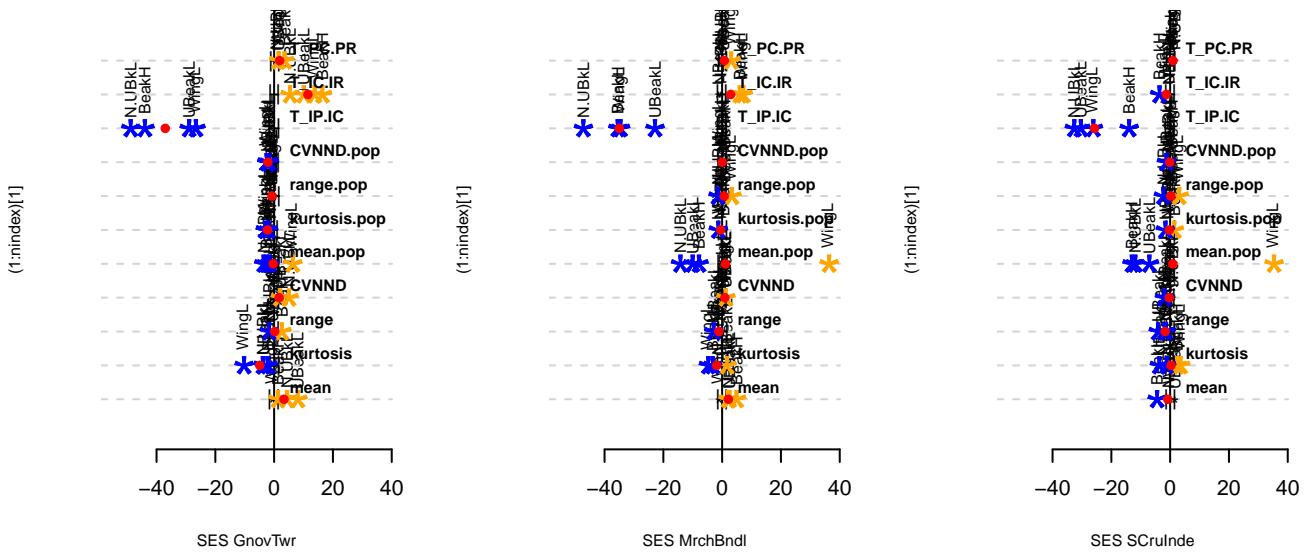
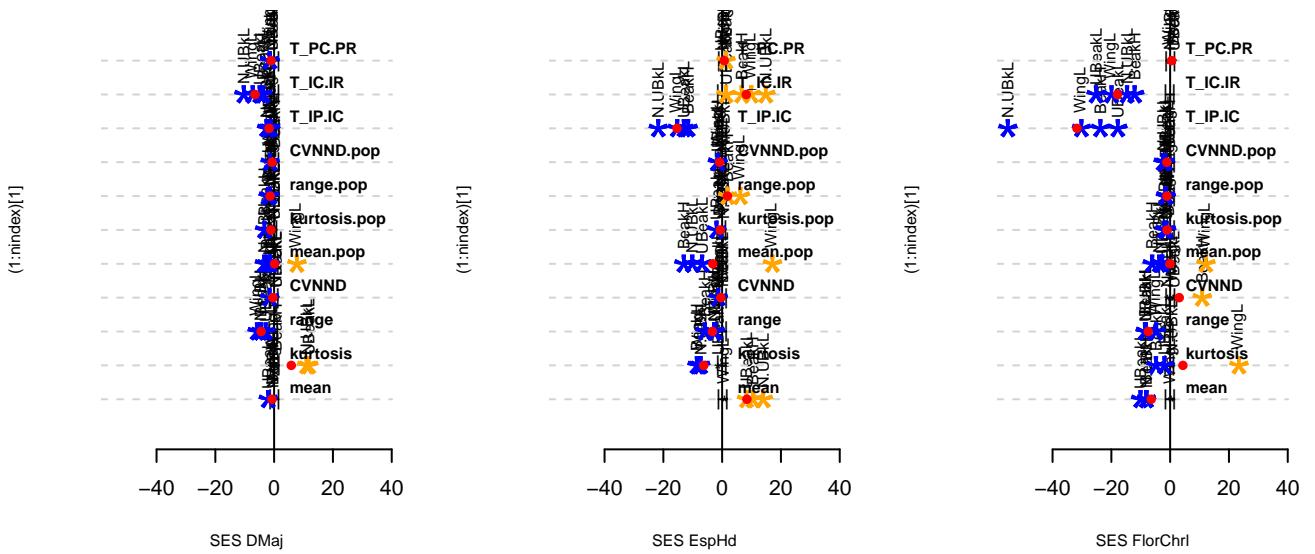
```
list.ind<-list(res.finch.withIV, res.finch.withoutIV, res.finch)
namesindex.i.l11=c("mean", "kurtosis", "range", "CVNND",
                  "mean.pop", "kurtosis.pop", "range.pop", "CVNND.pop",
                  "T_IP.IC", "T_IC.IR", "T_PC.PR")

i.l11<-as.listofindex(list.ind, namesindex=namesindex.i.l11)
```

```
class(i.l1)
## [1] "listofindex"
```

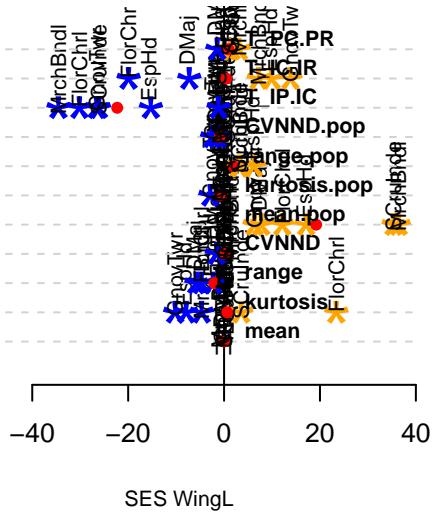
The plot type bytraits allows to plot all SES traits values for all sites or all traits

```
par(mfrow=c(2,3))
plot(i.l1,type="bysites")
```

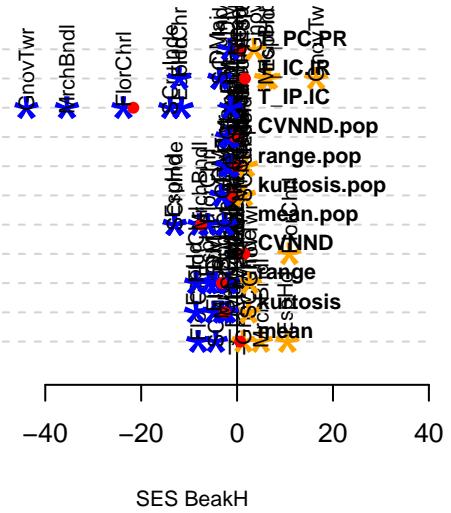


```
par(mfrow=c(2,2))
plot(i.l1,type="bytraits")
```

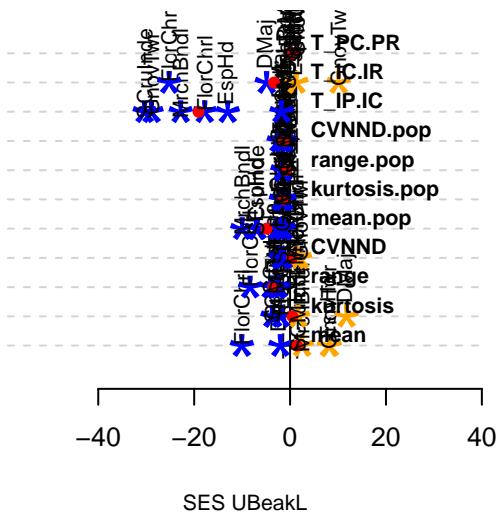
(1:nindex)[i]



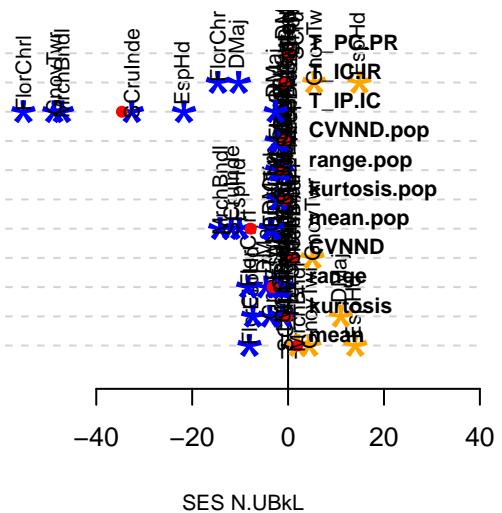
(1:nindex)[i]



(1:nindex)[i]



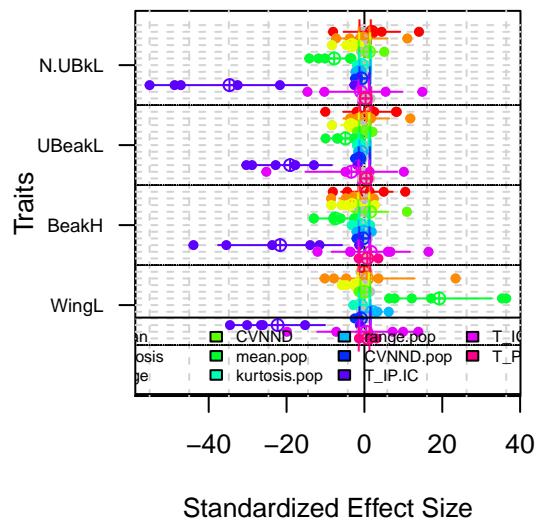
(1:nindex)[i]



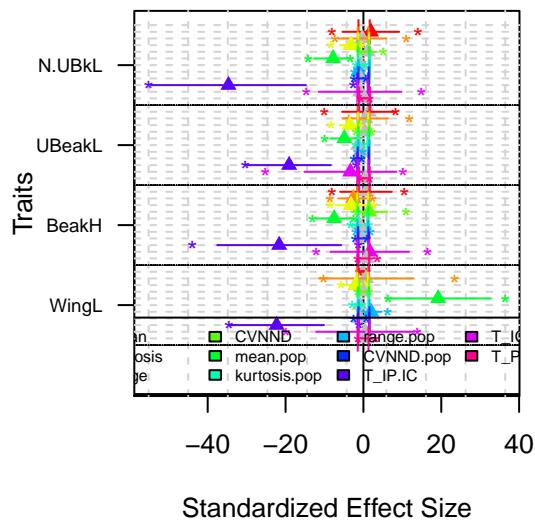
```
par(mfrow=c(1,1))
```

The other plot type are the same as plot.Tstats

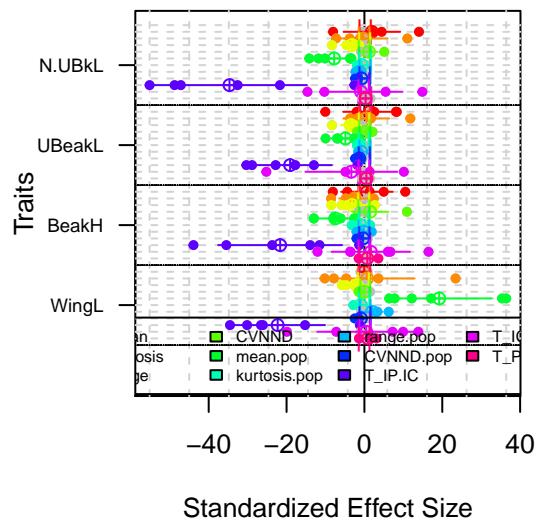
```
par(mfrow=c(2,2))
plot(i.11)
```



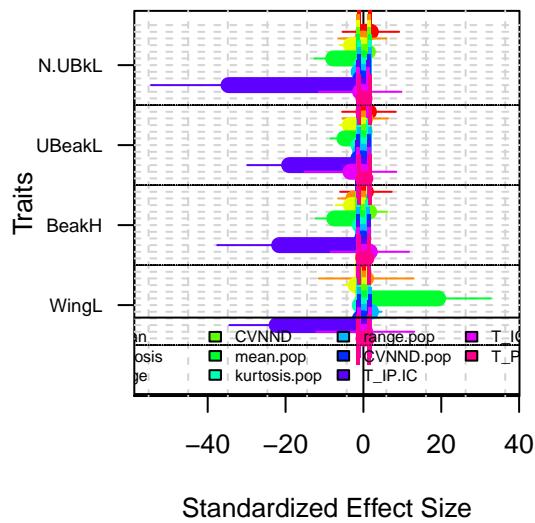
```
plot(i.l1,type="simple_range")
```



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



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



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

5.3 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)
```

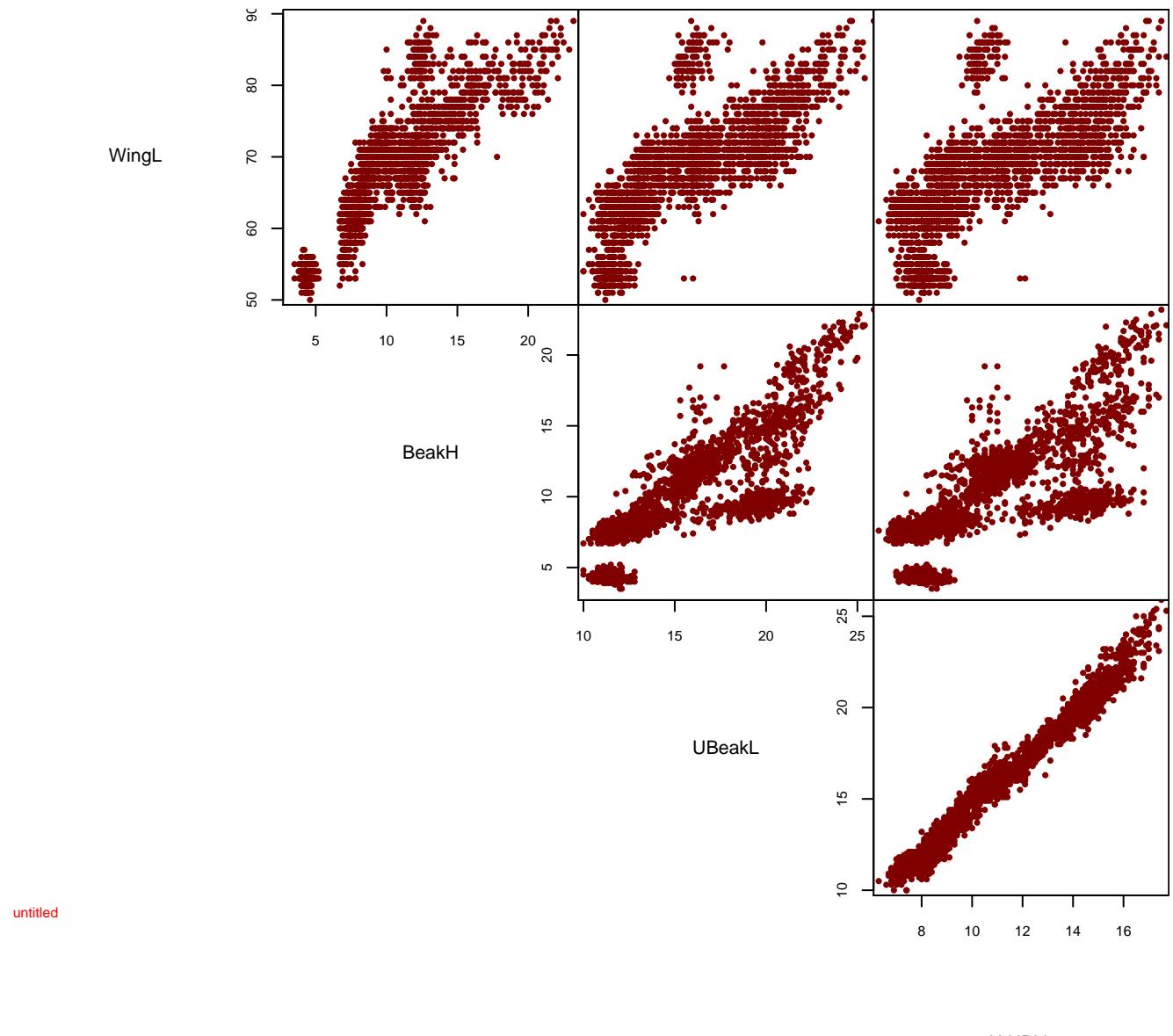
A simple example to illustrate the concept of the function ComIndexMulti

```
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=c(2,2),  
                           ind.plot=ind.plot.finch, nperm=9, sp=sp.finch)  
  
## [1] "creating null models"  
## [1] "nm.2 25 %"  
## [1] "nm.2 50 %"  
## [1] "nm.2 75 %"  
## [1] "nm.2 100 %"  
## [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 %"  
  
attributes(ses.listofindex(as.listofindex(list(res.sum.1))))  
  
## $names  
## [1] "index_1_1" "index_1_2"  
##  
## $class  
## [1] "ses.list"
```

A more interesting example using the function hypervolume from the package ...
hypervolume. We show here several results which differ 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)
}

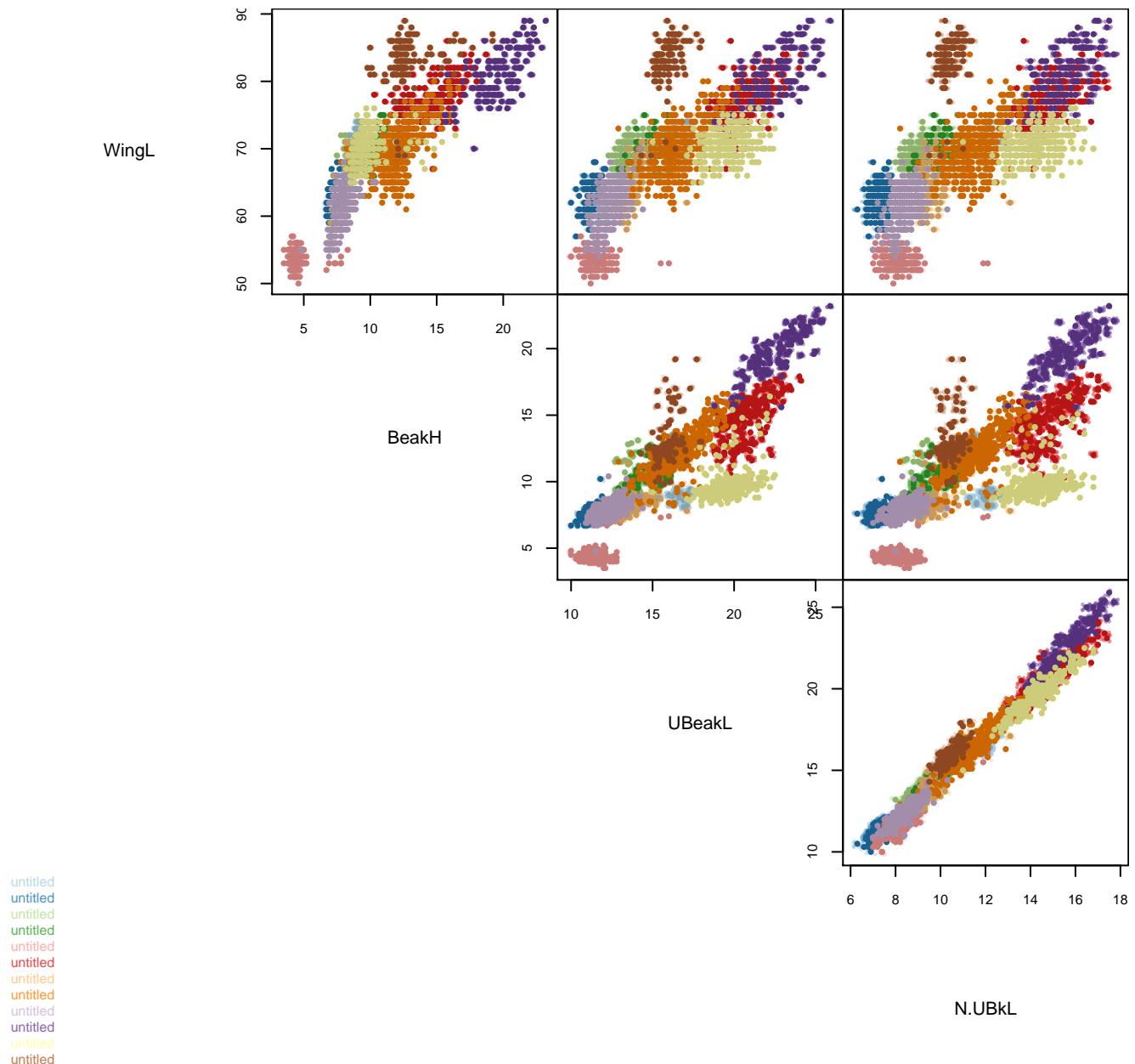
hv.list@HVList<-hv.list2
require(adegenet)

## 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

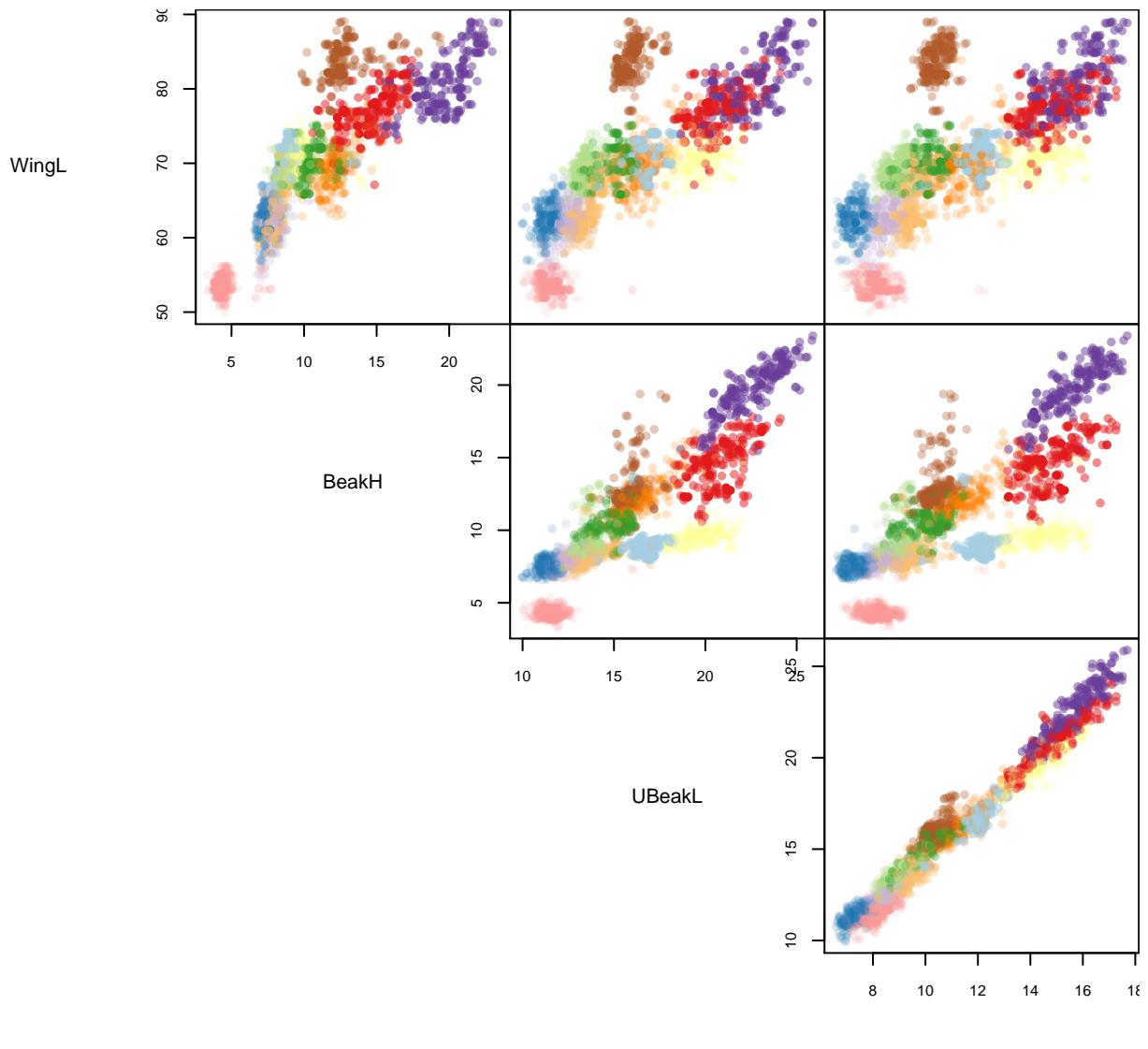
colorhv<-transp(funky(nlevels(sp.finch)), alpha=0.8)

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

```



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



```
untitled
```

N.UBkL

```
summary(hv.list)

## HypervolumeList with 12 elements:
## 
## Hypervolume
##   Name: untitled
##   Nr. of observations: 23
##   Dimensionality: 4
##   Volume: 0.581274
##   Bandwidth: 0.2 0.2 0.2 0.2
##   Disjunct factor: 0.987217
##   Quantile desired: 0.000000
##   Quantile obtained: 0.000000
```

```
## Nr. of repetitions per point: 1000
## Number of random points: 14385
## Hypervolume
## Name: untitled
## Nr. of observations: 172
## Dimensionality: 4
## Volume: 3.508501
## Bandwidth: 0.2 0.2 0.2 0.2
## Disjunct factor: 0.796807
## Quantile desired: 0.000000
## Quantile obtained: 0.000000
## Nr. of repetitions per point: 1000
## Number of random points: 91104
## Hypervolume
## Name: untitled
## Nr. of observations: 142
## Dimensionality: 4
## Volume: 2.957552
## Bandwidth: 0.2 0.2 0.2 0.2
## Disjunct factor: 0.813587
## Quantile desired: 0.000000
## Quantile obtained: 0.000000
## Nr. of repetitions per point: 1000
## Number of random points: 76385
## Hypervolume
## Name: untitled
## Nr. of observations: 73
## Dimensionality: 4
## Volume: 1.729685
## Bandwidth: 0.2 0.2 0.2 0.2
## Disjunct factor: 0.925559
## Quantile desired: 0.000000
## Quantile obtained: 0.000000
## Nr. of repetitions per point: 1000
## Number of random points: 43564
## Hypervolume
## Name: untitled
## Nr. of observations: 299
## Dimensionality: 4
## Volume: 4.127026
## Bandwidth: 0.2 0.2 0.2 0.2
## Disjunct factor: 0.539170
## Quantile desired: 0.000000
## Quantile obtained: 0.000000
## Nr. of repetitions per point: 1000
## Number of random points: 114079
## Hypervolume
## Name: untitled
```

```
## Nr. of observations: 206
## Dimensionality: 4
## Volume: 5.070588
## Bandwidth: 0.2 0.2 0.2 0.2
## Disjunct factor: 0.961504
## Quantile desired: 0.000000
## Quantile obtained: 0.000000
## Nr. of repetitions per point: 1000
## Number of random points: 126546
## Hypervolume
## Name: untitled
## Nr. of observations: 125
## Dimensionality: 4
## Volume: 2.734825
## Bandwidth: 0.2 0.2 0.2 0.2
## Disjunct factor: 0.854633
## Quantile desired: 0.000000
## Quantile obtained: 0.000000
## Nr. of repetitions per point: 1000
## Number of random points: 69799
## Hypervolume
## Name: untitled
## Nr. of observations: 548
## Dimensionality: 4
## Volume: 11.785994
## Bandwidth: 0.2 0.2 0.2 0.2
## Disjunct factor: 0.840128
## Quantile desired: 0.000000
## Quantile obtained: 0.000000
## Nr. of repetitions per point: 1000
## Number of random points: 302349
## Hypervolume
## Name: untitled
## Nr. of observations: 386
## Dimensionality: 4
## Volume: 6.293490
## Bandwidth: 0.2 0.2 0.2 0.2
## Disjunct factor: 0.636890
## Quantile desired: 0.000000
## Quantile obtained: 0.000000
## Nr. of repetitions per point: 1000
## Number of random points: 170580
## Hypervolume
## Name: untitled
## Nr. of observations: 126
## Dimensionality: 4
## Volume: 3.180147
## Bandwidth: 0.2 0.2 0.2 0.2
```

```

## Disjunct factor: 0.985909
## Quantile desired: 0.000000
## Quantile obtained: 0.000000
## Nr. of repetitions per point: 1000
## Number of random points: 78794
## Hypervolume
## Name: untitled
## Nr. of observations: 284
## Dimensionality: 4
## Volume: 6.331289
## Bandwidth: 0.2 0.2 0.2 0.2
## Disjunct factor: 0.870831
## Quantile desired: 0.000000
## Quantile obtained: 0.000000
## Nr. of repetitions per point: 1000
## Number of random points: 161250
## Hypervolume
## Name: untitled
## Nr. of observations: 129
## Dimensionality: 4
## Volume: 2.871520
## Bandwidth: 0.2 0.2 0.2 0.2
## Disjunct factor: 0.869525
## Quantile desired: 0.000000
## Quantile obtained: 0.000000
## Nr. of repetitions per point: 1000
## Number of random points: 72987

```

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

```

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

```



```

## +   message('at the R command line prompt.')
## + }

## Demo does not run by default to meet CRAN runtime requirements.
## This demo requires approximately 3 minutes to run.
## To run the demo, type
## doHypervolumeFinchDemo=TRUE
## demo(finch)
## at the R command line prompt.

```

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: calcul the hypervolume without by.factor
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=c(2,2),
                      ind.plot=ind.plot.finch, nperm=9, sp=sp.finch)

## [1] "creating null models"
## [1] "nm.2 25 %"
## [1] "nm.2 50 %"
## [1] "nm.2 75 %"
## [1] "nm.2 100 %"
## [1] "calculation of null values using null models"
## [1] "as.numeric(try(hypervolume(na.omit(x), reps=100, \n
## [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=c(2,2),
                      ind.plot=ind.plot.finch, nperm=9, sp=sp.finch)

## [1] "creating null models"
## [1] "nm.2 25 %"
## [1] "nm.2 50 %"
## [1] "nm.2 75 %"
## [1] "nm.2 100 %"
## [1] "calculation of null values using null models"
## [1] "as.numeric(try(hypervolume(na.omit(x), reps=100, \n
## [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=c(2,2),
                      ind.plot=ind.plot.finch, nperm=9, sp=sp.finch)

```

```

## [1] "creating null models"
## [1] "nm.2 25 %"
## [1] "nm.2 50 %"
## [1] "nm.2 75 %"
## [1] "nm.2 100 %"
## [1] "calculation of null values using null models"
## [1] "as.numeric(try(hypervolume(na.omit(x), reps=100,\n## [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.finч, nullmodels=c(2,2),
                      ind.plot=ind.plot.finч, nperm=9, sp=sp.finч)

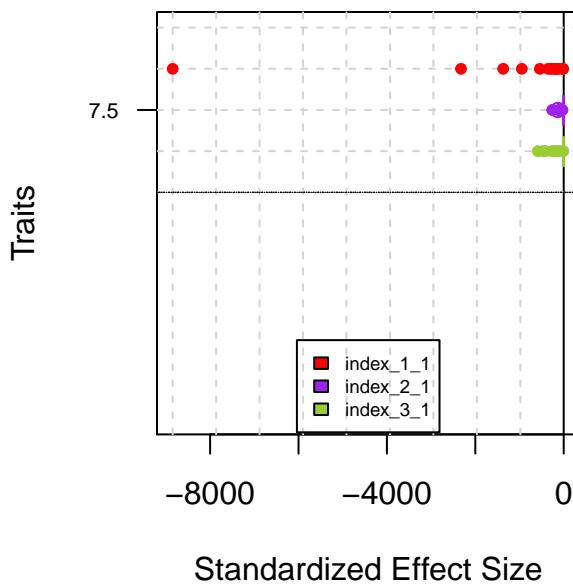
## [1] "creating null models"
## [1] "nm.2 25 %"
## [1] "nm.2 50 %"
## [1] "nm.2 75 %"
## [1] "nm.2 100 %"
## [1] "calculation of null values using null models"
## [1] "as.numeric(try(hypervolume(na.omit(x), reps=100, \n
## [1] "calculation of observed values"
## [1] "100 %"

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

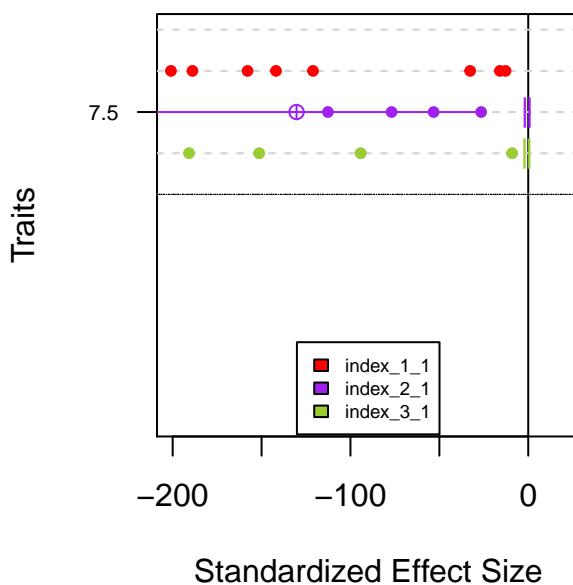
ses.list.multi<-ses.listofindex(list.ind.multi)

```

```
plot(list.ind.multi)
```



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



Compare hypervolume to Villéger 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 1 is trivial for this function
##because randomisation is within community only
Fdis.finch<-ComIndexMulti(traits.finch.mice,
                           index=funct,
                           by.factor=ind.plot.finch, nullmodels=c(2,2),
                           ind.plot=ind.plot.finch, nperm=9, sp=sp.finch)

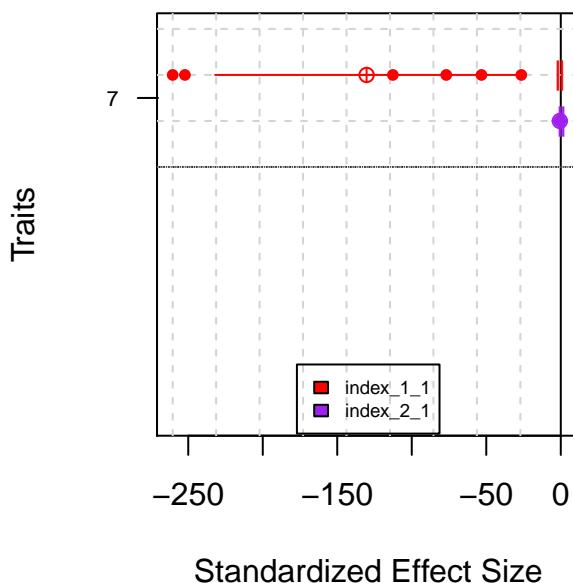
## [1] "creating null models"
## [1] "nm.2 25 %"
## [1] "nm.2 50 %"
## [1] "nm.2 75 %"
## [1] "nm.2 100 %"
## [1] "calculation of null values using null models"
## [1] "round(convhulln(x,FA)$vol,6) 100 %"
## [1] "calculation of observed values"
## [1] "100 %"

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

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

```

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



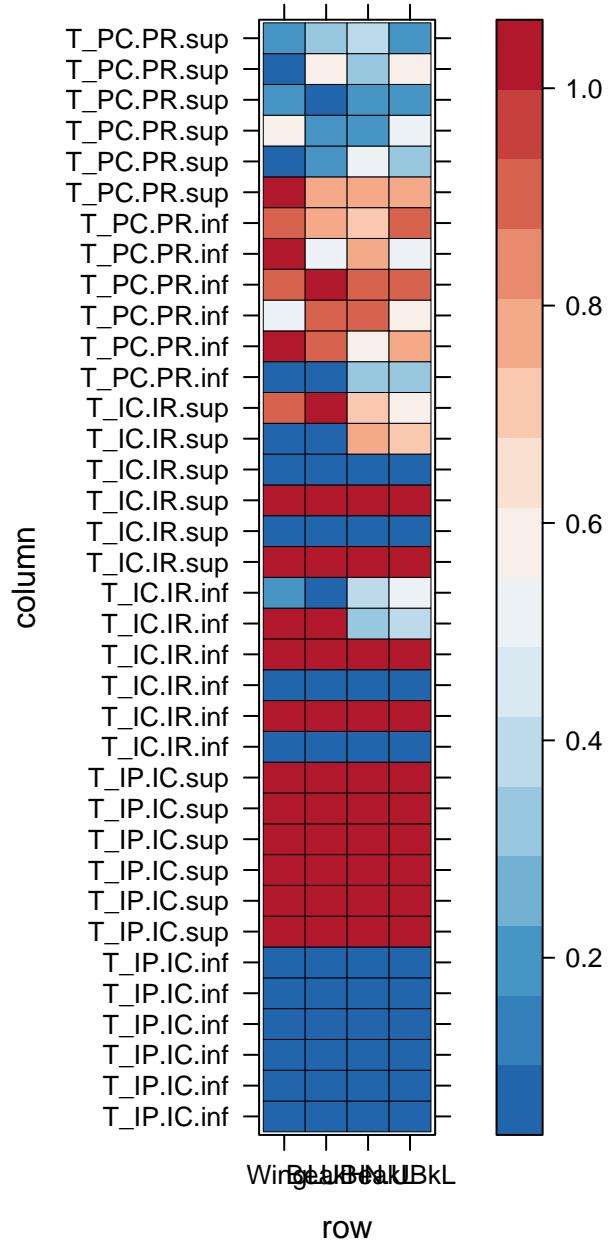
6 Others graphics functions

Using rasterVis to obtain more color schemes.

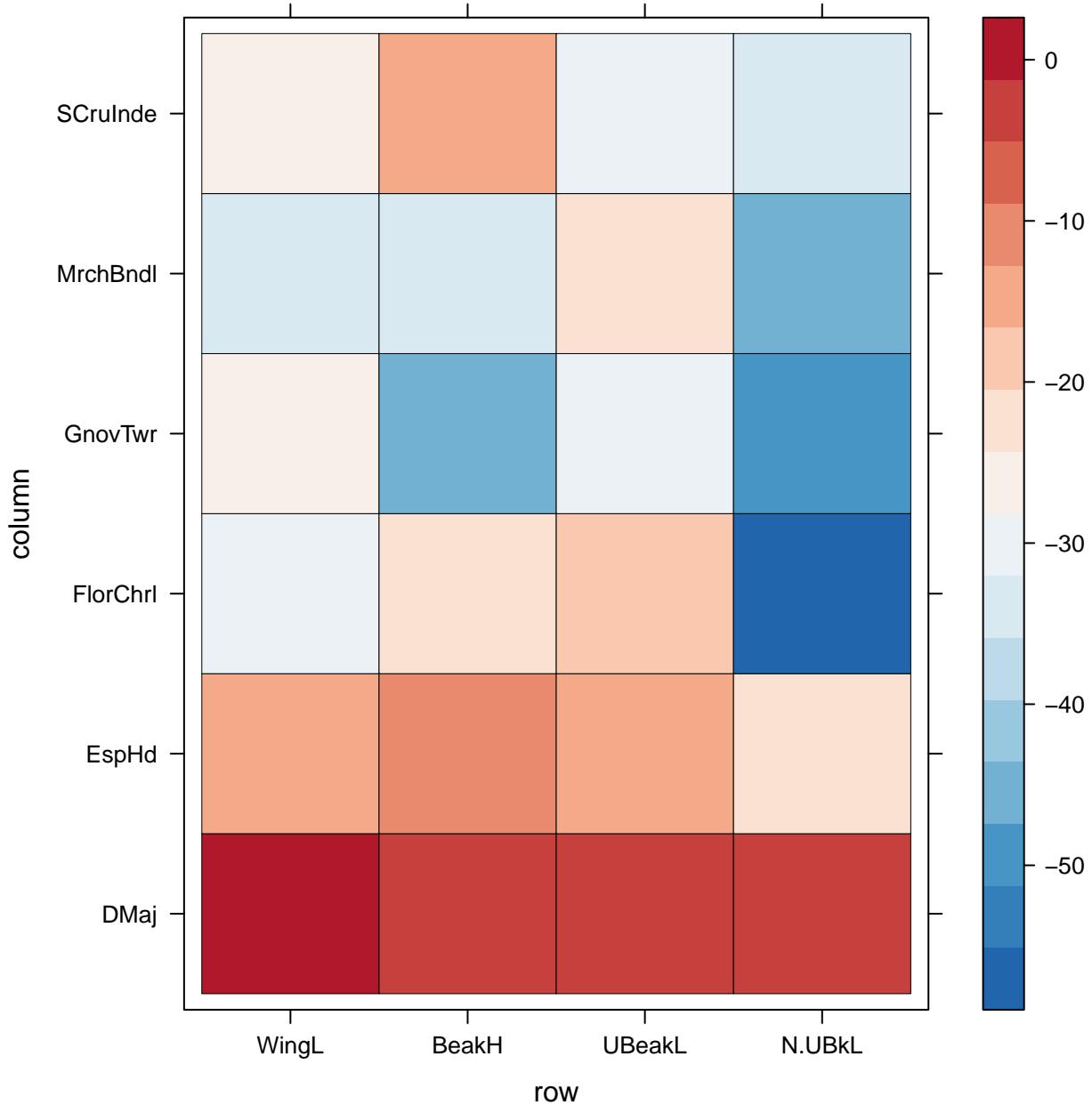
```
## Loading required package: rasterVis
## Loading required package: raster
## Loading required package: sp
##
## Attaching package: 'raster'
##
## The following object is masked from 'package:magic':
## 
##     shift
## 
## The following objects are masked from 'package:ape':
## 
##     edges, rotate,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

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

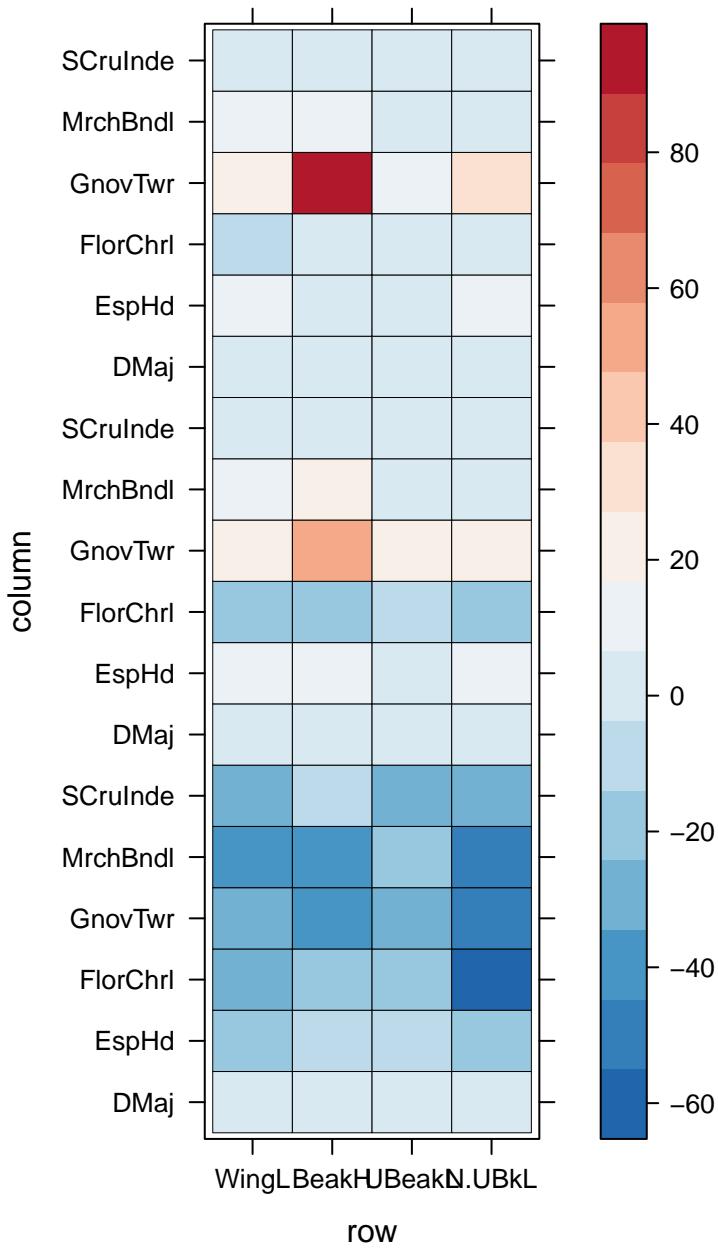
```
levelplot(t(sum_Tstats(res.finch)$p.value),
          colorkey=my.ckey, par.settings=my.theme, border="black")
```



```
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")
```



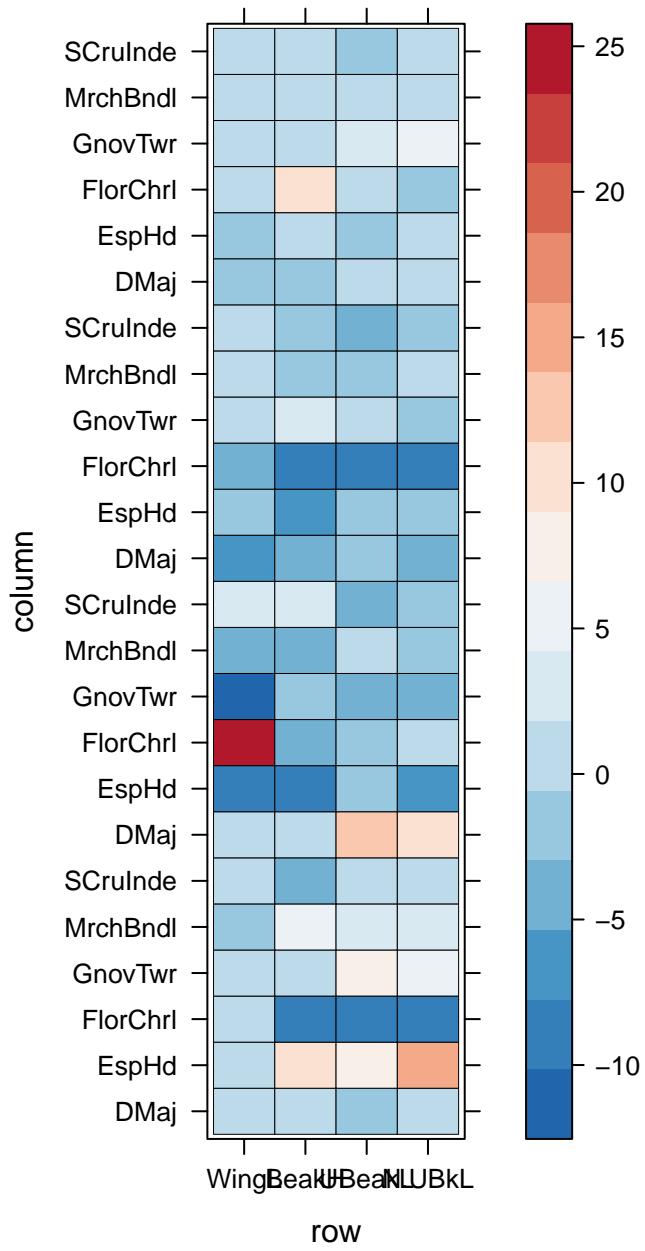
```
levelplot(cbind(t ses(res.finch$Tstats$T_IP.IC, res.finch$Tstats$T_IP.IC_nm)$ses),
          t ses(res.finch$Tstats$T_IC.IR, res.finch$Tstats$T_IP.IC_nm)$ses),
          t ses(res.finch$Tstats$T_PC.PR, res.finch$Tstats$T_IP.IC_nm)$ses))
, colorkey=my.ckey, par.settings=my.theme, border="black")
```



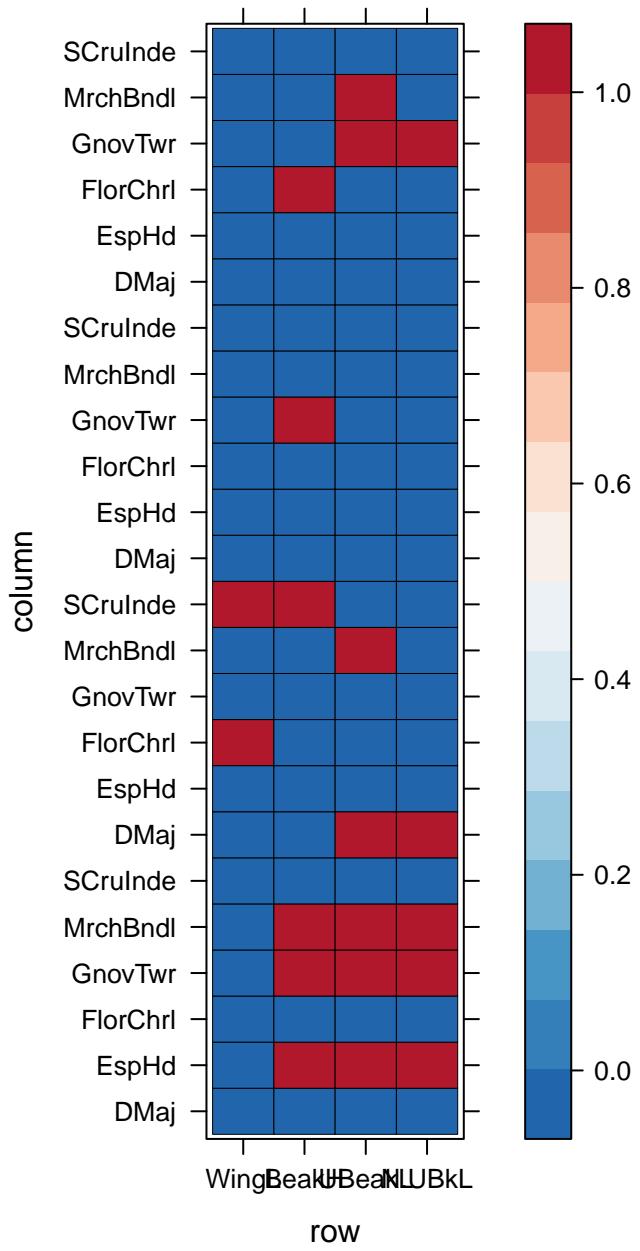
An other example using `ses.listofindex`. The first plot represent "ses" values and the second one the result of a test with H0: observed index value are greater than what we can expect using the null model (alpha=2.5%).

```
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

```

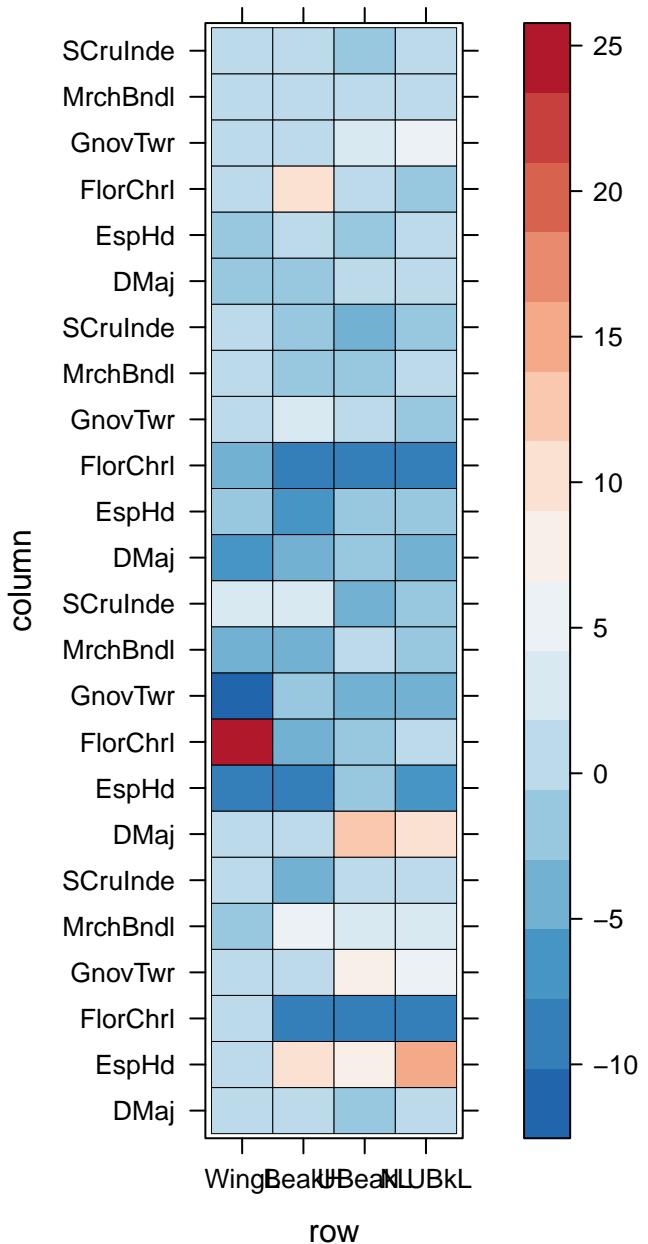
ses.ind<-t(rbind(ses.list[[1]]$ses,
                    ses.list[[2]]$ses,
                    ses.list[[3]]$ses,
                    ses.list[[4]]$ses))

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

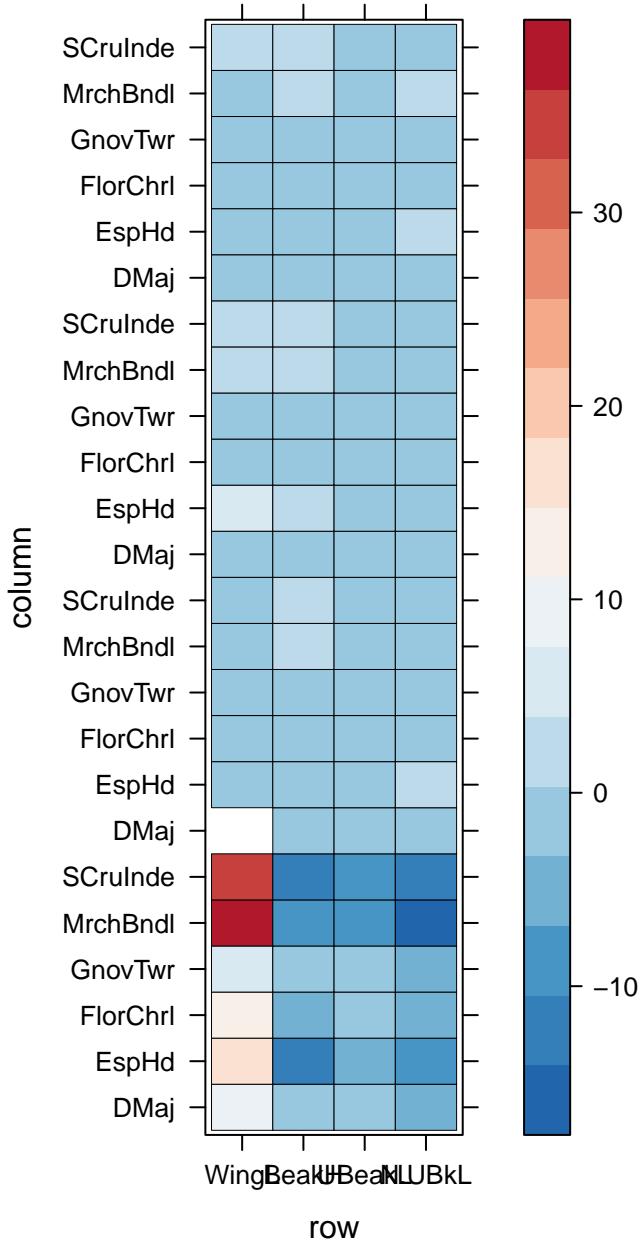
levelplot(ses.ind, colorkey=my.ckey,

```

```
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 put together all traits by meaning the SES values for each metrics in each sites whereas analysis dudi 2 analyse 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

```

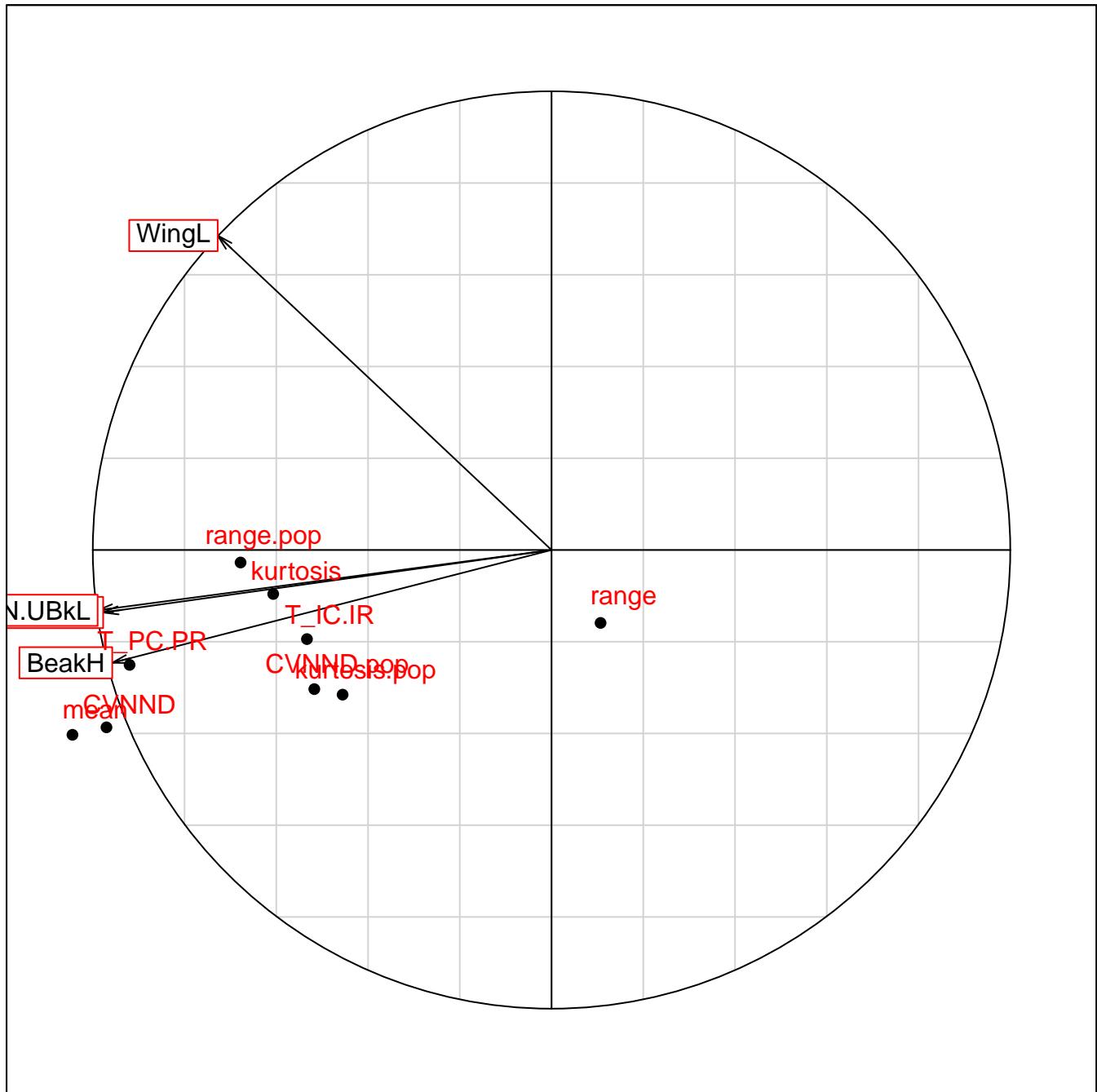
matfordudi<-complete(mice(matfordudi))
matfordudi2<-complete(mice(matfordudi2))

```

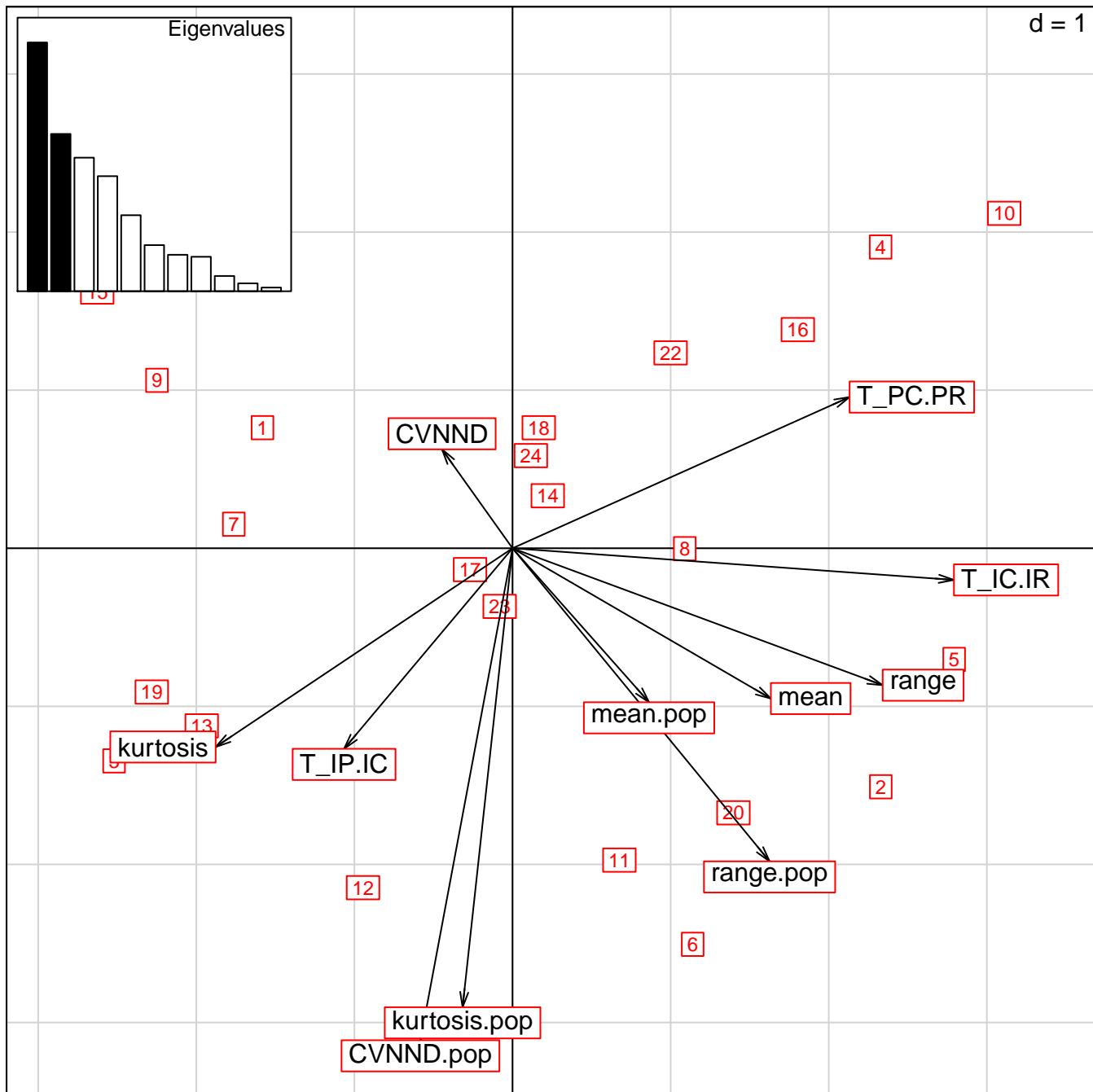
```

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)

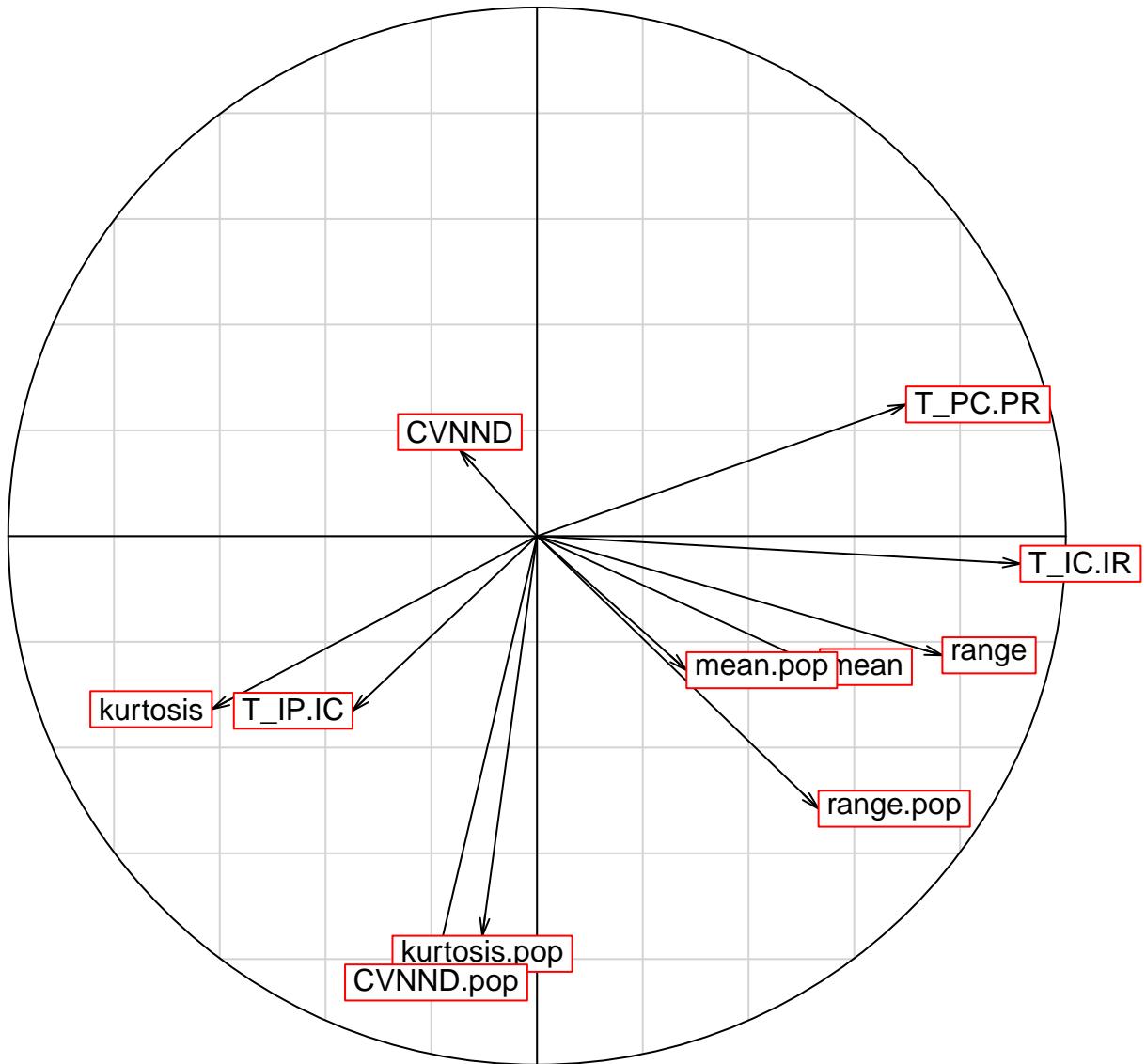
```



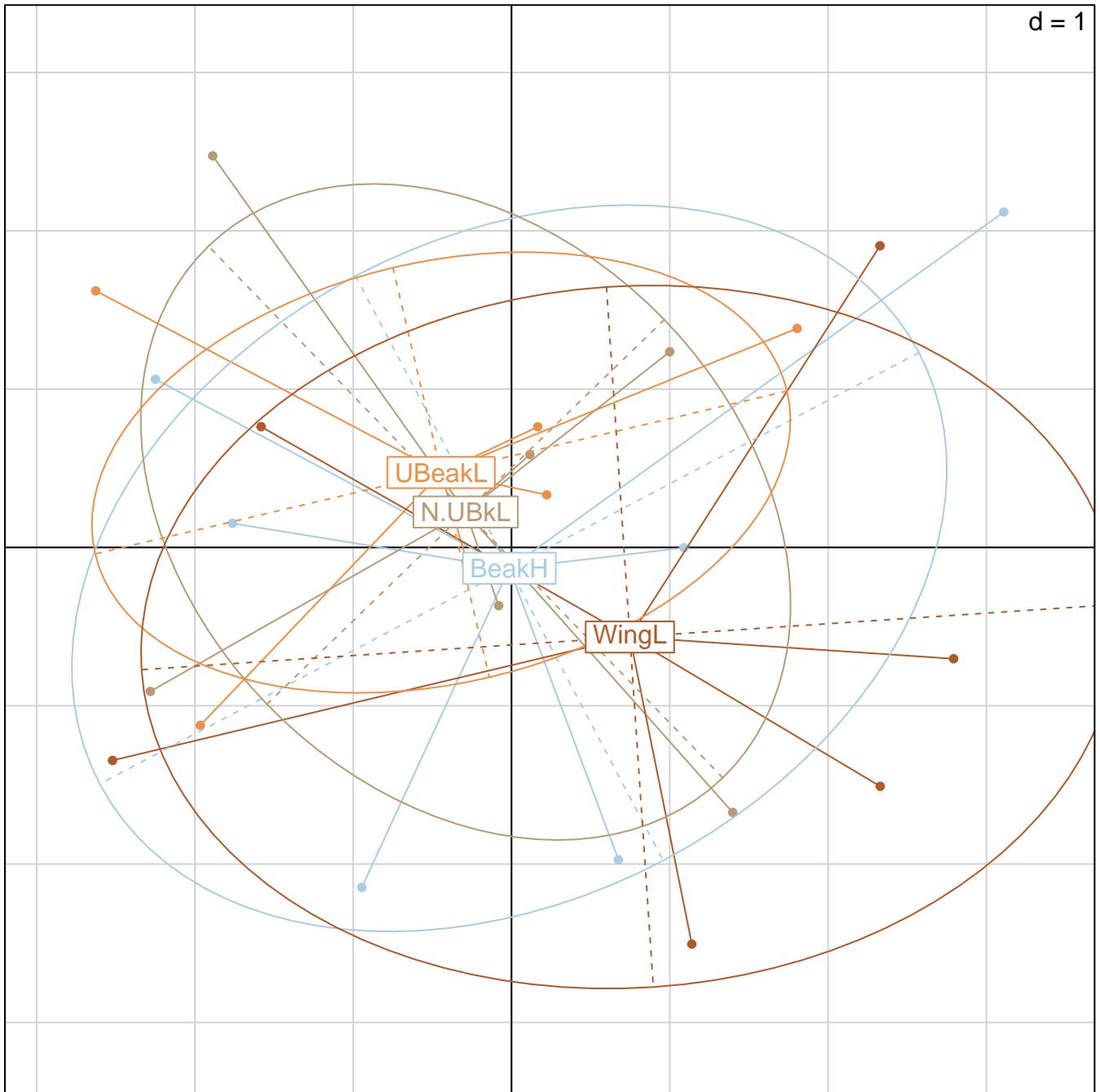
```
res.dudi2<-dudi.pca(matfordudi2, scan=F, nf=2)
scatter(res.dudi2)
```



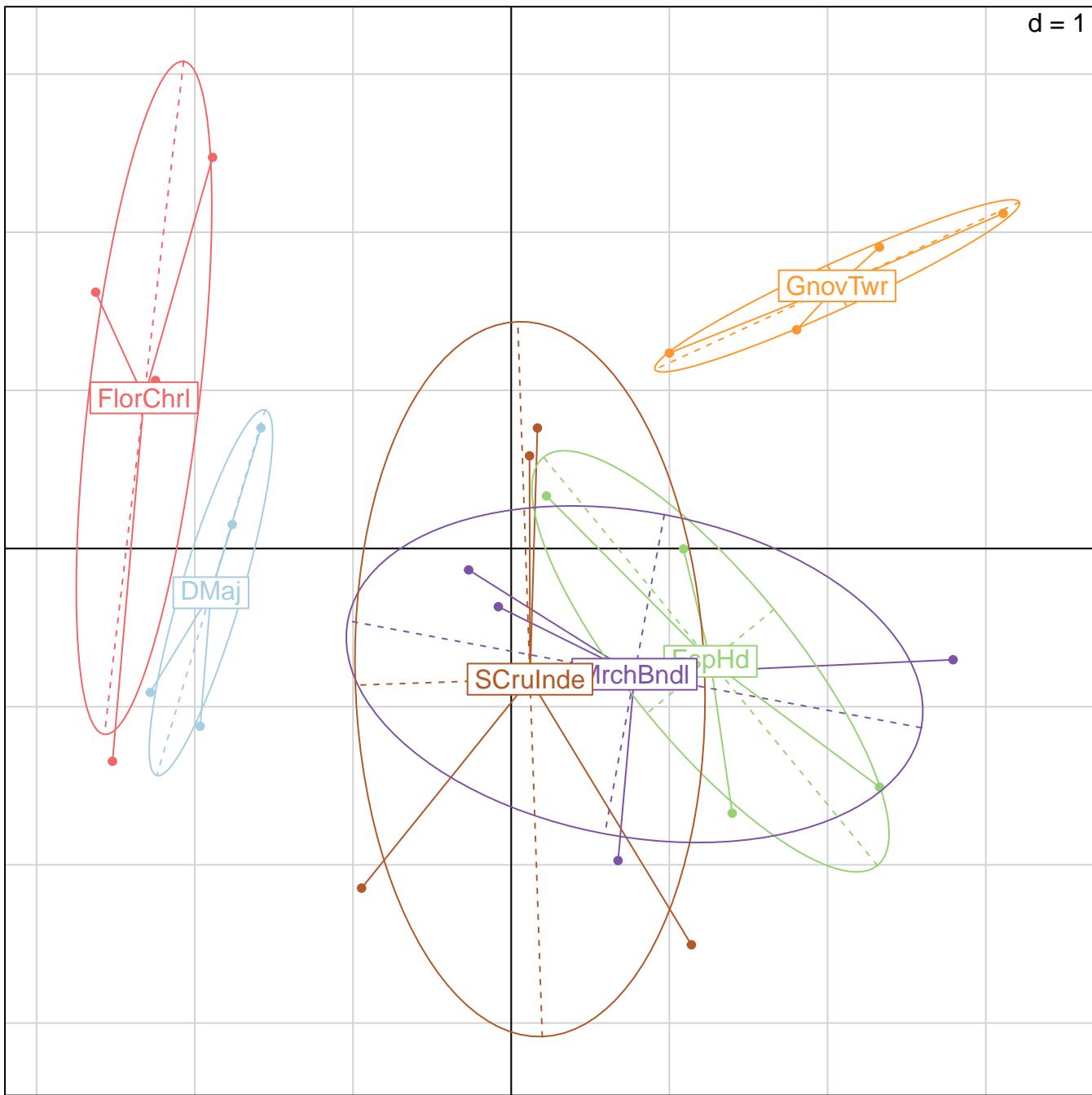
```
s.corcircle(res.dudi2$co)
```



```
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",
```



8 Conclusion

9 Acknowledgment