

Appendix C. Manual for R scripts

C.1. Package adiv

We have made available in package adiv version 2.1.1 (Pavoine 2020, 2021) all the functions used in our study. The data given in Appendices D and E have also been integrated in adiv: dataset named `batcomm`.

Functions in adiv where our new framework is developed are:

- Function `FPdivparam` that calculates functional or phylogenetic (FP-)diversity in communities using parametric indices ${}^{\alpha}K$, ${}^{\alpha}K^*$, ${}^{\alpha}Y$ and ${}^{\alpha}I$ discussed and developed in the main text.
- Function `plot.FPdivparam` that plots the results of function `FPdivparam`.
- Function `distinctAb` that calculates parametric indices of species' rarity and functional or phylogenetic distinctiveness and effective originality as in Tables 1 and 2 of the main text.
- Function `distinctDis` that calculates five indices of species' distinctiveness including the parametric index ${}^{\alpha}\Delta_{eq}$ developed in the main text (see Appendix B).
- Function `distinctTree` that calculates indices of species' distinctiveness that rely on the structure and branch lengths of (phylogenetic) trees including index ${}^{\alpha}\Delta_{eq}$ developed in the main text (see also Appendix B) (Trees with polytomies are allowed).

Complete guides through the functions are available in the associated help files and the manual available at <https://CRAN.R-project.org/package=adiv>. A vignette associated with package adiv can be obtained with the following script: `browseVignettes("adiv")`

C.2. Scripts used in the main text

```
install.packages("adephylo") # Jombart et al. (2010)
install.packages("adiv") # Pavoine et al. (2020, 2021)
install.packages("ape")
install.packages("phylobase")

library(adephylo)
library(adiv)
library(ape)
library(phylobase)

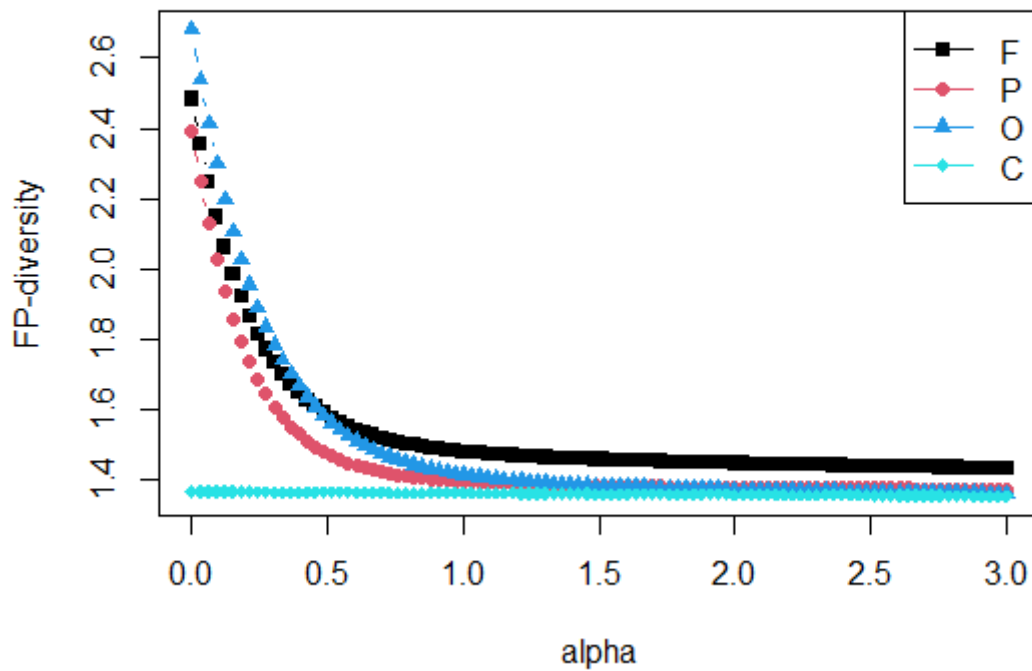
# The dataset available in Appendices D and E has been integrated in
package adiv (see section C.1). The following scripts can be used to
obtain the phylogenetic tree and species abundance:

data(batcomm)
phy <- read.tree(text = batcomm$tre2)
ab <- batcomm$ab2[, phy$tip.label]

# Figure 4 of the main text:

divY <- FPdivparam(comm = ab, disORtree = phy, palpha=seq(0, 3,
length=100), equivalent = TRUE)
plot(divY, col=c(1,2,4, 5), pch=c(15:18))
title("Phylogenetic diversity, Index alphaY")
```

Phylogenetic diversity, Index alphaY



F = rainforest
P = cacao plantation
O = old fields
C = cornfields

```
divI <- FPdivparam(comm = ab, disORtree = phy, method = "KstarI",  
palph=seq(0, 3, length=100) , equivalent = TRUE)  
plot(divI, col=c(1,2,4, 5), pch=c(15:18))  
title("Phylogenetic diversity, Index alphaI")
```

Phylogenetic diversity, Index alpha

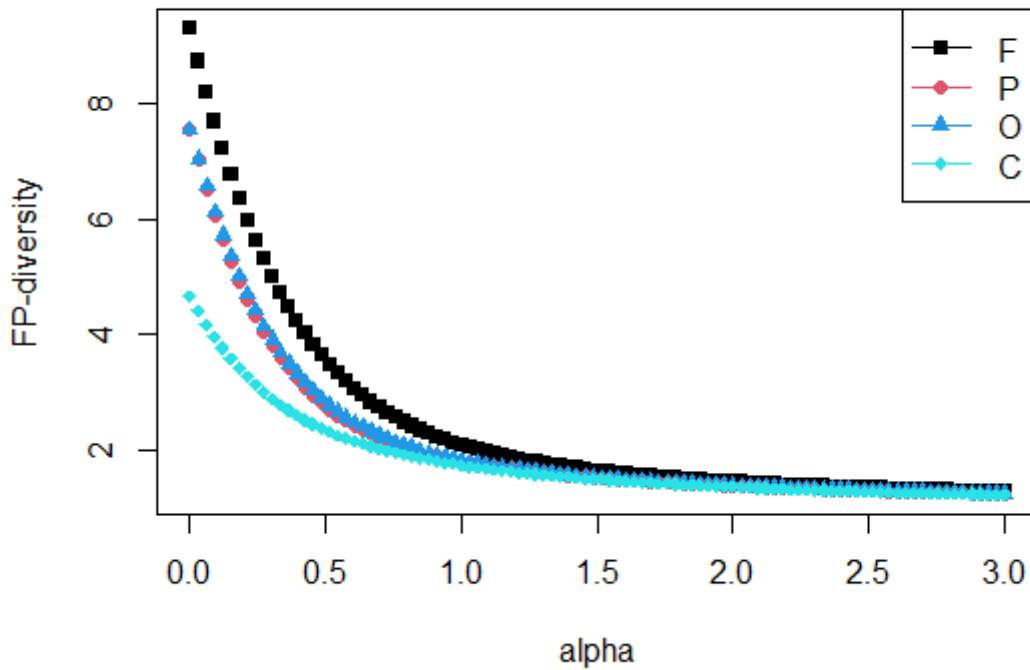


Figure 3 of the main text:

```
U <- distinctTree(phy, method = c("ED", "Delta*"), palpha = c(-3, -
2, -1, 0, 1, 2, 3))
U.4d <- phylo4d(phy, as.matrix(U))
dotp4d(U.4d, center = FALSE, scale = FALSE, trait.labels = c("ED",
"-3Delta*", "-2Delta*", "-1Delta*", "0Delta*", "1Delta*", "2Delta*",
"3Delta*"))
```

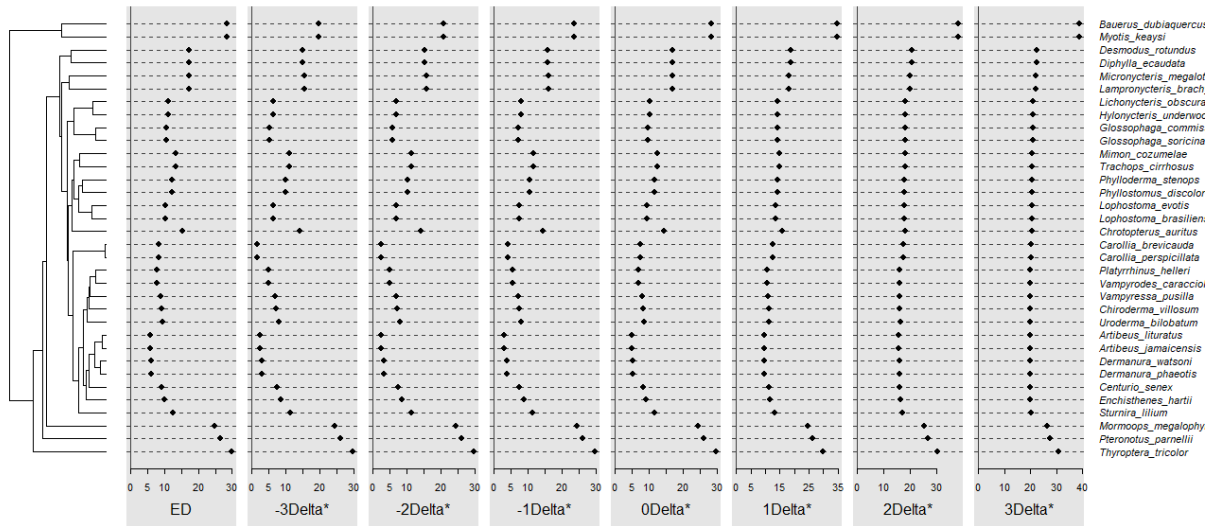
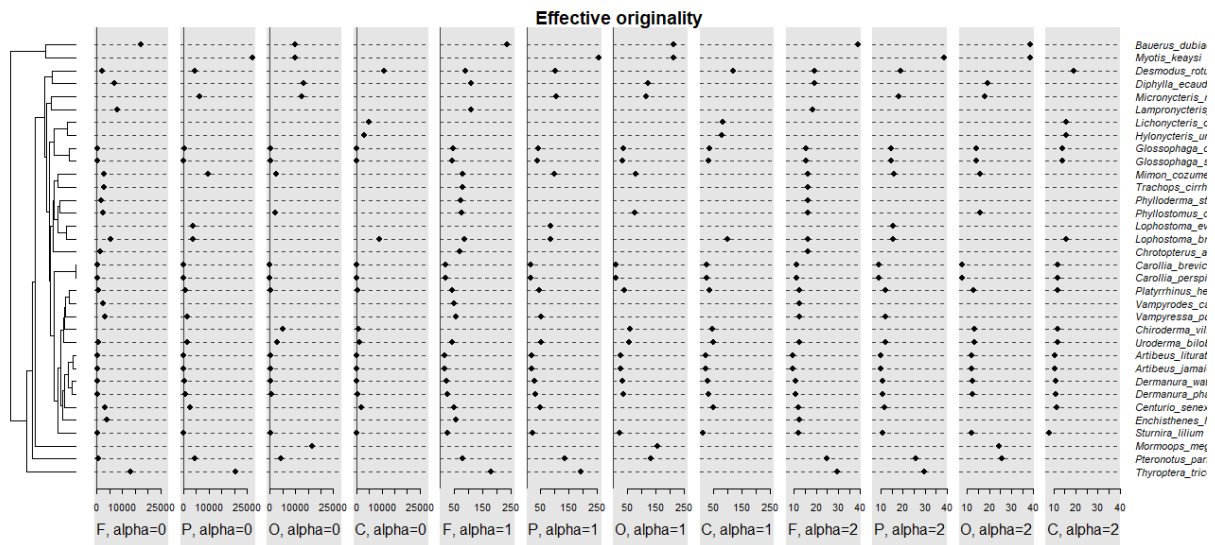


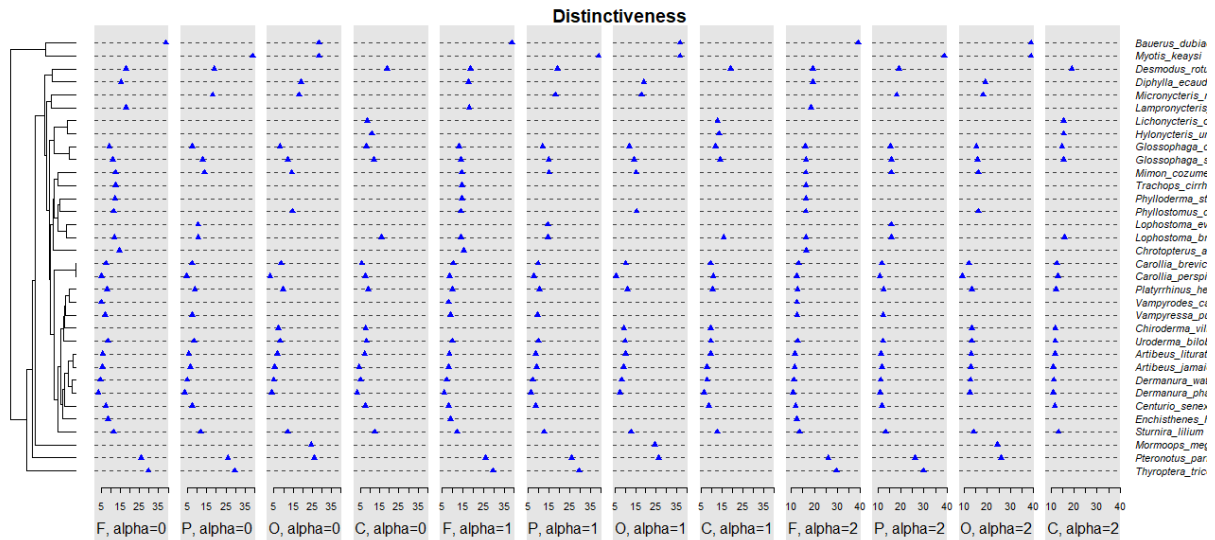
Figure 5 of the main text:

```
REStotalQ <- distinctAb(ab, phy)
REStotalKstar0 <- distinctAb(ab, phy, method="KstarI", palpha=0)
REStotalKstar1 <- distinctAb(ab, phy, method="KstarI", palpha=1)

MATT <- as.matrix(cbind.data.frame(t(REStotalKstar0[[2]]),
t(REStotalKstar1[[2]]), t(REStotalQ[[2]])))
colnames(MATT) <- paste("v", 1:12)
U.4d <- phylo4d(phy,MATT)
dotp4d(U.4d, center = FALSE, scale = FALSE,
  data.xlim = matrix(c(rep(range(MATT[, 1:4], na.rm=TRUE), 4),
  rep(range(MATT[, 5:8], na.rm=TRUE), 4),
  rep(range(MATT[, 9:12], na.rm=TRUE), 4))), 2, 12),
  trait.labels = c("F, alpha=0", "P, alpha=0", "O, alpha=0",
  "C, alpha=0", "F, alpha=1", "P, alpha=1", "O, alpha=1",
  "C, alpha=1", "F, alpha=2", "P, alpha=2", "O, alpha=2",
  "C, alpha=2"))
title("Effective originality")
```



```
MATT2 <- as.matrix(cbind.data.frame(t(REStotalKstar0[[3]]),
t(REStotalKstar1[[3]]), t(REStotalQ[[4]])))
colnames(MATT2) <- paste("v", 1:12)
U.4d2 <- phylo4d(phy,MATT2)
dotp4d(U.4d2, dot.pch = 17, dot.col="blue", dot.cex=1.2,
  center = FALSE, scale = FALSE,
  data.xlim = matrix(c(rep(range(MATT2[, 1:4], na.rm=TRUE), 4),
  rep(range(MATT2[, 5:8], na.rm=TRUE), 4),
  rep(range(MATT2[, 9:12], na.rm=TRUE), 4))), 2, 12),
  trait.labels = c("F, alpha=0", "P, alpha=0", "O, alpha=0",
  "C, alpha=0", "F, alpha=1", "P, alpha=1", "O, alpha=1",
  "C, alpha=1", "F, alpha=2", "P, alpha=2", "O, alpha=2",
  "C, alpha=2"))
title("Distinctiveness")
```



References

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