Appendix 1. R functions to calculate *h*p indexes of species (commonness of species), the *h*h of the community (the proportion of common species) and the list of common species. These are calculated from a typical composition matrix *M* based on abundances, with one row per plot and one column per species.

> hp.function <- function(M) # two-dimensional commonness of species

{

hp <- apply(M /rowSums(M), 2, function(x) max((1:nrow(M)/nrow(M))[sort(x, decreasing=T)>=(1:nrow(M)/nrow(M))]))

hp [which(hp =="-Inf")] <- 0 # assigns *h*p=0 to very uncommon species

names(hp) <- colnames(M) # assigns the name of the species

return(hp)

}

> hh.function <- function(M) # observed proportion of common species, and ordered list of common species

{

hp <- hp.function(M) # calculates *h*p indexes

hh <- max(((1:ncol(M))/ncol(M))[(sort(hp, decreasing=T)/max(hp)) >= ((1:ncol(M))/ncol(M))]) # calculates *h*h index

if(!is.na(hh)) a <- cbind(hp, colSums(M))

if(!is.na(hh)) common <- rownames(a[order(-a[, 1], -a[, 2]), ])[1:(hh\*ncol(M))] # names of common species (ordered by *h*p indexes and total abundances)

if(is.na(hh)) common <- NULL

return(list(hh=hh, common=common)) # output with the *h*h index of the community and the names of the common species

}