# THE 'rarefy.rich' FUNCTION

# The 'rarefy.rich' function using resampling to generate rarefaction curves whereby points along the 'curve' represent estimated species richness for a given sample size and given number of permutations. Confidence intervals and standard deviations for these points are also given. The input matrix consists of a table whereby columns represent samples (plots or time periods) and rows species. The values in each cell represent the number of times a given species was observed in that cell.

# This function is a quick way of generating rarefaction curves for multiple samples at a range of sample sizes.

# bootsize is the 'bootstrap size', that is the number of times a sample is drawn from the complete population of species. A reasonable value for bootsize is between 200 and 1000.

# sampsize is the 'sample size', the number of individuals for which, species richness is calculated. This can include a single number or a vector of numbers, which will produce values to visualise sampling (rarefaction) curves.

# group is a vector, which has the same length as the columns in rawdata and identifies groups of samples

# col is a character vector, which has the same length as the columns in rawdata that can be used to colour code the groups

# the output 'rarefac' is a 'long' table that includes 5 columns, namely, the sample size, sample name, mean, standard deviation, and 95% confidence intervals. These mean, standard deviation and 95% confidence interval values are estimated by the bootstrap procedure. Each row represents the values for the points along the rarefaction curve. The number of points is determined by the sampsize vector.


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# FUNCTION BEGINS HERE

"rarefy.rich" <- function(rawdata, bootsize=NULL, sampsize=NULL, group=NULL, col=NULL){
  if(is.null(bootsize)) {bootsize=1000}
  if(is.null(sampsize)) {sampsize=10}
  if(is.null(group)) {group="NA"
  if(is.null(col)) {col="black"}
  rarefac = array(NA, dim=c(3, ncol(rawdata), length(sampsize)),
    dimnames = list(c("Mean","SD","CI"), colnames(rawdata),NULL))

  # internal function to calculate rarefied species richness and other indices
  rarefirst<- function (rawdata.in, bootsize.in, sampsize.in) {
    apply(rawdata,2, function(x) {
      }
ci_norm <- function(x) { se <- sqrt(var(x) / length(x))
    tvalue <- qt(.975, length(x))
    tvalue * se}

# creating the 'unfolded' vector representing the number of occurrences of each 'species'
reareout = matrix(NA, 3, ncol(rawdata))

nrunique = rep(NA, bootsize.in)
unfolded = rep(NA, sum(x))

p = 1

for (i in 1:length(x)) {
    if (x[i] > 0) {
        nrindiv = x[i]
        unfolded[p:(p + nrindiv - 1)] = rep(i, nrindiv)
        p = p + nrindiv
    }
}

nrunfold = length(unfolded)
sampsize.in = min(nrunfold, sampsize.in)

# the actual sampling out of the unfolded vector, and repeating this 'bootsize' times
for (j in 1:bootsize.in) {
    nrunique[j] = length(unique(sample(1:nrunfold, sampsize.in)))
}

rareout[] <- rbind(mean(nrunique), sd(nrunique), ci_norm(nrunique))

rarefold = length(unfolded)
sampsize.in = min(rarefold, sampsize.in)

# Repeating the index calculation for all values of 'sampsize'
for (k in 1:length(sampsize)) {
    rarefac[, k] <- rarefirst(rawdata, bootsize, sampsize[k])
}

rarefac.sd <- rarefac[2, ,]
rarefac.ci <- rarefac[3, ,]
rarefac.mean <- rarefac[1, ,]
rarefac.mean.fin <- as.vector(ifelse(rarefac.sd == 0, NA, rarefac.mean))
rarefac.sd.fin <- as.vector(ifelse(rarefac.sd == 0, NA, rarefac.sd))
rarefac.ci.fin<-as.vector(ifelse(rarefac.sd==0,NA,rarefac.ci))

groups<-rep(group,length(sampsize))
cols<-rep(col,length(sampsize))
sites<-rep(colnames(rawdata),length(sampsize))
sample.size<-rep(sampsize,each=length(colnames(rawdata)))

rarefac<-data.frame(groups,sites,cols,sample.size,rarefac.mean.fin, rarefac.sd.fin,rarefac.ci.fin)
colnames(rarefac)<-c("Groups","Sample","Colours","Sample_size","Mean","SD","CI")

return(rarefac)
}

# FUNCTION ENDS HERE

# TEST FUNCTION BEGINS HERE

# In order to test the function we'll use the 'output.clust.matrix' object created previously with the 'Matrix.clust' function. Be careful to have modified the colnames as indicated.

# CREATE VECTORS OF GROUP NAMES AND COLOUR CODES FOR EACH GROUP

Col.rar<-c("Green","Green","Green","Green","Blue","Blue","Blue","Blue","Red","Red","Red","Brown","Brown","Brown","Brown")

# EXECUTE FUNCTION

output.rarefaction.results<-rarefy.rich(output.clust.matrix,bootsize=999, sampsize=seq(from=100,to=2000,by=100),group=Group.rar,col=Col.rar)

# PRODUCE FIGURE SHOWING RAREFACTION CRUVES

library(plotrix)

plotCI(output.rarefaction.results$Sample_size,output.rarefaction.results$Mean, pch=21, pt.bg=(as.character(output.rarefaction.results$Colours)),xlab= "size",ylab="Rarefied richness", ui=output.rarefaction.results$Mean + output.rarefaction.results$SD,li= output.rarefaction.results$Mean - output.rarefaction.results$SD) legend(1800,110,legend=unique(output.rarefaction.results$Groups),pch=21, pt.bg=unique(as.character(output.rarefaction.results$Colours)), bty="n")