Appendix 2.

Custom R scripts:

Loading packages and calling the data

```
library(vegan)

library(ggplot2)

setwd(choose.dir())

data<-read.table("sucessao_ABUND.txt", header=T) ### data containing abundances of the 10 most abundant ethnospecies in each plot

species<-data [, 3:49] ### removing the columns “Area” and “Environment”

data2<-read.table("sucessão_final_tudo3.txt", header=T) ### data containing abundances of all 230 ethnospecies

species2<-data2[, 3:232] ### removing the columns “Area” and “Environment”
```

Gradient of relative abundance of ethnospecies ordered by the one-dimensional NMDS (Figure 3)

```
### 1 – Generic function that sorts data###

generic<-function(tabel,gradient,at,grad,axisY,axisX){

tabel<-as.matrix(tabel)

gradient<-as.matrix(gradient)

weighted.average <-colSums(tabel*gradient[,1])/colSums(tabel)

sub.orden<-tabel[order(gradient[,1],decreasing=F),]          # sort plots according to the gradient

sub.orde<-sub.orden[,order(weighted.average,decreasing=T)] # put species sorted by the weighted average

data.pa<-matrix(0,nrow(tabel),ncol(tabel))

data.pa[tabel>0]<-1

ordered<-sub.orde[,which(colSums(data.pa)>0)] ## to delete possible empty columns (species that did not occur)

par(mfrow=c(ncol(ordenado)+1,1),mar=c(0,4,0.2,10),oma=c(3,1,1,6))

layout(matrix(1:(ncol(ordered)+1)),heights=c(3,rep(1,ncol(ordered))))

plot(sort(gradient[,1]),axes=F,ylab="",mfg=c(21,1),lwd=10,las=2,lend="butt",frame.plot=F,xaxt="n",type="h",col="black",ylim=c(min(gradient),max(gradient)))
```

```
axis(side=2,at=c(0,max(gradient)),las=2)
mtext(grad,4,outer=T,font=2,line=-10,padj=-18.5,las=2)
for(i in 1:ncol(ordered)){
barplot(ordered[,i],bty="l",axisnames=F,axes=FALSE,col="black")
#axis(side=2,at=max(ordered[,i]),las=2)
mtext(colnames(ordered)[i],3,line=-1.0,adj=0,at=at,cex=.8,font=3)
}
mtext(axisX,1,outer=T,font=2,line=1.2)
mtext(axisY,2,font=2,outer=T,line=-2)
}

### 2 – NMDS ###
parc1<-decostand(species,"total",MARGIN=1) ### standardization method for ordering rows (ethnospecies abundances)
resu<-metaMDS(parc1,distance = "bray", k=1,trymax=100,autotransform=F)
scor.nmds<-resu$points
summary(lm(vegdist(parc1)~vegdist(scor.nmds,"euclid")))
plot(scor.nmds, type="n", main="NMDS with Vegan") ### NMDS plot
text(scor.nmds)
generic(parc1,scor.nmds, 9.75, "") ### ordering plots by ethnospecies abundances
```

Dendrogram of the hierarchical clustering analysis to compare floristic composition (Figure 4)

```
cluster<-vegdist(species2, method="jaccard", binary=T)
phylogeny<-hclust(cluster, method="average")
plot(phylogeny, hang=-1)
matrix_cof<-cophenetic(phylogeny)
cor(matrix_cof, dist.jac) ### Cophenetic correlation coefficient
```

Comparison among plots in terms of ethnospecies richness (Figure 5)

```
### 1 – Rarefaction curves ###
```

```
rarecurve(species2, lty=1, xlab = "Number of stems", ylab="Expected richness",
      xlim=c(0,280), ylim=c(0,85), col=c("red", "black")[Environment], label=F)


### Expected richness with 95% confidence intervals ###

min(rowSums(species2)) ### minimum value of abundance showed in the rarefaction curves (value = 135)

Srar<-rarefy(species2, 135, se=T) ### average values of expected richness for each plot (standardized by the minimum value) and their standard errors

rarefaction <-read.table("Rarefação_Confiança.txt", header=T) ### data containing the average values of expected richness for each plot and their 95% confidence intervals (1.96 * standard error)

ggplot(rarefaction, aes(x=Group, y=Average, group=1)) +
    geom_errorbar(aes(ymin= Average-IC, ymax= Average+IC), width=.1) +
    geom_point() +
    theme_bw() +
    theme(panel.border = element_blank(), panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(), axis.line = element_line(colour = "black")) +
    scale_x_discrete(limits=c("1","2","3","4","5","6","7","8")) +
    scale_y_continuous(breaks=seq(0, 70, 5)) +
    labs(x="Forest age", y="Expected richness")
```

Diversity profiles using Hill's series (Figure 6)

Naret, Kuruwaty, Missão, Bikut, Dipisow, MataKoporuhu, MataKuruwaty and MataDipisowNaret are the names of the sampled forest areas

```
Naret<-data2[1, 3:232]

Kuruwaty<- data2 [2, 3:232]

Missão<- data2 [3, 3:232]

Bikut<- data2 [4, 3:232]

Dipisow<- data2[5, 3:232]

MataKoporuhu<- data2[6, 3:232]

MataKuruwaty<- data2[7, 3:232]
```

```
MataDipisowNaret<- data2[8, 3:232]


nine<-renyi(Naret, hill=T)
seventeen<-renyi(Kuruwaty, hill=T)
twentyeight<-renyi(Missão, hill=T)
seventy <-renyi(Bikut, hill=T)
onehundredforty <-renyi(Dipisow, hill=T)
oldforest1<-renyi(MataKoporuhu, hill=T)
oldforest2<-renyi(MataKuruwaty, hill=T)
oldforest3<-renyi(MataDipisowNaret, hill=T)


plot.default(nine, type="l", lty=2, xlab="Alpha", ylab="Hill number", ylim=c(0,90))
points(nine, pch=16)
points(seventeen, type="l", lty=2)
points(seventeen, pch=16)
points(twentyeight, type="l", lty=2)
points(twentyeight, pch=16)
points(seventy, type="l", lty=2)
points(seventy, pch=16)
points(onehundredforty, type="l", lty=2)
points(onehundredforty, pch=16)
points(oldforest1, type="l", lty=2, col="red")
points(oldforest1, col="red", pch=16)
points(oldforest2, type="l", lty=2, col="red")
points(oldforest2, col="red", pch=16)
points(oldforest3, type="l", lty=2, col="red")
points(oldforest3, col="red", pch=16)
```