# To read the data

wlr<-read.xlsx("WL\_U1356.xlsx",1,header=TRUE,as.data.frame=T)

wlsub<-wlr[,-(1:11)]##### only mid-depth for row.names

wlsub<-data.frame(wlsub,row.names=1)

wilkesna<-replace(wlsub,is.na(wlsub),0)#### 0 when there is no data

wlsub2<-wilkesna[,1:156]#### selection of taxa (no re-worked)

# Species accumulation curves

wlme<-wlsub2[(1:28),]#### subset of the mid-Eocene samples

wlee<- wlsub2[(29:145),]####### subset of the early Eocene samples

wlmerar<-specaccum(wlme,"exact", gamma="chao")

wleerar<-specaccum(wlee, "exact", gamma="chao")

plot(wleerar, ci.type="bar", ci.col="light gray")

plot(wlmerar, add=TRUE, ci.type="bar", ci.col="light gray")

# Rarefaction and diversity indices

wlt<-t(wlsub2)

wlsubsetb<-subset(wlt,select=which(apply(wlt,2,sum)>=100)) ####### subset samples >100 individuals

wtt<-t(wlsubsetb)

wl100<-rarefy(wtt,99,se=TRUE)##### rarefaction analysis

wl100

H<-diversity(wtt)##### Shannon index

H

J<-H/log(specnumber(wtt))###### Evenness

J

# Detrended Correspondence Analyses

wlsum<-apply(wtt,1,sum)###### relative abundances (%)

wlperc<-sweep(wtt,1,FUN="/",wlsum)\*100### relative abundances (%)

essaydca<-as.matrix(wlperc)

dca<-decorana(essaydca)

summary(dca)

sitescores<-scores(dca,display=c("sites"),choices=1)##### to extract sample scores Axis 1

sitescores2<-scores(dca,display=c("sites"))##### to extract sample scores

write.csv(sitescores2,file="sitesdca.csv")

# t-test

rarefy100ee<-wl100[1,1:13]##### subset mid-Eocene samples

rarefy100me<-wl100[1, 14:60]##### subset early Eocene samples

t.test(rarefy100ee,rarefy100me)#### t-test rarefaction values

Hee<-H[1:13]

Hme<-H[14:60]

t.test(Hee,Hme)###### t-test Shannon index

Jee<-J[1:13]

Jme<-J[14:60]

t.test(Jee,Jme)##### t-test Evenness

dcame<-sitescores[1:13]

dcaee<-sitescores[14:60

t.test(dcaee,dcame)##### t-test for DCA values