#R script for estimating species richness and sampling completeness ratio

data <- read.csv("final.csv",row.names=1)

library(SpadeR)

#using Chao2 estimation (we cannot use abundance)

#we use frequency (absence and presence following suggestion from Prosser & Hebert 2017)

ChaoSpecies(data,datatype="incidence\_raw",conf=0.95)

#rarefaction and extrapolation analyses

library(iNEXT)

library (ggplot2)

library(gridExtra)

ChaoRichness(data, datatype = "incidence\_raw", conf = 0.95)

out<-iNEXT(data,q=0,"incidence\_raw",se=TRUE,endpoint=52,conf=0.95, nboot=100)

#plot sample-size-based curve

p1<-ggiNEXT(out, type=1,se=T)+ xlab("Number of\nSampling Weeks")+ylab("Number of Plant Species")+scale\_colour\_manual(values=c("black"))+scale\_fill\_manual(values=c("gray25"))+ theme(panel.background = element\_rect(fill = 'white', colour="gray19"),panel.grid.major = element\_line(colour = "gray89"))

p11<-p1+ theme(plot.margin = unit(c(1,0.2,-1.1,1), "cm"))

#plot sample completeness curve

p2<-ggiNEXT(out, type=2, se=T)+ xlab("Number of\nSampling Weeks")+ylab("Sampling\nCompleteness Ratio")+scale\_colour\_manual(values=c("black"))+scale\_fill\_manual(values=c("gray25"))+ theme(panel.background = element\_rect(fill = 'white', colour="gray19"),panel.grid.major = element\_line(colour = "gray89"))

p22<-p2+ theme(plot.margin = unit(c(1,0.2,-1.1,0), "cm"))

grid.arrange(p11,p22,ncol=2,nrow=1)