##Soil contamination in nearby natural areas mirrors that in urban greenspaces worldwide ##

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####1. Gmulti model assessing the relative importance of predictors on HM, PEST, MPs, and ARGs in Figure 2B####

##install and library packages##

install.packages("rJava")

install.packages(“rfPermute”)

install.packages("glmulti")

library(rJava)

library(rfPermute)

library(glmulti)

##difine the function##

cor.sig = function(test) {

res.cor = cor(test)

res.sig = res.cor

res.sig[abs(res.sig) > 0] = NA

nx = dim(test)[2]

for (i in 1:nx) {

for (j in 1:nx) {

res.cor1 = as.numeric(cor.test(test[, i], test[, j])$est)

res.sig1 = as.numeric(cor.test(test[, i], test[, j])$p.value)

if (res.sig1 <= 0.001) {

sig.mark = "\*\*\*"

}

if (res.sig1 <= 0.01 & res.sig1 > 0.001) {

sig.mark = "\*\* "

}

if (res.sig1 <= 0.05 & res.sig1 > 0.01) {

sig.mark = "\* "

}

if (res.sig1 > 0.05) {

sig.mark = " "

}

if (res.cor1 > 0) {

res.sig[i, j] = paste(" ", as.character(round(res.cor1, 3)),

sig.mark, sep = "")

} else {

res.sig[i, j] = paste(as.character(round(res.cor1, 3)), sig.mark,

sep = "")

}

}

}

as.data.frame(res.sig)

}

##HM##

train<-read.csv("HM.csv",row.names=1)

head(train)

str(train)

cor.sig(train[, 1:19])

global.model <- lm(Heavy\_metals~HDI+GDP+Population+Population\_density+Irrigated+Fertilized+Mowed+Urban+MAT+MAP+Plant+TN+TP+SOC+pH, data = train)

Priori.model <- glmulti(global.model, level = 1, crit = "aicc")

summary(Priori.model)

plot(Priori.model,type="s")

##PEST##

train<-read.csv("PEST.csv",row.names=1)

head(train)

str(train)

cor.sig(train[, 1:18])

global.model <- lm(Pesticides~HDI+GDP+Population+Population\_density+Irrigated+Fertilized+Mowed+Urban+MAT+MAP+Plant+TN+TP+SOC+pH, data = train)

Priori.model <- glmulti(global.model, level = 1, crit = "aicc")

summary(Priori.model)

plot(Priori.model,type="s")

##MPs##

train<-read.csv("MP.csv",row.names=1)

head(train)

str(train)

cor.sig(train[, 1:18])

global.model <- lm(MPs~HDI+GDP+Population+Population\_density+Irrigated+Fertilized+Mowed+Urban+MAT+MAP+Plant+TN+TP+SOC+pH, data = train)

Priori.model <- glmulti(global.model, level = 1, crit = "aicc")

summary(Priori.model)

plot(Priori.model,type="s")

##ARGs##

train<-read.csv("ARG.csv",row.names=1)

head(train)

str(train)

cor.sig(train[, 1:21])

global.model <- lm(ARGs~HDI+GDP+Population+Population\_density+Irrigated+Fertilized+Mowed+Urban+MAT+MAP+Plant+TN+TP+SOC+pH, data = train)

Priori.model <- glmulti(global.model, level = 1, crit = "aicc")

summary(Priori.model)

plot(Priori.model,type="s")

####2. Nested PERMANOVA testing the differences of HM, PEST, MPs, and ARGs between urban greenspaces and natural areas in Figure S3, S10, and S11####

##load dataset##

data1<-read.csv("dataset1.csv",header=T,sep=",")

data2<-data1[,c(1:3,14:18)];data2<-na.omit(data2)

data3<-data1[,c(1:3,19:23)];data3<-na.omit(data3)

data4<-data1[,c(1:3,29:31)];data4<-na.omit(data4)

data5<-data1[,c(1:3,37)];data5<-na.omit(data5)

## Nested PERMANOVA test##

adonis(Multicontamination~LaNdUse4A,permutations = 999, method = "euclidean",strata=data1$Paired\_ID\_v4,data1)

adonis(Heavy\_metal~LaNdUse4A,permutations = 999, method = "euclidean",strata=data1$Paired\_ID\_v4,data1)

adonis(As~LaNdUse4A,permutations = 999, method = "euclidean",strata=data1$Paired\_ID\_v4,data1)

adonis(Cd~LaNdUse4A,permutations = 999, method = "euclidean",strata=data1$Paired\_ID\_v4,data1)

adonis(Pb~LaNdUse4A,permutations = 999, method = "euclidean",strata=data1$Paired\_ID\_v4,data1)

adonis(Cr~LaNdUse4A,permutations = 999, method = "euclidean",strata=data1$Paired\_ID\_v4,data1)

adonis(Cu~LaNdUse4A,permutations = 999, method = "euclidean",strata=data1$Paired\_ID\_v4,data1)

adonis(Ni~LaNdUse4A,permutations = 999, method = "euclidean",strata=data1$Paired\_ID\_v4,data1)

adonis(Zn~LaNdUse4A,permutations = 999, method = "euclidean",strata=data1$Paired\_ID\_v4,data1)

adonis(Hg~LaNdUse4A,permutations = 999, method = "euclidean",strata=data1$Paired\_ID\_v4,data1)

adonis(Pesticides~LaNdUse4A,permutations = 999, method = "euclidean",strata=data2$Paired\_ID\_v4,data2)

adonis(Atrazine\_and\_transformation\_products~LaNdUse4A,permutations = 999, method = "euclidean",strata=data2$Paired\_ID\_v4,data2)

adonis(Fungicide~LaNdUse4A,permutations = 999, method = "euclidean",strata=data2$Paired\_ID\_v4,data2)

adonis(Herbicide~LaNdUse4A,permutations = 999, method = "euclidean",strata=data2$Paired\_ID\_v4,data2)

adonis(Insecticide~LaNdUse4A,permutations = 999, method = "euclidean",strata=data2$Paired\_ID\_v4,data2)

adonis(MPs~LaNdUse4A,permutations = 999, method = "euclidean",strata=data3$Paired\_ID\_v4,data3)

adonis(Fragments~LaNdUse4A,permutations = 999, method = "euclidean",strata=data3$Paired\_ID\_v4,data3)

adonis(Films~LaNdUse4A,permutations = 999, method = "euclidean",strata=data3$Paired\_ID\_v4,data3)

adonis(PP~LaNdUse4A,permutations = 999, method = "euclidean",strata=data3$Paired\_ID\_v4,data3)

adonis(Poliester~LaNdUse4A,permutations = 999, method = "euclidean",strata=data3$Paired\_ID\_v4,data3)

adonis(ARG\_abundance~LaNdUse4A,permutations = 999, method = "euclidean",strata=data1$Paired\_ID\_v4,data1)

adonis(Multidrug\_abundance~LaNdUse4A,permutations = 999, method = "euclidean",strata=data1$Paired\_ID\_v4,data1)

adonis(MLSB\_abundance~LaNdUse4A,permutations = 999, method = "euclidean",strata=data1$Paired\_ID\_v4,data1)

adonis(Tetracycline\_abundance~LaNdUse4A,permutations = 999, method = "euclidean",strata=data1$Paired\_ID\_v4,data1)

adonis(Vancomycin\_abundance~LaNdUse4A,permutations = 999, method = "euclidean",strata=data1$Paired\_ID\_v4,data1)

adonis(HDPE~LaNdUse4A,permutations = 999, method = "euclidean",strata=data4$Paired\_ID\_v4,data4)

adonis(LDPE~LaNdUse4A,permutations = 999, method = "euclidean",strata=data4$Paired\_ID\_v4,data4)

adonis(Fibers~LaNdUse4A,permutations = 999, method = "euclidean",strata=data4$Paired\_ID\_v4,data4)

adonis(Richness\_of\_ARGs~LaNdUse4A,permutations = 999, method = "euclidean",strata=data1$Paired\_ID\_v4,data1)

adonis(Aminoglycoside\_abundance~LaNdUse4A,permutations = 999, method = "euclidean",strata=data1$Paired\_ID\_v4,data1)

adonis(Beta\_Lactamase\_abundance~LaNdUse4A,permutations = 999, method = "euclidean",strata=data1$Paired\_ID\_v4,data1)

adonis(Sulfonamide\_abundance~LaNdUse4A,permutations = 999, method = "euclidean",strata=data1$Paired\_ID\_v4,data1)

adonis(Others\_abundance~LaNdUse4A,permutations = 999, method = "euclidean",strata=data1$Paired\_ID\_v4,data1)

adonis(Multicontamination2~LaNdUse4A,permutations = 999, method = "euclidean",strata=data5$Paired\_ID\_v4,data5)

####3. Random sampling testing the differences of HM, PEST, MPs, and ARGs between urban greenspaces and Antarctica in Figure S8####

##load dataset##

data<-read.csv("dataset.csv",header=T,sep=",")

##random sampling test##

results1=NA

for (i in 1:100){

x <- sample(data$Cr[data$LaNdUse4A=="Urban"],size = 3,replace = T)

y <- sample(data$Cr[data$LaNdUse4A=="Antarctica"],size = 3,replace = T)

diference1=mean(x)-mean(y)

results1[i]=diference1

}

hist(results1) #These are the obtained results (bootstrapped differences urban - antarctica)

fg1=ecdf(results1) #create cumulative distribution function

fg1(0) #the probability of this difference being 0 is this (this is your p-Val)