# Two-way ANOVA

setwd('C:\\Users\\ygh\\Desktop')

data=read.csv('sysfc.csv')

str(data)

data$year=as.factor(data$year)

data$treatment=as.factor(data$treatment)

data$S=as.numeric(data$S)

str(data)

table(data$year, data$treatment)

aovS=aov(S~treatment+year+treatment\*year, data=data)

aovH=aov(H~treatment+year+treatment\*year,data=data)

summary(aovH)

aovJ=aov(J~treatment+year+treatment\*year,data=data)

summary(aovJ)

# One-way ANOVA

da=read.csv('S-YEAR.csv')

da$YEAR=as.factor(da$YEAR)

da$Treatment=as.factor(da$Treatment)

bartlett.test(da$S~da$YEAR)

aov1=aov(da$S~da$YEAR)

summary(aov1)

library(agricolae)

MC <- LSD.test(aov(S~YEAR, data= da), 'YEAR', p.adj = 'bonferroni')$groups

MC

#Diversity index

library('vegan')

library(reshape2)

mydata <- read.csv('seeding.csv')

mydata <- read.csv('1.csv')

S <- specnumber(herb.mat)

plot(S)

#HP

install.packages("hier.part")

library(hier.part)

data<-read.csv("CB.csv")

env<-data[,6:12];env

hier.part(data$S,env,fam="gaussian",gof="Rsqu")

#Cor

library(tidyverse)

library(corrplot)

setwd("C:\\Users\\ygh\\Desktop\\D-20230709")

mydata1<-read.csv('cor.csv',header = T,sep =",")

library(Hmisc)

cor\_new<-cor(mydata1)

res2 <- rcorr(as.matrix(mydata1))

res2

write.csv(res2, 'C:\\Users\\ygh\\Desktop\\P.csv')

# linear mixed model, LME

library(nlme)

setwd('C:\\Users\\yg\\Desktop')

a=read.csv('yg.csv')

m=lme(S~YEAR+TREAT, random = ~ 1|plot,data = a)

summary(m)