library(nlme)

library(lme4)

library(Matrix)

library(piecewiseSEM)

library(QuantPsyc)

library(boot)

library(dplyr)

d1<-read.csv("SOCD.csv", header = T, row.names = 1)

model1<-lm(SOCD~NDVI+diversity+richness, d1)

d1

coefs(model1, standardize = 'scale')

beta\_NDVI<- summary(model1)$coefficients[2, 1]

beta\_diversity<- summary(model1)$coefficients[3, 1]

beta\_richness<- summary(model1)$coefficients[4, 1]

plant community<-beta\_NDVI \* d1$NDVI+beta\_diversity \* d1$diversity+beta\_richness \* d1$richness

d1$plant community<-plant community

summary(lm(SOCD ~ plant community, d1))

coefs(lm(SOCD~ plant community, d1))

model2<-lm(SOCD~MAT, d1)

d1

coefs(model2, standardize = 'scale')

beta\_MAT<- summary(model1)$coefficients[2, 1]

climate<- MAT \* d1$MAT

d1$climate<-climate

summary(lm(SOCD ~ climate, d1))

coefs(lm(SOCD~ climate, d1))

model3<-lm(SOCD~BD+N, d1)

d1

coefs(model3, standardize = 'scale')

beta\_BD<- summary(model3)$coefficients[2, 1]

beta\_N<- summary(model3)$coefficients[3, 1]

soil<- beta\_BD \* d1$BD+beta\_N \* d1$N

d1$soil<-soil

summary(lm(SOCD ~ soil, d1))

coefs(lm(SOCD~ soil, d1))

microbe.list <- list(

lme(plant community ~ elevation, random = ~ 1| site, na.action = na.omit,

data = d1),

lme(climate ~ elevation, random = ~ 1| site, na.action = na.omit,

data = d1),

lme(soil ~ elevation, random = ~ 1| site, na.action = na.omit,

data = d1),

lme(SOCD ~ elevation, random = ~ 1| site, na.action = na.omit,

data = d1),

lme(SOCD ~ plant community+climate+soil, random = ~ 1| site, na.action = na.omit,

data = d1),

microbe.psem <- as.psem(microbe.list)

(new.summary <- summary(microbe.psem, .progressBar = F))

plot(microbe.psem)

coefs(microbe.psem)