rm(list=ls(all=TRUE))

#install.packages("metafor",dep=TRUE)

library(metafor)

SeHENH<-read.table("C:/Frontiers/R1/Drafts/Data\_file\_S7.txt",header=TRUE,dec=",")

SeHENH2 <- escalc("SMD",m1i=Hedgerow.Value,sd1i=Hedgerow.SD+0.1,n1i=nHedgerow,

m2i=Natural.habitat.Value,sd2i=Natural.habitat.SD+0.1,n2i=nControl,data=SeHENH)

SeHENH2$yi<-SeHENH2$yi\*SeHENH2$New.sign

#Vote counting

nrow(SeHENH2[SeHENH2$yi<0,]) # Natural habitat better than Hedgerow

nrow(SeHENH2[SeHENH2$yi>0,]) # Hedgerow better than natural habitat

nrow(SeHENH[SeHENH2$yi==0,]) # Hedgerow similar as natural habitat

##Null model

rem <- rma.mv(yi, vi, random = ~ 1 | Identifier, data=SeHENH2)

rem # The difference is significant(p < 0.01) and negative(-0.4450 +- 0.1280). Natural habitats are better!

sav <- confint(rem)

W <- diag(1/SeHENH2$vi)

X <- model.matrix(rem)

P <- W - W %\*% X %\*% solve(t(X) %\*% W %\*% X) %\*% t(X) %\*% W

100 \* sum(rem$sigma2) / (sum(rem$sigma2) + (rem$k-rem$p)/sum(diag(P))) # % heterogeneidad

100 \* sav$random[1,2:3] / (sav$random[1,2:3] + (rem$k-rem$p)/sum(diag(P))) # Confident interval of %

##Total I^2 is moderate to high 22.76 - 81.39 % #### This justifies the inclusion of moderators

#Next lines select for relevant variables

datm <- SeHENH2[,c(1,2,9,10,11,12,13,14,15)]

#and delete rows with any NAs

datm <- datm[complete.cases(datm),]

rma.mv.Overall<-rma.mv(yi,vi,mods=~Response+Climate.type+Spatial.Scale.Focus,

random=~1|Identifier,data=datm)

summary(rma.mv.Overall)

rma.mv.Response<-rma.mv(yi,vi,mods=~0+Response,random=~1|Identifier,data=SeHENH2)

summary(rma.mv.Response)

anova(rma.mv.Response, L=c(1,-1,0))#(QM = 0.07, p = 0.78; non-significant, Nitrogen cycling vs pest regulation).

anova(rma.mv.Response, L=c(1,0,-1))#(QM = 0.03, p = 0.85; non-significant, Nitrogen cycling vs soil formation).

anova(rma.mv.Response, L=c(0,1,-1))#(QM = 0.20, p = 0.65; non-significant, Pest regulation vs soil formation).

rma.mv.Climate.type<-rma.mv(yi,vi,mods=~0+Climate.type,random=~1|Identifier,data=SeHENH2)

summary(rma.mv.Climate.type)

anova(rma.mv.Climate.type, L=c(1,-1)) #(QM = 23.37, p < 0.01 ; significant)

rma.mv.Focus.of.spatial.scale<-rma.mv(yi,vi,mods=~0+Spatial.Scale.Focus,random=~1|Identifier,data=SeHENH2)

summary(rma.mv.Focus.of.spatial.scale)

anova(rma.mv.Focus.of.spatial.scale, L=c(1,-1)) #(QM = 2.92, p = 0.08; non-significant)

datg1 <- as.data.frame(matrix(,nrow=3,ncol=6)) # This line creates an empty dataset

datg1[3,1] <- "cPests"

datg1[3,2] <- length(SeHENH2$Response[SeHENH2$Response=="Pests"])

datg1[3,3] <- as.numeric(rma.mv.Response$beta[3])

datg1[3,4] <- as.numeric(rma.mv.Response$se[3])

datg1[3,5] <- as.numeric(rma.mv.Response$ci.lb[3])

datg1[3,6] <- as.numeric(rma.mv.Response$ci.ub[3])

datg1[2,1] <- "dNitrogen"

datg1[2,2] <- length(SeHENH2$Response[SeHENH2$Response=="Nitrogen"])

datg1[2,3] <- as.numeric(rma.mv.Response$beta[2])

datg1[2,4] <- as.numeric(rma.mv.Response$se[2])

datg1[2,5] <- as.numeric(rma.mv.Response$ci.lb[2])

datg1[2,6] <- as.numeric(rma.mv.Response$ci.ub[2])

datg1[1,1] <- "eSoilF"

datg1[1,2] <- length(SeHENH2$Response[SeHENH2$Response=="Nitrogen"])

datg1[1,3] <- as.numeric(rma.mv.Response$beta[1])

datg1[1,4] <- as.numeric(rma.mv.Response$se[1])

datg1[1,5] <- as.numeric(rma.mv.Response$ci.lb[1])

datg1[1,6] <- as.numeric(rma.mv.Response$ci.ub[1])

colnames(datg1) <- c("var","n","estimate","se","cil","ciu")

datg1$var <- as.factor(datg1$var)

library(ggplot2)

library(ggstance)

plot <- ggplot(data=datg1, aes(y=var, x=estimate, xmin=datg1$cil,xmax=datg1$ciu))

mains <- plot + geom\_point(size = 2.5,fatten=2,position=position\_dodgev(height=0.60))+

geom\_errorbarh(aes(xmin=datg1$cil,

xmax=datg1$ciu),

size=1.1,position=position\_dodgev(height=0.60)) +

geom\_vline(aes(xintercept=0),linetype="dashed",colour="red")+

geom\_hline(aes(yintercept=1.5),colour="grey80")+

xlab(label = "Effect size") + #Cambiar con cada predictor

ylab(label = "") +

scale\_y\_discrete(labels=c("eSoilF"="Soil formation","dNitrogen"="Nitrogen cycling",

"cPests"="Pest regulation"))+

scale\_x\_continuous(limits=c(-2.5,2.5),breaks=c(-2,-1,0,1,2))+

geom\_text(x=-2.4,y=3,label = datg1[1,2],size=4)+

geom\_text(x=-2.4,y=2,label = datg1[2,2],size=4)+

geom\_text(x=-2.4,y=1,label = datg1[3,2],size=4)+

theme\_bw()+

theme(legend.position="none")+

theme(panel.grid.major.y = element\_blank(), panel.grid.minor.y = element\_blank(),

panel.grid.major.x = element\_blank(), panel.grid.minor.x = element\_blank())+

theme(axis.text=element\_text(size=14),axis.title=element\_text(size=16,face="bold"))

mains

ggsave(filename="C:/Frontiers/R1/FigureS3.jpg",dpi = 1200, plot=mains, width = 150, height = 150, units = "mm")