##Unfortunately text files (.txt) are not supporting as a Data sheet by Frontiers submission system##########

######First of all, please transform Data\_file\_S2.xlsx into Data\_file\_S2.txt separated by tabulator##########

rm(list=ls(all=TRUE))

library(metafor)

BioHENH<-read.table("C:/Frontiers/Data\_file\_S3.txt",header=TRUE,dec=",")

BioHENH2 <- 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=BioHENH)

BioHENH2$New.Taxa<-factor(BioHENH2$New.Taxa,levels=c("Plants","Invertebrates","Vertebrates"))

BioHENH2$yi<-BioHENH2$yi\*BioHENH2$New.sign

##Vote counting

nrow(BioHENH2[BioHENH2$yi<0,]) # Natural habitat better than hedgerows

nrow(BioHENH2[BioHENH2$yi>0,]) # Hedgerow better than natural habitat

nrow(BioHENH2[BioHENH2$yi==0,]) #Hedgerows similar as natural habitats

##Null model

rem <- rma.mv(yi, vi, random = ~ 1 | Identifier, data=BioHENH2)

rem #The difference is not significant (p = 0.4261) and positive (0.1086 +- 0.1365) #Hedgerows are similar as natural habitats!

sav <- confint(rem)

W <- diag(1/BioHENH2$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))) # Intervalo de confianza del %

##Total I^2 is high 87.05 - 94.94%. This justifies to include moderators ####

##Next lines select for relevant variables (Identifier,New.Response,New.Taxa,

#Natural.habitat.type,Climate.type,Spatial.Scale.Focus,yi,vi)

datm <- BioHENH2[,c(1,2,4,15,16,17,18,19)]

#and deleted rows with any NA

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

rma.mv.Overall<-rma.mv(yi,vi,mods=~New.Response+New.Taxa+Natural.habitat.type+

 Climate.type+Spatial.Scale.Focus,random=~1|Identifier,data=datm)

summary(rma.mv.Overall)

rma.mv.New.Response<-rma.mv(yi,vi,mods=~0+New.Response,random=~1|Identifier,data=BioHENH2)

summary(rma.mv.New.Response)

anova(rma.mv.New.Response, L=c(1,-1)) # Esta es la Q que vale (QM = 128.7768, p < 0.01; significant)

rma.mv.New.Taxa<-rma.mv(yi,vi,mods=~0+New.Taxa,random=~1|Identifier,data=BioHENH2)

summary(rma.mv.New.Taxa)

anova(rma.mv.New.Taxa, L=c(1,-1,0)) # No differences (p-val= 0.0663)

anova(rma.mv.New.Taxa, L=c(1,0,-1)) # No differences (p-val = 0.2630)

anova(rma.mv.New.Taxa, L=c(0,1,-1)) # Differences (p-val = 0.0042)

rma.mv.Natural.habitat.type<-rma.mv(yi,vi,mods=~0+Natural.habitat.type,random=~1|Identifier,data=BioHENH2)

summary(rma.mv.Natural.habitat.type)

anova(rma.mv.Natural.habitat.type, L=c(1,-1))#(QM= 5.2086, p = 0.0203; significant)

rma.mv.Climate.type<-rma.mv(yi,vi,mods=~0+Climate.type,random=~1|Identifier,data=BioHENH2)

summary(rma.mv.Climate.type)

anova(rma.mv.Climate.type, L=c(1,-1)) # Ésta es la Q que vale (QM = 4.4933, p-val = 0.0658; non-significant).

rma.mv.Focus.of.spatial.scale<-rma.mv(yi,vi,mods=~0+Spatial.Scale.Focus,random=~1|Identifier,data=BioHENH2)

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

anova(rma.mv.Focus.of.spatial.scale, L=c(1,-1)) # Esta es la Q que vale (QM = 0.6641, p = 0.4151; non-significant)

datg1 <- as.data.frame(matrix(,nrow=12,ncol=6)) # Creo una base de datos vacia

datg1[12,1] <- "aLandscape"

datg1[12,2] <- length(BioHENH2$Spatial.Scale.Focus[BioHENH2$Spatial.Scale.Focus=="Landscape"])

datg1[12,3] <- as.numeric(rma.mv.Focus.of.spatial.scale$beta[2])

datg1[12,4] <- as.numeric(rma.mv.Focus.of.spatial.scale$se[2])

datg1[12,5] <- as.numeric(rma.mv.Focus.of.spatial.scale$ci.lb[2])

datg1[12,6] <- as.numeric(rma.mv.Focus.of.spatial.scale$ci.ub[2])

datg1[11,1] <- "bField"

datg1[11,2] <- length(BioHENH2$Spatial.Scale.Focus[BioHENH2$Spatial.Scale.Focus=="Field"])

datg1[11,3] <- as.numeric(rma.mv.Focus.of.spatial.scale$beta[1])

datg1[11,4] <- as.numeric(rma.mv.Focus.of.spatial.scale$se[1])

datg1[11,5] <- as.numeric(rma.mv.Focus.of.spatial.scale$ci.lb[1])

datg1[11,6] <- as.numeric(rma.mv.Focus.of.spatial.scale$ci.ub[1])

datg1[10,1] <- "cTemperate"

datg1[10,2] <- length(BioHENH2$Climate.type[BioHENH2$Climate.type=="Temperate"])

datg1[10,3] <- as.numeric(rma.mv.Climate.type$beta[2])

datg1[10,4] <- as.numeric(rma.mv.Climate.type$se[2])

datg1[10,5] <- as.numeric(rma.mv.Climate.type$ci.lb[2])

datg1[10,6] <- as.numeric(rma.mv.Climate.type$ci.ub[2])

datg1[9,1] <- "dTropical"

datg1[9,2] <- length(BioHENH2$Climate.type[BioHENH2$Climate.type=="Tropical"])

datg1[9,3] <- as.numeric(rma.mv.Climate.type$beta[1])

datg1[9,4] <- as.numeric(rma.mv.Climate.type$se[1])

datg1[9,5] <- as.numeric(rma.mv.Climate.type$ci.lb[1])

datg1[9,6] <- as.numeric(rma.mv.Climate.type$ci.ub[1])

datg1[8,1] <- "eForest/Woodland"

datg1[8,2] <- length(BioHENH2$Natural.habitat.type[BioHENH2$Natural.habitat.type=="Forest/Woodland"])

datg1[8,3] <- as.numeric(rma.mv.Natural.habitat.type$beta[1])

datg1[8,4] <- as.numeric(rma.mv.Natural.habitat.type$se[1])

datg1[8,5] <- as.numeric(rma.mv.Natural.habitat.type$ci.lb[1])

datg1[8,6] <- as.numeric(rma.mv.Natural.habitat.type$ci.ub[1])

datg1[7,1] <- "fGrasslands/Meadow"

datg1[7,2] <- length(BioHENH2$Natural.habitat.type[BioHENH2$Natural.habitat.type=="Grasslands/Meadow"])

datg1[7,3] <- as.numeric(rma.mv.Natural.habitat.type$beta[2])

datg1[7,4] <- as.numeric(rma.mv.Natural.habitat.type$se[2])

datg1[7,5] <- as.numeric(rma.mv.Natural.habitat.type$ci.lb[2])

datg1[7,6] <- as.numeric(rma.mv.Natural.habitat.type$ci.ub[2])

datg1[6,1] <- "gVertebrates"

datg1[6,2] <- length(BioHENH2$New.Taxa[BioHENH2$New.Taxa=="Vertebrates"])

datg1[6,3] <- as.numeric(rma.mv.New.Taxa$beta[3])

datg1[6,4] <- as.numeric(rma.mv.New.Taxa$se[3])

datg1[6,5] <- as.numeric(rma.mv.New.Taxa$ci.lb[3])

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

datg1[5,1] <- "hInvertebrates"

datg1[5,2] <- length(BioHENH2$New.Taxa[BioHENH2$New.Taxa=="Invertebrates"])

datg1[5,3] <- as.numeric(rma.mv.New.Taxa$beta[2]) ##E: Ojo tenías cambiados Invertebrados y plantas (corregido)

datg1[5,4] <- as.numeric(rma.mv.New.Taxa$se[2])

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

datg1[5,6] <- as.numeric(rma.mv.New.Taxa$ci.ub[2])

datg1[4,1] <- "iPlants"

datg1[4,2] <- length(BioHENH2$New.Taxa[BioHENH2$New.Taxa=="Plants"])

datg1[4,3] <- as.numeric(rma.mv.New.Taxa$beta[1])

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

datg1[4,5] <- as.numeric(rma.mv.New.Taxa$ci.lb[1])

datg1[4,6] <- as.numeric(rma.mv.New.Taxa$ci.ub[1])

datg1[3,1] <- "jDiversity"

datg1[3,2] <- length(BioHENH2$New.Response[BioHENH2$New.Response=="Diversity"])

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

datg1[3,4] <- as.numeric(rma.mv.New.Response$se[2])

datg1[3,5] <- as.numeric(rma.mv.New.Response$ci.lb[2])

datg1[3,6] <- as.numeric(rma.mv.New.Response$ci.ub[2])

datg1[2,1] <- "kAbundance"

datg1[2,2] <- length(BioHENH2$New.Response[BioHENH2$New.Response=="Abundance"])

datg1[2,3] <- as.numeric(rma.mv.New.Response$beta[1])

datg1[2,4] <- as.numeric(rma.mv.New.Response$se[1])

datg1[2,5] <- as.numeric(rma.mv.New.Response$ci.lb[1])

datg1[2,6] <- as.numeric(rma.mv.New.Response$ci.ub[1])

datg1[1,1] <- "lMain effect"

datg1[1,2] <- length(BioHENH2$yi)

datg1[1,3] <- as.numeric(rem$beta[1])

datg1[1,4] <- as.numeric(rem$se[1])

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

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

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

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

#install.packages("ggplot2",dep=TRUE)

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

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=2.5),colour="grey80")+

 geom\_hline(aes(yintercept=4.5),colour="grey80")+

 geom\_hline(aes(yintercept=6.5),colour="grey80")+

 geom\_hline(aes(yintercept=9.5),colour="grey80")+

 geom\_hline(aes(yintercept=11.5),colour="grey80")+

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

 ylab(label = "") +

 scale\_y\_discrete(labels=c("lMain effect"="Main effect","kAbundance"="Abundance","jDiversity"="Diversity",

 "iPlants"="Plants","hInvertebrates"="Invertebrates","gVertebrates"="Vertebrates",

 "fGrasslands/Meadow"="Grasslands/Meadow","eForest/Woodland"="Forest/Woodland",

 "dTropical"="Tropical","cTemperate"="Temperate",

 "bField"="Field","aLandscape"="Landscape"))+

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

 geom\_text(x=-2.4,y=12,label = datg1[1,2],size=4)+

 geom\_text(x=-2.4,y=11,label = datg1[2,2],size=4)+

 geom\_text(x=-2.4,y=10,label = datg1[3,2],size=4)+

 geom\_text(x=-2.4,y=9,label = datg1[4,2],size=4)+

 geom\_text(x=-2.4,y=8,label = datg1[5,2],size=4)+

 geom\_text(x=-2.4,y=7,label = datg1[6,2],size=4)+

 geom\_text(x=-2.4,y=6,label = datg1[7,2],size=4)+

 geom\_text(x=-2.4,y=5,label = datg1[8,2],size=4)+

 geom\_text(x=-2.4,y=4,label = datg1[9,2],size=4)+

 geom\_text(x=-2.4,y=3,label = datg1[10,2],size=4)+

 geom\_text(x=-2.4,y=2,label = datg1[11,2],size=4)+

 geom\_text(x=-2.4,y=1,label = datg1[12,2],size=4)+

 geom\_text(x=-1.5,y=10.5,label = "\*",size=6)+

 geom\_text(x=-1.5,y=5.5,label = "\*",size=6)+

 geom\_text(x=-1.5,y=9,label = "ab",size=4)+##E:

 geom\_text(x=-1.5,y=8,label = "a",size=4)+##E:

 geom\_text(x=-1.5,y=7,label = "b",size=4)+##E:

 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/Figure3.jpeg",dpi = 1200, plot=mains, width = 150, height = 150, units = "mm")