## R script for analysis in the article "How does infection alter animal migration? A meta-analysis across experimental and observational studies"

##Have tried to annotate it so it makes sense… but cannot always account for the logic of past Alice,

#especially when it comes object names

### Updated 26/4/17

##contact riselya@gmail.com

library(metafor)

library(ggplot2)

library(tidyr)

library(dplyr)

library(glmulti)

##import data file "Risely\_etal\_data.csv" (Data table 1) as 'basic'

basic <- read.csv("Risely\_etal\_data.csv")

####################### DATA

### "Basic" is all data combined for infection status and intensity

###explanations for all columns

names(basic)

#[1] "id" ##study ID

#[2] "rowid" ##row ID (not continuous)

#[3] "authors"

#[4] "title"

#[5] "journal"

#[6] "year"

#[7] "abstract"

#[8] "type" ##study design - observational or experimental

#[9] "trait" ##performance trait

#[10] "measure" ##how trait was actually measured

#[11] "exp.methods" ##the experimental methods used where relevant

#[12] "species" ##host species

#[13] "latin" ##host latin name

#[14] "taxa" ##host kingdon

#[15] "Order" ##host order

#[16] "Family" ##host family

#[17] "strain" ##parasite strain

#[18] "parasite.taxa" ##parasite type

#[19] "life.history.measured" ##list history of host when sampled

#[20] "setting" ## host sampled in field or lab

#[21] "subset" ##if analyses were split by age/sex, which grouping was used

#[22] "Infection.type" ## single or multiple infection measured

#[23] "migratory.leg2" ##whether a migratory leg occured before infection and sampling

#[24] "ss" ##sample size

#[25] "ss\_infected" ## sample size of infected group

#[26] "ss\_healthy" ##sample size of uninfected group

#[27] "slope" ##slope of relationship if presented

#[28] "effect" ##effect size presented

#[29] "stat" ##statistic used

#[30] "presented.p" ##p value presented

#[31] "adj.p" ## adjusted p - exact p value used in this study based on presented.p

#[32] "sig0.05" ##whether study was significat to 0.05

#[33] "infection.measure" ## whether observation on infection status or infection intensity

#[34] "z" ##Fisher's z

#[35] "var.z" ## variation in Fisher's Z

#[36] "g" ## Hedges' g

#[37] "var.g" ## variation in Hedges' g

#[38] "var.g1" ##capped var.g at 0.01

#[39] "function." ## the compute.es function used to calculate Fisher's z, Hedges' g and their variances

#[40] "Effect.direction" ##effect direction (negative/positive)

unique(basic$id) ##44 studies

str(basic)

##recatgorise some variables

basic$id<-factor(basic$id)

basic$rowid<-factor(basic$rowid)

basic$ss<-as.character(basic$ss)

basic$ss<-as.numeric(basic$ss)

basic$ss\_infected<-as.character(basic$ss\_infected)

basic$ss\_infected<-as.numeric(basic$ss\_infected)

basic$ss\_healthy<-as.character(basic$ss\_healthy)

basic$ss\_healthy<-as.numeric(basic$ss\_healthy)

basic$sig0.05<-factor(basic$sig0.05)

################### METAANALYSIS ON EFFECT OF **INFECTION STATUS** ON PEFORMANCE

##subset observations on infection status

effect<-subset(basic, infection.measure=="Infection status") ##subset observations on infection status

unique(effect$id) ##35 studies included

unique(effect$measure) ##20 measures

table(effect$Effect.direction)

table(effect$sig0.05)

###order categories

effect$trait<-factor(effect$trait, levels=c("Body stores","Refuelling","Movement","Phenology","Survival"))

effect$life.history.measured<-factor(effect$life.history.measured, levels=c("Migration","Breeding","Non-breeding","Lab"))

effect$parasite.taxa<-factor(effect$parasite.taxa, levels=c("Protozoa","Virus","Mites","Helminth","Multiple"))

effect$Order<-factor(effect$Order, levels=c("Passeriformes","Anseriformes","Salmoniformes","Lepidoptera","Falconiformes",

"Anguilliformes","Clupeiformes","Coraciiformes","Charadriiformes"))

effect<-effect[order(effect$trait, effect$g),]

###forest plot

forest.default(effect$g, effect$var.g1, slab = effect$id)

##change names of cohens d and variance to standardized names

effect$yi<-effect$g

effect$vi<-effect$var.g ##variance not capped

effect$vi1<-effect$var.g1 ##capped to 0.01

####exclude data points that use same animals and same trait as non-independent

effect\_independent<-subset(effect, rowid!=27 & rowid!= 28 &

rowid!= 10 & rowid!= 11 & rowid!= 12 & rowid!= 61 &

rowid!= 84 & rowid!= 106 & rowid!= 64 & rowid!= 66 &

rowid!= 68 & rowid!= 160 & rowid!= 158 & rowid!= 156 & rowid!= 51 )

##repeat with different set of points

#effect\_independent1<-subset(effect, rowid!=26 & rowid!= 28 &

# rowid!= 9 & rowid!= 11 & rowid!= 12 & rowid!= 60 &

# rowid!= 83 & rowid!= 105 & rowid!= 63 & rowid!= 65 &

# rowid!= 67 & rowid!= 159 & rowid!= 157 & rowid!= 155 & rowid!= 50 )

effect<-effect\_independent

##forest plots by trait

forest.default(effect$g, effect$vi1, cex=1, xlab="Hedges g", col=effect$trait)

forest.default(effect$g, effect$vi1, cex=1, xlab="Hedges g", col=effect$sig0.05)

forest.default(effect$g, effect$vi1)

##Kendall rank correlation test

cor.test(effect$yi, effect$vi, method="kendall", alternative="less")

coef(lm(yi ~ vi, data = effect))

##supplementary figure S6

ggplot(data=effect, aes(x=vi, y = yi))+geom\_point(size = 3)+ labs(x="Variance in Hedges' g", y = "Hedges' g")+

geom\_abline(intercept= -0.0562, slope = -2.58) +

theme\_bw() +

theme(text = element\_text(size=25),plot.background = element\_blank(),

panel.grid.major = element\_blank(),

panel.grid.minor = element\_blank() )+

theme(panel.border= element\_blank())+

theme(axis.text=element\_text(size = 14))+

theme(axis.line.x = element\_line(color="black", size = 0.5),

axis.line.y = element\_line(color="black", size = 0.5))

############################################ MODEL FITTING AND SELECTION ##################################################################################

##see Methods section

##explore which variables have an impact on effect size by comparing all models

rma.glmulti <- function(formula, data, ...) {

rma.mv(as.formula(paste(deparse(formula))), vi1, data=data, method="ML", ...)

}

### global model with 6 ecologically relevant variables. Max number of variables allowed in model is 2. Study ID as #random effect

res <- glmulti(yi ~ trait+ parasite.taxa+ Order +life.history.measured+type+migratory.leg2,random = ~ 1 | id, data=effect,

level=1, fitfunction=rma.glmulti, crit="aicc", maxsize= 2)

tmp <- weightable(res)

tmp

#write.csv(tmp, "aic.csv")

##Phylogeny important

##variable importance

plot(res, type="s")

plot(res, type="w")

print(res)

## lets check out the best models

summary(res@objects[[1]])

funnel(res@objects[[1]], yaxis="wi")

summary(res@objects[[2]])

funnel(res@objects[[2]], yaxis="wi")

summary(res@objects[[3]])

funnel(res@objects[[3]], yaxis="wi")

##################### best model###########################################

## first null model

null.model<-rma.mv(yi, vi1,random = ~ 1 | id, data=effect, method="REML")

summary(null.model)

funnel(null.model, xlab = "Hedges' g", cex.lab = 1.5, cex.axis=1.5)

#I2 = 100 \* (Q - df)/Q

#==52%

#######best model - include trait with host order as a covariable (see Methods section)

## using capped variance (vi1)

best.model1<-rma.mv(yi, vi1, mods=~ trait + Order ,random = ~ 1 | id, data=effect)

summary(best.model1)

#I2 = 40%

funnel(best.model1)

funnel(best.model1, yaxis="wi") ##weighting of points

##make table of best model (table 3a)

best.model.table<-data.frame(best.model1$b)

best.model.table$se<-best.model1$se

best.model.table$zval<-best.model1$zval

best.model.table$p<-best.model1$pval

best.model.table$l.ci<-best.model1$ci.lb

best.model.table$u.ci<-best.model1$ci.ub

#write.csv(best.model.table, "best.model.csv")

##plot resids

F1 <- fitted(best.model1)

E1 <- resid(best.model1)

plot(x = F1,

y = E1,

xlab = "Fitted values",

ylab = "Pearson residuals",

cex.lab = 1.5)

abline(h = 0, lty = 2)

##some outliers.

hist(E1, breaks=10)

##save fitted and residuals and hat values

effect$resids<-resid(best.model1, type ="pearson")

effect$predicted<-fitted(best.model1)

effect$leverage<-hatvalues(best.model1)

mean(effect$leverage)

plot(effect$leverage)

subset(effect, resids < -1)

##three outliers in residuals are from the van gils paper on avian influenza on phenology, movement and refuelling

##exclude these and rerun from line 205 - doesnt make much difference although reduces model residual heterogeneity

#effect<-subset(effect, resids > -1) ##rerun without outliers

##PLOT ESTIMATES (Figure 3)

best.model1<-rma.mv(yi, vi1, mods=~ trait+Order,random = ~ 1 | id, data=effect)

summary(best.model1)

trait.pred<-predict(best.model1, newmods=rbind(c(0,0,0,0,0,0,0,0,0,0,0,0),c(1,0,0,0,0,0,0,0,0,0,0,0),c(0,1,0,0,0,0,0,0,0,0,0,0),

c(0,0,1,0,0,0,0,0,0,0,0,0),c(0,0,0,1,0,0,0,0,0,0,0,0)))

trait<-data.frame(trait.pred$pred)

trait$se<-trait.pred$se

trait$l.ci<-trait.pred$ci.lb

trait$u.ci<-trait.pred$ci.ub

trait$level<-factor(c("Body stores","Refuelling","Movement","Phenology","Survival"))

trait$level<-factor(trait$level, levels=c("Body stores","Refuelling","Movement","Phenology","Survival"))

colnames(trait)[1]<-"predicted"

predictedvalues<-trait

predictedvalues$l.se<-predictedvalues$predicted - predictedvalues$se

predictedvalues$u.se<-predictedvalues$predicted + predictedvalues$se

##boxplot

##overlayed with raw data with proportional weights

###################fig 3a

ggplot(data=predictedvalues, aes(x=level, y = predicted, fill = Order))+

geom\_boxplot(aes(ymin=l.ci, lower=l.se,

middle = predicted, upper = u.se, ymax=u.ci, width = 0.5), stat="identity", fill="lightgray", lwd=0.7)+

geom\_jitter(data = effect, aes(x= trait, y = yi, size = 1/vi1, col = Order),width=0.15, alpha=1/2)+

labs(y="Predicted Hedges' g", x ="")+geom\_hline(yintercept=0, linetype="longdash")+

theme\_bw() + theme(text = element\_text(size=22),axis.text.x = element\_text(angle=45, vjust=0.5),

plot.background = element\_blank(),

panel.grid.major = element\_blank(),

panel.grid.minor = element\_blank() )+

theme(panel.border= element\_blank())+

theme(axis.line.x = element\_line(color="black", size = 0.4),

axis.line.y = element\_line(color="black", size = 0.4))+

scale\_y\_continuous(breaks=seq(-2,0.5, 0.5))+scale\_color\_brewer(type = "qual", palette = "Set1")+

guides(colour = guide\_legend(override.aes = list(size=6)))

#############################################################################################################

#########################modelling traits separately

survival<-subset(effect, trait=="Survival")

Bodystores<-subset(effect, trait=="Body stores")

phenology<-subset(effect, trait=="Phenology")

movement<-subset(effect, trait=="Movement")

refuelling<-subset(effect, trait=="Refuelling")

null1<-rma.mv(yi, vi1, random = ~ 1 | id, data=Bodystores) ##null model

summary(null1)

#I2 = 100 \* (28.7-16)/28.7

#I2 = 38

null2<-rma.mv(yi, vi1, random = ~ 1 | id, data=refuelling) ##null model

summary(null2)

#I2 = 44%

null3<-rma.mv(yi, vi1, random = ~ 1 | id, data=movement) ##null model

summary(null3)

#I2 = 65%

null4<-rma.mv(yi, vi1, random = ~ 1 | id, data=phenology) ##null model

summary(null4)

#I2 = 58%

null5<-rma.mv(yi, vi1, random = ~ 1 | id, data=survival) ##null model

summary(null5)

# I2 = 18%

pred1<-predict(null1)

pred2<-predict(null2)

pred3<-predict(null3)

pred4<-predict(null4)

pred5<-predict(null5)

trait<-data.frame(rbind(pred1,pred2,pred3,pred4,pred5))

trait$pred<-as.numeric(trait$pred)

trait$se<-as.numeric(trait$se)

trait$ci.lb<-as.numeric(trait$ci.lb)

trait$ci.ub<-as.numeric(trait$ci.ub)

trait<-trait[,1:4]

trait$level<-factor(c("Body stores","Refuelling","Movement","Phenology","Survival"))

trait$level<-factor(trait$level, levels=c("Body stores","Refuelling","Movement","Phenology","Survival"))

colnames(trait)[1]<-"predicted"

colnames(trait)[3]<-"l.ci"

colnames(trait)[4]<-"u.ci"

predictedvalues<-trait

str(predictedvalues)

predictedvalues$l.se<-predictedvalues$predicted - predictedvalues$se

predictedvalues$u.se<-predictedvalues$predicted + predictedvalues$se

##Figure 3b

ggplot(data=predictedvalues, aes(x=level, y = predicted, fill = parasite.taxa))+

geom\_boxplot(aes(ymin=l.ci, lower=l.se,

middle = predicted, upper = u.se, ymax=u.ci, width = 0.5), stat="identity", fill="lightgray", lwd=0.7)+

geom\_jitter(data = effect, aes(x= trait, y = yi, size = 1/vi1, col = parasite.taxa),width=0.15, alpha=1/2)+

labs(y="Predicted Hedges' g", x ="")+geom\_hline(yintercept=0, linetype="longdash")+

theme\_bw() + theme(text = element\_text(size=22),axis.text.x = element\_text(angle=45, vjust=0.5),

plot.background = element\_blank(),

panel.grid.major = element\_blank(),

panel.grid.minor = element\_blank() )+

theme(panel.border= element\_blank())+

theme(axis.line.x = element\_line(color="black", size = 0.4),

axis.line.y = element\_line(color="black", size = 0.4))+

scale\_y\_continuous(breaks=seq(-2,0.5, 0.5))+scale\_color\_manual(values=c("red","blue","cyan3", "gold","magenta"))+

guides(colour = guide\_legend(override.aes = list(size=6)))

#model with just trait

best.model2<-rma.mv(yi, vi1, mods=~ trait,random = ~ 1 | id, data=effect)

summary(best.model2)

trait.pred<-predict(best.model2, newmods=rbind(c(0,0,0,0),c(1,0,0,0),c(0,1,0,0),

c(0,0,1,0),c(0,0,0,1)))

trait<-data.frame(trait.pred$pred)

trait$se<-trait.pred$se

trait$l.ci<-trait.pred$ci.lb

trait$u.ci<-trait.pred$ci.ub

trait$level<-factor(c("Body stores","Refuelling","Movement","Phenology","Survival"))

trait$level<-factor(trait$level, levels=c("Body stores","Refuelling","Movement","Phenology","Survival"))

colnames(trait)[1]<-"predicted"

predictedvalues<-trait

predictedvalues$l.se<-predictedvalues$predicted - predictedvalues$se

predictedvalues$u.se<-predictedvalues$predicted + predictedvalues$se

##boxplot

##overlayed with raw data with proportional weights

ggplot(data=predictedvalues, aes(x=level, y = predicted, fill = parasite.taxa))+

geom\_boxplot(aes(ymin=l.ci, lower=l.se,

middle = predicted, upper = u.se, ymax=u.ci, width = 0.5), stat="identity", fill="lightgray", lwd=0.7)+

geom\_jitter(data = effect, aes(x= trait, y = yi, size = 1/vi1, col = parasite.taxa),width=0.15, alpha=1/2)+

labs(y="Predicted Hedges' g", x = "")+geom\_hline(yintercept=0, linetype="longdash")+

theme\_bw() + theme(text = element\_text(size=22),axis.text.x = element\_text(angle=45, vjust=0.5),

plot.background = element\_blank(),

panel.grid.major = element\_blank(),

panel.grid.minor = element\_blank() )+

theme(panel.border= element\_blank())+

theme(axis.line.x = element\_line(color="black", size = 0.4),

axis.line.y = element\_line(color="black", size = 0.4))+

scale\_y\_continuous(breaks=seq(-2,0.5, 0.5))+scale\_color\_manual(values=c("red3","royalblue3","darkgreen", "orange","yellow"))+

guides(colour = guide\_legend(override.aes = list(size=6)))

##very similar to that of plot where all traits are modelled separately.

###########################################SENSITIVITY ANALYSES##################################

###use uncapped variance instead of capped variance (replace vi1 with vi in all models) and rerun

#best.model1<-rma.mv(yi, vi, mods=~ trait + Order, random = ~ 1 | id, data=effect)

#summary(best.model1)

##exclude insects in case this biases models and rerun

#effect<-subset(effect, taxa!=”Insect”)

##exclude outliers for best model and rerun

#effect<-subset(effect, resids > -1)

###Does not change models overall

##################################################################################################################################

#################################### INTENSITY META-ANALYSIS ######################################

intensity<-subset(basic, infection.measure=="Intensity")

table(intensity$sig0.05)

###exclude points that use the same animals

#intensity<-subset(intensity, rowid != 4 & rowid!=5 & rowid!=134 & rowid!=22)

intensity<-intensity[order(intensity$trait, intensity$z),]

forest.default(intensity$z, intensity$var.z)

forest.default(intensity$z, intensity$var.z, col = intensity$sig0.05)

forest.default(intensity$z, intensity$var.z, col = intensity$trait)

##order categories

intensity$trait<-factor(intensity$trait, levels=c("Body stores","Movement","Phenology","Survival"))

intensity$parasite.taxa<-factor(intensity$parasite.taxa, levels=c("Protozoa","Virus","Mites","Helminth","Myxospora"))

intensity$Order<-factor(intensity$Order, levels=c("Passeriformes","Anseriformes","Salmoniformes","Lepidoptera","Falconiformes",

"Anguilliformes","Clupeiformes","Coraciiformes","Charadriiformes"))

###univariate models with each of the six explanatory variables

model.intensity<-rma.mv(z, var.z, mods = ~ trait, random = ~1|id, data=intensity)

model.intensity1<-rma.mv(z, var.z, mods = ~ Order, random = ~1|id, data=intensity)

model.intensity2<-rma.mv(z, var.z, mods = ~ parasite.taxa, random = ~1|id, data=intensity)

model.intensity3<-rma.mv(z, var.z, mods = ~ life.history.measured, random = ~1|id, data=intensity)

model.intensity4<-rma.mv(z, var.z, mods = ~ migratory.leg2, random = ~1|id, data=intensity)

model.intensity5<-rma.mv(z, var.z, mods = ~ type, random = ~1|id, data=intensity)

model.intensity6<-rma.mv(z, var.z, random = ~1|id, data=intensity) #null model

aicc(model.intensity)

aicc(model.intensity1)

aicc(model.intensity2)

aicc(model.intensity3)

aicc(model.intensity4)

aicc(model.intensity5)

aicc(model.intensity6)

##best model includes just trait (AICC = 6.8)

summary(model.intensity) #best model

funnel(model.intensity6) #null model funnel plot

##table - Table 4a

best.model.table<-data.frame(model.intensity$b)

best.model.table$se<-model.intensity$se

best.model.table$zval<-model.intensity$zval

best.model.table$p<-model.intensity$pval

best.model.table$l.ci<-model.intensity$ci.lb

best.model.table$u.ci<-model.intensity$ci.ub

#write.csv(best.model.table, "best.model.intensity.csv")

##plot model estimates (Fig 4)

trait.pred<-predict(model.intensity, newmods=rbind(c(0,0,0),c(1,0,0),c(0,1,0),

c(0,0,1)))

trait<-data.frame(trait.pred$pred)

trait$se<-trait.pred$se

trait$l.ci<-trait.pred$ci.lb

trait$u.ci<-trait.pred$ci.ub

trait$level<-factor(c("Body stores","Movement","Phenology","Survival"))

trait$level<-factor(trait$level, levels=c("Body stores","Movement","Phenology","Survival"))

colnames(trait)[1]<-"predicted"

predictedvalues<-trait

predictedvalues$l.se<-predictedvalues$predicted - predictedvalues$se

predictedvalues$u.se<-predictedvalues$predicted + predictedvalues$se

##boxplot

##overlayed with raw data with proportional weights

##Figure 4a

ggplot(data=predictedvalues, aes(x=level, y = predicted, fill = parasite.taxa))+

geom\_boxplot(aes(ymin=l.ci, lower=l.se,

middle = predicted, upper = u.se, ymax=u.ci, width = 0.5), stat="identity", fill="lightgray", lwd=0.7)+

geom\_jitter(data = intensity, aes(x= trait, y = z, size = 1/var.z, col = parasite.taxa),width=0.15, alpha=1/2)+

labs(y="Fisher's z", x = "")+geom\_hline(yintercept=0, linetype="longdash")+

theme\_bw() + theme(text = element\_text(size=22),axis.text.x = element\_text(angle=45, vjust=0.5),

plot.background = element\_blank(),

panel.grid.major = element\_blank(),

panel.grid.minor = element\_blank() )+

theme(panel.border= element\_blank())+

theme(axis.line.x = element\_line(color="black", size = 0.4),

axis.line.y = element\_line(color="black", size = 0.4))+

scale\_color\_manual(values=c("red3","royalblue3","cyan3", "orange","magenta"))+

guides(colour = guide\_legend(override.aes = list(size=6)))

######################model intensity separately

survival<-subset(intensity, trait=="Survival")

Bodystores<-subset(intensity, trait=="Body stores")

phenology<-subset(intensity, trait=="Phenology")

movement<-subset(intensity, trait=="Movement")

null1<-rma.mv(z, var.z, random = ~ 1 | id, data=Bodystores) ##null model

summary(null1)

#I2 = 100 \* (28.7-16)/28.7

#I2 = 38

null3<-rma.mv(z, var.z, random = ~ 1 | id, data=movement) ##null model

summary(null3)

#I2 = 65%

null4<-rma.mv(z, var.z, random = ~ 1 | id, data=phenology) ##null model

summary(null4)

#I2 = 58%

null5<-rma.mv(z, var.z, random = ~ 1 | id, data=survival) ##null model

summary(null5)

# I2 = 18%

pred1<-predict(null1)

pred3<-predict(null3)

pred4<-predict(null4)

pred5<-predict(null5)

trait<-data.frame(rbind(pred1,pred3,pred4,pred5))

trait$pred<-as.numeric(trait$pred)

trait$se<-as.numeric(trait$se)

trait$ci.lb<-as.numeric(trait$ci.lb)

trait$ci.ub<-as.numeric(trait$ci.ub)

trait<-trait[,1:4]

trait$level<-factor(c("Body stores","Movement","Phenology","Survival"))

trait$level<-factor(trait$level, levels=c("Body stores","Movement","Phenology","Survival"))

colnames(trait)[1]<-"predicted"

colnames(trait)[3]<-"l.ci"

colnames(trait)[4]<-"u.ci"

predictedvalues<-trait

str(predictedvalues)

predictedvalues$l.se<-predictedvalues$predicted - predictedvalues$se

predictedvalues$u.se<-predictedvalues$predicted + predictedvalues$se

##Fig 4b

ggplot(data=predictedvalues, aes(x=level, y = predicted))+

geom\_boxplot(aes(ymin=l.ci, lower=l.se,

middle = predicted, upper = u.se, ymax=u.ci, width = 0.5), stat="identity", fill="lightgray", lwd=0.7)+

geom\_jitter(data = intensity, aes(x= trait, y = z, size = 1/var.z, col = id),width=0.15, alpha=2/3)+

labs(y="Fisher's z", x = "")+geom\_hline(yintercept=0, linetype="longdash")+

theme\_bw() + theme(text = element\_text(size=22),axis.text.x = element\_text(angle=45, vjust=0.5),

plot.background = element\_blank(),

panel.grid.major = element\_blank(),

panel.grid.minor = element\_blank() )+

theme(panel.border= element\_blank())+

theme(axis.line.x = element\_line(color="black", size = 0.4),

axis.line.y = element\_line(color="black", size = 0.4))+

scale\_color\_manual(values=c("green","royalblue3","cyan", "red","magenta","gray40","black","sienna","purple","pink","green4","blue","gold"))+

guides(colour = guide\_legend(override.aes = list(size=6)))

##coloured by host phylogeny

ggplot(data=predictedvalues, aes(x=level, y = predicted))+

geom\_boxplot(aes(ymin=l.ci, lower=l.se,

middle = predicted, upper = u.se, ymax=u.ci, width = 0.5), stat="identity", fill="lightgray", lwd=0.7)+

geom\_jitter(data = intensity, aes(x= trait, y = z, size = 1/var.z, col = Order),width=0.15, alpha=1/2)+

labs(y="Fisher's z", x = "")+geom\_hline(yintercept=0, linetype="longdash")+

theme\_bw() + theme(text = element\_text(size=22),axis.text.x = element\_text(angle=45, vjust=0.5),

plot.background = element\_blank(),

panel.grid.major = element\_blank(),

panel.grid.minor = element\_blank() )+

theme(panel.border= element\_blank())+

theme(axis.line.x = element\_line(color="black", size = 0.4),

axis.line.y = element\_line(color="black", size = 0.4))+

scale\_color\_brewer(type = "qual", palette = "Set1")+

guides(colour = guide\_legend(override.aes = list(size=6)))