

Risely_etal_Rscript.R

arisely

Wed Jun 21 10:56:22 2017

```
## 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 do it makes sense
```

```
### Updated 26/4/17
```

```
library(metafor)
```

```
## Warning: package 'metafor' was built under R version 3.3.3
```

```
## Loading required package: Matrix
```

```
## Warning: package 'Matrix' was built under R version 3.3.3
```

```
## Loading 'metafor' package (version 1.9-9). For an overview  
## and introduction to the package please type: help(metafor).
```

```
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 3.3.3
```

```
library(tidyr)
```

```
##
```

```
## Attaching package: 'tidyr'
```

```
## The following object is masked from 'package:Matrix':
```

```
##
```

```
##      expand
```

```
library(dplyr)
```

```
##
```

```
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
```

```
##
```

```
##      filter, lag
```

```

## The following objects are masked from 'package:base':
##
## intersect, setdiff, setequal, union

library(glmulti)

## Loading required package: rJava

##import data file "Data_table2_data.csv" (Data table 2) as 'basic'

basic <- read.csv("C:/Users/arisely/Dropbox/PhD/Lit Review/R/LitReviewR/Meta-
analysis/Working datasheets/Risely_etal_data.csv")

##### METAANALYSIS FOR INFECTION INTENSITY

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

###explanations for all columns

names(basic)

## [1] "id" "rowid"
## [3] "authors" "title"
## [5] "journal" "year"
## [7] "abstract" "type"
## [9] "trait" "measure"
## [11] "exp.methods" "species"
## [13] "latin" "taxa"
## [15] "Order" "Family"
## [17] "strain" "parasite.taxa"
## [19] "life.history.measured" "setting"
## [21] "subset" "Infection.type"
## [23] "migratory.leg2" "ss"
## [25] "ss_infected" "ss_healthy"
## [27] "slope" "effect"
## [29] "stat" "presented.p"
## [31] "adj.p" "sig0.05"
## [33] "infection.measure" "z"
## [35] "var.z" "g"
## [37] "var.g" "var.g1"
## [39] "function." "Effect.direction"

#[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 kingdom
#[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 occurred 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 significant 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

```

```

## [1] 99 75 39 1 2 81 3 80 59 82 70 71 36 72 12 29 76
## [18] 25 101 53 31 17 41 15 30 77 19 62 60 69 65 10 11 78
## [35] 48 40 79 13 6 5 50

```

```

str(basic)

```

```

## 'data.frame': 99 obs. of 40 variables:
## $ id : int 99 75 75 75 75 39 39 39 1 1 ...
## $ rowid : int 153 119 120 121 122 49 50 51 2 3 ...
## $ authors : Factor w/ 41 levels "Altizer, SM; Hobson, KA;

```

```

Davis, AK; De Roode, JC, Wassenaar, LI",...: 1 2 2 2 2 3 3 3 4 4 ...
## $ title : Factor w/ 41 levels "A rare study from the
wintering grounds provides insight into the costs of malaria infection for
migratory birds",...: 9 16 16 16 16 8 8 8 4 4 ...
## $ journal : Factor w/ 28 levels "ARDEOLA","AUK",...: 24 19 19
19 19 1 1 1 15 15 ...
## $ year : int 2015 1999 1999 1999 1999 2009 2009 2009
2011 2011 ...
## $ abstract : Factor w/ 41 levels "Animal movements may
contribute to the spread of pathogens. In the case of avian influenza virus,
[migratory] birds have been s"| __truncated__,...: 17 36 36 36 36 6 6 6 20 20
...
## $ type : Factor w/ 2 levels "E","O": 2 1 1 1 1 2 2 2 2 2
...
## $ trait : Factor w/ 5 levels "Body stores",...: 2 5 5 1 1 4
1 1 3 3 ...
## $ measure : Factor w/ 20 levels "Annual survival",...: 5 11
11 3 3 13 7 2 17 17 ...
## $ exp.methods : Factor w/ 5 levels "", "na", "Parasite
addition",...: 2 3 3 3 3 2 2 2 2 2 ...
## $ species : Factor w/ 27 levels "Altantic herring",...: 19 18
18 18 18 7 7 7 13 13 ...
## $ latin : Factor w/ 25 levels "Acrocephalus
arundinaceus",...: 9 9 9 9 9 24 24 24 1 1 ...
## $ taxa : Factor w/ 3 levels "Bird","Fish",...: 3 3 3 3 3 1
1 1 1 1 ...
## $ Order : Factor w/ 9 levels "Anguilliformes",...: 7 7 7 7
7 8 8 8 8 8 ...
## $ Family : Factor w/ 13 levels "Acrocephalidae",...: 9 9 9 9
9 13 13 13 1 1 ...
## $ strain : Factor w/ 22 levels "Anguillicola crassus",...:
18 18 18 18 18 10 10 10 7 7 ...
## $ parasite.taxa : Factor w/ 5 levels "Helminth","Mites",...: 4 4 4
4 4 4 4 4 4 ...
## $ life.history.measured: Factor w/ 4 levels "Breeding","Lab",...: 4 2 2 2
2 3 3 3 1 1 ...
## $ setting : Factor w/ 3 levels "", "Field", "Lab": 2 3 3 3 3 2
2 2 2 2 ...
## $ subset : Factor w/ 7 levels "Adults","all",...: 2 5 3 5 3
2 2 2 3 5 ...
## $ Infection.type : Factor w/ 2 levels "Multiple","Single": 2 2 2 2
2 2 2 2 2 2 ...
## $ migratory.leg2 : Factor w/ 2 levels "N","Y": 2 1 1 1 1 2 2 2 2 2
...
## $ ss : int 175 98 100 98 100 53 53 53 37 34 ...
## $ ss_infected : Factor w/ 47 levels "10","100","11",...: 2 46 46
46 46 12 12 12 46 46 ...
## $ ss_healthy : Factor w/ 47 levels "10","102","1070",...: 39 46
46 46 46 25 25 25 46 46 ...
## $ slope : Factor w/ 23 levels "-0.016","-0.022",...: 23 23

```

```

23 23 23 23 23 23 23 23 ...
## $ effect : Factor w/ 73 levels "-0.21","-0.414",...: 50 69
40 22 9 17 35 13 57 33 ...
## $ stat : Factor w/ 12 levels "%","Beta","F",...: 10 3 3 3
3 7 7 3 3 3 ...
## $ presented.p : Factor w/ 63 levels "<0.0000001","<0.0001",...: 2
3 34 58 19 59 41 61 25 43 ...
## $ adj.p : num 0.0001 0.001 0.23 0.89 0.03 0.9 0.33 0.93
0.07 0.4 ...
## $ sig0.05 : int 1 1 0 0 1 0 0 0 0 0 ...
## $ infection.measure : Factor w/ 2 levels "Infection status",...: 1 2 2
2 2 1 1 1 2 2 ...
## $ z : num -0.28 -0.34 -0.12 0.01 0.22 0.02 -0.13 -
0.01 -0.3 -0.15 ...
## $ var.z : num 0.01 0.01 0.01 0.01 0.01 0.02 0.02 0.02
0.03 0.03 ...
## $ g : num -0.56 -0.68 -0.24 0.03 0.44 0.04 -0.28 -
0.03 -0.6 -0.29 ...
## $ var.g : num 0.02 0.04 0.04 0.04 0.04 0.08 0.08 0.08
0.11 0.11 ...
## $ var.g1 : num 0.02 0.04 0.04 0.04 0.04 0.08 0.08 0.08
0.11 0.11 ...
## $ function. : Factor w/ 98 levels "chies(1.89,173)",...: 8 12
42 76 25 77 49 82 36 51 ...
## $ Effect.direction : Factor w/ 4 levels "Negative","None",...: 1 1 1 2
3 3 1 1 1 1 ...

##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)

## Warning: NAs introduced by coercion

basic$ss_healthy<-as.character(basic$ss_healthy)
basic$ss_healthy<-as.numeric(basic$ss_healthy)

## Warning: NAs introduced by coercion

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

## [1] 99 39 2 81 3 59 82 70 71 36 72 29 76 25 101 53 31
## [18] 17 41 15 77 19 62 69 65 10 11 78 48 40 79 13 6 5
## [35] 50
## 41 Levels: 1 2 3 5 6 10 11 12 13 15 17 19 25 29 30 31 36 39 40 41 ... 101

unique(effect$measure) ##20 measures

## [1] Distance travelled      Mass change
## [3] Fat score                Body mass
## [5] Lifespan                  Local movements
## [7] Annual survival          Endurance
## [9] Speed                     plasma triglyceride concentration
## [11] Condition index          Stop-over arrival
## [13] Body mass change         Migration survival
## [15] Feeding rate             Staging time
## [17] Spring arrival           Growth rate
## [19] Lean mass                Spring departure
## 20 Levels: Annual survival Body mass Body mass change ... Stop-over
arrival

table(effect$Effect.direction)

##
##          Negative          None          Positive Probably negative
##              42              3              18              3

table(effect$sig0.05)

##
## 0 1
## 37 29

###order categories

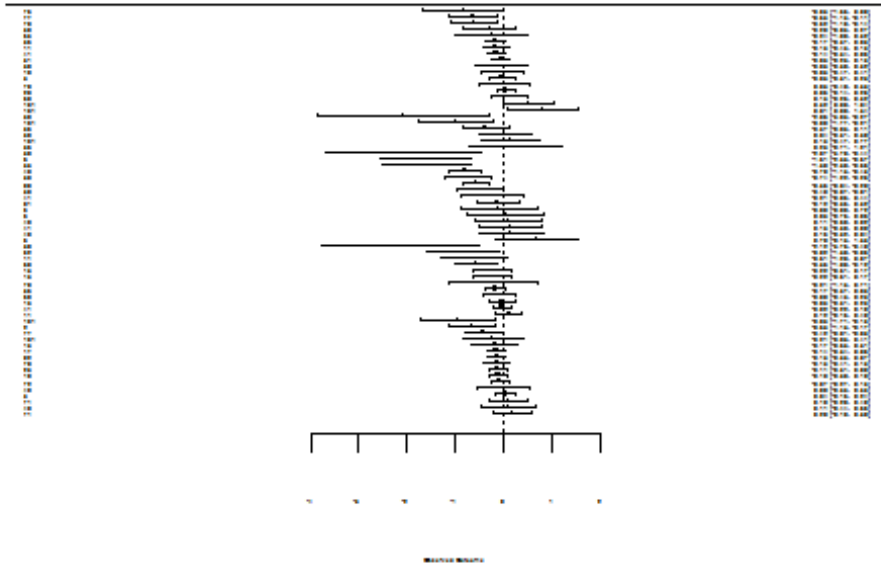
effect$trait<-factor(effect$trait, levels=c("Body
stores","Refuelling","Movement","Phenology","Survival"))
effect$life.history.measured<-factor(effect$life.history.measured,
levels=c("Migration","Breeding","Non-breeding","Lab"))
effect$parasite.taxa<-factor(effect$parasite.taxa,
levels=c("Protozoa","Virus","Mites","Helminth","Multiple"))
effect$Order<-factor(effect$Order,
levels=c("Passeriformes","Anseriformes","Salmoniformes","Lepidoptera","Falcon
iformes",

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

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

```

```
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
```

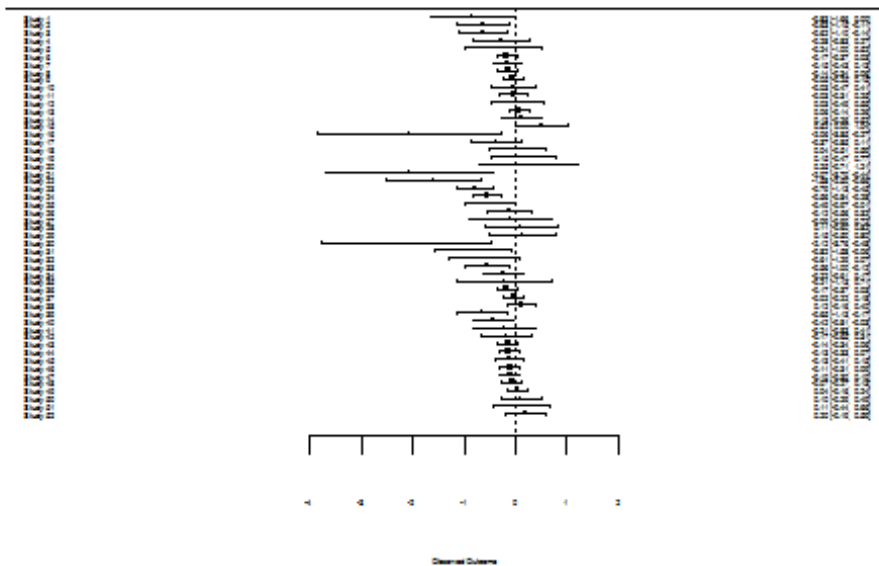
```
#effect_independent1<-subset(effect, rowid!=26 & rowid!= 28 &
#                             rowid!= 9 & rowid!= 11 & rowid!= 12 & rowid!= 60
#                             &
```

```
#           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")
```

```
##
```

```
## Kendall's rank correlation tau
```

```
##
```

```
## data: effect$yi and effect$vi
```

```
## z = -2.1837, p-value = 0.01449
```



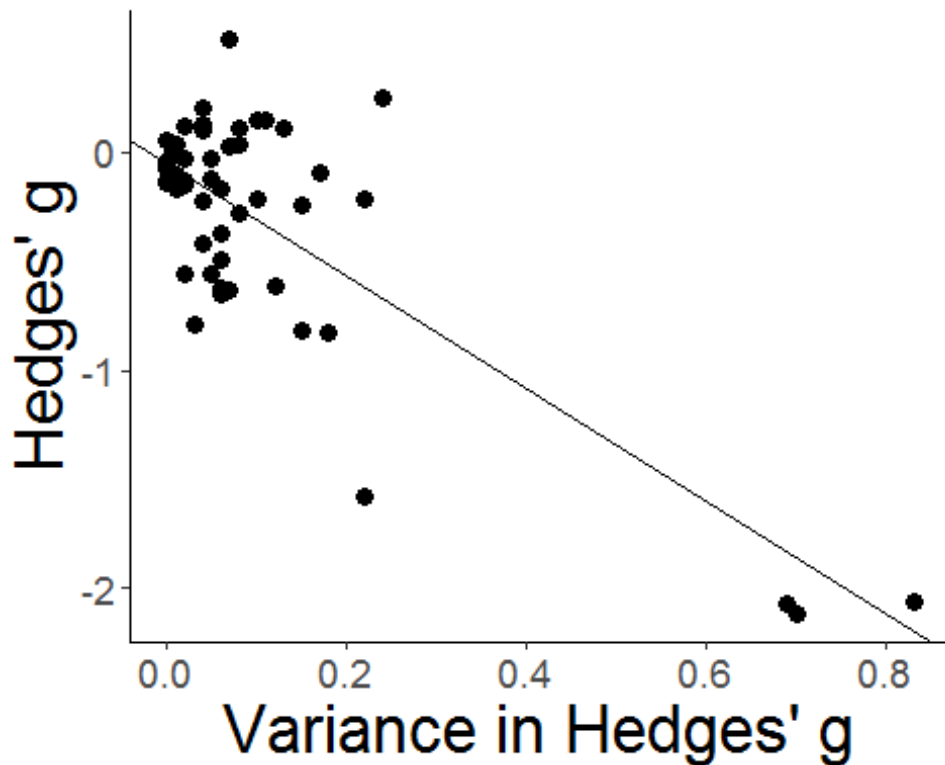
```
## alternative hypothesis: true tau is less than 0
## sample estimates:
##      tau
## -0.2129025

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

## (Intercept)          vi
## -0.03994311 -2.61193433

##supplementary fig

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
#####
#####
```

```
##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",  
  ...)  
}
```

```
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)
```

```
## Initialization...
```

```
## TASK: Exhaustive screening of candidate set.
```

```
## Fitting...
```

```
## Warning in rma.mv(as.formula(paste(deparse(formula))), vi1, data = data, :  
## Redundant predictors dropped from the model.
```

```
## Completed.
```

```
tmp <- weightable(res)
```

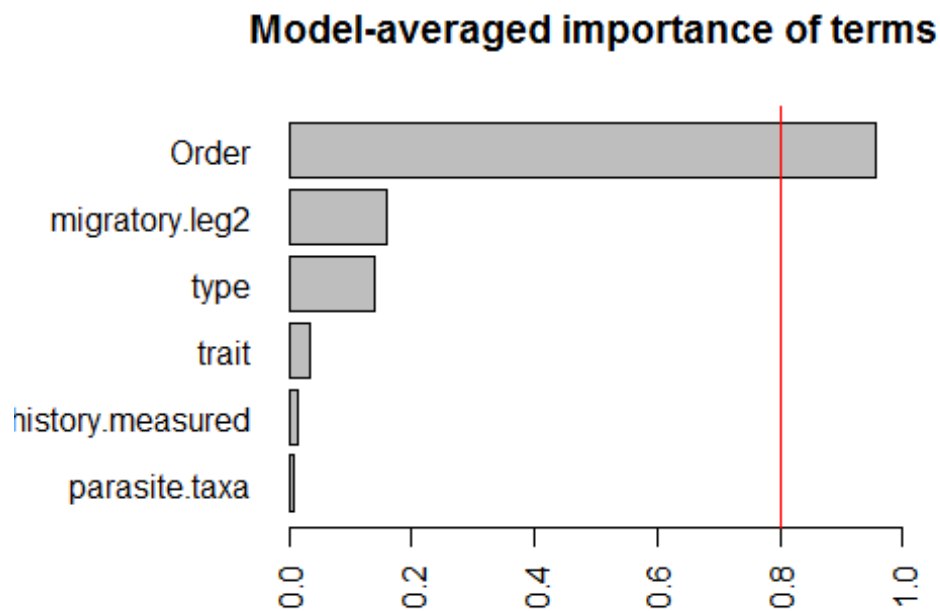
```
tmp
```

##	model	aicc	weights
## 1	yi ~ 1 + Order	30.62552	6.671356e-01
## 2	yi ~ 1 + Order + migratory.leg2	33.78642	1.373515e-01
## 3	yi ~ 1 + Order + type	33.85538	1.326962e-01
## 4	yi ~ 1 + trait + migratory.leg2	38.28193	1.450933e-02
## 5	yi ~ 1 + trait	38.45283	1.332096e-02
## 6	yi ~ 1 + Order + life.history.measured	38.93838	1.044961e-02
## 7	yi ~ 1 + parasite.taxa + Order	39.53281	7.762858e-03
## 8	yi ~ 1 + trait + type	40.75564	4.211994e-03
## 9	yi ~ 1 + life.history.measured + migratory.leg2	41.72978	2.587949e-03
## 10	yi ~ 1 + migratory.leg2	41.99198	2.269966e-03
## 11	yi ~ 1	42.14224	2.105672e-03
## 12	yi ~ 1 + type + migratory.leg2	42.68849	1.602408e-03
## 13	yi ~ 1 + trait + Order	43.39864	1.123481e-03
## 14	yi ~ 1 + life.history.measured	43.54038	1.046617e-03
## 15	yi ~ 1 + type	44.26675	7.278791e-04
## 16	yi ~ 1 + trait + life.history.measured	45.06469	4.884148e-04
## 17	yi ~ 1 + life.history.measured + type	45.96663	3.111251e-04
## 18	yi ~ 1 + trait + parasite.taxa	47.05605	1.804558e-04
## 19	yi ~ 1 + parasite.taxa	49.70407	4.801315e-05
## 20	yi ~ 1 + parasite.taxa + type	50.18962	3.766376e-05

```
## 21      yi ~ 1 + parasite.taxa + migratory.leg2 51.29744 2.164536e-05
## 22  yi ~ 1 + parasite.taxa + life.history.measured 52.71685 1.064494e-05

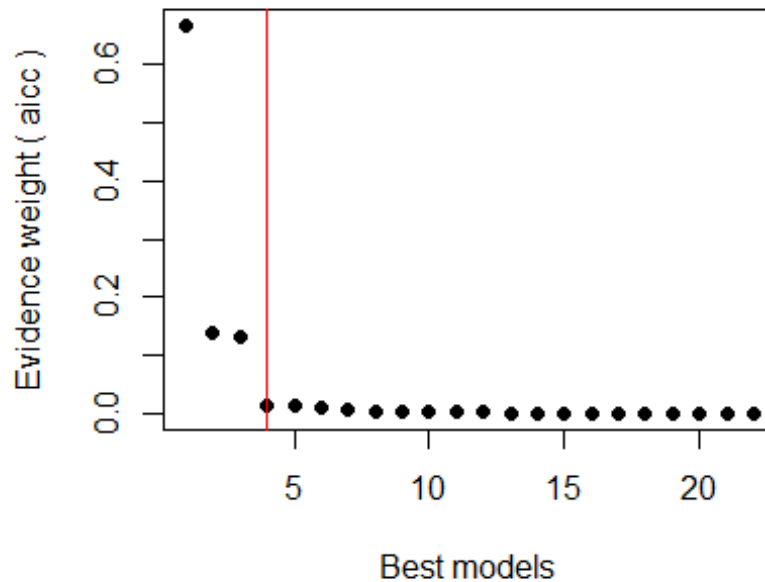
#write.csv(tmp, "aic.csv")
##Phylogeny important

##variable importance
plot(res, type="s")
```



```
plot(res, type="w")
```

Profile of model weights



```
print(res)

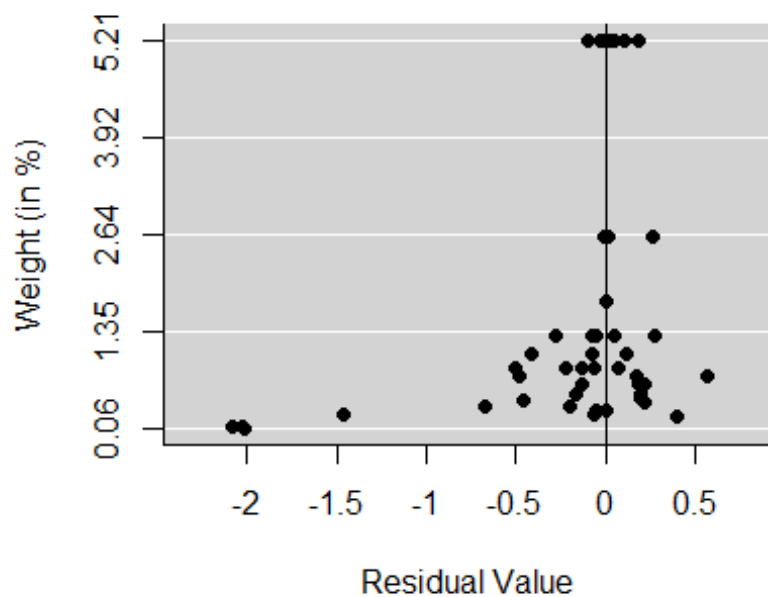
## glmulti.analysis
## Method: h / Fitting: rma.glmulti / IC used: aicc
## Level: 1 / Marginality: FALSE
## From 22 models:
## Best IC: 30.6255221455606
## Best model:
## [1] "yi ~ 1 + Order"
## Evidence weight: 0.667135594334537
## Worst IC: 52.7168492698264
## 1 models within 2 IC units.
## 3 models to reach 95% of evidence weight.

##best model
summary(res@objects[[1]])

##
## Multivariate Meta-Analysis Model (k = 52; method: ML)
##
##   logLik  Deviance      AIC      BIC      AICc
##   -2.6298   66.3457   25.2597   44.7721   30.6255
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed  factor
## sigma^2    0.0000   0.0000    35    no     id
```

```
##
## Test for Residual Heterogeneity:
## QE(df = 43) = 66.3457, p-val = 0.0127
##
## Test of Moderators (coefficient(s) 2,3,4,5,6,7,8,9):
## QM(df = 8) = 40.8521, p-val < .0001
##
## Model Results:
##
##               estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          -0.1477  0.0359  -4.1144  <.0001  -0.2181  -0.0774
## OrderAnseriformes    0.1048  0.0594   1.7642  0.0777  -0.0116   0.2212
## OrderSalmoniformes   0.0339  0.0661   0.5131  0.6079  -0.0956   0.1635
## OrderLepidoptera    -0.4103  0.1153  -3.5589  0.0004  -0.6362  -0.1843
## OrderFalconiformes   0.2977  0.1459   2.0405  0.0413   0.0118   0.5837
## OrderAnguilliformes -0.6423  0.1769  -3.6309  0.0003  -0.9890  -0.2956
## OrderClupeiformes    0.0977  0.1063   0.9198  0.3577  -0.1105   0.3060
## OrderCoraciiformes  -0.6823  0.4258  -1.6024  0.1091  -1.5168   0.1522
## OrderCharadriiformes 0.0477  0.1063   0.4492  0.6533  -0.1605   0.2560
##
## intrcpt          ***
## OrderAnseriformes      .
## OrderSalmoniformes
## OrderLepidoptera      ***
## OrderFalconiformes     *
## OrderAnguilliformes    ***
## OrderClupeiformes
## OrderCoraciiformes
## OrderCharadriiformes
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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



```
summary(res@objects[[2]])
```

```
##
## Multivariate Meta-Analysis Model (k = 52; method: ML)
```

```
##
##   logLik  Deviance      AIC      BIC      AICc
## -2.5932   66.2725   27.1864   48.6501   33.7864
```

```
## Variance Components:
```

```
##
##           estim      sqrt  nlvls  fixed  factor
## sigma^2    0.0000   0.0000    35    no     id
```

```
## Test for Residual Heterogeneity:
```

```
## QE(df = 42) = 66.2725, p-val = 0.0099
```

```
## Test of Moderators (coefficient(s) 2,3,4,5,6,7,8,9,10):
```

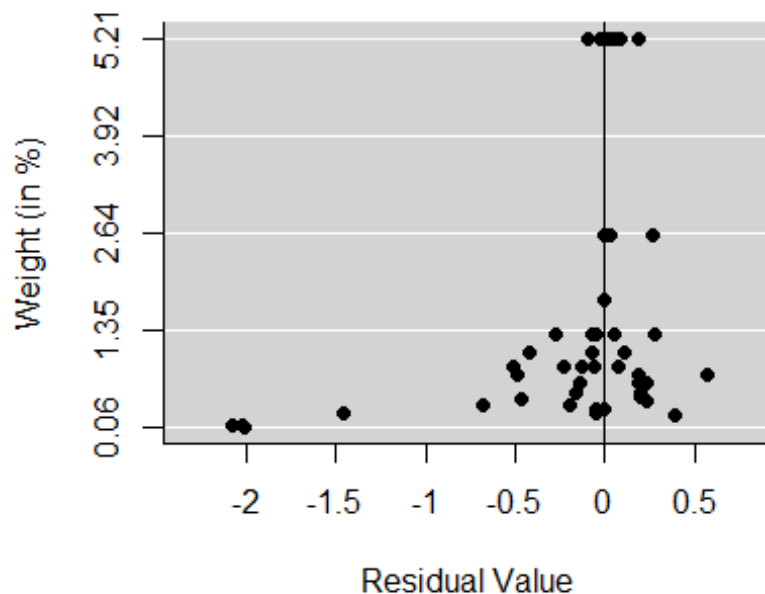
```
## QM(df = 9) = 40.9253, p-val < .0001
```

```
## Model Results:
```

```
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          -0.1601  0.0582  -2.7526  0.0059  -0.2741  -0.0461
## OrderAnseriformes    0.1136  0.0678   1.6763  0.0937  -0.0192   0.2465
## OrderSalmoniformes   0.0414  0.0717   0.5779  0.5633  -0.0991   0.1819
## OrderLepidoptera    -0.4105  0.1153  -3.5612  0.0004  -0.6365  -0.1846
## OrderFalconiformes   0.3101  0.1529   2.0280  0.0426   0.0104   0.6098
```

```
## OrderAnguilliformes    -0.6457  0.1773  -3.6410  0.0003  -0.9933  -0.2981
## OrderClupeiformes      0.1101  0.1157   0.9519  0.3412  -0.1166   0.3369
## OrderCoraciiformes    -0.6699  0.4282  -1.5643  0.1177  -1.5092   0.1694
## OrderCharadriiformes   0.0601  0.1157   0.5197  0.6033  -0.1666   0.2869
## migratory.leg2Y        0.0158  0.0585   0.2706  0.7867  -0.0988   0.1305
##
## intrcpt                **
## OrderAnseriformes      .
## OrderSalmoniformes
## OrderLepidoptera       ***
## OrderFalconiformes     *
## OrderAnguilliformes    ***
## OrderClupeiformes
## OrderCoraciiformes
## OrderCharadriiformes
## migratory.leg2Y
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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



```
summary(res@objects[[3]])

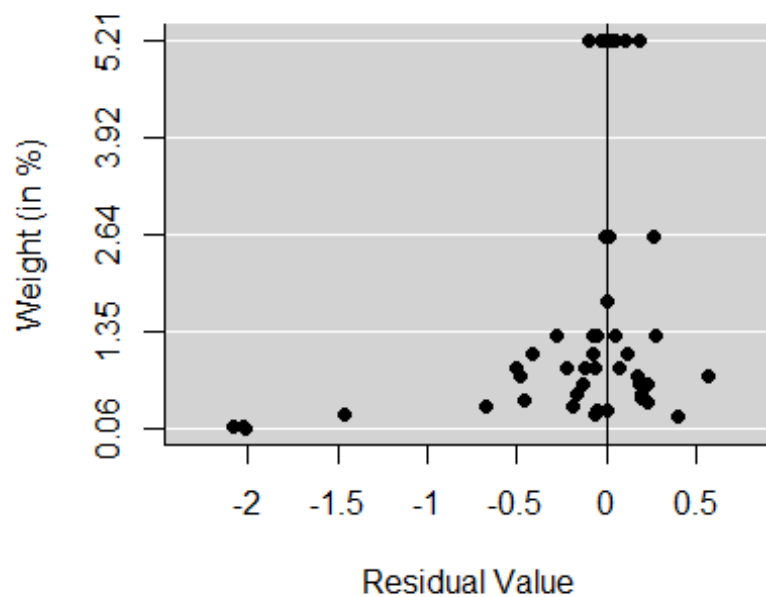
##
## Multivariate Meta-Analysis Model (k = 52; method: ML)
##
```

```

##   logLik   Deviance      AIC      BIC      AICc
## -2.6277   66.3415   27.2554   48.7191   33.8554
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed  factor
## sigma^2    0.0000   0.0000    35    no     id
##
## Test for Residual Heterogeneity:
## QE(df = 42) = 66.3415, p-val = 0.0097
##
## Test of Moderators (coefficient(s) 2,3,4,5,6,7,8,9,10):
## QM(df = 9) = 40.8564, p-val < .0001
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          -0.1519  0.0724  -2.0965  0.0360  -0.2938  -0.0099
## OrderAnseriformes    0.1044  0.0597   1.7505  0.0800  -0.0125   0.2214
## OrderSalmoniformes   0.0366  0.0776   0.4713  0.6374  -0.1155   0.1887
## OrderLepidoptera    -0.4099  0.1154  -3.5525  0.0004  -0.6361  -0.1838
## OrderFalconiformes   0.2971  0.1462   2.0322  0.0421   0.0106   0.5837
## OrderAnguilliformes -0.6429  0.1771  -3.6293  0.0003  -0.9900  -0.2957
## OrderClupeiformes    0.0971  0.1067   0.9106  0.3625  -0.1119   0.3062
## OrderCoraciiformes  -0.6781  0.4304  -1.5756  0.1151  -1.5217   0.1654
## OrderCharadriiformes 0.0471  0.1067   0.4418  0.6586  -0.1619   0.2562
## type0               0.0047  0.0722   0.0655  0.9478  -0.1368   0.1463
##
## intrcpt          *
## OrderAnseriformes .
## OrderSalmoniformes
## OrderLepidoptera  ***
## OrderFalconiformes *
## OrderAnguilliformes ***
## OrderClupeiformes
## OrderCoraciiformes
## OrderCharadriiformes
## type0
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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

```

```
#####best
model#####

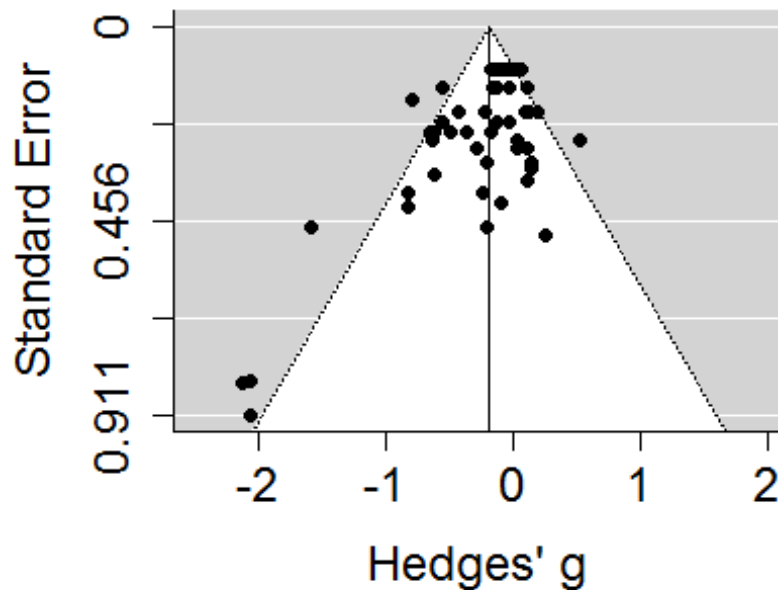
##null model

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

##
## Multivariate Meta-Analysis Model (k = 52; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -19.2159   38.4319   42.4319   46.2955   42.6819
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed  factor
## sigma^2    0.0342   0.1850    35     no      id
##
## Test for Heterogeneity:
## Q(df = 51) = 107.1978, p-val < .0001
##
## Model Results:
##
```

```
## estimate      se      zval      pval      ci.lb      ci.ub      ***
## -0.1850      0.0431     -4.2967     <.0001     -0.2694     -0.1006
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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)
##capped variance (vi1)

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

##
## Multivariate Meta-Analysis Model (k = 52; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -12.0233   24.0467   52.0467   75.3366   69.5467
##
## Variance Components:
##
```

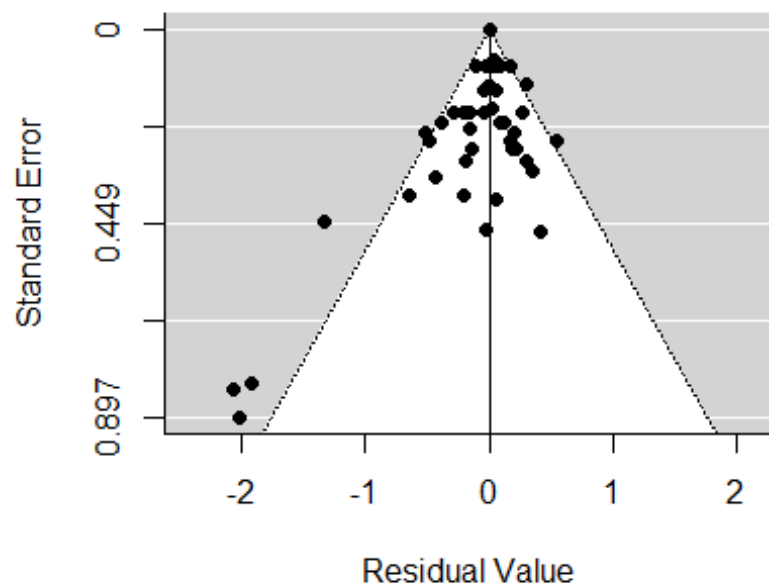
```

##          estim      sqrt  nlvls  fixed  factor
## sigma^2    0.0000  0.0000    35    no      id
##
## Test for Residual Heterogeneity:
## QE(df = 39) = 65.1334, p-val = 0.0054
##
## Test of Moderators (coefficient(s) 2,3,4,5,6,7,8,9,10,11,12,13):
## QM(df = 12) = 42.0645, p-val < .0001
##
## Model Results:
##
##          estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          -0.1414  0.0563  -2.5130  0.0120  -0.2517  -0.0311
## traitRefuelling    -0.0137  0.1573  -0.0871  0.9306  -0.3220  0.2946
## traitMovement      -0.1206  0.1330  -0.9068  0.3645  -0.3814  0.1401
## traitPhenology     -0.0359  0.0728  -0.4925  0.6224  -0.1785  0.1068
## traitSurvival       0.0111  0.0758   0.1469  0.8832  -0.1374  0.1597
## OrderAnseriformes   0.1161  0.0651   1.7830  0.0746  -0.0115  0.2438
## OrderSalmoniformes  0.0214  0.0777   0.2757  0.7828  -0.1309  0.1738
## OrderLepidoptera    -0.3201  0.1574  -2.0337  0.0420  -0.6285  -0.0116
## OrderFalconiformes  0.2803  0.1520   1.8442  0.0652  -0.0176  0.5782
## OrderAnguilliformes -0.5279  0.2207  -2.3921  0.0168  -0.9605  -0.0954
## OrderClupeiformes   0.0914  0.1147   0.7967  0.4256  -0.1335  0.3163
## OrderCoraciiformes -0.6886  0.4280  -1.6089  0.1076  -1.5274  0.1502
## OrderCharadriiformes 0.0303  0.1144   0.2646  0.7913  -0.1940  0.2546
##
## intrcpt          *
## traitRefuelling
## traitMovement
## traitPhenology
## traitSurvival
## OrderAnseriformes  .
## OrderSalmoniformes
## OrderLepidoptera   *
## OrderFalconiformes .
## OrderAnguilliformes *
## OrderClupeiformes
## OrderCoraciiformes
## OrderCharadriiformes
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

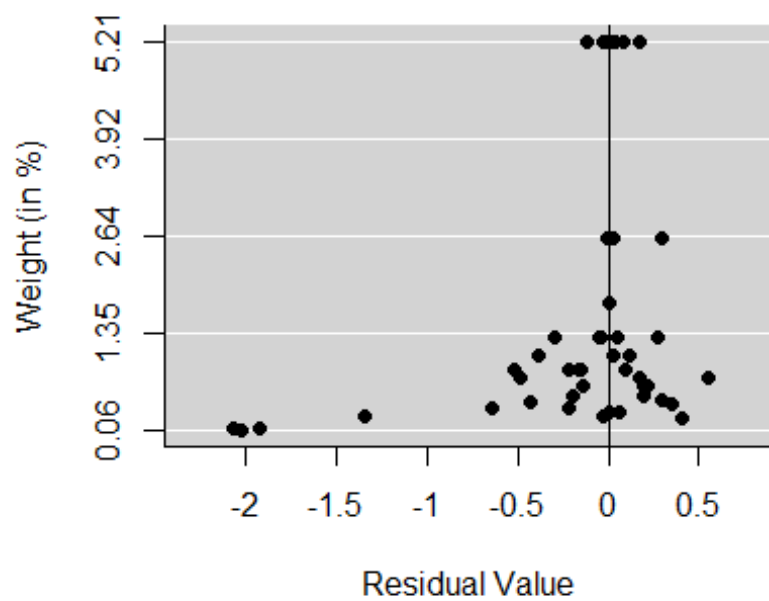
#I2 = 40%

funnel(best.model1)

```



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



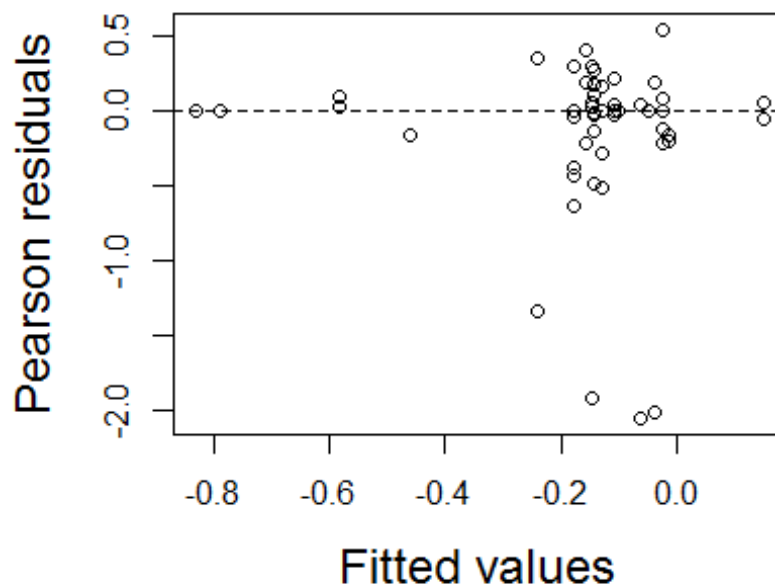
```
##make table of best model (table 3a)

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")

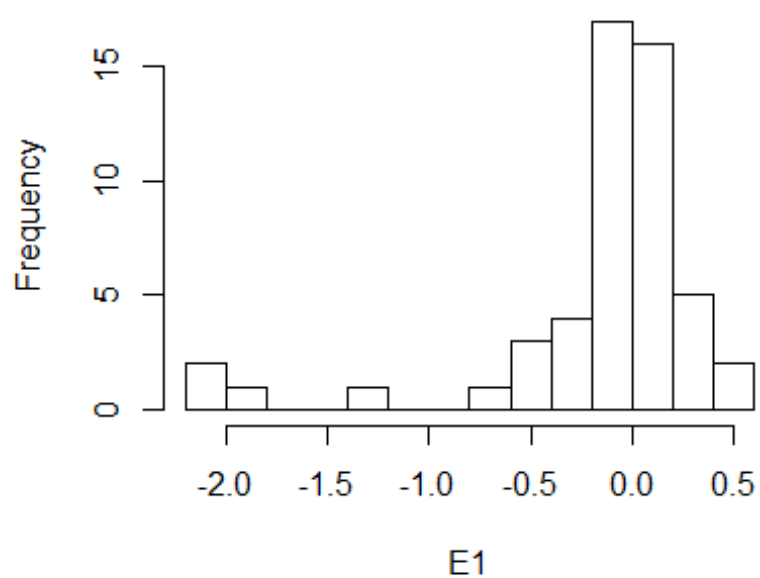
##plot resid

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)
```

Histogram of E1



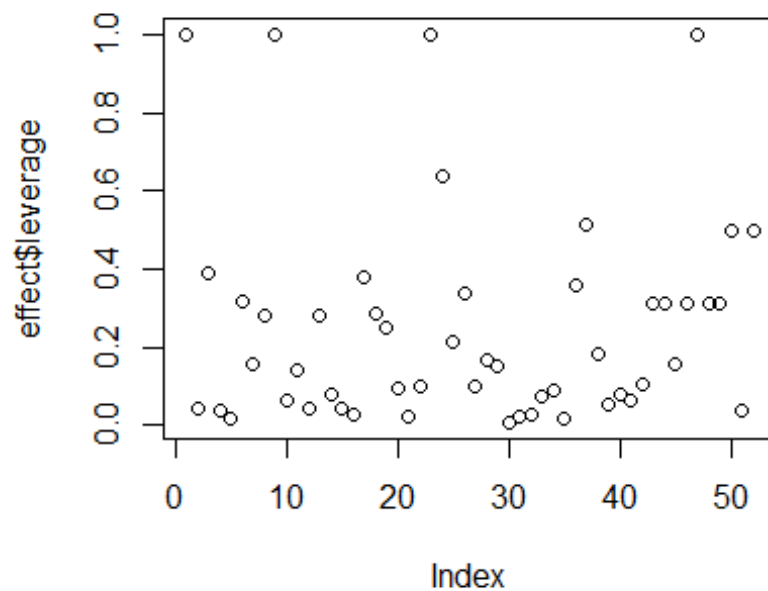
```
##save fitted and residuals and hat values

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

mean(effect$leverage)

## [1] 0.25

plot(effect$leverage)
```



```
subset(effect, resid < -1)
```

```
##      id rowid
## 99 50      73
## 98 50      72
## 46 53      79
## 97 50      71
##
## authors
## 99 van Gils, JA; Munster, VJ; Radersma, R; Liefhebber, D; Fouchier, RAM;
Klaassen, M
## 98 van Gils, JA; Munster, VJ; Radersma, R; Liefhebber, D; Fouchier, RAM;
Klaassen, M
## 46                                Kocan, R; LaPatra, S; Gregg, J; Winton, J;
Hershberger, P
## 97 van Gils, JA; Munster, VJ; Radersma, R; Liefhebber, D; Fouchier, RAM;
Klaassen, M
##
## title
## 99 Hampered Foraging and Migratory Performance in Swans Infected with Low-
Pathogenic Avian Influenza A Virus
## 98 Hampered Foraging and Migratory Performance in Swans Infected with Low-
Pathogenic Avian Influenza A Virus
## 46                                Ichthyophonus-induced cardiac damage: a mechanism for
reduced swimming stamina in salmonids
## 97 Hampered Foraging and Migratory Performance in Swans Infected with Low-
Pathogenic Avian Influenza A Virus
```

journal year
99 PLOS ONE 2007
98 PLOS ONE 2007
46 JOURNAL OF FISH DISEASES 2006
97 PLOS ONE 2007
##

abstract

99 It is increasingly acknowledged that migratory birds, notably waterfowl, play a critical role in the maintenance and spread of influenza A viruses. In order to elucidate the epidemiology of influenza A viruses in their natural hosts, a better understanding of the pathological effects in these hosts is required. Here we report on the feeding and migratory performance of wild migratory Bewick's swans (*Cygnus columbianus bewickii* Yarrell) naturally infected with low-pathogenic avian influenza (LPAI) A viruses of subtypes H6N2 and H6N8. Using information on geolocation data collected from Global Positioning Systems fitted to neck-collars, we show that infected swans experienced delayed migration, leaving their wintering site more than a month after uninfected animals. This was correlated with infected birds travelling shorter distances and fuelling and feeding at reduced rates. The data suggest that LPAI virus infections in wild migratory birds may have higher clinical and ecological impacts than previously recognised.

98 It is increasingly acknowledged that migratory birds, notably waterfowl, play a critical role in the maintenance and spread of influenza A viruses. In order to elucidate the epidemiology of influenza A viruses in their natural hosts, a better understanding of the pathological effects in these hosts is required. Here we report on the feeding and migratory performance of wild migratory Bewick's swans (*Cygnus columbianus bewickii* Yarrell) naturally infected with low-pathogenic avian influenza (LPAI) A viruses of subtypes H6N2 and H6N8. Using information on geolocation data collected from Global Positioning Systems fitted to neck-collars, we show that infected swans experienced delayed migration, leaving their wintering site more than a month after uninfected animals. This was correlated with infected birds travelling shorter distances and fuelling and feeding at reduced rates. The data suggest that LPAI virus infections in wild migratory birds may have higher clinical and ecological impacts than previously recognised.

46

Swimming stamina, measured as time-to-fatigue, was reduced by approximately two-thirds in rainbow trout experimentally infected with *Ichthyophonus*. Intensity of *Ichthyophonus* infection was most severe in cardiac muscle but multiple organs were infected to a lesser extent. The mean heart weight of infected fish was 40% greater than that of uninfected fish, the result of parasite biomass, infiltration of immune cells and fibrotic (granuloma) tissue surrounding the parasite. Diminished swimming stamina is hypothesized to be due to cardiac failure resulting from the combination of parasite-damaged heart muscle and low myocardial oxygen supply during sustained aerobic exercise. Loss of stamina in *Ichthyophonus*-infected salmonids could explain the poor performance previously reported for wild Chinook and sockeye salmon stocks during their spawning migration.

97 It is increasingly acknowledged that migratory birds, notably waterfowl, play a critical role in the maintenance and spread of influenza A viruses. In order to elucidate the epidemiology of influenza A viruses in their natural hosts, a better understanding of the pathological effects in these hosts is required. Here we report on the feeding and migratory performance of wild migratory Bewick's swans (*Cygnus columbianus bewickii* Yarrell) naturally infected with low-pathogenic avian influenza (LPAI) A viruses of subtypes H6N2 and H6N8. Using information on geolocation data collected from Global Positioning Systems fitted to neck-collars, we show that infected swans experienced delayed migration, leaving their wintering site more than a month after uninfected animals. This was correlated with infected birds travelling shorter distances and fuelling and feeding at reduced rates. The data suggest that LPAI virus infections in wild migratory birds may have higher clinical and ecological impacts than previously recognised.

##	type	trait	measure	exp.methods	species
## 99	0	Refuelling	Feeding rate	na	Bewick swan
## 98	0	Movement	Distance travelled	na	Bewick swan
## 46	E	Movement	Endurance	Parasite addition	Rainbow trout
## 97	0	Phenology	Spring departure	na	Bewick swan

##	latin taxa	Order	Family	strain
## 99	<i>Cygnus columbianus bewickii</i>	Bird Anseriformes	Anatidae	LPAIV
## 98	<i>Cygnus columbianus bewickii</i>	Bird Anseriformes	Anatidae	LPAIV
## 46	<i>Oncorhynchus mykiss</i>	Fish Salmoniformes	Salmonidae	Ichthyophonous
## 97	<i>Cygnus columbianus bewickii</i>	Bird Anseriformes	Anatidae	LPAIV

##	parasite.taxa	life.history.measured	setting	subset	Infection.type
## 99	Virus	Non-breeding	Field	all	Single
## 98	Virus	Migration	Field	all	Single
## 46	Protozoa	Lab	Lab	all	Single
## 97	Virus	Non-breeding	Field	all	Single

##	migratory.leg2	ss	ss_infected	ss_healthy	slope	effect
## 99	N 6	2	4	Not presented	22.96	
## 98	N 12	2	10	Not presented	11.03	
## 46	N 22	11	11	6.5	Not presented	
## 97	N 12	2	10	Not presented	10.53	

##	stat	presented.p	adj.p	sig0.05	infection.measure	z	var.z	g
## 99	F	<0.05	0.0410	1	Infection status	-1.02	0.33	-2.06
## 98	F	<0.05	0.0160	1	Infection status	-0.76	0.11	-2.07
## 46	t	0.001	0.0010	1	Infection status	-0.75	0.05	-1.58
## 97	F	<0.05	0.0142	1	Infection status	-0.78	0.11	-2.12

##	var.g	var.g1	function.	Effect.direction	yi	vi	vil
## 99	0.83	0.83	pes(0.041,2,4)	Negative	-2.06	0.83	0.83
## 98	0.69	0.69	pes(0.016,2,10)	Negative	-2.07	0.69	0.69
## 46	0.22	0.22	pes(0.001,11,11)	Negative	-1.58	0.22	0.22
## 97	0.70	0.70	pes(0.0142,2,10)	Negative	-2.12	0.70	0.70

##	resids	predicted	leverage
## 99	-2.021023	-0.03897662	0.029914145
## 98	-1.924077	-0.14592324	0.024298957
## 46	-1.339376	-0.24062372	0.098078320
## 97	-2.058862	-0.06113818	0.007315035

```

##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)

##PLOT ESTIMATES (Figure 3)

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

##
## Multivariate Meta-Analysis Model (k = 52; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -12.0233   24.0467   52.0467   75.3366   69.5467
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed  factor
## sigma^2    0.0000   0.0000    35    no     id
##
## Test for Residual Heterogeneity:
## QE(df = 39) = 65.1334, p-val = 0.0054
##
## Test of Moderators (coefficient(s) 2,3,4,5,6,7,8,9,10,11,12,13):
## QM(df = 12) = 42.0645, p-val < .0001
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          -0.1414  0.0563  -2.5130  0.0120  -0.2517  -0.0311
## traitRefuelling   -0.0137  0.1573  -0.0871  0.9306  -0.3220  0.2946
## traitMovement     -0.1206  0.1330  -0.9068  0.3645  -0.3814  0.1401
## traitPhenology     -0.0359  0.0728  -0.4925  0.6224  -0.1785  0.1068
## traitSurvival       0.0111  0.0758   0.1469  0.8832  -0.1374  0.1597
## OrderAnseriformes   0.1161  0.0651   1.7830  0.0746  -0.0115  0.2438
## OrderSalmoniformes  0.0214  0.0777   0.2757  0.7828  -0.1309  0.1738
## OrderLepidoptera    -0.3201  0.1574  -2.0337  0.0420  -0.6285  -0.0116
## OrderFalconiformes  0.2803  0.1520   1.8442  0.0652  -0.0176  0.5782
## OrderAnguilliformes -0.5279  0.2207  -2.3921  0.0168  -0.9605  -0.0954
## OrderClupeiformes   0.0914  0.1147   0.7967  0.4256  -0.1335  0.3163
## OrderCoraciiformes  -0.6886  0.4280  -1.6089  0.1076  -1.5274  0.1502
## OrderCharadriiformes 0.0303  0.1144   0.2646  0.7913  -0.1940  0.2546
##
## intrcpt          *
## traitRefuelling
## traitMovement
## traitPhenology

```

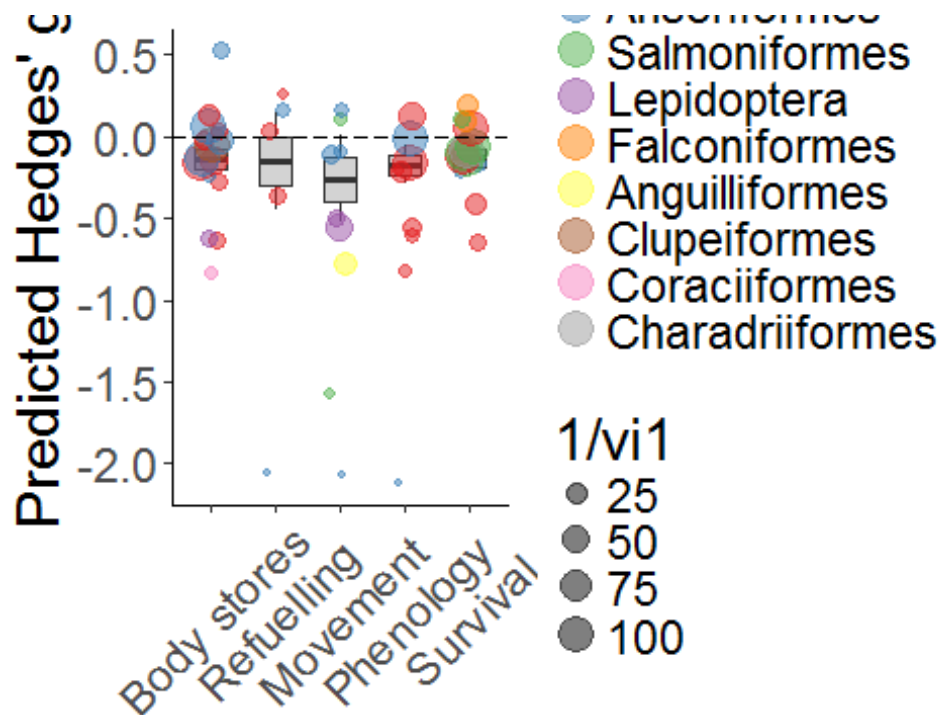
```
## traitSurvival  
## OrderAnseriformes .  
## OrderSalmoniformes  
## OrderLepidoptera *  
## OrderFalconiformes .  
## OrderAnguilliformes *  
## OrderClupeiformes  
## OrderCoraciiformes  
## OrderCharadriiformes  
##  
## ---  
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1  
  
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)))

## Warning: Ignoring unknown aesthetics: width

```



#####fig 3b

```

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 = effect, aes(x= trait, y = yi, size = 1/vi1, col =
parasite.taxa),width=0.1, alpha=1/2)+
  labs(y="Hedges' g", x = "")+geom_hline(yintercept=0, linetype="longdash")+
  theme_bw() + theme(text = element_text(size=22),axis.text.x =

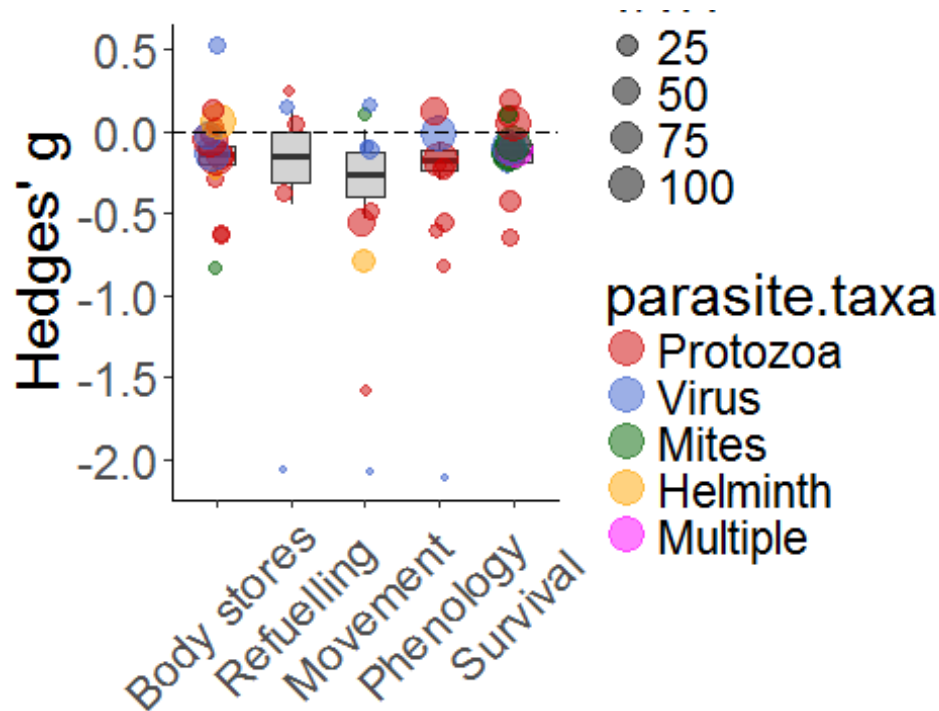
```

```

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", "magenta", "cyan3"))+
  guides(colour = guide_legend(override.aes = list(size=6)))

```

```
## Warning: Ignoring unknown aesthetics: width
```



```
#####
#####
```

```
#####modelling traits seperately
```

```

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)
```

```
##
## Multivariate Meta-Analysis Model (k = 15; method: REML)
##
```

```
##   logLik  Deviance      AIC      BIC      AICc
## -1.4741    2.9483    6.9483    8.2264    8.0392
##
```

```
## Variance Components:
```

```
##
##           estim      sqrt  nlvls  fixed  factor
## sigma^2    0.0030  0.0544     15     no      id
##
```

```
## Test for Heterogeneity:
```

```
## Q(df = 14) = 22.9530, p-val = 0.0610
##
```

```
## Model Results:
```

```
##
## estimate      se      zval      pval      ci.lb      ci.ub
## -0.0943    0.0439   -2.1490    0.0316   -0.1803   -0.0083      *
```

```
## ---
##
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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

```
#I2 = 38
```

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

```
##
## Multivariate Meta-Analysis Model (k = 5; method: REML)
##
```

```
##   logLik  Deviance      AIC      BIC      AICc
## -3.7386    7.4772   11.4772   10.2498   23.4772
##
```

```
## Variance Components:
```

```
##
##           estim      sqrt  nlvls  fixed  factor
## sigma^2    0.0000  0.0000      4     no      id
##
```

```
## Test for Heterogeneity:
```

```
## Q(df = 4) = 7.1940, p-val = 0.1260
##
```

```
## Model Results:
```

```
##
## estimate      se      zval      pval      ci.lb      ci.ub
```

```
## -0.1259  0.1498 -0.8402  0.4008 -0.4196  0.1678
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#I2 = 44%

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

##
## Multivariate Meta-Analysis Model (k = 9; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -7.6154  15.2308  19.2308  19.3897  21.6308
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed  factor
## sigma^2    0.1414  0.3760      9     no      id
##
## Test for Heterogeneity:
## Q(df = 8) = 22.4334, p-val = 0.0042
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub      **
## -0.4664    0.1642  -2.8397    0.0045  -0.7883  -0.1445
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#I2 = 65%

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

##
## Multivariate Meta-Analysis Model (k = 9; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -5.7714  11.5428  15.5428  15.7017  17.9428
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed  factor
## sigma^2    0.0230  0.1516      8     no      id
##
## Test for Heterogeneity:
```

```

## Q(df = 8) = 19.1443, p-val = 0.0141
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## -0.1983      0.0890     -2.2298     0.0258     -0.3727     -0.0240      *
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#I2 = 58%

null15<-rma.mv(yi, vi1, random = ~ 1 | id, data=survival) ##null model
summary(null15)

##
## Multivariate Meta-Analysis Model (k = 14; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
##   4.8968   -9.7936   -5.7936   -4.6637   -4.5936
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed  factor
## sigma^2      0.0000   0.0000     13     no      id
##
## Test for Heterogeneity:
## Q(df = 13) = 13.9475, p-val = 0.3775
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## -0.0959      0.0358     -2.6801     0.0074     -0.1661     -0.0258      **
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# I2 = 18%

pred1<-predict(null11)
pred2<-predict(null12)
pred3<-predict(null13)
pred4<-predict(null14)
pred5<-predict(null15)

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)

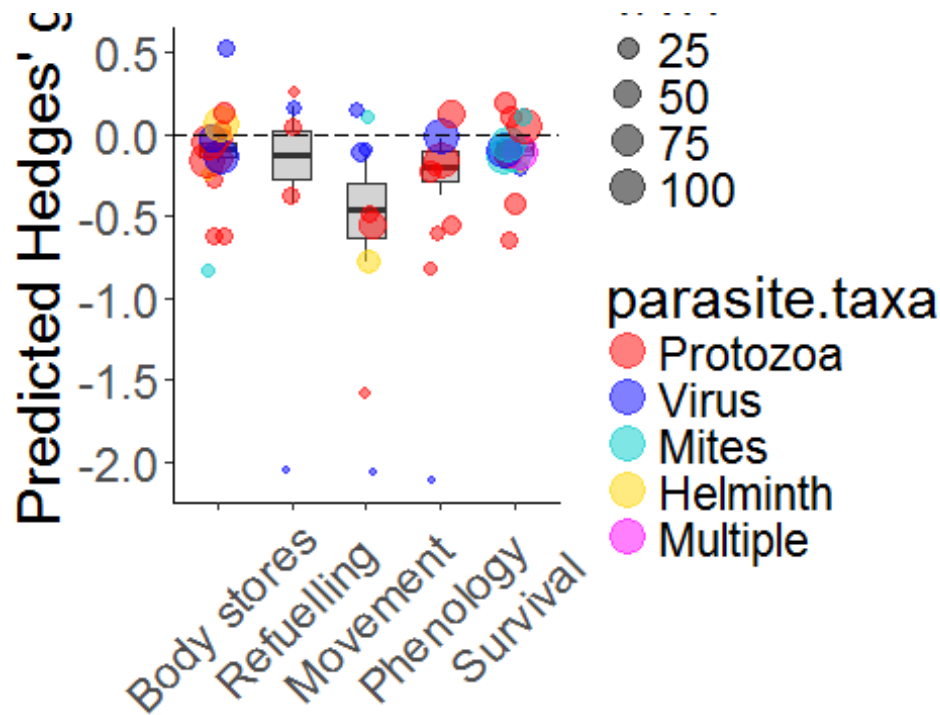
## 'data.frame':    5 obs. of  5 variables:
## $ predicted: num  -0.0943 -0.1259 -0.4664 -0.1983 -0.0959
## $ se       : num   0.0439 0.1498 0.1642 0.089 0.0358
## $ l.ci     : num  -0.18 -0.42 -0.788 -0.373 -0.166
## $ u.ci     : num  -0.0083 0.1678 -0.1445 -0.024 -0.0258
## $ level    : Factor w/ 5 levels "Body stores",...: 1 2 3 4 5

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

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)))

## Warning: Ignoring unknown aesthetics: width

```



#model with just trait

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

```
##
## Multivariate Meta-Analysis Model (k = 52; method: REML)
##
##   logLik  Deviance      AIC      BIC     AICc
## -15.6441   31.2882   43.2882   54.3891   45.3882
##
## Variance Components:
##
##           estim      sqrt nlvls  fixed  factor
## sigma^2    0.0045   0.0674    35    no     id
##
## Test for Residual Heterogeneity:
## QE(df = 47) = 85.6722, p-val = 0.0005
##
## Test of Moderators (coefficient(s) 2,3,4,5):
## QM(df = 4) = 17.4304, p-val = 0.0016
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      -0.1048  0.0456  -2.3004  0.0214  -0.1942  -0.0155
## traitRefuelling -0.0169  0.1582  -0.1071  0.9147  -0.3270  0.2931
```

*

```

## traitMovement      -0.3826  0.0980  -3.9051  <.0001  -0.5747  -0.1906  ***
## traitPhenology      -0.0400  0.0719  -0.5569  0.5776  -0.1809   0.1009
## traitSurvival       0.0044  0.0618   0.0720  0.9426  -0.1167   0.1256
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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

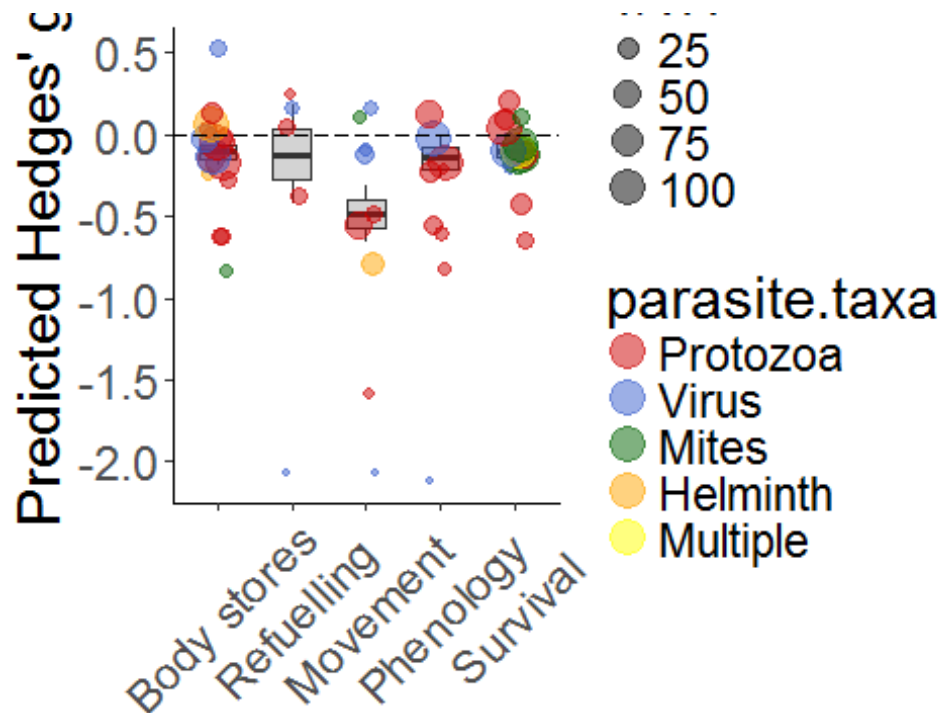
##overlayed with raw data with proportional weights

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)))
```

```
## Warning: Ignoring unknown aesthetics: width
```



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

```
#####SENSITIVITY
ANALYSES#####
```

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

```
##exlude insects in case this biases biases models and rerun
```

```
##exlude outliers and rerun
```

```
###Does not change models overall
```

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

```

##exclude moller as as 9 datapoints so might bias results because so many
#intensity<-subset(intensity, id != "62")

##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","Falcon
iformes",

"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)

## Warning in rma.mv(z, var.z, mods = ~Order, random = ~1 | id, data =
## intensity): Redundant predictors dropped from the model.

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

## Warning in rma.mv(z, var.z, mods = ~parasite.taxa, random = ~1 | id, data
=
## intensity): Redundant predictors dropped from the model.

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)

aicc(model.intensity)

## [1] 42.39734

aicc(model.intensity1)

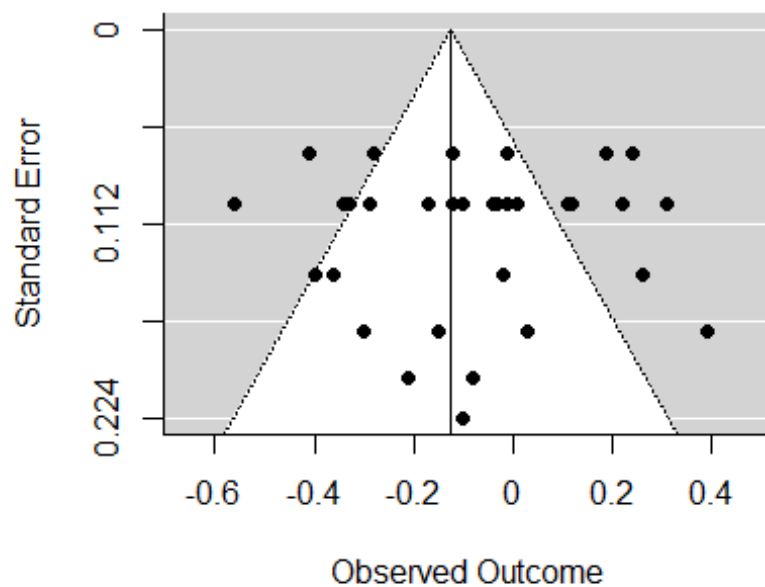
## [1] 67.73933

```

```

aicc(model.intensity2)
## [1] 59.73878
aicc(model.intensity3)
## [1] 65.42541
aicc(model.intensity4)
## [1] 49.45543
aicc(model.intensity5)
## [1] 57.37388
aicc(model.intensity6)
## [1] 54.04641
funnel(model.intensity6)

```



```

summary(model.intensity6)
##
## Multivariate Meta-Analysis Model (k = 33; method: REML)
##
##   logLik  Deviance    AIC    BIC   AICc
## -24.8163  49.6326  53.6326  56.5641  54.0464

```

```
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed  factor
## sigma^2    0.0142  0.1190    13    no     id
##
## Test for Heterogeneity:
## Q(df = 32) = 166.2538, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## -0.1251    0.0405   -3.0904    0.0020   -0.2044   -0.0457      **
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

##best model includes just trait (AICC = 42.4)

summary(model.intensity)

##
## Multivariate Meta-Analysis Model (k = 33; method: REML)
##
##      logLik  Deviance      AIC      BIC      AICC
## -14.8943    29.7886    39.7886    46.6251    42.3973
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed  factor
## sigma^2    0.0239  0.1546    13    no     id
##
## Test for Residual Heterogeneity:
## QE(df = 29) = 155.5302, p-val < .0001
##
## Test of Moderators (coefficient(s) 2,3,4):
## QM(df = 3) = 25.0563, p-val < .0001
##
## Model Results:
##
##      estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          0.0893  0.0677    1.3177    0.1876   -0.0435    0.2221
## traitMovement   -0.2897  0.1338   -2.1645    0.0304   -0.5520   -0.0274      *
## traitPhenology  -0.3297  0.0784   -4.2037 <.0001   -0.4834   -0.1760    ***
## traitSurvival   -0.2817  0.0817   -3.4475  0.0006   -0.4418   -0.1215    ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```
##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
```

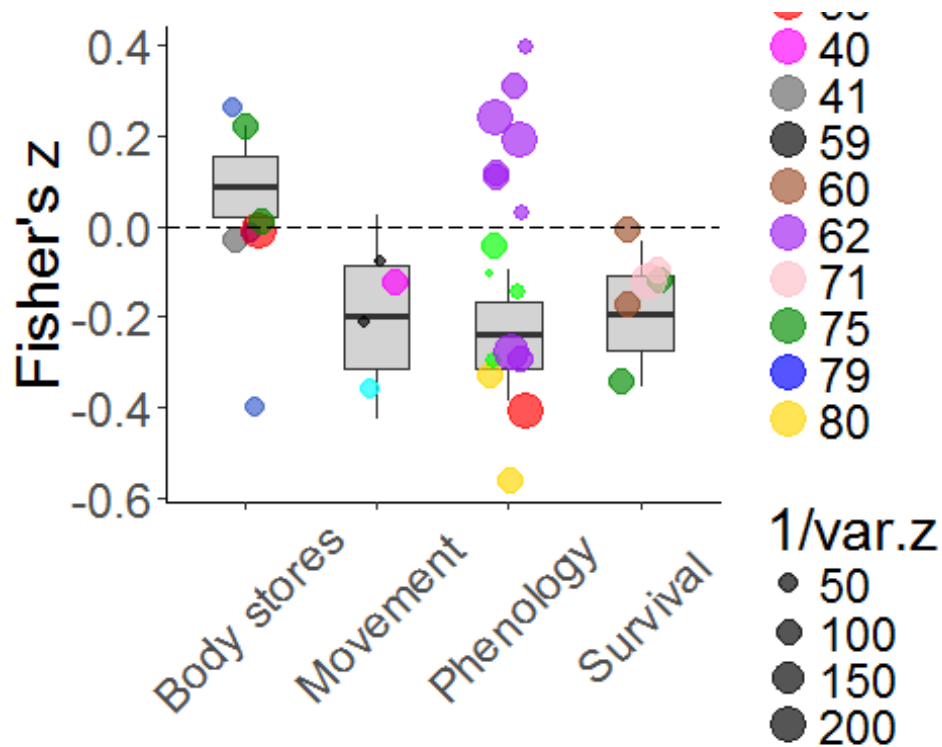
```
ggplot(data=predictedvalues, aes(x=level, y = predicted))+
  geom_boxplot(aes(ymin=l.ci, lower=l.se,
                  middle = predicted, upper = u.se, ymax=u.ci, width = 0.5),
stat="identity", fill="lightgray", lwd=0.7)+
  geom_jitter(data = intensity, aes(x= trait, y = z, size = 1/var.z, col =
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)))

```

```
## Warning: Ignoring unknown aesthetics: width
```



```
#####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)

```

```

##
## Multivariate Meta-Analysis Model (k = 7; method: REML)
##
##   logLik  Deviance      AIC      BIC     AICc

```

```

## -0.4555    0.9110    4.9110    4.4945    8.9110
##
## Variance Components:
##
##          estim    sqrt  nlvls  fixed  factor
## sigma^2    0.0003  0.0165     5     no     id
##
## Test for Heterogeneity:
## Q(df = 6) = 16.2062, p-val = 0.0127
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##   0.0148    0.0401    0.3683    0.7127   -0.0637    0.0932
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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

#I2 = 38

#I2 = 44%

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

##
## Multivariate Meta-Analysis Model (k = 4; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
##   1.6423   -3.2846    0.7154   -1.0874    12.7154
##
## Variance Components:
##
##          estim    sqrt  nlvls  fixed  factor
## sigma^2    0.0000  0.0000     3     no     id
##
## Test for Heterogeneity:
## Q(df = 3) = 2.2447, p-val = 0.5232
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##  -0.1863    0.0707   -2.6340    0.0084   -0.3248   -0.0477      **
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

#I2 = 65%

```
null14<-rma.mv(z, var.z, random = ~ 1 | id, data=phenology) ##null model  
summary(null14)
```

```
##  
## Multivariate Meta-Analysis Model (k = 16; method: REML)  
##  
##   logLik  Deviance      AIC      BIC      AICc  
## -16.6213  33.2426  37.2426  38.6587  38.2426  
##  
## Variance Components:  
##  
##           estim      sqrt  nlvls  fixed  factor  
## sigma^2    0.0576  0.2401     4    no     id  
##  
## Test for Heterogeneity:  
## Q(df = 15) = 131.0194, p-val < .0001  
##  
## Model Results:  
##  
## estimate      se      zval      pval      ci.lb      ci.ub  
## -0.2209    0.1242   -1.7792    0.0752   -0.4643    0.0224      .  
##  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

#I2 = 58%

```
null15<-rma.mv(z, var.z, random = ~ 1 | id, data=survival) ##null model  
summary(null15)
```

```
##  
## Multivariate Meta-Analysis Model (k = 6; method: REML)  
##  
##   logLik  Deviance      AIC      BIC      AICc  
##   4.1603  -8.3207  -4.3207  -5.1018   1.6793  
##  
## Variance Components:  
##  
##           estim      sqrt  nlvls  fixed  factor  
## sigma^2    0.0004  0.0188     3    no     id  
##  
## Test for Heterogeneity:  
## Q(df = 5) = 6.0600, p-val = 0.3004  
##  
## Model Results:  
##  
## estimate      se      zval      pval      ci.lb      ci.ub
```

```
## -0.1404  0.0394 -3.5640  0.0004 -0.2176 -0.0632      ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# 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)

## 'data.frame':  4 obs. of  5 variables:
## $ predicted: num  0.0148 -0.1863 -0.2209 -0.1404
## $ se       : num  0.0401 0.0707 0.1242 0.0394
## $ l.ci     : num  -0.0637 -0.3248 -0.4643 -0.2176
## $ u.ci     : num  0.0932 -0.0477 0.0224 -0.0632
## $ level    : Factor w/ 4 levels "Body stores",...: 1 2 3 4

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

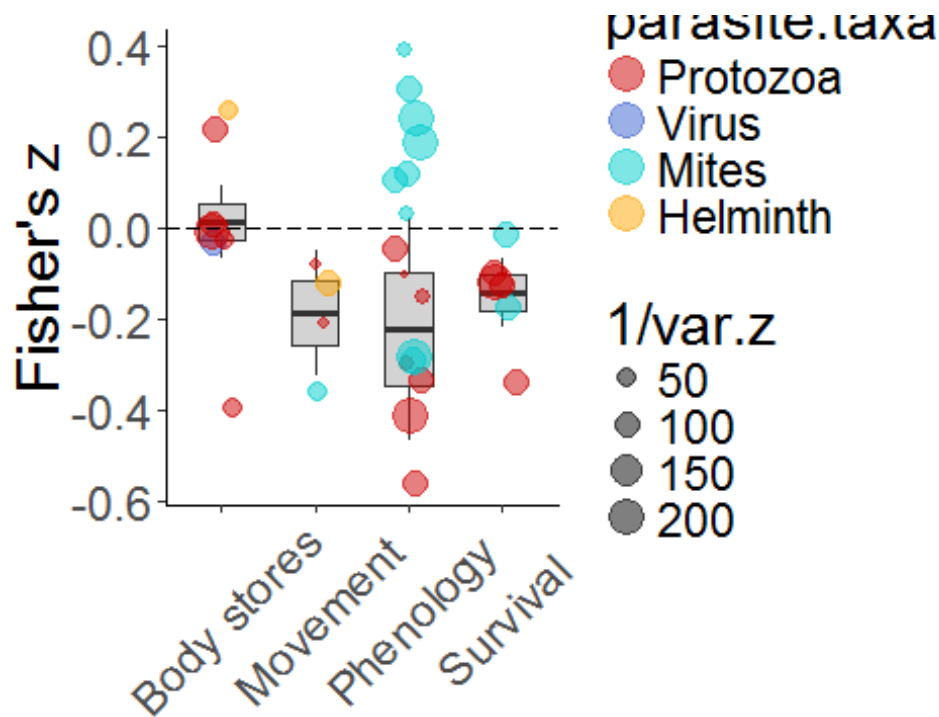
ggplot(data=predictedvalues, aes(x=level, y = predicted, fill =
parasite.taxa))+
  geom_boxplot(aes(ymin=l.ci, lower=l.se,
                    middle = predicted, upper = u.se, ymax=u.ci, width = 0.5),
stat="identity", fill="lightgray", lwd=0.7)+
  geom_jitter(data = intensity, aes(x= trait, y = z, size = 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)))

## Warning: Ignoring unknown aesthetics: width

```



##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 =

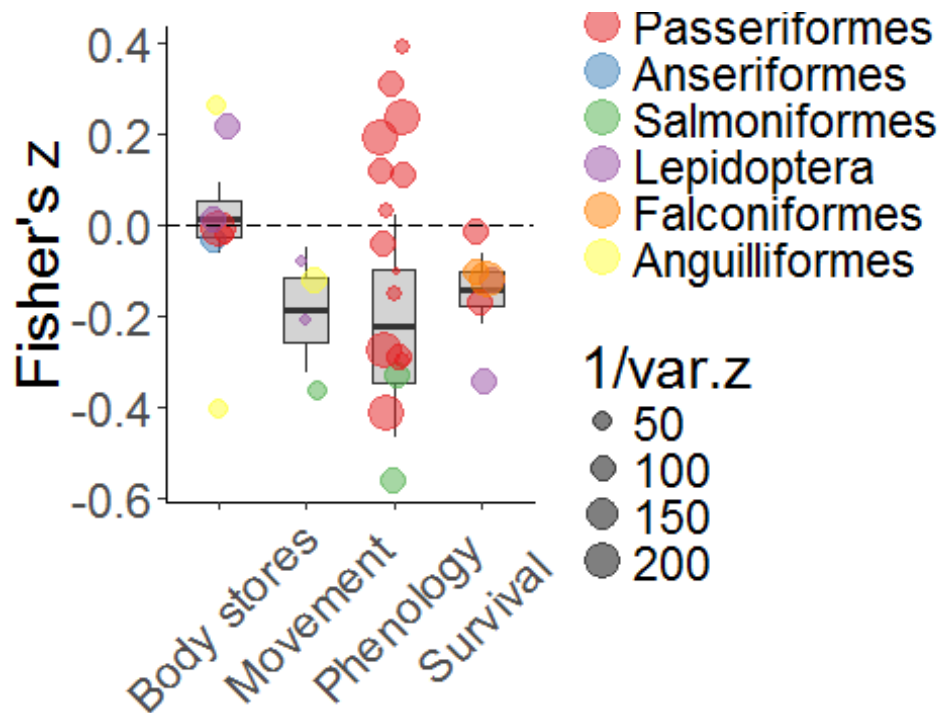
```

```

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)))

```

```
## Warning: Ignoring unknown aesthetics: width
```



```
#####END#####
```