

Rcode.R

arisely

Fri Sep 08 11:57:26 2017

```
## R script for analysis in the article "Migratory animals feel the cost of infection: a meta-
analysis across species"
#Alice Risely, Marcel Klaassen, & Bethany Hoyer
# For full data sets (including excluded points due to unclear effect direction, etc), go to g
ithub.com/Riselya

##R version 3.4.1
##contact riselya@gmail.com

library(metafor)

## Loading required package: Matrix

## Loading 'metafor' package (version 2.0-0). For an overview
## and introduction to the package please type: help(metafor).

library(ggplot2)
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

#for phylogenetic tree
library(rotl)
library(ape)

##
## Attaching package: 'ape'

## The following object is masked from 'package:glmulti':
##
##      consensus

##import data file "Supplementary File 3.csv" as 'all_data'

all_data <- read.csv("Supplementary File 3.csv")

##### DATA

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

###definitions for all variable

names(all_data)

## [1] "id" "rowid"
## [3] "authors" "title"
## [5] "journal" "year"
## [7] "abstract" "type"
## [9] "trait" "measure"
## [11] "exp.methods" "species"
## [13] "species_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] "species_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" ##estimation of whether a migratory leg occurred before infection and sampling (Y/N)
#[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. For info only
#[40] "Effect.direction" ##effect direction (negative/positive)

unique(all_data$id) ##41 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(all_data)
```

```
## '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 prov
ides 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 1
5 ...
## $ year : int 2015 1999 1999 1999 1999 2009 2009 2009 2011 2011 ...
## $ abstract : Factor w/ 41 levels "Animal movements may contribute to the sprea
d of pathogens. In the case of avian influenza virus, [migratory] b"| __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 1
7 ...
## $ 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 1
3 13 ...
## $ species_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 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 5
7 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.gl : 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
all_data$id<-factor(all_data$id)
all_data$rowid<-factor(all_data$rowid)
all_data$ss<-as.character(all_data$ss) #two step conversion
all_data$ss<-as.numeric(all_data$ss)
all_data$ss_infected<-as.character(all_data$ss_infected) #two step conversion
all_data$ss_infected<-as.numeric(all_data$ss_infected)
```

```
## Warning: NAs introduced by coercion
```

```
all_data$ss_healthy<-as.character(all_data$ss_healthy)
all_data$ss_healthy<-as.numeric(all_data$ss_healthy)
```

```
## Warning: NAs introduced by coercion
```

```
all_data$sig0.05<-factor(all_data$sig0.05)

##### get phylogenetic tree for all host species to add OTT_ID (Tree of life)
to dataframe. Need for later analyses.

##### supplementary material

## create seperate phylo trees for each status and intesity dataset

species<-unique(all_data$species_latin)

taxa<-tnrs_match_names(names= c("Acrocephalus arundinaceus",
                                "Anas crecca",
                                "Anas platyrhynchos",
                                "Anguilla anguilla",
                                "Arenaria interpres",
                                "Chen caerulescens",
                                "Clupea harengus",
                                "Cygnus columbianus",
                                "Danaus plexippus",
                                "Delichon urbica",
                                "Falco sparverius",
                                "Ficedula hypoleuca",
                                "Hirundo pyrrhonota",
                                "Hirundo rustica",
                                "Luscinia svecica",
                                "Merops apiaster",
                                "Oncorhynchus gorbusha",
                                "Oncorhynchus mykiss",
                                "Oncorhynchus nerka",
                                "Progne subis",
```

```
"Salmo salar",
"Setophaga coronata",
"Setophaga magnolia",
"Sylvia atricapilla",
"Sylvia borin"))
```

taxa #all species assigned correctly

```
##          search_string
## 1  acrocephalus arundinaceus
## 2          anas crecca
## 3  anas platyrhynchos
## 4  anguilla anguilla
## 5  arenaria interpres
## 6  chen caerulescens
## 7  clupea harengus
## 8  cygnus columbianus
## 9  danaus plexippus
## 10  delichon urbica
## 11  falco sparverius
## 12  ficedula hypoleuca
## 13  hirundo pyrrhonota
## 14  hirundo rustica
## 15  luscinia svecica
## 16  merops apiaster
## 17  oncorhynchus gorbusha
## 18  oncorhynchus mykiss
## 19  oncorhynchus nerka
## 20  progne subis
## 21  salmo salar
## 22  setophaga coronata
## 23  setophaga magnolia
## 24  sylvia atricapilla
## 25  sylvia borin
##
##          unique_name approximate_match
## 1  Acrocephalus arundinaceus          FALSE
## 2  Anas crecca                      FALSE
## 3  Anas platyrhynchos                FALSE
## 4  Anguilla anguilla                 FALSE
## 5  Arenaria interpres                FALSE
## 6  Anser caerulescens                FALSE
## 7  Clupea harengus                  FALSE
## 8  Cygnus columbianus                FALSE
## 9  Danaus plexippus                  FALSE
## 10 Delichon urbicum                  FALSE
## 11 Falco sparverius                  FALSE
## 12 Ficedula hypoleuca                FALSE
## 13 Petrochelidon pyrrhonota          FALSE
## 14 Hirundo rustica                   FALSE
## 15 Luscinia svecica                   FALSE
## 16 Merops apiaster                   FALSE
## 17 Oncorhynchus gorbusha              FALSE
## 18 Oncorhynchus mykiss (species in domain Eukaryota) FALSE
```

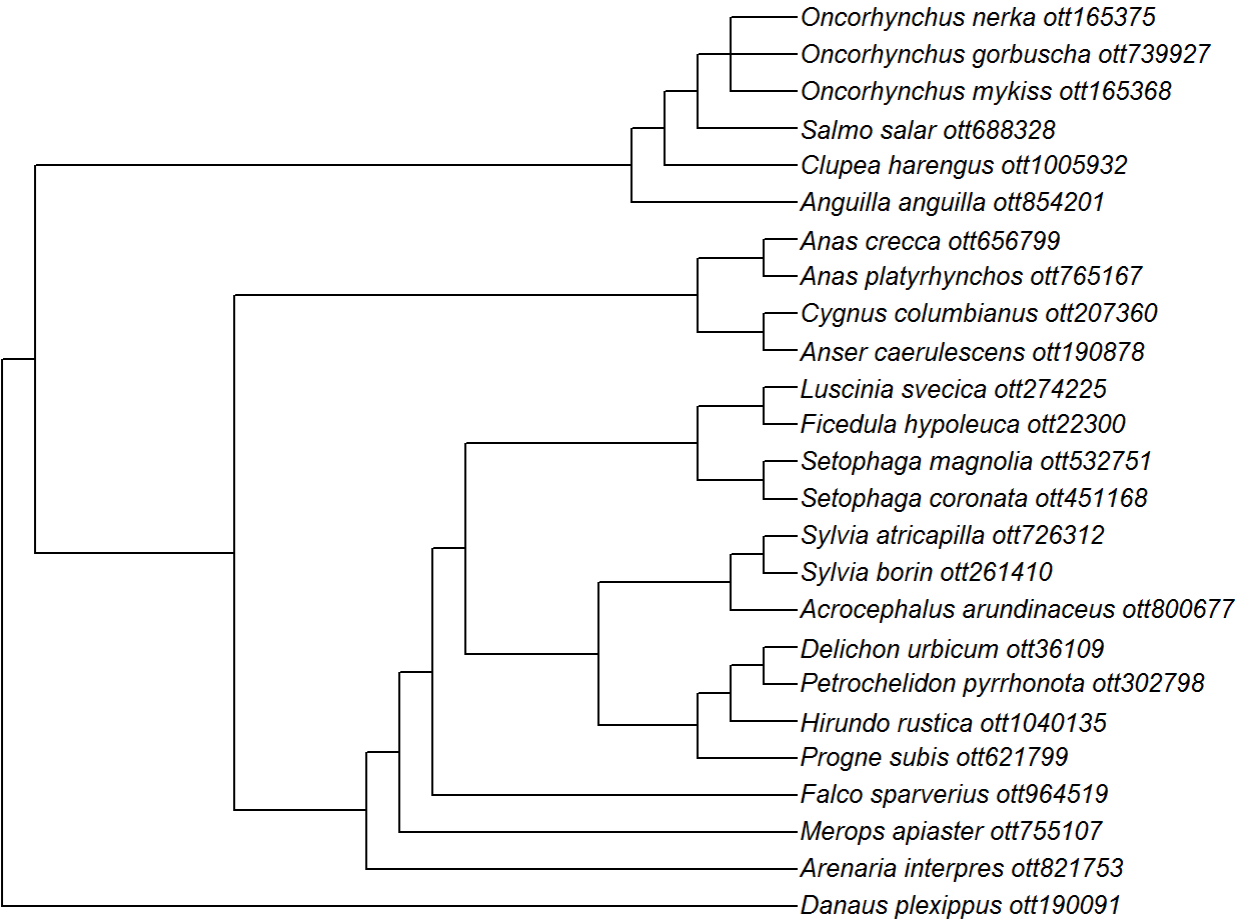
##	19		Oncorhynchus nerka	FALSE
##	20		Progne subis	FALSE
##	21		Salmo salar	FALSE
##	22		Setophaga coronata	FALSE
##	23		Setophaga magnolia	FALSE
##	24		Sylvia atricapilla	FALSE
##	25		Sylvia borin	FALSE
##		ott_id is_synonym	flags number_matches	
##	1	800677	FALSE SIBLING_HIGHER	1
##	2	656799	FALSE SIBLING_HIGHER	1
##	3	765167	FALSE SIBLING_HIGHER	1
##	4	854201	FALSE	1
##	5	821753	FALSE	1
##	6	190878	TRUE	1
##	7	1005932	FALSE	1
##	8	207360	FALSE	1
##	9	190091	FALSE	1
##	10	36109	TRUE	1
##	11	964519	FALSE	1
##	12	22300	FALSE SIBLING_HIGHER	1
##	13	302798	TRUE	1
##	14	1040135	FALSE	1
##	15	274225	FALSE	1
##	16	755107	FALSE	1
##	17	739927	FALSE	1
##	18	165368	FALSE	2
##	19	165375	FALSE	1
##	20	621799	FALSE	1
##	21	688328	FALSE SIBLING_HIGHER	1
##	22	451168	FALSE	1
##	23	532751	FALSE	1
##	24	726312	FALSE	1
##	25	261410	FALSE	1

```
#make phylo tree

tree <- tol_induced_subtree(ott_ids = ott_id(taxa))
str(tree)
```

```
## List of 4
## $ edge      : int [1:47, 1:2] 26 34 36 36 35 37 38 38 40 40 ...
## $ tip.label : chr [1:25] "Danaus_plexippus_ott190091" "Progne_subis_ott621799" "Petrocheli
don_pyrrhonota_ott302798" "Delichon_urbicum_ott36109" ...
## $ Nnode     : int 23
## $ node.label: chr [1:23] "" "Euteleostomi ott114654" "Neognathae ott241846" "" ...
## - attr(*, "class")= chr "phylo"
```

```
#plot
plot(tree, cex = .8, label.offset = .1, no.margin = TRUE)
```



```
##add species ott_ids to dataframe so that models can match correlation matrix phylo IDs to sp
species in dataframe

tree$tip.label
```

```
## [1] "Danaus_plexippus_ott190091"
## [2] "Progne_subis_ott621799"
## [3] "Petrochelidon_pyrrhonota_ott302798"
## [4] "Delichon_urbicum_ott36109"
## [5] "Hirundo_rustica_ott1040135"
## [6] "Acrocephalus_arundinaceus_ott800677"
## [7] "Sylvia_borin_ott261410"
## [8] "Sylvia_atricapilla_ott726312"
## [9] "Setophaga_coronata_ott451168"
## [10] "Setophaga_magnolia_ott532751"
## [11] "Ficedula_hypoleuca_ott22300"
## [12] "Luscinia_svecica_ott274225"
## [13] "Falco_sparverius_ott964519"
## [14] "Merops_apiaster_ott755107"
## [15] "Arenaria_interpres_ott821753"
## [16] "Anser_caerulescens_ott190878"
## [17] "Cygnus_columbianus_ott207360"
## [18] "Anas_platyrhynchos_ott765167"
## [19] "Anas_crecca_ott656799"
## [20] "Oncorhynchus_mykiss_ott165368"
```



```
## [21] "Oncorhynchus_gorbuscha_ott739927"
## [22] "Oncorhynchus_nerka_ott165375"
## [23] "Salmo_salar_ott688328"
## [24] "Clupea_harengus_ott1005932"
## [25] "Anguilla_anguilla_ott854201"

all_data$species_ott[all_data$species_latin=="Acrocephalus arundinaceus"]<-"Acrocephalus_arund
inaceus_ott800677"
all_data$species_ott[all_data$species_latin=="Anas crecca"]<-"Anas_crecca_ott656799"
all_data$species_ott[all_data$species_latin=="Anas platyrhynchos"]<-"Anas_platyrhynchos_ott765
167"
all_data$species_ott[all_data$species_latin=="Anguilla anguilla"]<-"Anguilla_anguilla_ott85420
1"
all_data$species_ott[all_data$species_latin=="Arenaria interpres"]<-"Arenaria_interpres_ott821
753"
all_data$species_ott[all_data$species_latin=="Chen caerulescens"]<-"Anser_caerulescens_ott1908
78"
all_data$species_ott[all_data$species_latin=="Clupea harengus"]<-"Clupea_harengus_ott1005932"
all_data$species_ott[all_data$species_latin=="Cygnus columbianus"]<-"Cygnus_columbianus_ott207
360"
all_data$species_ott[all_data$species_latin=="Danaus plexippus"]<-"Danaus_plexippus_ott190091"
all_data$species_ott[all_data$species_latin=="Delichon urbica"]<-"Delichon_urbicum_ott36109"
all_data$species_ott[all_data$species_latin=="Falco sparverius"]<-"Falco_sparverius_ott964519"
all_data$species_ott[all_data$species_latin=="Ficedula hypoleuca"]<-"Ficedula_hypoleuca_ott223
00"
all_data$species_ott[all_data$species_latin=="Hirundo pyrrhonota"]<-"Petrochelidon_pyrrhonota_
ott302798"
all_data$species_ott[all_data$species_latin=="Hirundo rustica"]<-"Hirundo_rustica_ott1040135"
all_data$species_ott[all_data$species_latin=="Luscinia svecica"]<-"Luscinia_svecica_ott274225"
all_data$species_ott[all_data$species_latin=="Merops apiaster"]<-"Merops_apiaster_ott755107"
all_data$species_ott[all_data$species_latin=="Oncorhynchus gorbuscha"]<-"Oncorhynchus_gorbusch
a_ott739927"
all_data$species_ott[all_data$species_latin=="Oncorhynchus mykiss"]<-"Oncorhynchus_mykiss_ott1
65368"
all_data$species_ott[all_data$species_latin=="Oncorhynchus nerka"]<-"Oncorhynchus_nerka_ott165
375"
all_data$species_ott[all_data$species_latin=="Progne subis"]<-"Progne_subis_ott621799"
all_data$species_ott[all_data$species_latin=="Salmo salar"]<-"Salmo_salar_ott688328"
all_data$species_ott[all_data$species_latin=="Setophaga coronata"]<-"Setophaga_coronata_ott451
168"
all_data$species_ott[all_data$species_latin=="Setophaga magnolia"]<-"Setophaga_magnolia_ott532
751"
all_data$species_ott[all_data$species_latin=="Sylvia atricapilla"]<-"Sylvia_atricapilla_ott726
312"
all_data$species_ott[all_data$species_latin=="Sylvia borin"]<-"Sylvia_borin_ott261410"

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

##subset observations on infection status
```

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

unique(status$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(status$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(status$Effect.direction)
```

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

```
table(status$sig0.05)
```

```
##
##  0  1
## 37 29
```

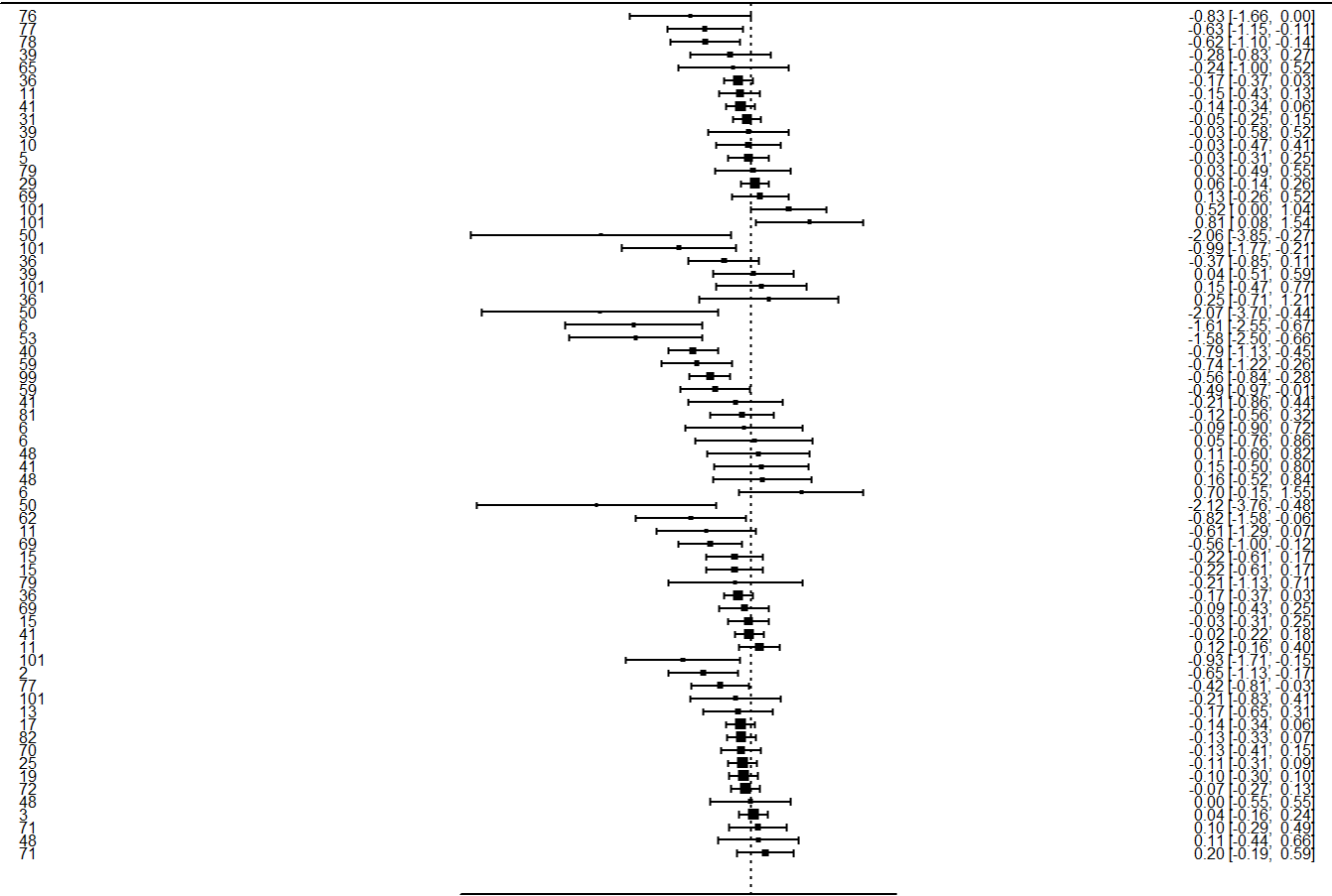
```
###order categories

status$trait<-factor(status$trait, levels=c("Body stores","Refuelling","Movement","Phenology",
"Survival"))
status$life.history.measured<-factor(status$life.history.measured, levels=c("Migration","Breeding",
"Non-breeding","Lab"))
status$parasite.taxa<-factor(status$parasite.taxa, levels=c("Protozoa","Virus","Mites","Helminth",
"Multiple"))
status$Order<-factor(status$Order, levels=c("Passeriformes","Anseriformes","Salmoniformes","Lepidoptera",
"Falconiformes",
"Anguilliformes","Clupeiformes","Coraciiformes","Charadriiformes"))
status$species latin<-factor(status$species latin)
```

```
status<-status[order(status$trait, status$g),]

###forest plot

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



```
##change names of hedges' g and variance to standardized names

status$yi<-status$g
status$vi<-status$var.g ##variance not capped
status$vil<-status$var.g1 ##capped to 0.01

####exclude data points that use same animals and same trait as non-independent
##Rowid's that use same animals and same traits

# 9 + 10 + 11 + 12 van Dijk et al. OIKOS
# 26 + 27 +28 Lopez et al. PLOS ONE
# 50 + 51 Arizaga et al. ARDEOLA
# 60 + 61 Latorre-Margalef et al. PROC B
# 63 + 64 Silvertsgard et al. HYDROBIOGIA
# 65 + 66 Silvertsgard et al. HYDROBIOGIA
# 83 + 84 Bradley et al ECOLOGY
# 105 + 106 Ratii OECOLOGIA
# 155 + 156 Hoyer et al. INTEGRATIVE & COMP BIOLOGY
# 157 + 158 Hoyer et al. INTEGRATIVE & COMP BIOLOGY
```

```
# 159 + 160 Hoyer et al. INTEGRATIVE & COMP BIOLOGY

status_independent<-subset(status, rowid!=27 & rowid!= 28 &
                             rowid!= 10 & rowid!= 11 & rowid!= 12 & rowid!= 61 &
                             rowid!= 84 & rowid!= 106 & rowid!= 64 & rowid!= 66 &
                             rowid!= 160 & rowid!= 158 & rowid!= 156 & rowid!= 51 )

##repeat with different set of points

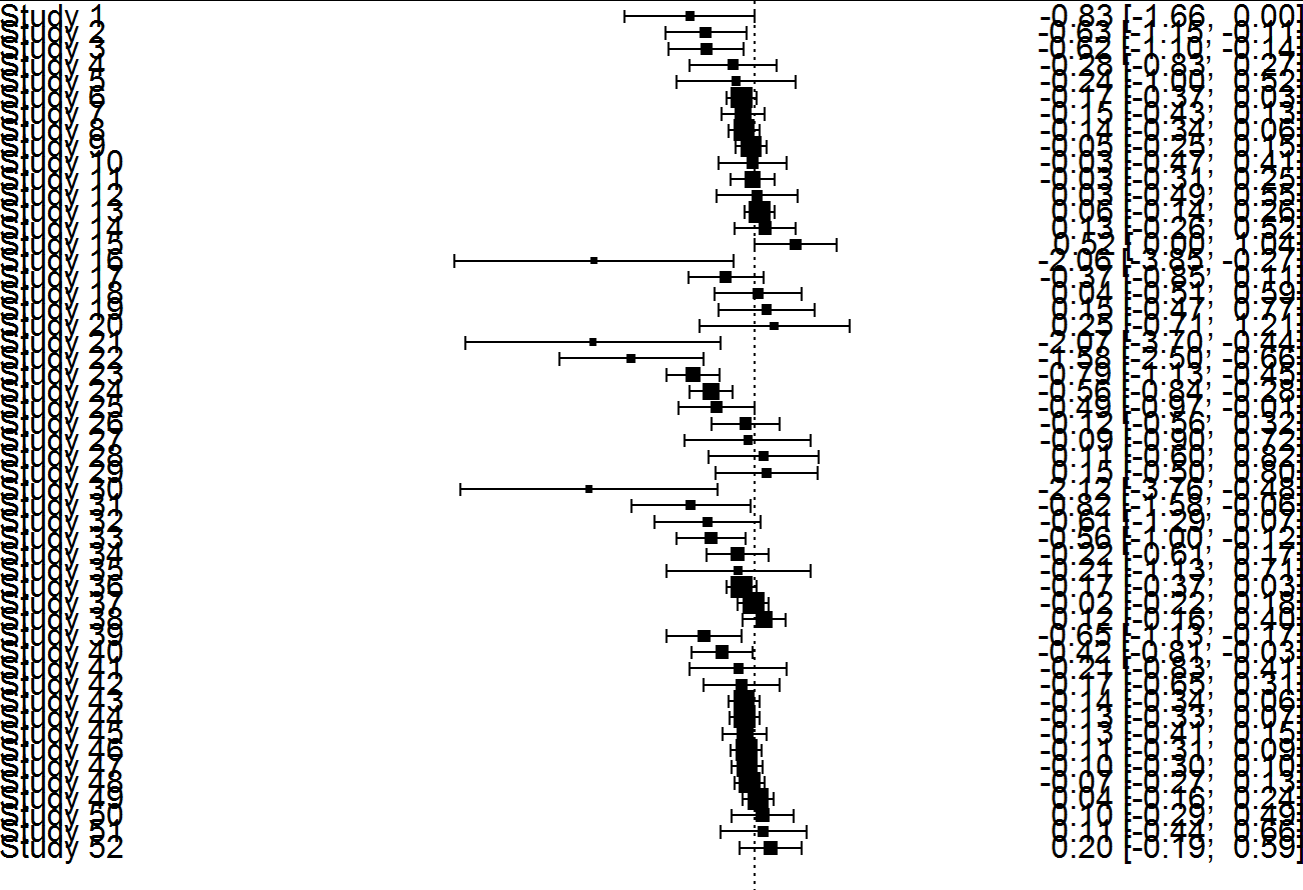
#status_independent1<-subset(status, rowid!=26 & rowid!= 28 &
#                             rowid!= 9 & rowid!= 11 & rowid!= 12 & rowid!= 60 &
#                             rowid!= 83 & rowid!= 105 & rowid!= 63 & rowid!= 65 &
#                             rowid!= 159 & rowid!= 157 & rowid!= 155 & rowid!= 50 )

## run analysis excluding these points

status<-status_independent

##forest plots by trait

forest.default(status$g, status$vil, cex=1, xlab="Hedges g")
```



```
##Kendall rank correlation test
```

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

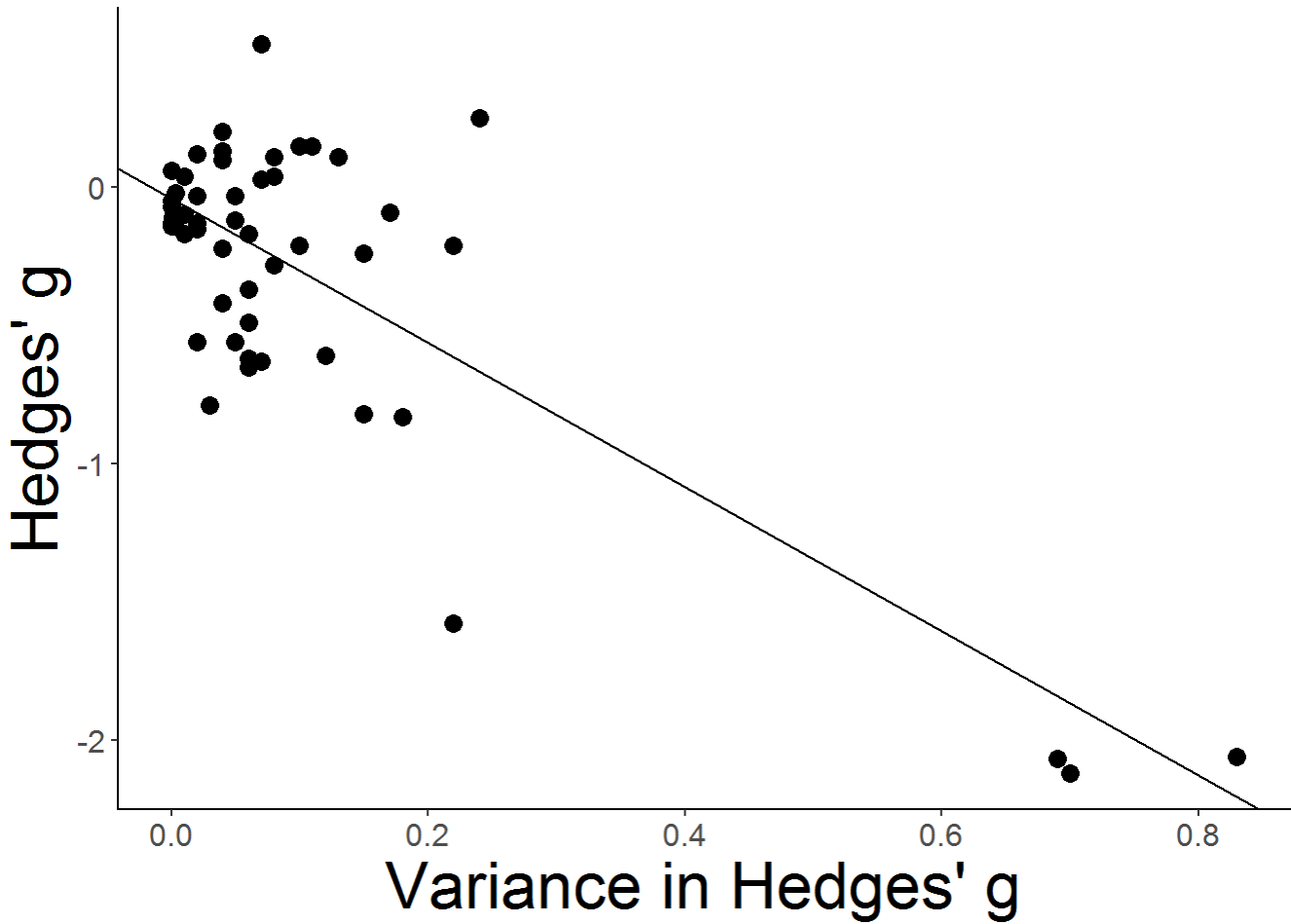
```
##
## Kendall's rank correlation tau
##
## data: status$yi and status$vi
## z = -2.1837, p-value = 0.01449
## alternative hypothesis: true tau is less than 0
## sample estimates:
##      tau
## -0.2129025
```

```
coef(lm(yi ~ vi, data = status))
```

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

```
##supplementary figure S7

ggplot(data=status, aes(x=vi, y = yi))+geom_point(size = 3)+ labs(x="Variance in Hedges' g", y
= "Hedges' g")+
  geom_abline(intercept= -0.0399, slope = -2.61)  +
  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 = 12))+
  theme(axis.line.x = element_line(color="black", size = 0.5),
        axis.line.y = element_line(color="black", size = 0.5))
```



```
#####create phylogentic correlation matrix to control for phylogeny

unique(status$species_ott)
```

```
## [1] "Merops_apiaster_ott755107"
## [2] "Delichon_urbicum_ott36109"
## [3] "Danaus_plexippus_ott190091"
## [4] "Sylvia_atricapilla_ott726312"
## [5] "Anser_caerulescens_ott190878"
## [6] "Setophaga_coronata_ott451168"
## [7] "Anas_platyrhynchos_ott765167"
## [8] "Clupea_harengus_ott1005932"
## [9] "Luscinia_svecica_ott274225"
## [10] "Acrocephalus_arundinaceus_ott800677"
## [11] "Anas_crecca_ott656799"
## [12] "Ficedula_hypoleuca_ott22300"
## [13] "Cygnus_columbianus_ott207360"
## [14] "Setophaga_magnolia_ott532751"
## [15] "Oncorhynchus_mykiss_ott165368"
## [16] "Anguilla_anguilla_ott854201"
## [17] "Salmo_salar_ott688328"
## [18] "Hirundo_rustica_ott1040135"
## [19] "Sylvia_borin_ott261410"
## [20] "Petrochelidon_pyrrhonota_ott302798"
## [21] "Progne_subis_ott621799"
```

```
## [22] "Arenaria_interpres_ott821753"
## [23] "Falco_sparverius_ott964519"
```

```
unique(status$species_latin)
```

```
## [1] Merops apiaster      Delichon urbica
## [3] Danaus plexippus     Sylvia atricapilla
## [5] Chen caerulescens    Setophaga coronata
## [7] Anas platyrhynchos   Clupea harengus
## [9] Luscinia svecica     Acrocephalus arundinaceus
## [11] Anas crecca          Ficedula hypoleuca
## [13] Cygnus columbianus   Setophaga magnolia
## [15] Oncorhynchus mykiss   Anguilla anguilla
## [17] Salmo salar          Hirundo rustica
## [19] Sylvia borin         Hirundo pyrrhonota
## [21] Progne subis         Arenaria interpres
## [23] Falco sparverius
## 23 Levels: Acrocephalus arundinaceus Anas crecca ... Sylvia borin
```

```
taxa<-tnrs_match_names(names= c("Danaus plexippus",
                                "Sylvia atricapilla",
                                "Acrocephalus arundinaceus",
                                "Anas platyrhynchos",
                                "Hirundo pyrrhonota",
                                "Progne subis",
                                "Falco sparverius",
                                "Setophaga magnolia",
                                "Setophaga coronata",
                                "Salmo salar",
                                "Anguilla anguilla",
                                "Anas crecca",
                                "Merops apiaster",
                                "Oncorhynchus mykiss",
                                "Cygnus columbianus",
                                "Clupea harengus",
                                "Sylvia borin",
                                "Delichon urbica",
                                "Arenaria interpres",
                                "Hirundo rustica",
                                "Ficedula hypoleuca",
                                "Chen caerulescens",
                                "Luscinia svecica"))
```

```
tree <- tol_induced_subtree(ott_ids = ott_id(taxa))
str(tree)
```

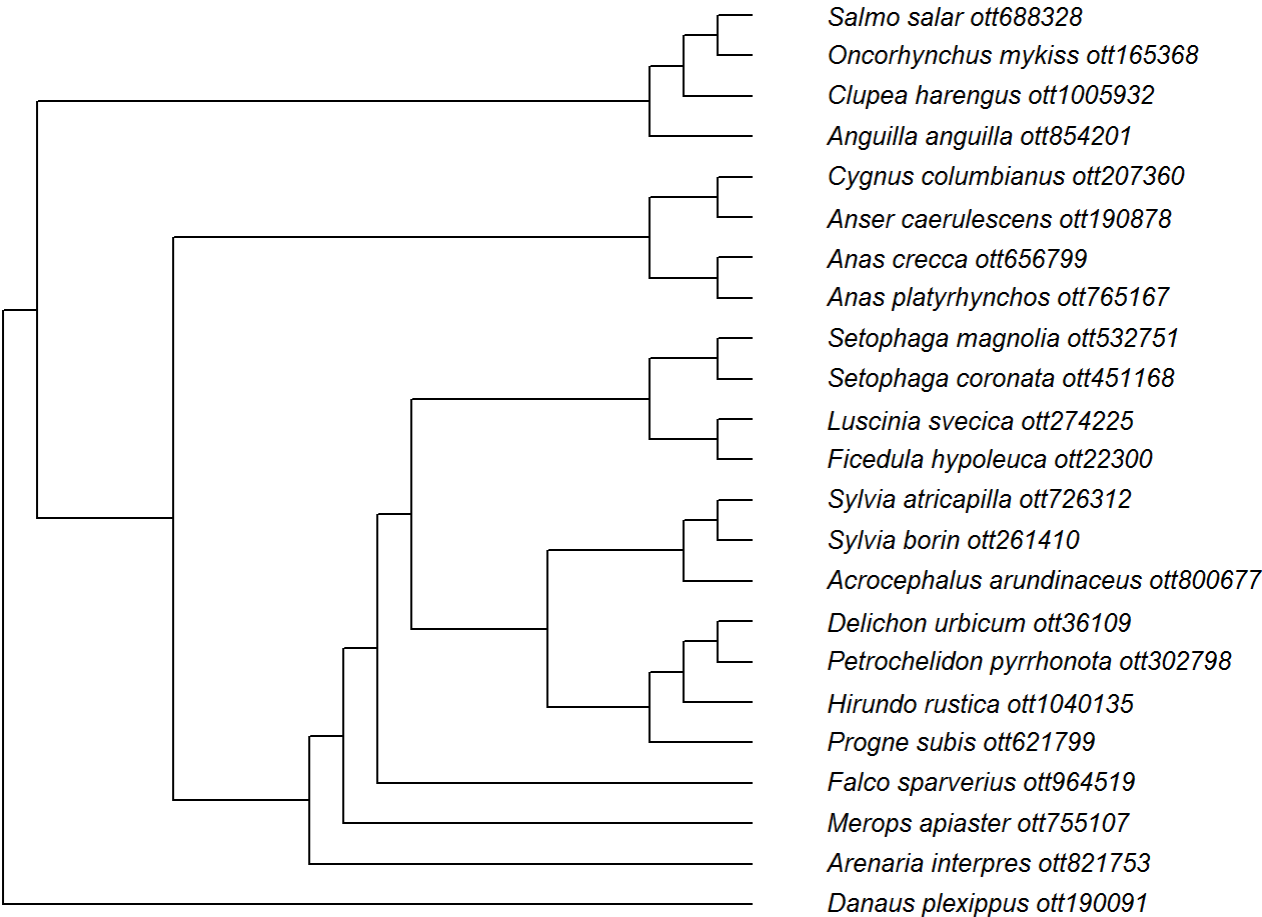
```
## List of 4
## $ edge      : int [1:44, 1:2] 24 32 34 34 33 35 36 36 38 38 ...
## $ tip.label : chr [1:23] "Danaus_plexippus_ott190091" "Progne_subis_ott621799" "Petrocheli
don_pyrrhonota_ott302798" "Delichon_urbicum_ott36109" ...
## $ Nnode     : int 22
```

```
## $ node.label: chr [1:22] "" "Euteleostomi ott114654" "Neognathae ott241846" "" ...
## - attr(*, "class")= chr "phylo"
```

```
##estimate branch lengths using APE
```

```
treel<-compute.brlen(tree, method = "Grafen", power = 1)
```

```
plot(treel, cex = .8, label.offset = .1, no.margin = TRUE)
```



```
str(treel)
```

```
## List of 5
## $ edge      : int [1:44, 1:2] 24 32 34 34 33 35 36 36 38 38 ...
## $ tip.label : chr [1:23] "Danaus_plexippus_ott190091" "Progne_subis_ott621799" "Petrochel
idon_pyrrhonota_ott302798" "Delichon_urbicum_ott36109" ...
## $ Nnode     : int 22
## $ node.label: chr [1:22] "" "Euteleostomi ott114654" "Neognathae ott241846" "" ...
## $ edge.length: num [1:44] 1 0.1364 0.0455 0.0455 0.0909 ...
## - attr(*, "class")= chr "phylo"
```

```
##create correlation matrix
```

```
corr_matrix<-vcv(treel, corr=TRUE)
```



```
#corr_matrix

##### MODEL SELECTION #####

# see Methods section
# explore which variables have an impact on effect size by comparing all models
# use capped variance (vil)

# use gmlmulti package for model selction
# see http://www.metafor-project.org/doku.php/tips:model\_selection\_with\_glmulti for coding methods

rma.glmulti <- function(formula, data, ...) {
  rma.mv(as.formula(paste(deparse(formula))), vil, data=data, method="ML", ...)
}

### global model with 4 ecologically relevant variables. Max number of variables allowed in model is 2. Study ID and species (phylogeny) as random effects

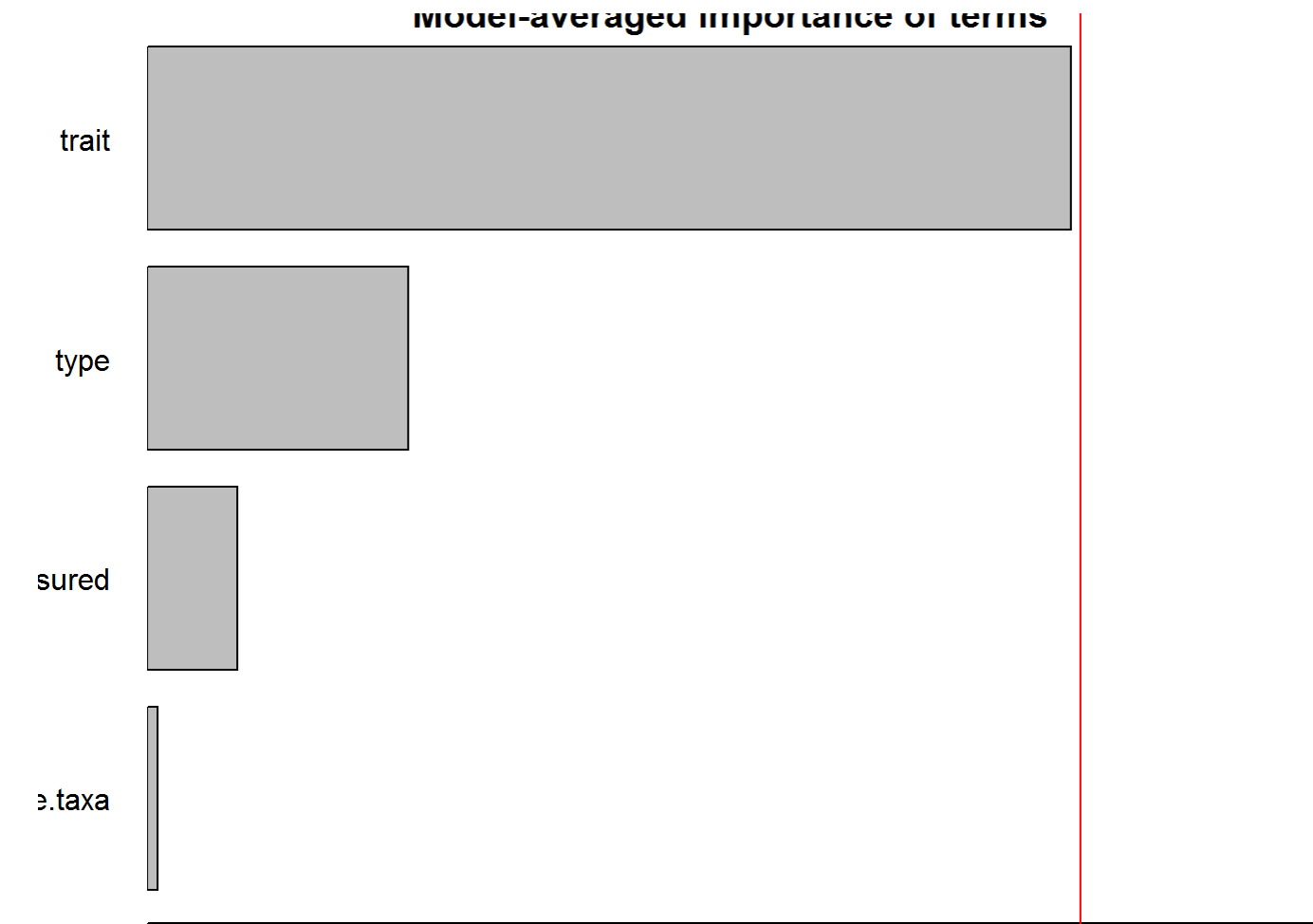
res <- glmulti(yi ~ trait+life.history.measured+type+parasite.taxa,random = list(~1 | id, ~ 1 | species_ott), R = list(species_ott = corr_matrix), data=status,
              level=1, fitfunction=rma.glmulti, crit="aicc", maxsize= 2)

## Initialization...
## TASK: Exhaustive screening of candidate set.
## Fitting...
## Completed.

tmp <- weightable(res)
tmp

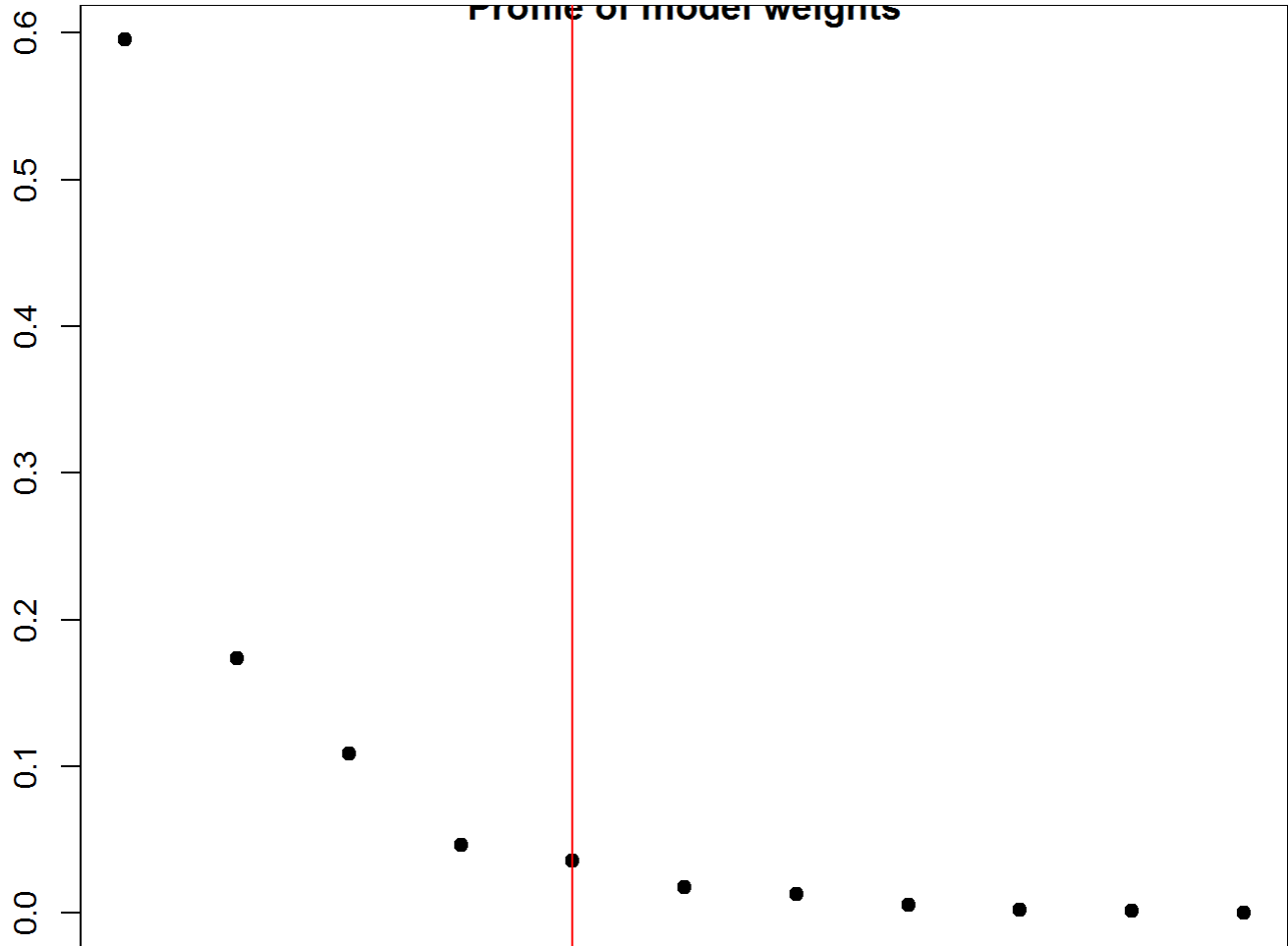
##           model      aicc      weights
## 1          yi ~ 1 + trait 40.99834 0.5954521060
## 2      yi ~ 1 + trait + type 43.46509 0.1734596573
## 3          yi ~ 1 44.39734 0.1088336167
## 4  yi ~ 1 + life.history.measured 46.10270 0.0463926197
## 5          yi ~ 1 + type 46.61781 0.0358586411
## 6  yi ~ 1 + trait + life.history.measured 48.06131 0.0174238196
## 7  yi ~ 1 + life.history.measured + type 48.64542 0.0130108392
## 8  yi ~ 1 + trait + parasite.taxa 50.29019 0.0057167158
## 9  yi ~ 1 + parasite.taxa 52.38286 0.0020078459
## 10 yi ~ 1 + type + parasite.taxa 52.99301 0.0014799208
## 11 yi ~ 1 + life.history.measured + parasite.taxa 55.79699 0.0003642179

##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 11 models:
## Best IC: 40.9983405584542
## Best model:
## [1] "yi ~ 1 + trait"
## Evidence weight: 0.595452106012837
## Worst IC: 55.7969886452856
## 1 models within 2 IC units.
## 4 models to reach 95% of evidence weight.
```

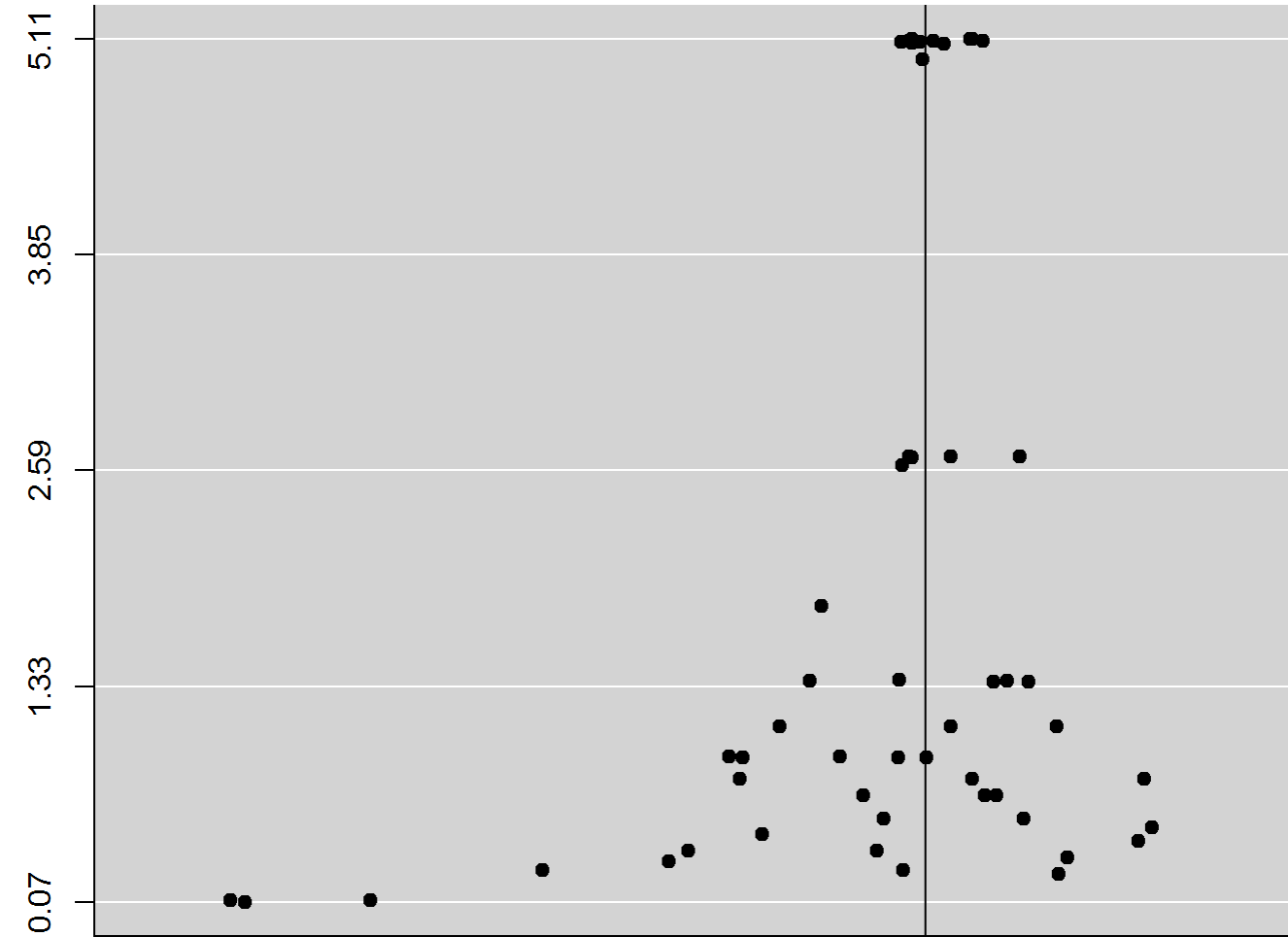
```
## lets check out the best models

summary(res@objects[[1]])
```

```
##
## Multivariate Meta-Analysis Model (k = 52; method: ML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -12.2264   85.5390   38.4529   52.1116   40.9983
##
```

```
## Variance Components:
##
##          estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1 0.0000  0.0000    35    no          id    no
## sigma^2.2 0.0013  0.0363    23    no species_ott yes
##
## Test for Residual Heterogeneity:
## QE(df = 47) = 85.6722, p-val = 0.0005
##
## Test of Moderators (coefficient(s) 2:5):
## QM(df = 4) = 20.1820, p-val = 0.0005
##
## Model Results:
##
##          estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt      -0.1030  0.0457  -2.2544  0.0242  -0.1925  -0.0134      *
## traitRefuelling -0.0262  0.1556  -0.1685  0.8662  -0.3311   0.2787
## traitMovement  -0.3913  0.0935  -4.1861 <.0001  -0.5745  -0.2081    ***
## traitPhenology  -0.0444  0.0696  -0.6382  0.5233  -0.1807   0.0919
## traitSurvival    0.0099  0.0560   0.1771  0.8595  -0.0999   0.1197
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

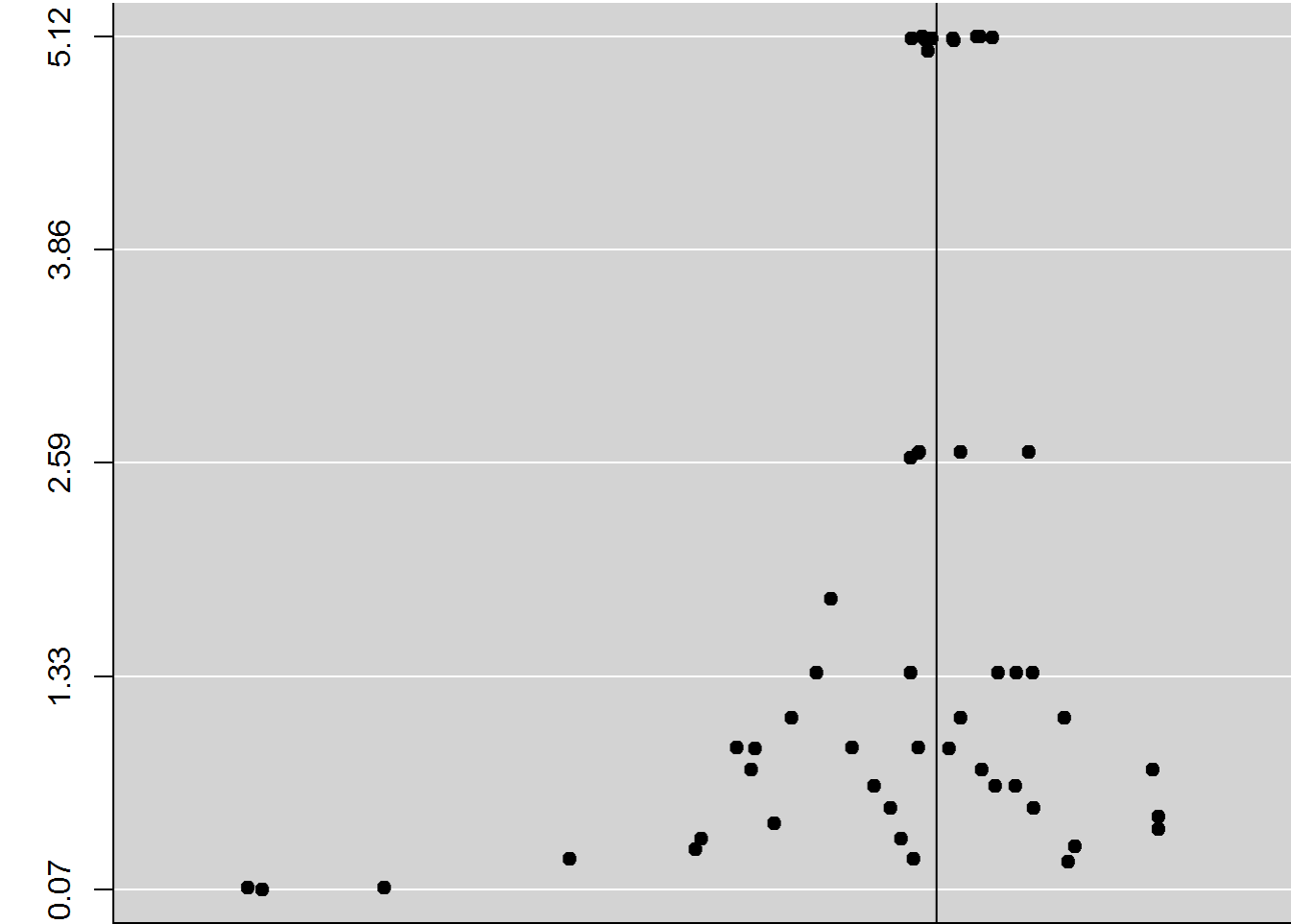
```
funnel(res@objects[[1]], yaxis="wi")
```



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

```
##
## Multivariate Meta-Analysis Model (k = 52; method: ML)
##
##      logLik  Deviance      AIC      BIC      AICc
## -12.0581    85.2023   40.1163   55.7262   43.4651
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0000   0.0000    35    no           id    no
## sigma^2.2  0.0010   0.0324    23    no species_ott  yes
##
## Test for Residual Heterogeneity:
## QE(df = 46) = 85.2963, p-val = 0.0004
##
## Test of Moderators (coefficient(s) 2:6):
## QM(df = 5) = 20.7741, p-val = 0.0009
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          -0.1396  0.0798  -1.7495  0.0802  -0.2961   0.0168      .
## traitRefuelling   -0.0275  0.1555  -0.1770  0.8595  -0.3323   0.2772
## traitMovement     -0.3872  0.0936  -4.1357  <.0001  -0.5708  -0.2037  ***
## traitPhenology     -0.0451  0.0695  -0.6492  0.5162  -0.1812   0.0911
## traitSurvival       0.0231  0.0616   0.3752  0.7075  -0.0976   0.1439
## typeO              0.0398  0.0681   0.5839  0.5593  -0.0937   0.1733
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

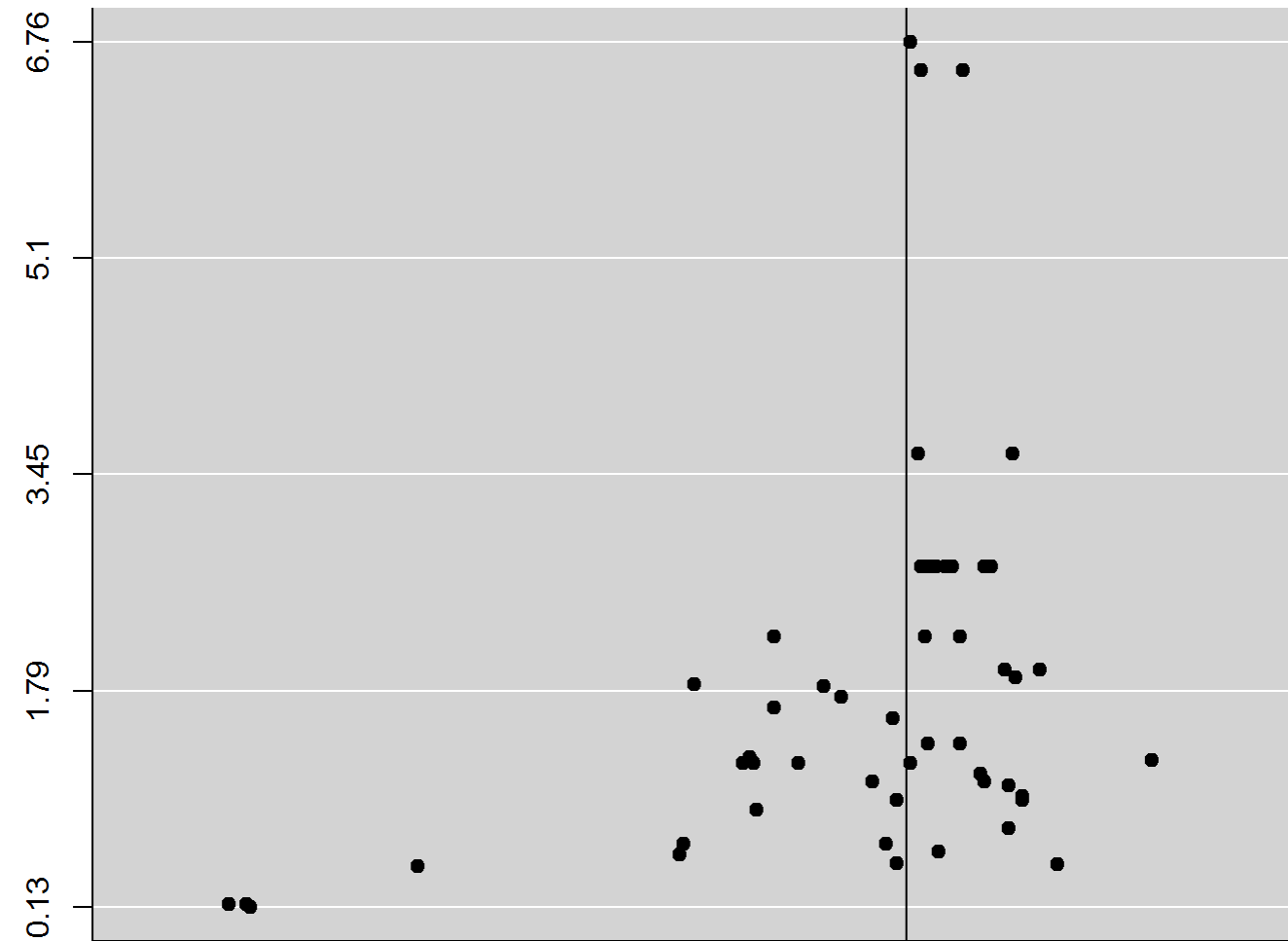
```
funnel(res@objects[[2]], yaxis="wi")
```



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

```
##
## Multivariate Meta-Analysis Model (k = 52; method: ML)
##
##   logLik  Deviance      AIC      BIC     AICc
## -18.9487   98.9834   43.8973   49.7511   44.3973
##
## Variance Components:
##
##           estim    sqrt  nlvls  fixed      factor    R
## sigma^2.1  0.0307  0.1753    35    no           id    no
## sigma^2.2  0.0000  0.0000    23    no species_ott  yes
##
## Test for Heterogeneity:
## Q(df = 51) = 107.1978, p-val < .0001
##
## Model Results:
##
## estimate      se      zval    pval    ci.lb    ci.ub    ***
## -0.1819  0.0417  -4.3682  <.0001  -0.2636  -0.1003
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

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



```
##### Fit null and best models #####

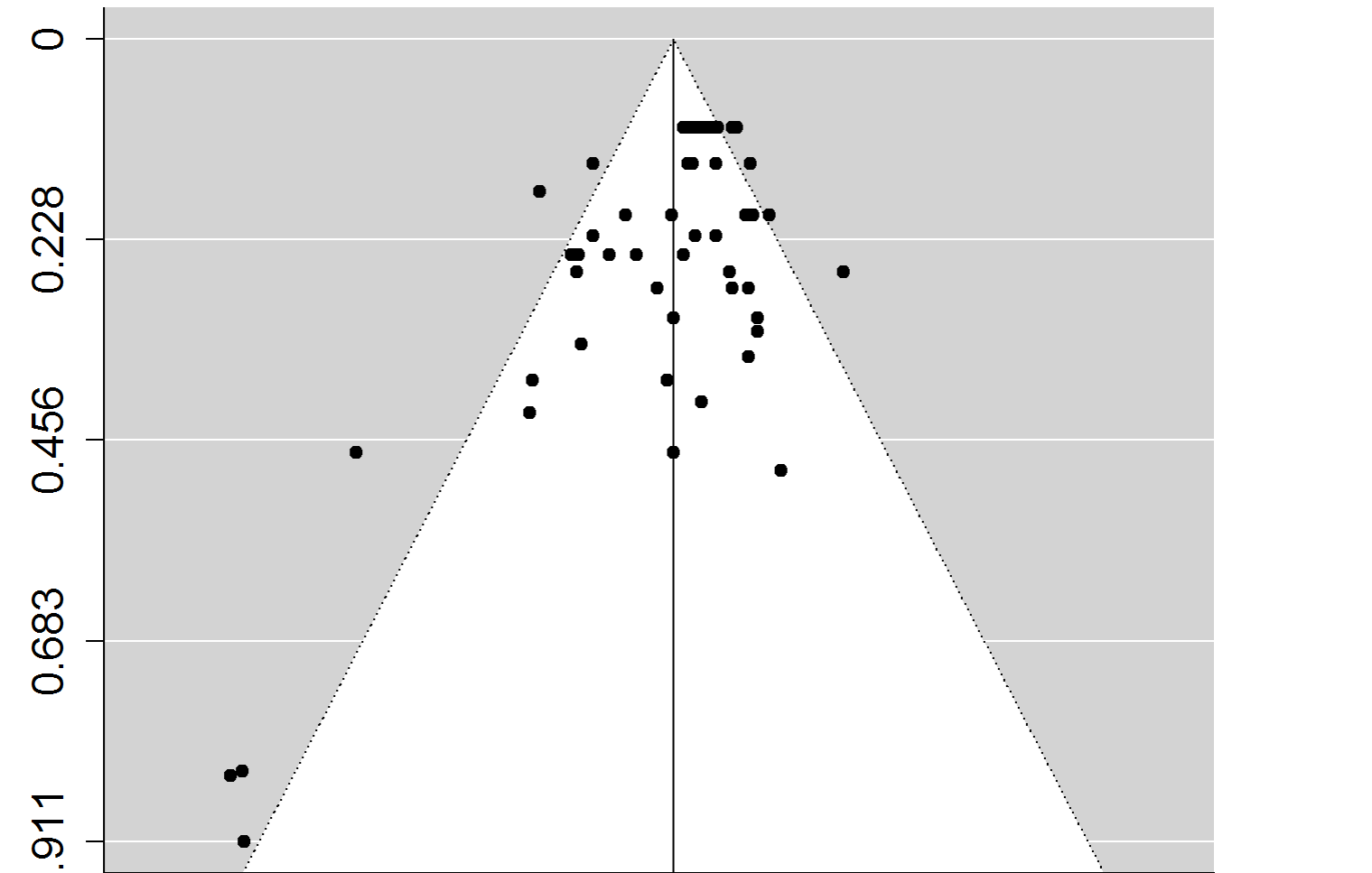
## first, null model (in text)

null.model<-rma.mv(yi, vi1,random = list(~1 | id, ~ 1 | species_ott), R = list(species_ott = c
orr_matrix), data=status, method="REML")
summary(null.model)

##
## Multivariate Meta-Analysis Model (k = 52; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -18.8690   37.7380   43.7380   49.5335   44.2487
##
## Variance Components:
##
##           estim    sqrt  nlvls  fixed      factor    R
## sigma^2.1  0.0180  0.1340    35    no          id    no
## sigma^2.2  0.0173  0.1316    23    no species_ott  yes
##
## Test for Heterogeneity:
## Q(df = 51) = 107.1978, p-val < .0001
```

```
##
## Model Results:
##
## estimate      se      zval    pval    ci.lb    ci.ub
## -0.2127  0.0778  -2.7358  0.0062  -0.3651  -0.0603  **
##
## ---
## 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)
```



```
## heterogeneity (see http://www.metafor-project.org/doku.php/tips:i2\_multilevel\_multivariate
for methods)

W <- diag(1/status$vi1)
X <- model.matrix(null.model)
P <- W - W %*% X %*% solve(t(X) %*% W %*% X) %*% t(X) %*% W
100 * sum(null.model$sigma2) / (sum(null.model$sigma2) + (null.model$k-null.model$p)/sum(diag(
P)))
```

```
## [1] 56.08345
```

```
# = 56.8% #Total variance
```



```
100 * null.model$sigma2 / (sum(null.model$sigma2) + (null.model$k-null.model$p)/sum(diag(P)))

## [1] 28.55393 27.52951

# sigma1 = 28.6%   sigma2 = 27.5 # all variance attributed to phylogeny

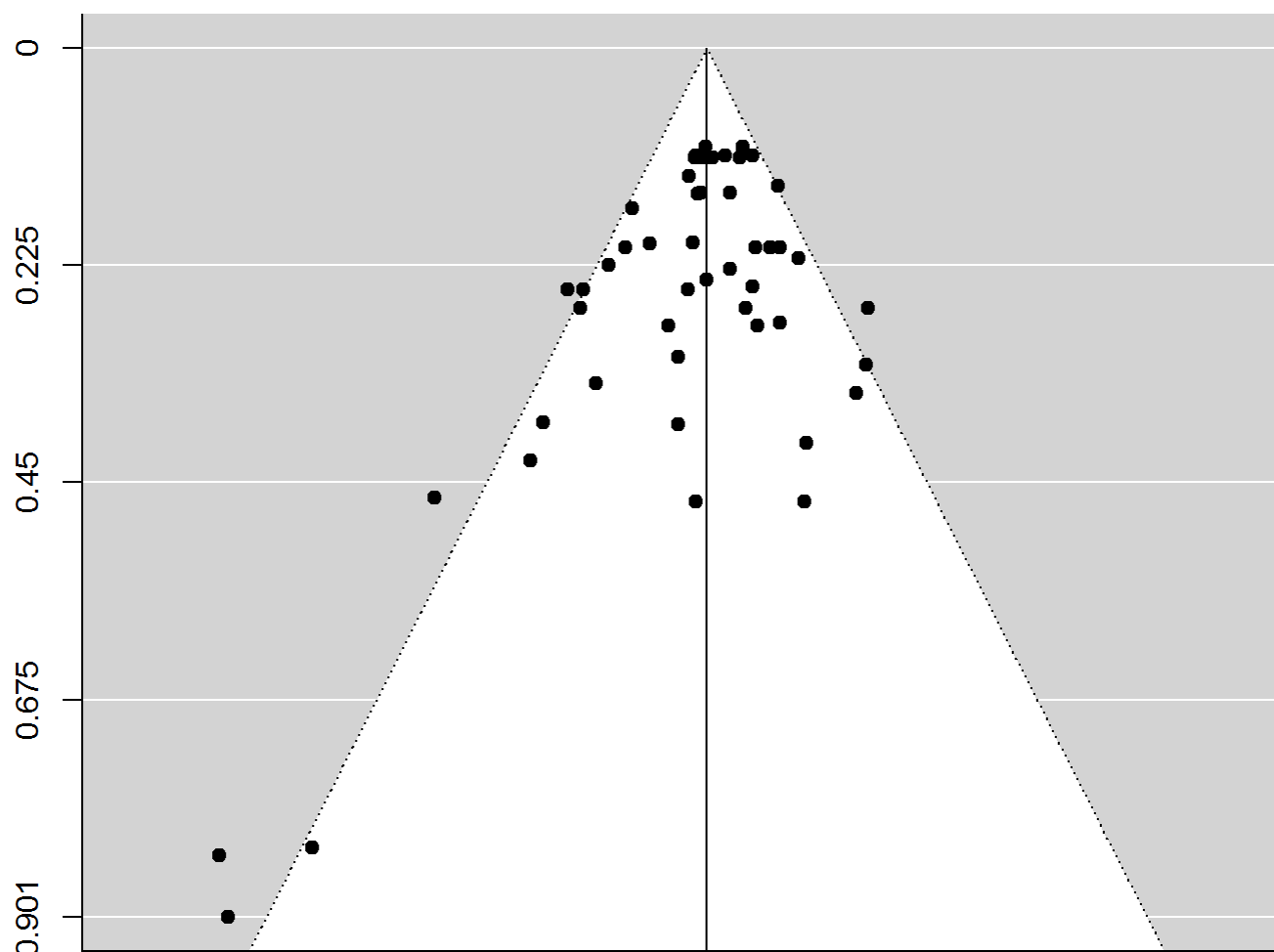
#with trait as moderator (best model)

best.model1<-rma.mv(yi, vi1, mods=~ trait, random = list(~1 | id, ~ 1 | species_ott), R = list
(species_ott = corr_matrix), data=status)

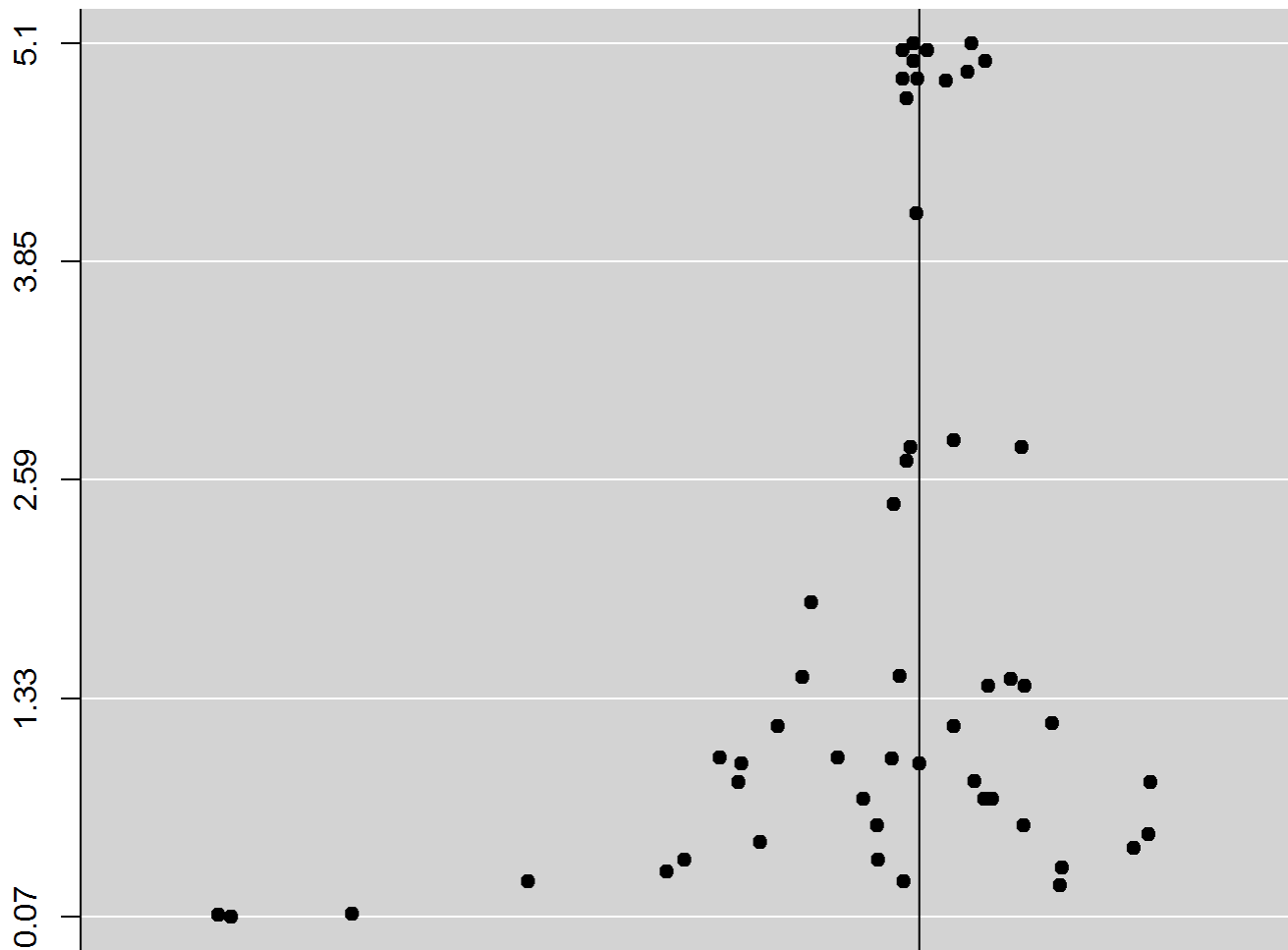
#Table 3a
summary(best.model1)

##
## Multivariate Meta-Analysis Model (k = 52; method: REML)
##
##      logLik  Deviance      AIC      BIC      AICc
## -15.0592   30.1184   44.1184   57.0694   46.9902
##
## Variance Components:
##
##           estim    sqrt  nlvls  fixed      factor    R
## sigma^2.1  0.0000  0.0000    35    no           id    no
## sigma^2.2  0.0062  0.0786    23    no species_ott  yes
##
## Test for Residual Heterogeneity:
## QE(df = 47) = 85.6722, p-val = 0.0005
##
## Test of Moderators (coefficient(s) 2:5):
## QM(df = 4) = 16.8404, p-val = 0.0021
##
## Model Results:
##
##           estimate      se    zval    pval    ci.lb    ci.ub
## intrcpt          -0.1253  0.0607  -2.0648  0.0389  -0.2443  -0.0064    *
## traitRefuelling   -0.0172  0.1564  -0.1097  0.9126  -0.3237   0.2894
## traitMovement     -0.3642  0.0987  -3.6912  0.0002  -0.5575  -0.1708   ***
## traitPhenology    -0.0409  0.0704  -0.5806  0.5615  -0.1790   0.0972
## traitSurvival      0.0316  0.0610   0.5181  0.6044  -0.0879   0.1511
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

funnel(best.model1)
```



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



```
## heterogeneity

W <- diag(1/status$vil)
X <- model.matrix(best.model1)
P <- W - W %*% X %*% solve(t(X) %*% W %*% X) %*% t(X) %*% W
100 * sum(best.model1$sigma2) / (sum(best.model1$sigma2) + (best.model1$k-best.model1$p)/sum(diag(P)))
```

```
## [1] 17.76046
```

```
# = 17.8% #Total variance

100 * best.model1$sigma2 / (sum(best.model1$sigma2) + (best.model1$k-best.model1$p)/sum(diag(P)))
```

```
## [1] 7.430091e-08 1.776046e+01
```

```
# sigma1 = 0%    sigma2 = 17.8 # all variance attributed to phylogeny

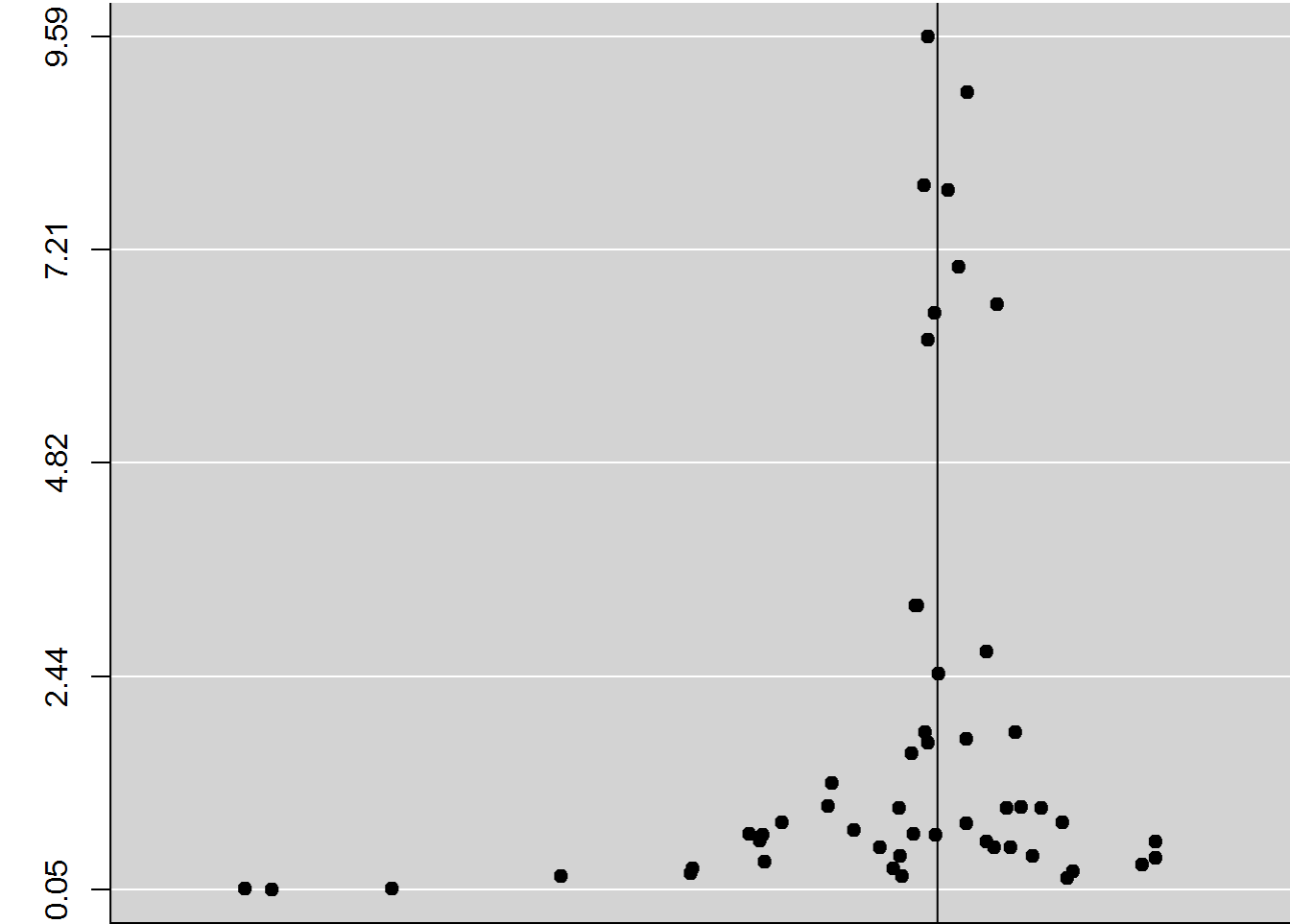
## use uncapped variance to compare (table S5)

best.model2<-rma.mv(yi, vi, mods=~ trait ,random = list(~1 | id, ~ 1 | species_ott), R = list(
species_ott = corr_matrix), data=status)
```

```
summary(best.model2)
```

```
##
## Multivariate Meta-Analysis Model (k = 52; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -14.9381   29.8761   43.8761   56.8272   46.7479
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0044   0.0660    35    no           id    no
## sigma^2.2  0.0048   0.0690    23    no  species_ott  yes
##
## Test for Residual Heterogeneity:
## QE(df = 47) = 191.3432, p-val < .0001
##
## Test of Moderators (coefficient(s) 2:5):
## QM(df = 4) = 15.8992, p-val = 0.0032
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          -0.1131  0.0529  -2.1374  0.0326  -0.2168  -0.0094      *
## traitRefuelling   -0.0136  0.1568  -0.0865  0.9311  -0.3210   0.2938
## traitMovement     -0.3718  0.0983  -3.7831  0.0002  -0.5644  -0.1792    ***
## traitPhenology      0.0054  0.0554   0.0981  0.9218  -0.1031   0.1140
## traitSurvival       0.0110  0.0527   0.2090  0.8344  -0.0922   0.1143
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
funnel(best.model2, yaxis="wi") ##weighting of points
```



```
#heterogeneity

W <- diag(1/status$vi)
X <- model.matrix(best.model2)
P <- W - W %*% X %*% solve(t(X) %*% W %*% X) %*% t(X) %*% W
100 * sum(best.model2$sigma2) / (sum(best.model2$sigma2) + (best.model2$k-best.model2$p)/sum(diag(P)))
```

[1] 88.96059

```
# = 89.0% #Total variance

100 * best.model2$sigma2 / (sum(best.model2$sigma2) + (best.model2$k-best.model2$p)/sum(diag(P)))
```

[1] 42.50226 46.45833

```
# sigma1 = 42.5%   sigma2 = 46.5 # all variance attributed to phylogeny

##### back to capped variaces

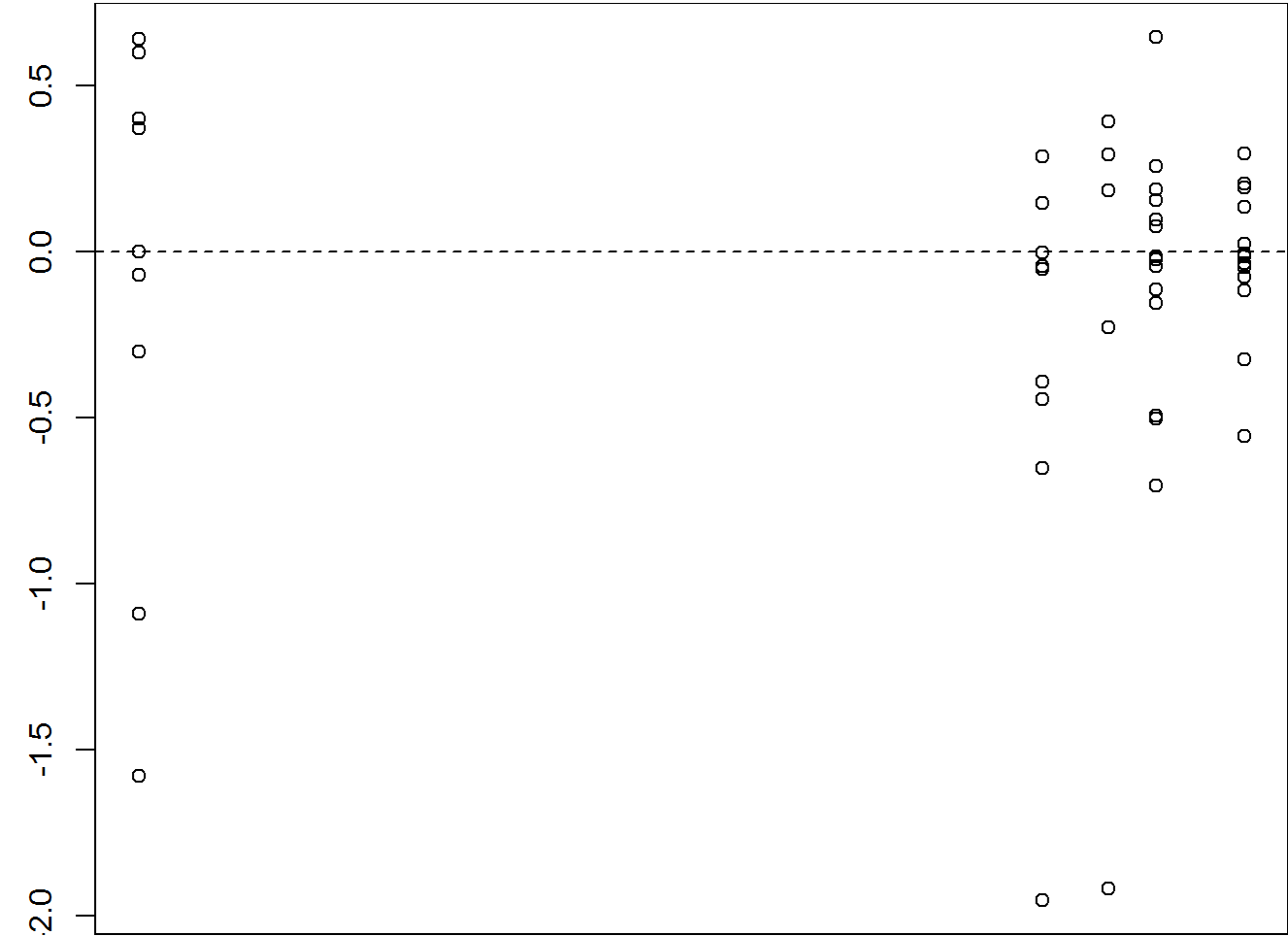
##make table of best model (table 3a) with capped variances
```

```
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")

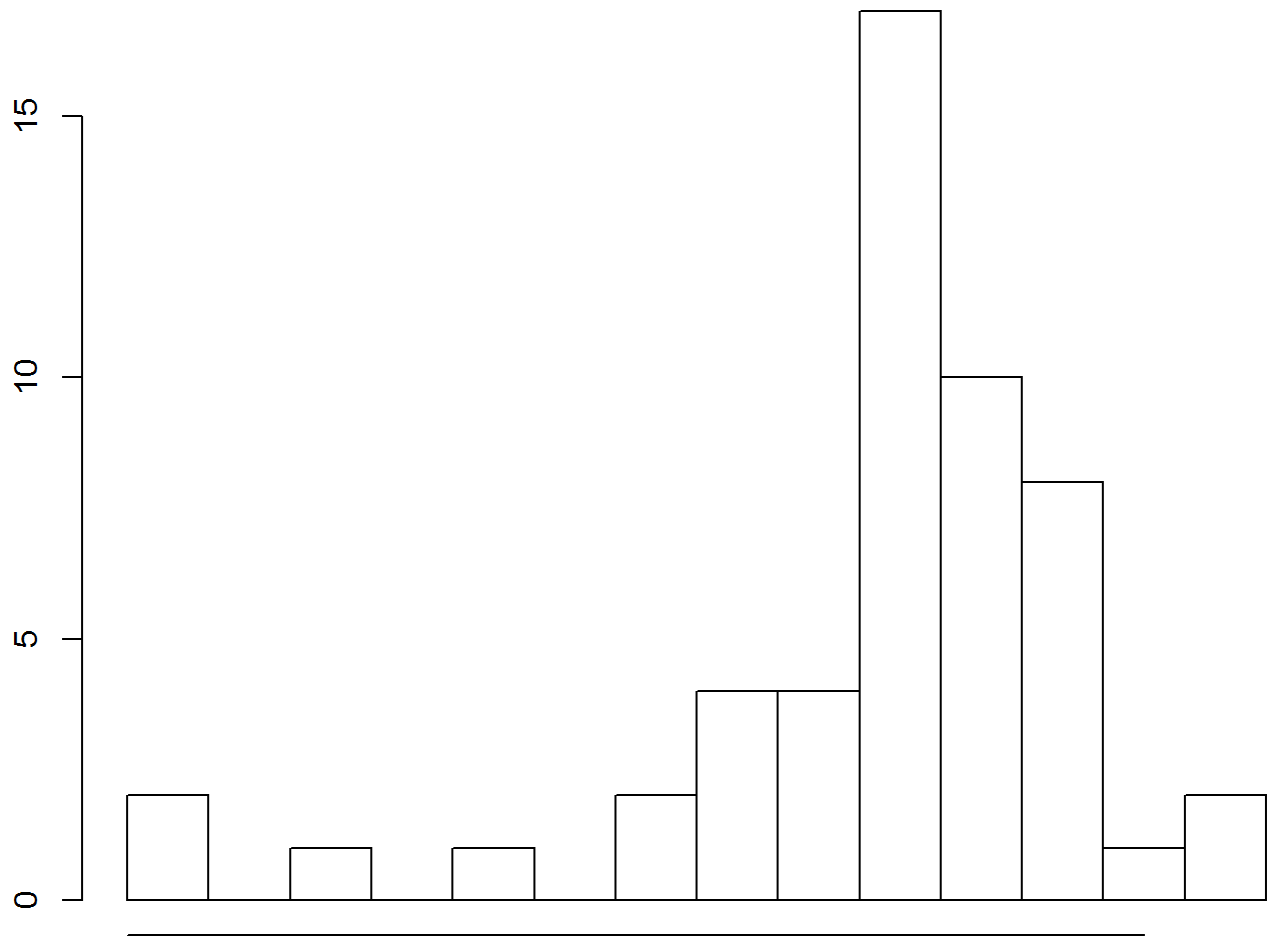
##plot resid

F1 <- fitted(best.model1)
E1 <- resid(best.model1)
plot(x = F1,
     y = E1,
     xlab = "Fitted values",
     ylab = "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

status$resids<-resid(best.model1)
status$predicted<-fitted(best.model1)
status$leverage<-hatvalues(best.model1)

mean(status$leverage)
```

```
## [1] 0.09615385
```

```
#plot(status$leverage)

#subset(status, resids < -1.0)

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

##PLOT ESTIMATES (Figure 3)

best.model1<-rma.mv(yi, vi1, mods=~ trait ,random = list(~1 | id, ~ 1 | species_ott), R = list(species_ott = corr matrix), data=status)
```

```
summary(best.model1)
```

```
##
## Multivariate Meta-Analysis Model (k = 52; method: REML)
##
##      logLik  Deviance      AIC      BIC      AICc
## -15.0592    30.1184    44.1184    57.0694    46.9902
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0000  0.0000    35     no           id     no
## sigma^2.2  0.0062  0.0786    23     no  species_ott  yes
##
## Test for Residual Heterogeneity:
## QE(df = 47) = 85.6722, p-val = 0.0005
##
## Test of Moderators (coefficient(s) 2:5):
## QM(df = 4) = 16.8404, p-val = 0.0021
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt          -0.1253  0.0607  -2.0648  0.0389  -0.2443  -0.0064      *
## traitRefuelling   -0.0172  0.1564  -0.1097  0.9126  -0.3237   0.2894
## traitMovement     -0.3642  0.0987  -3.6912  0.0002  -0.5575  -0.1708    ***
## traitPhenology    -0.0409  0.0704  -0.5806  0.5615  -0.1790   0.0972
## traitSurvival      0.0316  0.0610   0.5181  0.6044  -0.0879   0.1511
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# get predicted values for each trait to plot
# see http://www.metafor-project.org/doku.php/tips:testing\_factors\_lincoms

trait.pred<-predict(best.model1, 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

##create SE values
```



```

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

##boxplot

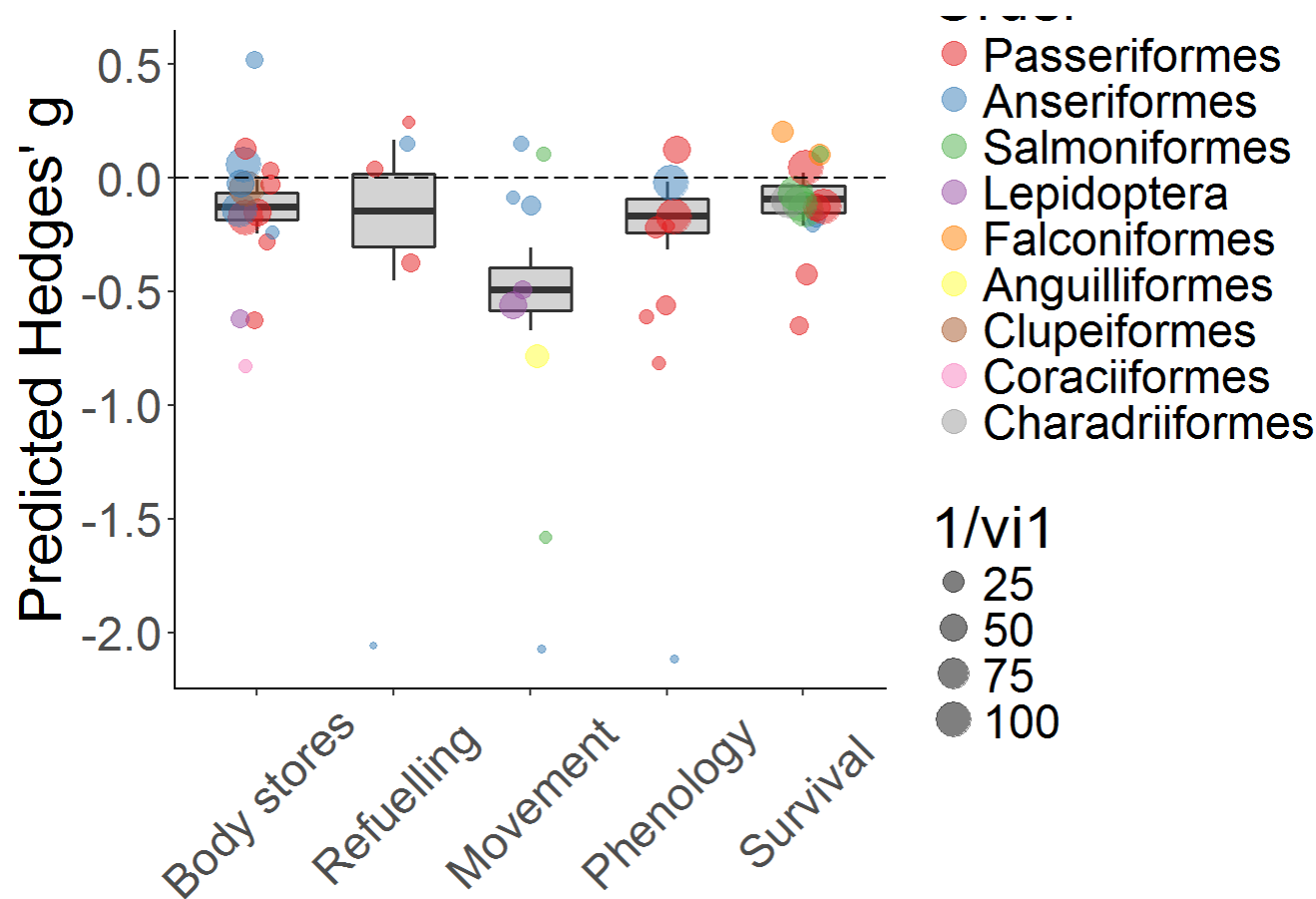
##overlayed with raw data with proportional weights

##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 = 0.6), stat="identity",
  fill="lightgray", lwd=0.7)+
  geom_jitter(data = status, 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=4)))

```

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



```
### Fig S8

##order parasite strains by type (Haemoparasites in birds, ectoparasites in birds, etc)

status$strain<-factor(status$strain, levels=c("Haemoparasites",
                                             "Leucocytozoon",
                                             "Trypanosoma",

                                             "Feather mites",
                                             "Ectoparasites",

                                             "Cestodes (general)",

                                             "LPAIV",

                                             "Anguillicola crassus",
                                             "Cloacotaenia megalops",
                                             "Ichthyophonus",
                                             "Ichthyophonus hoferi",
                                             "L. salmonis",

                                             "Ophryocystis elektroscirrha",

                                             "Multiple"))

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

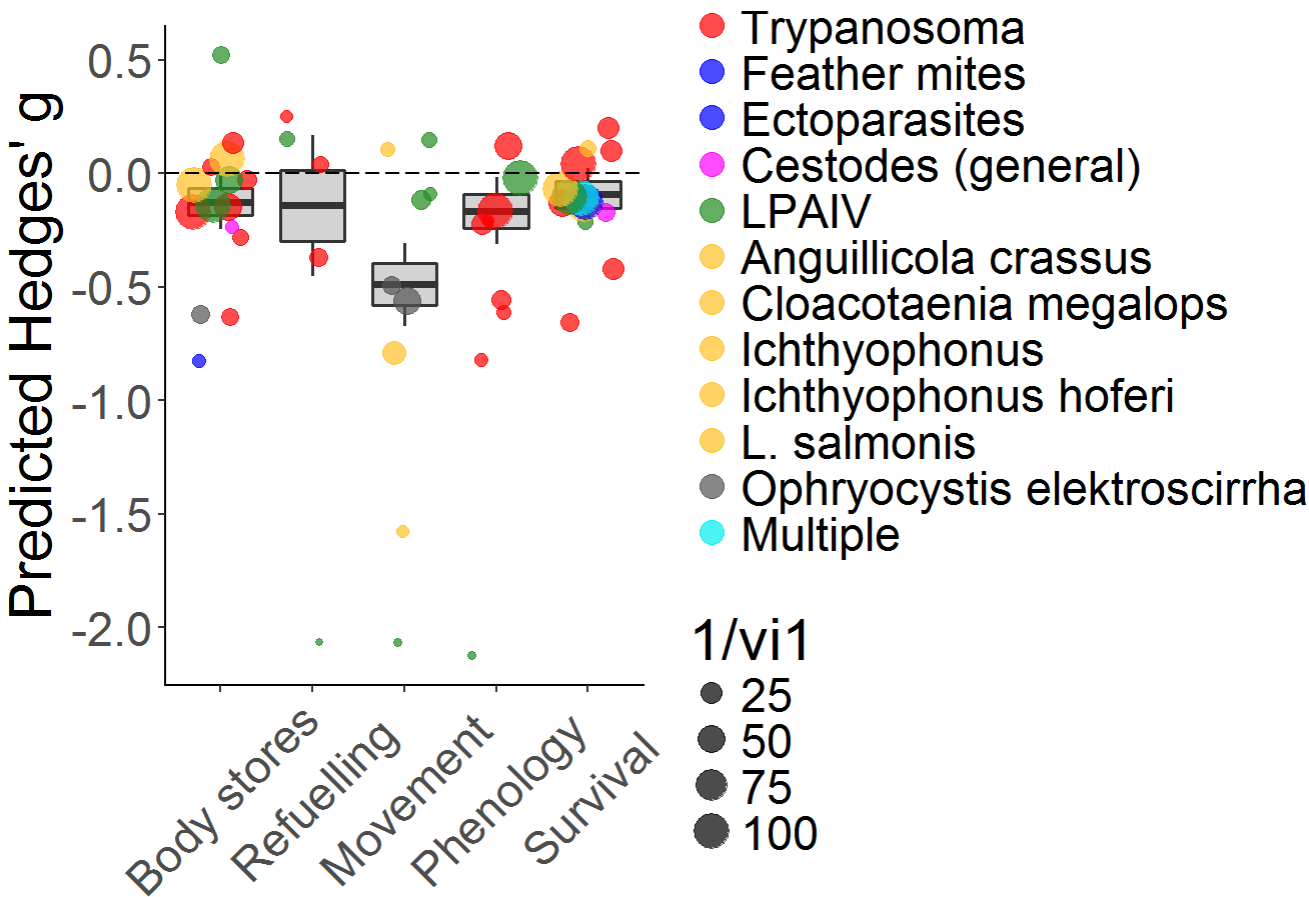
```
geom_boxplot(aes(ymin=l.ci, lower=l.se,
                 middle = predicted, upper = u.se, ymax=u.ci, width = 0.7), stat="identity",
fill="lightgray", lwd=0.7)+
geom_jitter(data = status, aes(x= trait, y = yi, size = 1/vi1, col = strain),width=0.3, alpha=0.7)+
labs(y="Predicted Hedges' g", x = "")+geom_hline(yintercept=0, 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","red","red","
blue","blue",

"magenta","forestgr
een","goldenrod1","goldenrod1",

"goldenrod1","golde
nrod1","goldenrod1","gray33","cyan2"))+
guides(colour = guide_legend(override.aes = list(size=4)))
```

Warning: Ignoring unknown aesthetics: width



#####

```
#####

#####modelling traits separately

survival<-subset(status, trait=="Survival")
Bodystores<-subset(status, trait=="Body stores")
phenology<-subset(status, trait=="Phenology")
movement<-subset(status, trait=="Movement")
refuelling<-subset(status, trait=="Refuelling")
#####

null1<-rma.mv(yi, vi1, random = list(~1 | id, ~ 1 | species_ott), R = list(species_ott = corr_
matrix), data=Bodystores) ##null model
summary(null1)
```

```
##
## Multivariate Meta-Analysis Model (k = 15; method: REML)
##
##   logLik   Deviance      AIC      BIC      AICc
##  -1.2761    2.5522    8.5522   10.4694   10.9522
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0007   0.0266    15    no           id    no
## sigma^2.2  0.0111   0.1055    13    no species_ott  yes
##
## Test for Heterogeneity:
## Q(df = 14) = 22.9530, p-val = 0.0610
##
## Model Results:
##
## estimate      se      zval    pval    ci.lb    ci.ub
##  -0.1280   0.0746  -1.7165   0.0861  -0.2741   0.0182
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
W <- diag(1/Bodystores$vi1)
X <- model.matrix(null1)
P <- W - W %*% X %*% solve(t(X) %*% W %*% X) %*% t(X) %*% W
100 * sum(null1$sigma2) / (sum(null1$sigma2) + (null1$k-null1$p)/sum(diag(P)))
```

```
## [1] 31.93163
```

```
# = 31.9% #Total variance

100 * null1$sigma2 / (sum(null1$sigma2) + (null1$k-null1$p)/sum(diag(P)))
```

```
## [1] 1.910757 30.020877

# signal = 1.9%    sigma2 = 30.02 # all variance attributed to phylogeny
#####

null2<-rma.mv(yi, vi1, random = list(~1 | id, ~ 1 | species_ott), R = list(species_ott = corr_
matrix), data=refuelling) ##null model
summary(null2)

##
## Multivariate Meta-Analysis Model (k = 5; method: REML)
##
##      logLik   Deviance      AIC      BIC      AICc
## -3.7386      7.4772    13.4772    11.6361    37.4772
##
## Variance Components:
##
##              estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0000  0.0000      4    no              id    no
## sigma^2.2  0.0000  0.0000      4    no  species_ott  yes
##
## 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

W <- diag(1/refuelling$vi1)
X <- model.matrix(null2)
P <- W - W %*% X %*% solve(t(X) %*% W %*% X) %*% t(X) %*% W
100 * sum(null2$sigma2) / (sum(null2$sigma2) + (null2$k-null2$p)/sum(diag(P)))

## [1] 1.356361e-07

# = 0% #Total variance

100 * null2$sigma2 / (sum(null2$sigma2) + (null2$k-null2$p)/sum(diag(P)))

## [1] 1.356361e-07 0.000000e+00

# signal = 0%    sigma2 = 0%

#####
```

```
null3<-rma.mv(yi, vil, random = list(~1 | id, ~ 1 | species_ott), R = list(species_ott = corr_
matrix), data=movement) ##null model
summary(null3)
```

```
##
## Multivariate Meta-Analysis Model (k = 9; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
##  -7.6154   15.2308   21.2308   21.4691   27.2308
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.1414   0.3760      9     no           id     no
## sigma^2.2  0.0000   0.0000      6     no  species_ott  yes
##
## 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
```

```
W <- diag(1/movement$vil)
X <- model.matrix(null3)
P <- W - W %*% X %*% solve(t(X) %*% W %*% X) %*% t(X) %*% W
100 * sum(null3$sigma2) / (sum(null3$sigma2) + (null3$k-null3$p)/sum(diag(P)))
```

```
## [1] 67.67498
```

```
# = 67.7% #Total variance

100 * null3$sigma2 / (sum(null3$sigma2) + (null3$k-null3$p)/sum(diag(P)))
```

```
## [1] 6.767498e+01 6.753964e-07
```

```
# signal = 67.7%   sigma2 = 0%

#####

null4<-rma.mv(yi, vil, random = list(~1 | id, ~ 1 | species_ott), R = list(species_ott = corr_
matrix), data=phenology) ##null model
summary(null4)
```

```
##
```

```
## Multivariate Meta-Analysis Model (k = 9; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
## -5.7714   11.5428   17.5428   17.7811   23.5428
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0230   0.1516      8     no           id     no
## sigma^2.2  0.0000   0.0000      8     no  species_ott  yes
##
## 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
```

```
W <- diag(1/phenology$vi1)
X <- model.matrix(null4)
P <- W - W %*% X %*% solve(t(X) %*% W %*% X) %*% t(X) %*% W
100 * sum(null4$sigma2) / (sum(null4$sigma2) + (null4$k-null4$p)/sum(diag(P)))
```

```
## [1] 40.93287
```

```
# = 40.9% #Total variance

100 * null4$sigma2 / (sum(null4$sigma2) + (null4$k-null4$p)/sum(diag(P)))
```

```
## [1] 4.093287e+01 9.640157e-08
```

```
# signal = 40.9%   sigma2 = 0%

#####

null5<-rma.mv(yi, vi1,random = list(~1 | id, ~ 1 | species_ott), R = list(species_ott = corr_m
atrix), data=survival) ##null model
summary(null5)
```

```
##
## Multivariate Meta-Analysis Model (k = 14; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
##  4.8968   -9.7936   -3.7936   -2.0987   -1.1269
##
## Variance Components:
```

```
##
##           estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0000   0.0000     13    no           id    no
## sigma^2.2  0.0000   0.0000     10    no  species_ott  yes
##
## 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
```

```
W <- diag(1/survival$vi1)
X <- model.matrix(null5)
P <- W - W %*% X %*% solve(t(X) %*% W %*% X) %*% t(X) %*% W
100 * sum(null5$sigma2) / (sum(null5$sigma2) + (null5$k-null5$p)/sum(diag(P)))
```

```
## [1] 2.767861e-08
```

```
# = 40.9% #Total variance

100 * null5$sigma2 / (sum(null5$sigma2) + (null5$k-null5$p)/sum(diag(P)))
```

```
## [1] 2.703191e-08 6.466953e-10
```

```
# signal = 40.9%    sigma2 = 0%

##### PLOT Fig 3b

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)
```

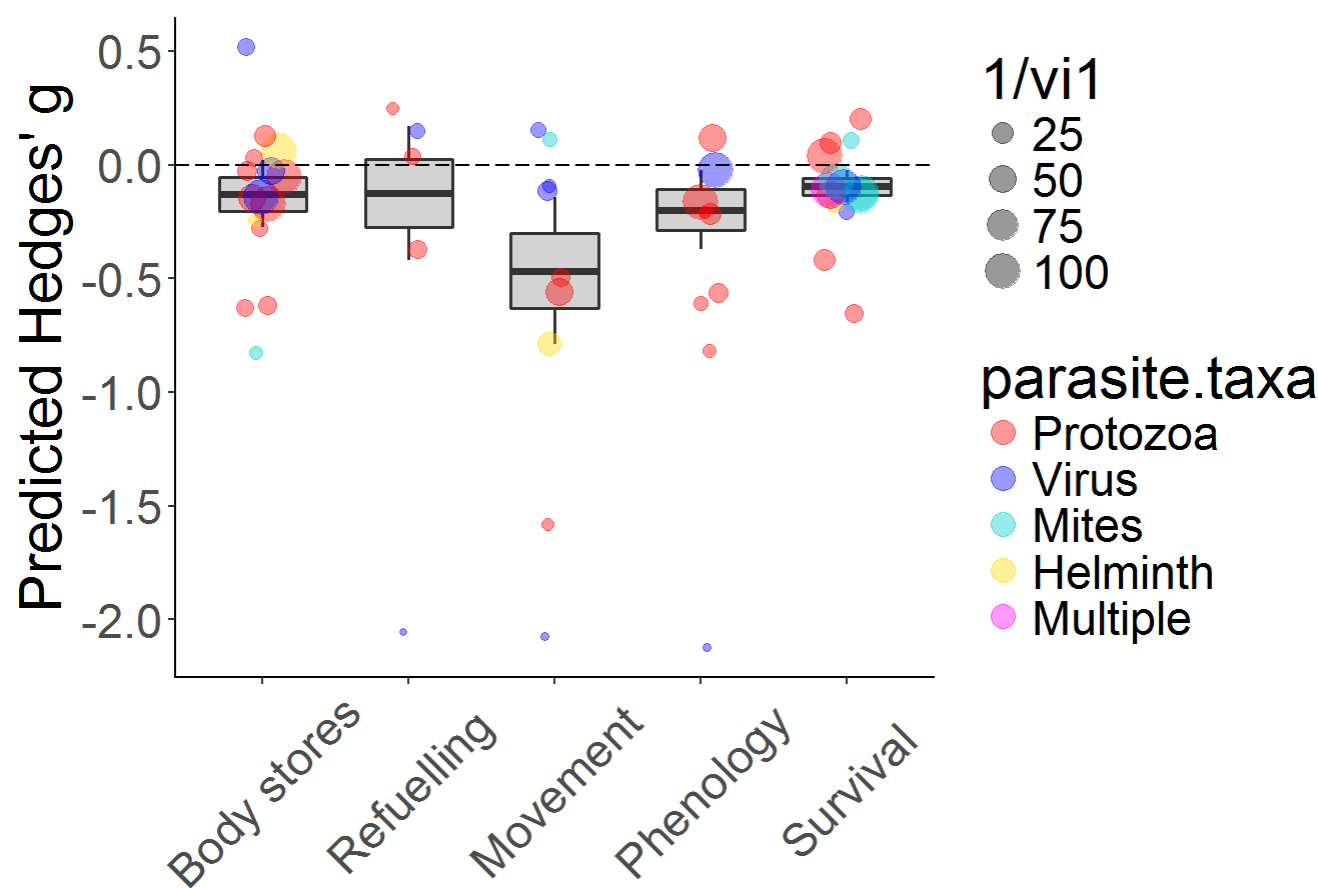
```
## 'data.frame':    5 obs. of  5 variables:
##  $ predicted: num  -0.128 -0.1259 -0.4664 -0.1983 -0.0959
##  $ se       : num   0.0746 0.1498 0.1642 0.089 0.0358
##  $ l.ci     : num  -0.274 -0.42 -0.788 -0.373 -0.166
##  $ u.ci     : num   0.0182 0.1678 -0.1445 -0.024 -0.0258
##  $ level    : Factor w/ 5 levels "Body stores",...: 1 2 3 4 5
```

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

##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 = 0.6), stat="identity",
  fill="lightgray", lwd=0.7)+
  geom_jitter(data = status, aes(x= trait, y = yi, size = 1/vi1, col = parasite.taxa),width=0.15, alpha=0.4)+
  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=4)))
```

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



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

###use uncapped variance instead of capped variance (replace vil with vi in all models) and re
run
#best.modell<-rma.mv(yi, vi, mods=~ trait + Order, random = ~ 1 | id, data=status)
#summary(best.modell)

##exclude insects in case this biases models and rerun
#status<-subset(status, taxa!="Insect")

##exclude outliers for best model and rerun
#status<-subset(status, resids > -1)

###Does not change models overall

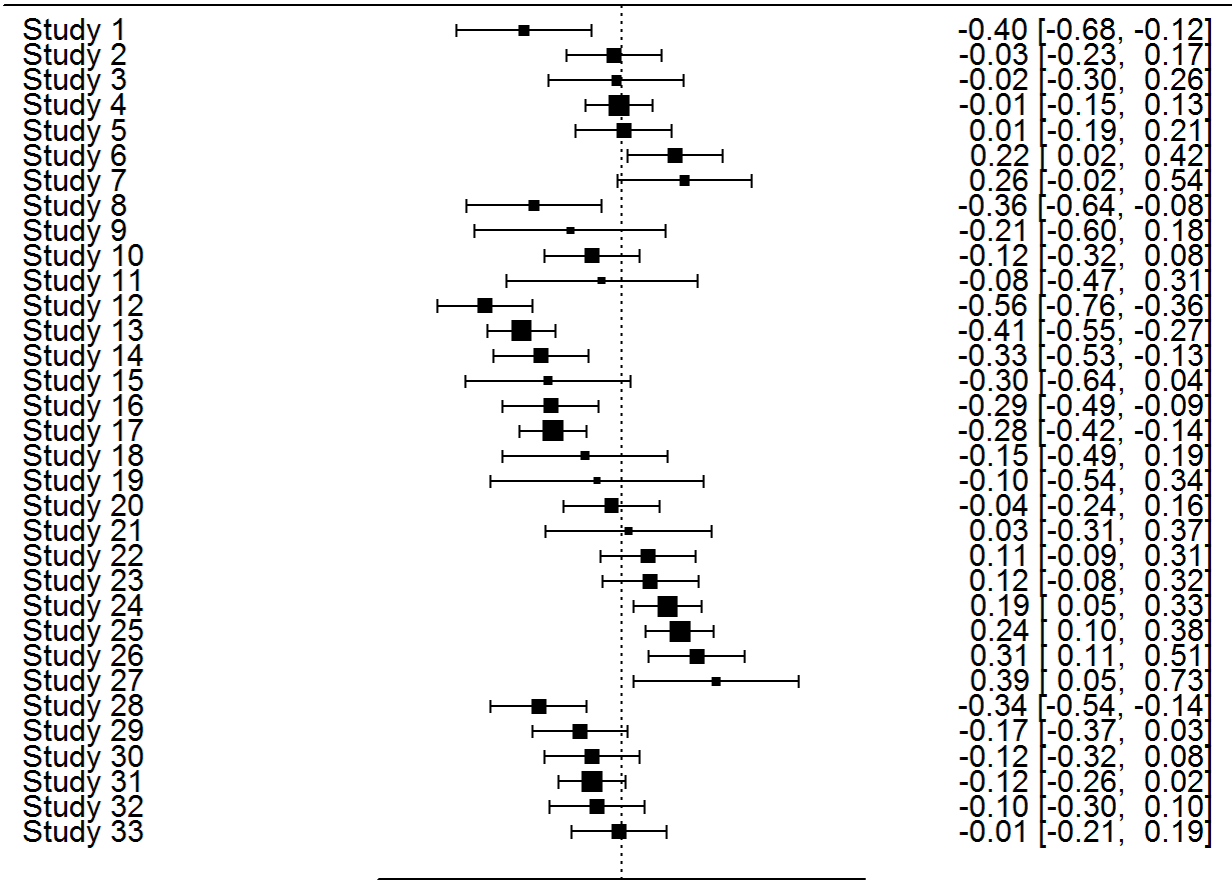
#####
#####

#####                                INTENSITY  META-ANALYSIS                                #####
#####
###same methods as with status
```

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

###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)
```



```
##order categories

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

intensity$parasite.taxon<-factor(intensity$parasite.taxon, levels=c("Protozoa","Virus","Mites","Helminth","Myxospora"))
intensity$Order<-factor(intensity$Order, levels=c("Passeriformes","Anseriformes","Salmoniformes","Lepidoptera","Falconiformes",
                                                    "Anguilliformes","Clupeiformes","Coraciiformes","Charadriiformes"))

##make phylo tree

intensity$species_latin<-factor(intensity$species_latin)

unique(intensity$species_latin)
```

```
## [1] Anguilla anguilla          Anas platyrhynchos
## [3] Acrocephalus arundinaceus Setophaga coronata
## [5] Danaus plexippus            Oncorhynchus gorboscha
## [7] Oncorhynchus nerka          Hirundo rustica
## [9] Falco sparverius
## 9 Levels: Acrocephalus arundinaceus ... Setophaga coronata
```

```
taxa<-tnrs_match_names(names= c("Acrocephalus arundinaceus",
                                "Anas platyrhynchos",
                                "Anguilla anguilla",
                                "Danaus plexippus",
                                "Falco sparverius",
                                "Hirundo rustica",
                                "Oncorhynchus gorboscha",
                                "Oncorhynchus nerka",
                                "Setophaga coronata"))

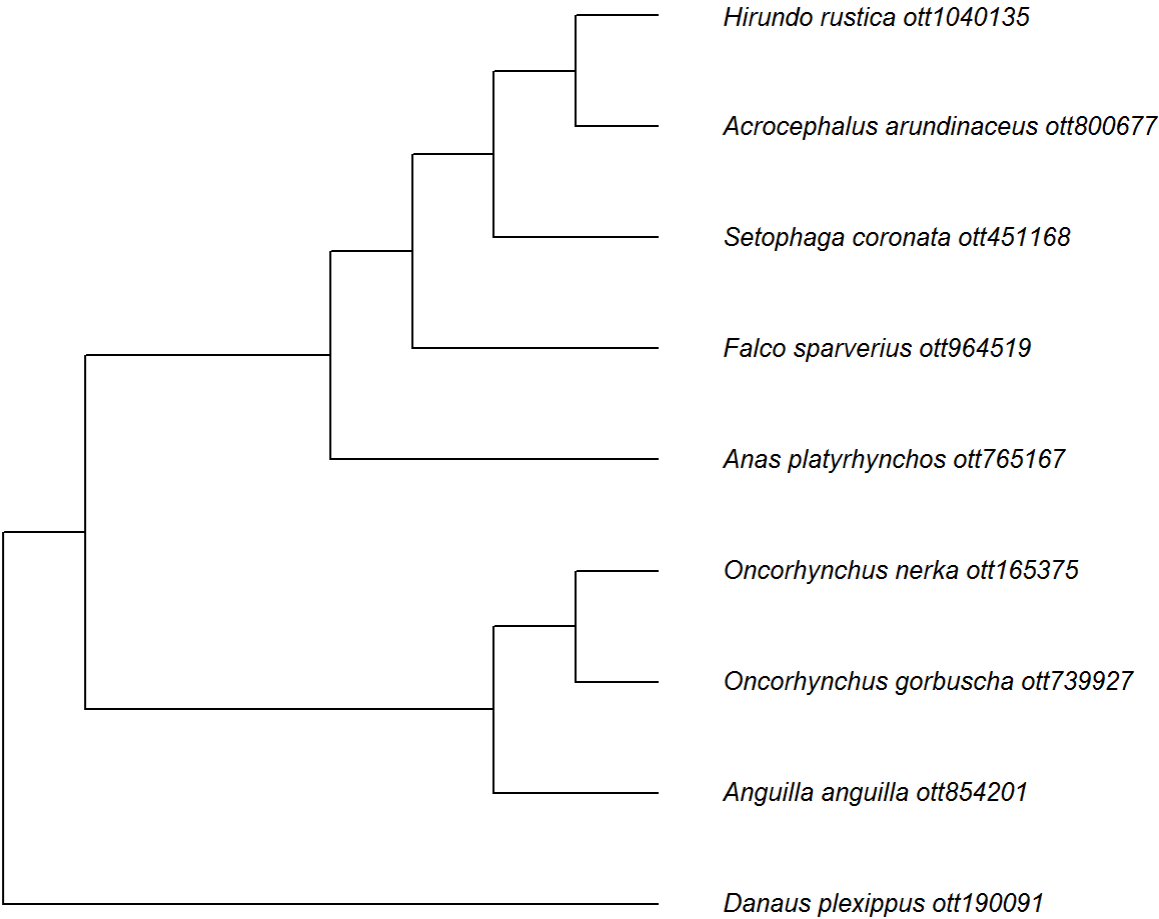
tree <- tol_induced_subtree(ott_ids = ott_id(taxa))
str(tree)
```

```
## List of 4
## $ edge      : int [1:16, 1:2] 10 12 13 13 17 17 16 15 14 10 ...
## $ tip.label : chr [1:9] "Danaus_plexippus_ott190091" "Anguilla_anguilla_ott854201" "Oncorh
ynchus_gorboscha_ott739927" "Oncorhynchus_nerka_ott165375" ...
## $ Nnode     : int 8
## $ node.label: chr [1:8] "" "Euteleostomi ott114654" "Teleostei ott212201" "Oncorhynchus ot
t739931" ...
## - attr(*, "class")= chr "phylo"
```

```
##estimate branch lengths

treel<-compute.brlen(tree, method = "Grafen", power = 1)

#plot
plot(treel, cex = .8, label.offset = .1, no.margin = TRUE)
```



```
str(treel)

## List of 5
## $ edge      : int [1:16, 1:2] 10 12 13 13 17 17 16 15 14 10 ...
## $ tip.label : chr [1:9] "Danaus_plexippus_ott190091" "Anguilla_anguilla_ott854201" "Oncorhynchus_gorbuscha_ott739927" "Oncorhynchus_nerka_ott165375" ...
## $ Nnode     : int 8
## $ node.label: chr [1:8] "" "Euteleostomi ott114654" "Teleostei ott212201" "Oncorhynchus ott739931" ...
## $ edge.length: num [1:16] 1 0.25 0.125 0.125 0.125 0.125 0.25 0.375 0.5 0.125 ...
## - attr(*, "class")= chr "phylo"

##create correlation matrix

corr_matrix<-vcv(treel, corr=TRUE)
str(corr_matrix)

## num [1:9, 1:9] 1 0 0 0 0 0 0 0 0 ...
## - attr(*, "dimnames")=List of 2
## ..$ : chr [1:9] "Danaus_plexippus_ott190091" "Anguilla_anguilla_ott854201" "Oncorhynchus_gorbuscha_ott739927" "Oncorhynchus_nerka_ott165375" ...
## ..$ : chr [1:9] "Danaus_plexippus_ott190091" "Anguilla_anguilla_ott854201" "Oncorhynchus_gorbuscha_ott739927" "Oncorhynchus_nerka_ott165375" ...
```

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

model.intensity<-rma.mv(z, var.z, mods = ~ trait, random = list(~1 | id, ~ 1 | species_ott), R
  = list(species_ott = corr_matrix), data=intensity)
model.intensity2<-rma.mv(z, var.z, mods = ~ parasite.taxa, random = list(~1 | id, ~ 1 | specie
s_ott), R = list(species_ott = corr_matrix), data=intensity)
```

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

```
model.intensity3<-rma.mv(z, var.z, mods = ~ life.history.measured, random = list(~1 | id, ~ 1
| species_ott), R = list(species_ott = corr_matrix), data=intensity)
model.intensity4<-rma.mv(z, var.z, mods = ~ type, random = list(~1 | id, ~ 1 | species_ott), R
  = list(species_ott = corr_matrix), data=intensity)
model.intensity5<-rma.mv(z, var.z, random = list(~1 | id, ~ 1 | species_ott), R = list(species
_ott = corr_matrix), data=intensity) #null model

aicc(model.intensity) #trait
```

```
## [1] 45.07104
```

```
aicc(model.intensity2) #parasite type
```

```
## [1] 57.72775
```

```
aicc(model.intensity3) # Life history
```

```
## [1] 67.40055
```

```
aicc(model.intensity4) #study design
```

```
## [1] 58.60323
```

```
aicc(model.intensity5) #null
```

```
## [1] 55.49761
```

```
##best model includes just trait (AICC = 45.1)
```

```
summary(model.intensity) #best model
```

```
##
## Multivariate Meta-Analysis Model (k = 33; method: REML)
##
```

```
##      logLik  Deviance      AIC      BIC      AICc
## -14.6264    29.2529    41.2529    49.4566    45.0710
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0155   0.1244     13     no           id     no
## sigma^2.2  0.0132   0.1150      9     no  species_ott  yes
##
## Test for Residual Heterogeneity:
## QE(df = 29) = 155.5302, p-val < .0001
##
## Test of Moderators (coefficient(s) 2:4):
## QM(df = 3) = 24.8116, p-val < .0001
##
## Model Results:
##
##           estimate      se      zval      pval      ci.lb      ci.ub
## intrcpt           0.0547  0.0907   0.6038  0.5460  -0.1230   0.2325
## traitMovement    -0.2086  0.1301  -1.6041  0.1087  -0.4635   0.0463
## traitPhenology   -0.3176  0.0758  -4.1922 <.0001  -0.4661  -0.1691 ***
## traitSurvival    -0.2893  0.0797  -3.6312  0.0003  -0.4455  -0.1332 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(model.intensity5) #null model
```

```
##
## Multivariate Meta-Analysis Model (k = 33; method: REML)
##
##      logLik  Deviance      AIC      BIC      AICc
## -24.3202    48.6405    54.6405    59.0377    55.4976
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0071   0.0842     13     no           id     no
## sigma^2.2  0.0140   0.1183      9     no  species_ott  yes
##
## Test for Heterogeneity:
## Q(df = 32) = 166.2538, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##  -0.1350  0.0750  -1.7992  0.0720  -0.2821  0.0121  .
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#I2 null model
```

```
W <- diag(1/intensity$var.z)
X <- model.matrix(model.intensity5)
P <- W - W %*% X %*% solve(t(X) %*% W %*% X) %*% t(X) %*% W
100 * sum(model.intensity5$sigma2) / (sum(model.intensity5$sigma2) + (model.intensity5$k-model
.intensity5$p)/sum(diag(P)))
```

```
## [1] 66.94903
```

```
# = 66.9% #Total variance
```

```
100 * model.intensity5$sigma2 / (sum(model.intensity5$sigma2) + (model.intensity5$k-model.inte
nsity5$p)/sum(diag(P)))
```

```
## [1] 22.49523 44.45379
```

```
# signal = 22.5 % sigma2 = 44.5%
```

```
##I2 best model
```

```
W <- diag(1/intensity$var.z)
X <- model.matrix(model.intensity)
P <- W - W %*% X %*% solve(t(X) %*% W %*% X) %*% t(X) %*% W
100 * sum(model.intensity$sigma2) / (sum(model.intensity$sigma2) + (model.intensity$k-model.in
tensity$p)/sum(diag(P)))
```

```
## [1] 73.08514
```

```
# = 73.08% #Total variance
```

```
100 * model.intensity$sigma2 / (sum(model.intensity$sigma2) + (model.intensity$k-model.intensi
ty$p)/sum(diag(P)))
```

```
## [1] 39.40730 33.67784
```

```
# signal = 39.4%   sigma2 = 33.7%
```

```
##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

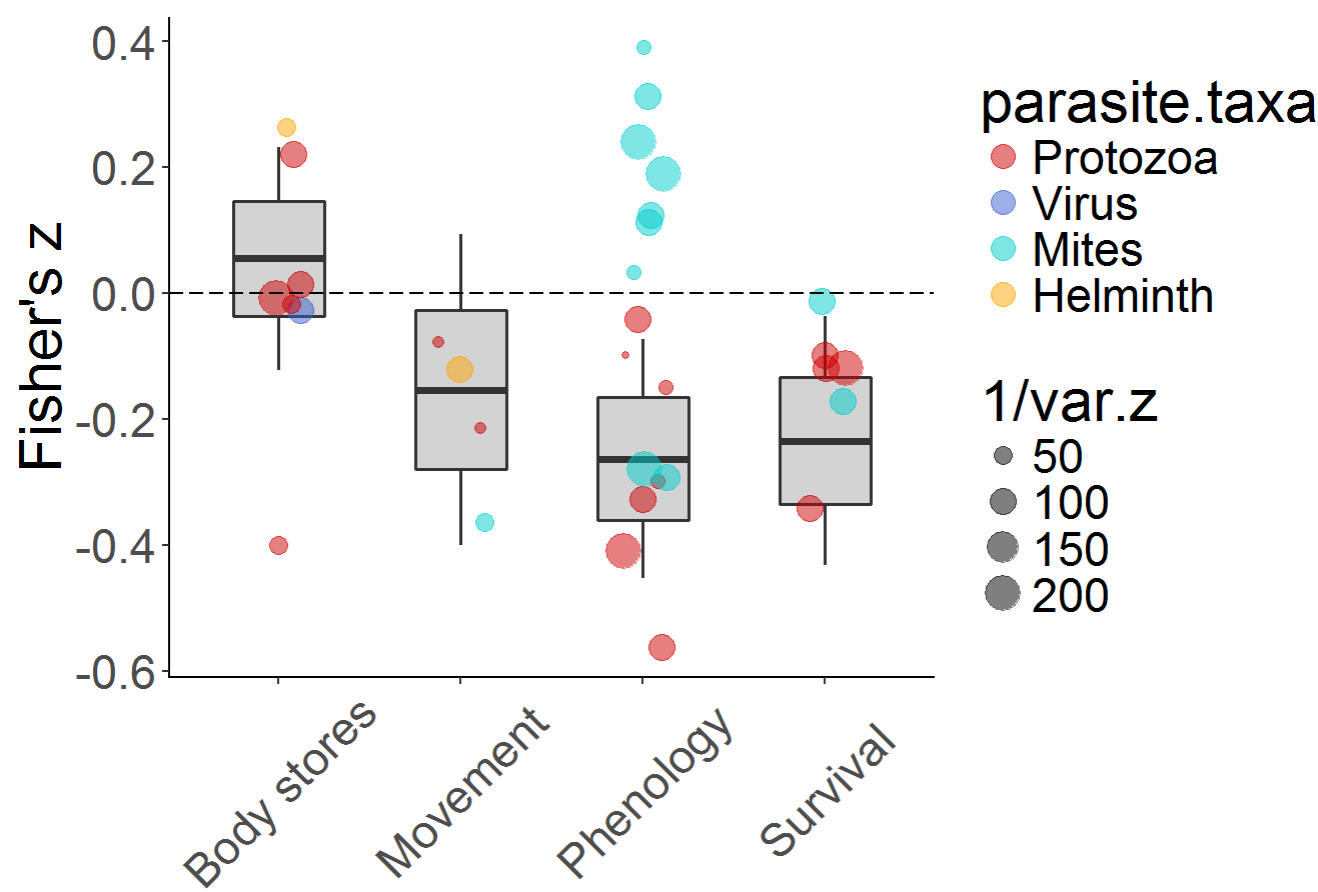
##boxplot

##overlaid with raw data with proportional weights

##Figure 4b

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
h=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=4)))
```

```
## 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 = list(~1 | id, ~ 1 | species_ott), R = list(species_ott = corr
_matrix), data=Bodystores) ##null model
summary(null1)
```

```
##
## Multivariate Meta-Analysis Model (k = 7; method: REML)
##
##   logLik  Deviance      AIC      BIC      AICc
##   -0.3996    0.7991    6.7991    6.1744    18.7991
##
## Variance Components:
##
##           estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0000  0.0000     5    no           id     no
## sigma^2.2  0.0016  0.0405     5    no  species_ott  yes
##
```

```
## Test for Heterogeneity:
## Q(df = 6) = 16.2062, p-val = 0.0127
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
##    0.0156    0.0460    0.3401    0.7338   -0.0745    0.1058
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##I2

W <- diag(1/Bodystores$var.z)
X <- model.matrix(null1)
P <- W - W %*% X %*% solve(t(X) %*% W %*% X) %*% t(X) %*% W
100 * sum(null1$sigma2) / (sum(null1$sigma2) + (null1$k-null1$p)/sum(diag(P)))
```

```
## [1] 12.6707
```

```
# = 17.34% #Total variance

100 * null1$sigma2 / (sum(null1$sigma2) + (null1$k-null1$p)/sum(diag(P)))
```

```
## [1] 4.412966e-09 1.267070e+01
```

```
# sigma1 = 0%      sigma2 = 17.34%

#####

#Does not converge with phylogeny as random effect, so removed.

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
W <- diag(1/movement$var.z)
X <- model.matrix(null3)
P <- W - W %*% X %*% solve(t(X) %*% W %*% X) %*% t(X) %*% W
100 * sum(null3$sigma2) / (sum(null3$sigma2) + (null3$k-null3$p)/sum(diag(P)))
```

```
## [1] 9.380134e-07
```

```
# = 0% #Total variance

100 * null3$sigma2 / (sum(null3$sigma2) + (null3$k-null3$p)/sum(diag(P)))
```

```
## [1] 9.380134e-07
```

```
# signal = 0%    # no sigma two

#####

null4<-rma.mv(z, var.z, random = list(~1 | id, ~ 1 | species_ott), R = list(species_ott = corr
_matrix), data=phenology) ##null model
summary(null4)
```

```
##
## Multivariate Meta-Analysis Model (k = 16; method: REML)
##
##      logLik  Deviance      AIC      BIC      AICc
## -16.5858   33.1715   39.1715   41.2957   41.3533
##
## Variance Components:
##
##      estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0364  0.1908     4    no           id    no
## sigma^2.2  0.0426  0.2064     4    no  species_ott  yes
##
## Test for Heterogeneity:
## Q(df = 15) = 131.0194, p-val < .0001
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## -0.2602  0.1839  -1.4146   0.1572  -0.6207   0.1003
##
## ---
```

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

```
#i2
W <- diag(1/phenology$var.z)
X <- model.matrix(null4)
P <- W - W %*% X %*% solve(t(X) %*% W %*% X) %*% t(X) %*% W
100 * sum(null4$sigma2) / (sum(null4$sigma2) + (null4$k-null4$p)/sum(diag(P)))
```

```
## [1] 88.83919
```

```
# = 88.8% #Total variance

100 * null4$sigma2 / (sum(null4$sigma2) + (null4$k-null4$p)/sum(diag(P)))
```

```
## [1] 40.92618 47.91301
```

```
# signal = 40.9%   # sigma2 = 47.9%

#####

null5<-rma.mv(z, var.z, random = list(~1 | id, ~ 1 | species_ott), R = list(species_ott = corr
_matrix), data=survival) ##null model
summary(null5)
```

```
##
## Multivariate Meta-Analysis Model (k = 6; method: REML)
##
##      logLik  Deviance      AIC      BIC      AICc
##      4.2548   -8.5096   -2.5096   -3.6812   21.4904
##
## Variance Components:
##
##              estim      sqrt  nlvls  fixed      factor      R
## sigma^2.1  0.0000  0.0000      3    no              id    no
## sigma^2.2  0.0022  0.0470      3    no species_ott  yes
##
## Test for Heterogeneity:
## Q(df = 5) = 6.0600, p-val = 0.3004
##
## Model Results:
##
## estimate      se      zval      pval      ci.lb      ci.ub
## -0.1473  0.0499  -2.9514  0.0032  -0.2451  -0.0495  **
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#i2
W <- diag(1/survival$var.z)
```

```
X <- model.matrix(null15)
P <- W - W %*% X %*% solve(t(X) %*% W %*% X) %*% t(X) %*% W
100 * sum(null15$sigma2) / (sum(null15$sigma2) + (null15$k-null15$p)/sum(diag(P)))
```

```
## [1] 20.1373
```

```
# = 20.1% #Total variance

100 * null15$sigma2 / (sum(null15$sigma2) + (null15$k-null15$p)/sum(diag(P)))
```

```
## [1] 6.321574e-08 2.013730e+01
```

```
# sigma1 = 0%    # sigma2 = 20.1%

##### plot Fig 4b

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  0.0156 -0.1863 -0.2602 -0.1473
## $ se       : num  0.046 0.0707 0.1839 0.0499
## $ l.ci     : num  -0.0745 -0.3248 -0.6207 -0.2451
## $ u.ci     : num  0.1058 -0.0477 0.1003 -0.0495
## $ level    : Factor w/ 4 levels "Body stores",...: 1 2 3 4
```

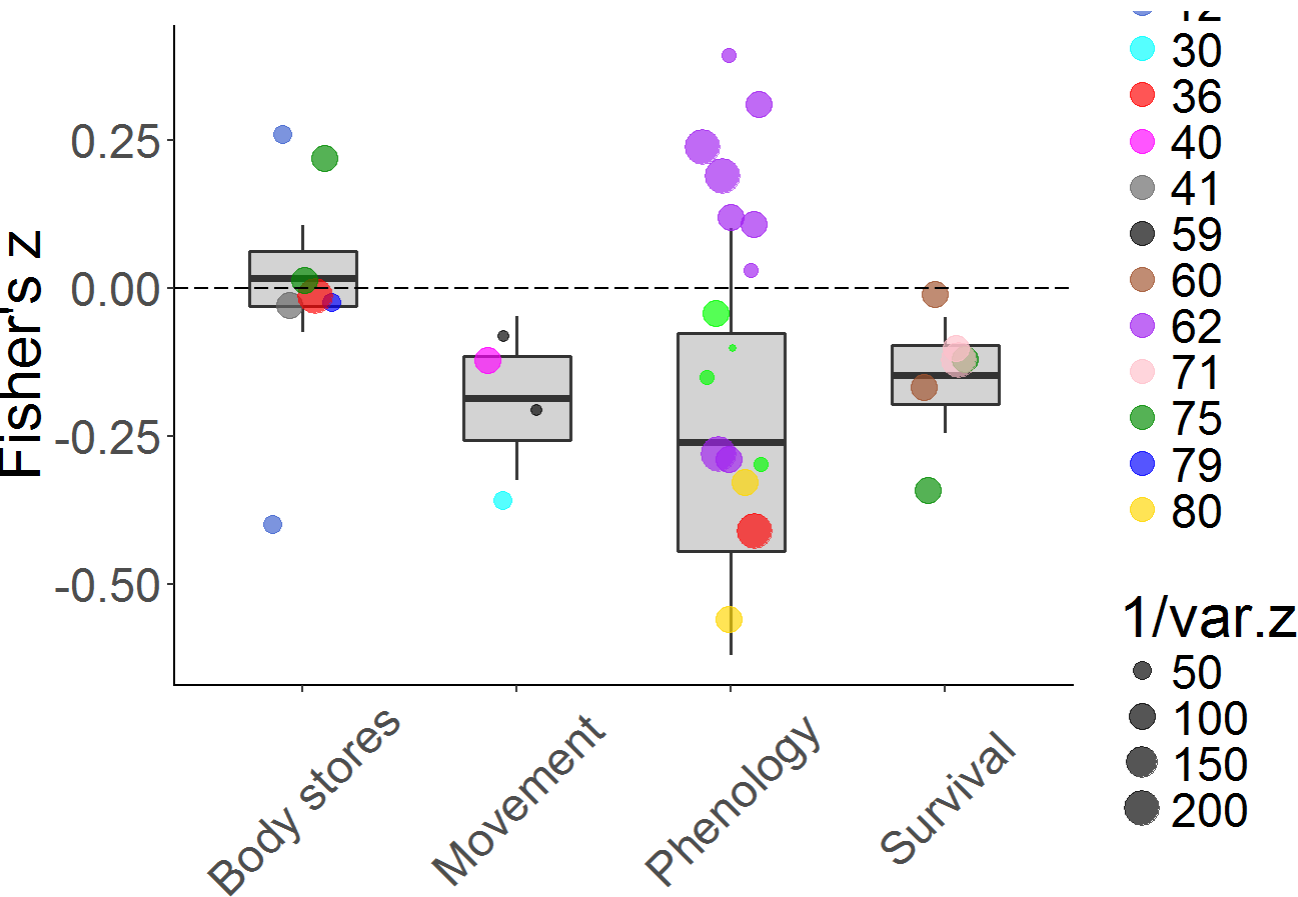
```
predictedvalues$l.se<-predictedvalues$predicted - predictedvalues$se
predictedvalues$u.se<-predictedvalues$predicted + predictedvalues$se

##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, alp
ha=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","s
ienna","purple","pink","green4","blue","gold"))+
  guides(colour = guide_legend(override.aes = list(size=4)))
```

Warning: Ignoring unknown aesthetics: width



END