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<html><head></head><body><pre style="word-wrap: break-word; white-space: pre-wrap;">#R
version 3.4.4
library(ape) #5.0
library(phytools) #0.6-44
library(ggplot2) #2.2.1
library(RcmdrMisc) #1.0-5

#Set your work directory
setwd("")

##### Louse families: Data and phylogeny subsets #####
#Importing family data
louse_data=read.table("Supplementary_Data_S1_Louse_family_data_Renschs_rule_in_avian_lice_con
tradictory_allometric_trends_for_sexual_size_dimorphism_I_S_PIROSS_A_HARNOS_L_ROZSA.csv",
sep=",", dec=".", quote = "'",header = T) #Importing data
louse_data$louse_family=factor(louse_data$louse_family) #Converting louse family variable to
factor
levels(louse_data$louse_family)=c("M","P","R") #Renaming factor levels: M: Menoponidae,
P:Phloptoridae, R: Ricinidae
louse_data$louse_family=relevel(louse_data$louse_family, ref="P") #Setting reference factor
level
row.names(louse_data) = louse_data[["louse_species"]] #Setting row names (louse species
names)

louse_data$log_male_total_body_length=log(louse_data$male_total_body_length) #Calculating log
body lengths
louse_data$log_female_total_body_length=log(louse_data$female_total_body_length) #Calculating
log body lengths
louse_data$m_f_rat=louse_data$male_total_body_length/louse_data$female_total_body_length
#Calculating male/female body lengths

#Importing family tree
louse_tree=read.caic("Supplementary_Data_S2_Louse_family_phylogeny_Renschs_rule_in_avian_lice
_contradictory_allometric_trends_for_sexual_size_dimorphism_I_S_PIROSS_A_HARNOS_L_ROZSA.csv",
fileEncoding = "UTF-8")
louse_tree2=drop.tip(louse_tree,
setdiff(as.character(louse_tree[["tip.label"]]),louse_data$louse_species))
louse_tree2
louse_tree3=compute.brlen(louse_tree2)
louse_tree3

#Family subsets
#Phloptoridae
louse_data_P=droplevels(louse_data[louse_data$louse_family=="P",]) #Data subset
louse_tree_P=drop.tip(louse_tree3,
setdiff(as.character(louse_tree3[["tip.label"]]),louse_data_P$louse_species)) #Phylogeny
subset
P_log_male=louse_data_P$log_male_total_body_length #log(male body length)
names(P_log_male)=louse_data_P$louse_species #naming vector elements
P_log_female=louse_data_P$log_female_total_body_length #log(female body length)
names(P_log_female)=louse_data_P$louse_species #naming vector elements

#Menoponidae
louse_data_M=droplevels(louse_data[louse_data$louse_family=="M",]) #Data subset
louse_tree_M=drop.tip(louse_tree3,
setdiff(as.character(louse_tree3[["tip.label"]]),louse_data_M$louse_species)) #Mhylogeny
subset
M_log_male=louse_data_M$log_male_total_body_length #log(male body length)
names(M_log_male)=louse_data_M$louse_species #naming vector elements
M_log_female=louse_data_M$log_female_total_body_length #log(female body length)
names(M_log_female)=louse_data_M$louse_species #naming vector elements

#Ricinidae
louse_data_R=droplevels(louse_data[louse_data$louse_family=="R",]) #Data subset
louse_tree_R=drop.tip(louse_tree3,
setdiff(as.character(louse_tree3[["tip.label"]]),louse_data_R$louse_species)) #Rhylogeny
subset
R_log_male=louse_data_R$log_male_total_body_length #log(male body length)
names(R_log_male)=louse_data_R$louse_species #naming vector elements

R_log_female=louse_data_R$log_female_total_body_length #log(female body length)
names(R_log_female)=louse_data_R$louse_species #naming vector elements

##### Louse families: Phylogenetic RMA regression #####
#Phloptoridae

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rensch_phyl_RMA_P=phyl.RMA(x=P_log_female,y=P_log_male, method="lambda",tree = louse_tree_P)
rensch_phyl_RMA_P

#Menoponidae
rensch_phyl_RMA_M=phyl.RMA(x=M_log_female,y=M_log_male, method="lambda",tree = louse_tree_M)
rensch_phyl_RMA_M

#Ricinidae
rensch_phyl_RMA_R=phyl.RMA(x=R_log_female,y=R_log_male, method="lambda",tree = louse_tree_R)
rensch_phyl_RMA_R

##### Louse families: Phylogenetic RMA regression - Jackknife influence diagnostics
#####
#Philopteridae
#Could take a long time to run!
rensch_phyl_RMA_P_jk_results=data.frame(row_num=1:length(P_log_female), beta1=NA, r2=NA,
p=NA)
for(i in 1:length(P_log_female)){
  louse_tree_P_jk=drop.tip(louse_tree_P,
setdiff(as.character(louse_tree_P[["tip.label"]]),names(P_log_female[-i]))) #Phylogeny subset
  rensch_phyl_RMA_P_jk=phyl.RMA(x=P_log_female[-i],y=P_log_male[-i], method="lambda",tree =
louse_tree_P_jk)

rensch_phyl_RMA_P_jk_results[i,2:4]=c(rensch_phyl_RMA_P_jk$RMA.beta[2],rensch_phyl_RMA_P_jk$t
est[c(1,4)])
  print(paste(i,"out of",length(P_log_female),"done."))
}
write.csv(rensch_phyl_RMA_P_jk_results,"rensch_phyl_RMA_P_jk_results.csv", row.names = F)

summary(rensch_phyl_RMA_P_jk_results[,-1])
#The effect (in %) on the slope of the most influential point in the model
(rensch_phyl_RMA_P_influence=max((rensch_phyl_RMA_P_jk_results$beta1-
rensch_phyl_RMA_P$RMA.beta[2])/rensch_phyl_RMA_P$RMA.beta[2]*100))

#Menoponidae
#Could take a long time to run!
rensch_phyl_RMA_M_jk_results=data.frame(row_num=1:length(M_log_female), beta1=NA, r2=NA,
p=NA)
for(i in 1:length(M_log_female)){
  louse_tree_M_jk=drop.tip(louse_tree_M,
setdiff(as.character(louse_tree_M[["tip.label"]]),names(M_log_female[-i]))) #Phylogeny subset
  rensch_phyl_RMA_M_jk=phyl.RMA(x=M_log_female[-i],y=M_log_male[-i], method="lambda",tree =
louse_tree_M_jk)

rensch_phyl_RMA_M_jk_results[i,2:4]=c(rensch_phyl_RMA_M_jk$RMA.beta[2],rensch_phyl_RMA_M_jk$t
est[c(1,4)])
  print(paste(i,"out of",length(M_log_female),"done."))
}
write.csv(rensch_phyl_RMA_M_jk_results,"rensch_phyl_RMA_M_jk_results.csv", row.names = F)

summary(rensch_phyl_RMA_M_jk_results[,-1])
#The effect (in %) on the slope of the most influential point in the model
(rensch_phyl_RMA_M_influence=max((rensch_phyl_RMA_M_jk_results$beta1-
rensch_phyl_RMA_M$RMA.beta[2])/rensch_phyl_RMA_M$RMA.beta[2]*100))

#Ricinidae
rensch_phyl_RMA_R_jk_results=data.frame(row_num=1:length(R_log_female), beta1=NA, r2=NA,
p=NA)
for(i in 1:length(R_log_female)){
  louse_tree_R_jk=drop.tip(louse_tree_R,
setdiff(as.character(louse_tree_R[["tip.label"]]),names(R_log_female[-i]))) #Phylogeny subset
  rensch_phyl_RMA_R_jk=phyl.RMA(x=R_log_female[-i],y=R_log_male[-i], method="lambda",tree =
louse_tree_R_jk)

rensch_phyl_RMA_R_jk_results[i,2:4]=c(rensch_phyl_RMA_R_jk$RMA.beta[2],rensch_phyl_RMA_R_jk$t
est[c(1,4)])
  print(paste(i,"out of",length(R_log_female),"done."))
}
write.csv(rensch_phyl_RMA_R_jk_results,"rensch_phyl_RMA_R_jk_results.csv", row.names = F)

summary(rensch_phyl_RMA_R_jk_results[,-1])
#The effect (in %) on the slope of the most influential point in the model
(rensch_phyl_RMA_R_influence=max((rensch_phyl_RMA_R_jk_results$beta1-
rensch_phyl_RMA_R$RMA.beta[2])/rensch_phyl_RMA_R$RMA.beta[2]*100))

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##### Philopteridae and Menoponidae by host orders: Data and phylogeny subsets
#####
#Louse families from different orders subsets
#Philopteridae - Passeriformes
louse_data_P_Passeriformes=droplevels(louse_data[louse_data$louse_family=="P"&louse_data$order=="Passeriformes",]) #Data subset
louse_tree_P_Passeriformes=drop.tip(louse_tree3,
setdiff(as.character(louse_tree3[["tip.label"]]),louse_data_P_Passeriformes$louse_species))
#Phylogeny subset
P_Passeriformes_log_male=log(louse_data_P_Passeriformes$male_total_body_length) #log(male
body length)
names(P_Passeriformes_log_male)=louse_data_P_Passeriformes$louse_species #naming vector
elements
P_Passeriformes_log_female=log(louse_data_P_Passeriformes$female_total_body_length)
#log(female body length)
names(P_Passeriformes_log_female)=louse_data_P_Passeriformes$louse_species #naming vector
elements

#Menoponidae - Passeriformes
louse_data_M_Passeriformes=droplevels(louse_data[louse_data$louse_family=="M"&louse_data$order=="Passeriformes",]) #Data subset
louse_tree_M_Passeriformes=drop.tip(louse_tree3,
setdiff(as.character(louse_tree3[["tip.label"]]),louse_data_M_Passeriformes$louse_species))
#Phylogeny subset
M_Passeriformes_log_male=log(louse_data_M_Passeriformes$male_total_body_length) #log(male
body length)
names(M_Passeriformes_log_male)=louse_data_M_Passeriformes$louse_species #naming vector
elements
M_Passeriformes_log_female=log(louse_data_M_Passeriformes$female_total_body_length)
#log(female body length)
names(M_Passeriformes_log_female)=louse_data_M_Passeriformes$louse_species #naming vector
elements

#Philopteridae - Charadriiformes
louse_data_P_Charadriiformes=droplevels(louse_data[louse_data$louse_family=="P"&louse_data$order=="Charadriiformes",]) #Data subset
louse_tree_P_Charadriiformes=drop.tip(louse_tree3,
setdiff(as.character(louse_tree3[["tip.label"]]),louse_data_P_Charadriiformes$louse_species))
#Phylogeny subset
P_Charadriiformes_log_male=log(louse_data_P_Charadriiformes$male_total_body_length) #log(male
body length)
names(P_Charadriiformes_log_male)=louse_data_P_Charadriiformes$louse_species #naming vector
elements
P_Charadriiformes_log_female=log(louse_data_P_Charadriiformes$female_total_body_length)
#log(female body length)
names(P_Charadriiformes_log_female)=louse_data_P_Charadriiformes$louse_species #naming vector
elements

#Menoponidae - Charadriiformes
louse_data_M_Charadriiformes=droplevels(louse_data[louse_data$louse_family=="M"&louse_data$order=="Charadriiformes",]) #Data subset
louse_tree_M_Charadriiformes=drop.tip(louse_tree3,
setdiff(as.character(louse_tree3[["tip.label"]]),louse_data_M_Charadriiformes$louse_species))
#Phylogeny subset
M_Charadriiformes_log_male=log(louse_data_M_Charadriiformes$male_total_body_length) #log(male
body length)
names(M_Charadriiformes_log_male)=louse_data_M_Charadriiformes$louse_species #naming vector
elements
M_Charadriiformes_log_female=log(louse_data_M_Charadriiformes$female_total_body_length)
#log(female body length)
names(M_Charadriiformes_log_female)=louse_data_M_Charadriiformes$louse_species #naming vector
elements

#Philopteridae - Galliformes
louse_data_P_Galliformes=droplevels(louse_data[louse_data$louse_family=="P"&louse_data$order=="Galliformes",]) #Data subset
louse_tree_P_Galliformes=drop.tip(louse_tree3,
setdiff(as.character(louse_tree3[["tip.label"]]),louse_data_P_Galliformes$louse_species))
#Phylogeny subset
P_Galliformes_log_male=log(louse_data_P_Galliformes$male_total_body_length) #log(male body
length)
names(P_Galliformes_log_male)=louse_data_P_Galliformes$louse_species #naming vector elements
P_Galliformes_log_female=log(louse_data_P_Galliformes$female_total_body_length) #log(female
body length)
names(P_Galliformes_log_female)=louse_data_P_Galliformes$louse_species #naming vector
elements
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elements

#Menoponidae - Galliformes
louse_data_M_Galliformes=droplevels(louse_data[louse_data$louse_family=="M"&louse_data$order=="Galliformes",]) #Data subset
louse_tree_M_Galliformes=drop.tip(louse_tree3,
setdiff(as.character(louse_tree3[["tip.label"]]),louse_data_M_Galliformes$louse_species))
#Phylogeny subset
M_Galliformes_log_male=log(louse_data_M_Galliformes$male_total_body_length) #log(male body
length)
names(M_Galliformes_log_male)=louse_data_M_Galliformes$louse_species #naming vector elements
M_Galliformes_log_female=log(louse_data_M_Galliformes$female_total_body_length) #log(female
body length)
names(M_Galliformes_log_female)=louse_data_M_Galliformes$louse_species #naming vector
elements

##### Philopteridae and Menoponidae by host orders: Phylogenetic RMA regression
#####
#Philopteridae - Passeriformes
rensch_phyl_RMA_P_Passeriformes=phyl.RMA(x=P_Passeriformes_log_female,y=P_Passeriformes_log_m
ale, method="lambda",tree = louse_tree_P_Passeriformes)
rensch_phyl_RMA_P_Passeriformes

#Menoponidae - Passeriformes
rensch_phyl_RMA_M_Passeriformes=phyl.RMA(x=M_Passeriformes_log_female,y=M_Passeriformes_log_m
ale, method="lambda",tree = louse_tree_M_Passeriformes)
rensch_phyl_RMA_M_Passeriformes

#Philopteridae - Charadriiformes
rensch_phyl_RMA_P_Charadriiformes=phyl.RMA(x=P_Charadriiformes_log_female,y=P_Charadriiformes
_log_male, method="lambda",tree = louse_tree_P_Charadriiformes)
rensch_phyl_RMA_P_Charadriiformes

#Menoponidae - Charadriiformes
rensch_phyl_RMA_M_Charadriiformes=phyl.RMA(x=M_Charadriiformes_log_female,y=M_Charadriiformes
_log_male, method="lambda",tree = louse_tree_M_Charadriiformes)
rensch_phyl_RMA_M_Charadriiformes

#Philopteridae - Galliformes
rensch_phyl_RMA_P_Galliformes=phyl.RMA(x=P_Galliformes_log_female,y=P_Galliformes_log_male,
method="lambda",tree = louse_tree_P_Galliformes)
rensch_phyl_RMA_P_Galliformes

#Menoponidae - Galliformes
rensch_phyl_RMA_M_Galliformes=phyl.RMA(x=M_Galliformes_log_female,y=M_Galliformes_log_male,
method="lambda",tree = louse_tree_M_Galliformes)
rensch_phyl_RMA_M_Galliformes

##### Philopteridae and Menoponidae by host orders: Phylogenetic RMA regression -
Jackknife influence diagnostics #####
#Philopteridae - Passeriformes
rensch_phyl_RMA_P_Passeriformes_jk_results=data.frame(row_num=1:length(P_Passeriformes_log_fe
male), beta1=NA, r2=NA, p=NA)
for(i in 1:length(P_Passeriformes_log_female)){
  louse_tree_P_Passeriformes_jk=drop.tip(louse_tree_P_Passeriformes,
setdiff(as.character(louse_tree_P_Passeriformes[["tip.label"]]),names(P_Passeriformes_log_fem
ale[-i]))) #Phylogeny subset
  rensch_phyl_RMA_P_Passeriformes_jk=phyl.RMA(x=P_Passeriformes_log_female[-
i],y=P_Passeriformes_log_male[-i], method="lambda",tree = louse_tree_P_Passeriformes_jk)

rensch_phyl_RMA_P_Passeriformes_jk_results[i,2:4]=c(rensch_phyl_RMA_P_Passeriformes_jk$RMA.be
ta[2],rensch_phyl_RMA_P_Passeriformes_jk$test[c(1,4)])
  print(paste(i,"out of",length(P_Passeriformes_log_female),"done. "))
}
write.csv(rensch_phyl_RMA_P_Passeriformes_jk_results,"rensch_phyl_RMA_P_Passeriformes_jk_resu
lts.csv", row.names = F)

summary(rensch_phyl_RMA_P_Passeriformes_jk_results[,-1])
#The effect (in %) on the slope of the most influential point in the model
(rensch_phyl_RMA_P_Passeriformes_influence=max((rensch_phyl_RMA_P_Passeriformes_jk_results$be
ta1-
rensch_phyl_RMA_P_Passeriformes$RMA.beta[2])/rensch_phyl_RMA_P_Passeriformes$RMA.beta[2]*100)
)

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#Menoponidae - Passeriformes
rensch_phyl_RMA_M_Passeriformes_jk_results=data.frame(row_num=1:length(M_Passeriformes_log_fem
male), betal=NA, r2=NA, p=NA)
for(i in 1:length(M_Passeriformes_log_female)){
  louse_tree_M_Passeriformes_jk=drop.tip(louse_tree_M_Passeriformes,
setdiff(as.character(louse_tree_M_Passeriformes[["tip.label"]]),names(M_Passeriformes_log_fem
ale[-i]))) #Phylogeny subset
  rensch_phyl_RMA_M_Passeriformes_jk=phyl.RMA(x=M_Passeriformes_log_female[-
i],y=M_Passeriformes_log_male[-i], method="lambda",tree = louse_tree_M_Passeriformes_jk)

rensch_phyl_RMA_M_Passeriformes_jk_results[i,2:4]=c(rensch_phyl_RMA_M_Passeriformes_jk$RMA.be
ta[2],rensch_phyl_RMA_M_Passeriformes_jk$test[c(1,4)])
  print(paste(i,"out of",length(M_Passeriformes_log_female),"done."))
}
write.csv(rensch_phyl_RMA_M_Passeriformes_jk_results,"rensch_phyl_RMA_M_Passeriformes_jk_resu
lts.csv", row.names = F)

summary(rensch_phyl_RMA_M_Passeriformes_jk_results[,-1])
#The effect (in %) on the slope of the most influential point in the model
(rensch_phyl_RMA_M_Passeriformes_influence=max((rensch_phyl_RMA_M_Passeriformes_jk_results$be
tal-
rensch_phyl_RMA_M_Passeriformes$RMA.beta[2])/rensch_phyl_RMA_M_Passeriformes$RMA.beta[2]*100)
)

#Philopteridae - Charadriiformes
rensch_phyl_RMA_P_Charadriiformes_jk_results=data.frame(row_num=1:length(P_Charadriiformes_lo
g_female), betal=NA, r2=NA, p=NA)
for(i in 1:length(P_Charadriiformes_log_female)){
  louse_tree_P_Charadriiformes_jk=drop.tip(louse_tree_P_Charadriiformes,
setdiff(as.character(louse_tree_P_Charadriiformes[["tip.label"]]),names(P_Charadriiformes_log
_female[-i]))) #Phylogeny subset
  rensch_phyl_RMA_P_Charadriiformes_jk=phyl.RMA(x=P_Charadriiformes_log_female[-
i],y=P_Charadriiformes_log_male[-i], method="lambda",tree = louse_tree_P_Charadriiformes_jk)

rensch_phyl_RMA_P_Charadriiformes_jk_results[i,2:4]=c(rensch_phyl_RMA_P_Charadriiformes_jk$RM
A.beta[2],rensch_phyl_RMA_P_Charadriiformes_jk$test[c(1,4)])
  print(paste(i,"out of",length(P_Charadriiformes_log_female),"done."))
}
write.csv(rensch_phyl_RMA_P_Charadriiformes_jk_results,"rensch_phyl_RMA_P_Charadriiformes_jk_
results.csv", row.names = F)

summary(rensch_phyl_RMA_P_Charadriiformes_jk_results[,-1])
#The effect (in %) on the slope of the most influential point in the model
(rensch_phyl_RMA_P_Charadriiformes_influence=max((rensch_phyl_RMA_P_Charadriiformes_jk_result
s$beta1-
rensch_phyl_RMA_P_Charadriiformes$RMA.beta[2])/rensch_phyl_RMA_P_Charadriiformes$RMA.beta[2]*
100))

#Menoponidae - Charadriiformes
rensch_phyl_RMA_M_Charadriiformes_jk_results=data.frame(row_num=1:length(M_Charadriiformes_lo
g_female), betal=NA, r2=NA, p=NA)
for(i in 1:length(M_Charadriiformes_log_female)){
  louse_tree_M_Charadriiformes_jk=drop.tip(louse_tree_M_Charadriiformes,
setdiff(as.character(louse_tree_M_Charadriiformes[["tip.label"]]),names(M_Charadriiformes_log
_female[-i]))) #Phylogeny subset
  rensch_phyl_RMA_M_Charadriiformes_jk=phyl.RMA(x=M_Charadriiformes_log_female[-
i],y=M_Charadriiformes_log_male[-i], method="lambda",tree = louse_tree_M_Charadriiformes_jk)

rensch_phyl_RMA_M_Charadriiformes_jk_results[i,2:4]=c(rensch_phyl_RMA_M_Charadriiformes_jk$RM
A.beta[2],rensch_phyl_RMA_M_Charadriiformes_jk$test[c(1,4)])
  print(paste(i,"out of",length(M_Charadriiformes_log_female),"done."))
}
write.csv(rensch_phyl_RMA_M_Charadriiformes_jk_results,"rensch_phyl_RMA_M_Charadriiformes_jk_
results.csv", row.names = F)

summary(rensch_phyl_RMA_M_Charadriiformes_jk_results[,-1])
#The effect (in %) on the slope of the most influential point in the model
(rensch_phyl_RMA_M_Charadriiformes_influence=max((rensch_phyl_RMA_M_Charadriiformes_jk_result
s$beta1-
rensch_phyl_RMA_M_Charadriiformes$RMA.beta[2])/rensch_phyl_RMA_M_Charadriiformes$RMA.beta[2]*
100))

#Philopteridae - Galliformes
rensch_phyl_RMA_P_Galliformes_jk_results=data.frame(row_num=1:length(P_Galliformes_log_femal
e), betal=NA, r2=NA, p=NA)

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for(i in 1:length(P_Galliformes_log_female)){
  louse_tree_P_Galliformes_jk=drop.tip(lobe_tree_P_Galliformes,
setdiff(as.character(lobe_tree_P_Galliformes[["tip.label"]]),names(P_Galliformes_log_female[
-i]))) #Phylogeny subset
  rensch_phyl_RMA_P_Galliformes_jk=phyl.RMA(x=P_Galliformes_log_female[-
i],y=P_Galliformes_log_male[-i], method="lambda",tree = louse_tree_P_Galliformes_jk)

rensch_phyl_RMA_P_Galliformes_jk_results[i,2:4]=c(rensch_phyl_RMA_P_Galliformes_jk$RMA.beta[2
],rensch_phyl_RMA_P_Galliformes_jk$test[c(1,4)])
  print(paste(i,"out of",length(P_Galliformes_log_female),"done."))
}
write.csv(rensch_phyl_RMA_P_Galliformes_jk_results,"rensch_phyl_RMA_P_Galliformes_jk_results.
csv", row.names = F)

summary(rensch_phyl_RMA_P_Galliformes_jk_results[,-1])
#The effect (in %) on the slope of the most influential point in the model
(rensch_phyl_RMA_P_Galliformes_influence=max((rensch_phyl_RMA_P_Galliformes_jk_results$beta1-
rensch_phyl_RMA_P_Galliformes$RMA.beta[2])/rensch_phyl_RMA_P_Galliformes$RMA.beta[2]*100))

#Menoponidae - Galliformes
rensch_phyl_RMA_M_Galliformes_jk_results=data.frame(row_num=1:length(M_Galliformes_log_female
), beta1=NA, r2=NA, p=NA)
for(i in 1:length(M_Galliformes_log_female)){
  louse_tree_M_Galliformes_jk=drop.tip(lobe_tree_M_Galliformes,
setdiff(as.character(lobe_tree_M_Galliformes[["tip.label"]]),names(M_Galliformes_log_female[
-i]))) #Phylogeny subset
  rensch_phyl_RMA_M_Galliformes_jk=phyl.RMA(x=M_Galliformes_log_female[-
i],y=M_Galliformes_log_male[-i], method="lambda",tree = louse_tree_M_Galliformes_jk)

rensch_phyl_RMA_M_Galliformes_jk_results[i,2:4]=c(rensch_phyl_RMA_M_Galliformes_jk$RMA.beta[2
],rensch_phyl_RMA_M_Galliformes_jk$test[c(1,4)])
  print(paste(i,"out of",length(M_Galliformes_log_female),"done."))
}
write.csv(rensch_phyl_RMA_M_Galliformes_jk_results,"rensch_phyl_RMA_M_Galliformes_jk_results.
csv", row.names = F)

summary(rensch_phyl_RMA_M_Galliformes_jk_results[,-1])
#The effect (in %) on the slope of the most influential point in the model
(rensch_phyl_RMA_M_Galliformes_influence=max((rensch_phyl_RMA_M_Galliformes_jk_results$beta1-
rensch_phyl_RMA_M_Galliformes$RMA.beta[2])/rensch_phyl_RMA_M_Galliformes$RMA.beta[2]*100))

##### Table 1: Descriptive statistics of male, female body lengths ( $\hat{\mu}$ m) and host
weights (g) #####
table_body_length_descriptives=data.frame(group=c("Philopteridae","Menoponidae","Ricinidae",
"Philopteridae_Passeriformes","Menoponidae_Passeriformes",
"Philopteridae_Charadriiformes","Menoponidae_Charadriiformes",
"Philopteridae_Galliformes","Menoponidae_Galliformes"),
male_mean=NA,male_sd=NA,female_mean=NA,female_sd=NA,male_female_ratio_mean=NA,male_female_rat
io_sd=NA,host_weight_mean=NA,host_weight_sd=NA,N=NA)

table_body_length_descriptives[1,2:10]=c(t(numSummary(lobe_data_P[,c("male_total_body_length
","female_total_body_length","m_f_rat","host_weight")],
statistics =
c("mean","sd"))$table),numSummary(lobe_data_P[,c("male_total_body_length","female_total_body
_length","m_f_rat","host_weight")],
statistics = c("mean","sd"))$n[1])
table_body_length_descriptives[2,2:10]=c(t(numSummary(lobe_data_M[,c("male_total_body_length
","female_total_body_length","m_f_rat","host_weight")],
statistics =
c("mean","sd"))$table),numSummary(lobe_data_M[,c("male_total_body_length","female_total_body
_length","m_f_rat","host_weight")],
statistics = c("mean","sd"))$n[1])
table_body_length_descriptives[3,2:10]=c(t(numSummary(lobe_data_R[,c("male_total_body_length
","female_total_body_length","m_f_rat","host_weight")],
statistics =
c("mean","sd"))$table),numSummary(lobe_data_R[,c("male_total_body_length","female_total_body
_length","m_f_rat","host_weight")],

```

```

statistics = c("mean","sd"))$n[1])
table_body_length_descriptives[4,2:10]=c(t(numSummary(louse_data_P_Passeriformes[,c("male_tot
al_body_length","female_total_body_length","m_f_rat","host_weight")],
statistics =
c("mean","sd"))$table),numSummary(louse_data_P_Passeriformes[,c("male_total_body_length","fem
ale_total_body_length","m_f_rat","host_weight")],
statistics = c("mean","sd"))$n[1])
table_body_length_descriptives[5,2:10]=c(t(numSummary(louse_data_M_Passeriformes[,c("male_tot
al_body_length","female_total_body_length","m_f_rat","host_weight")],
statistics =
c("mean","sd"))$table),numSummary(louse_data_M_Passeriformes[,c("male_total_body_length","fem
ale_total_body_length","m_f_rat","host_weight")],
statistics = c("mean","sd"))$n[1])
table_body_length_descriptives[6,2:10]=c(t(numSummary(louse_data_P_Charadriiformes[,c("male_t
otal_body_length","female_total_body_length","m_f_rat","host_weight")],
statistics =
c("mean","sd"))$table),numSummary(louse_data_P_Charadriiformes[,c("male_total_body_length","f
emale_total_body_length","m_f_rat","host_weight")],
statistics = c("mean","sd"))$n[1])
table_body_length_descriptives[7,2:10]=c(t(numSummary(louse_data_M_Charadriiformes[,c("male_t
otal_body_length","female_total_body_length","m_f_rat","host_weight")],
statistics =
c("mean","sd"))$table),numSummary(louse_data_M_Charadriiformes[,c("male_total_body_length","f
emale_total_body_length","m_f_rat","host_weight")],
statistics = c("mean","sd"))$n[1])
table_body_length_descriptives[8,2:10]=c(t(numSummary(louse_data_P_Galliformes[,c("male_total
_body_length","female_total_body_length","m_f_rat","host_weight")],
statistics =
c("mean","sd"))$table),numSummary(louse_data_P_Galliformes[,c("male_total_body_length","femal
e_total_body_length","m_f_rat","host_weight")],
statistics = c("mean","sd"))$n[1])
table_body_length_descriptives[9,2:10]=c(t(numSummary(louse_data_M_Galliformes[,c("male_total
_body_length","female_total_body_length","m_f_rat","host_weight")],
statistics =
c("mean","sd"))$table),numSummary(louse_data_M_Galliformes[,c("male_total_body_length","femal
e_total_body_length","m_f_rat","host_weight")],
statistics = c("mean","sd"))$n[1])
table_body_length_descriptives[c(2:5,8:9)]=round(table_body_length_descriptives[c(2:5,8:9)],
digits = 0)
table_body_length_descriptives[6:7]=round(table_body_length_descriptives[6:7], digits = 2)
table_body_length_descriptives
write.csv(table_body_length_descriptives,"Table_1_Body_length_descriptives.csv",row.names =
F)

```

```

##### Table 2: Species closest to different quantiles of male relative sizes with
male and female body lengths and host masses #####
#0.025 quantile of relative male size, relative male size, male body length, female body
length, host weight, louse species name, host species name
relative_male_size_quantiles_table=data.frame(groups=c(rep("Louse
families",9),rep("Philopterid and Menoponid lice from different host orders",18)),
family_hostorder_ecomorph=c("Philopteridae","Philopteridae","Philopteridae",
"Menoponidae","Menoponidae","Menoponidae",
"Ricinidae","Ricinidae","Ricinidae",
"Philopteridae from
Passeriformes","Philopteridae from Passeriformes","Philopteridae from Passeriformes",
"Menoponidae from
Passeriformes","Menoponidae from Passeriformes","Menoponidae from Passeriformes",
"Philopteridae from
Charadriiformes","Philopteridae from Charadriiformes","Philopteridae from Charadriiformes",
"Menoponidae from
Charadriiformes","Menoponidae from Charadriiformes","Menoponidae from Charadriiformes",
"Philopteridae from
Galliformes","Philopteridae from Galliformes","Philopteridae from Galliformes",
"Menoponidae from
Galliformes","Menoponidae from Galliformes","Menoponidae from Galliformes"),
quantile=c(rep(c("2.5%","50%","97.5%"),9)),

```

```
relative_male_size=NA,  
male_body_length=NA,  
female_body_length=NA,  
host_weight=NA,  
louse_species_name=NA,  
host_species_name=NA
```

```
)
```

#Philopteridae

```
louse_data_P$louse_species=as.character(louse_data_P$louse_species)  
louse_data_P$host_species=as.character(louse_data_P$host_species)  
P_quantiles=numSummary(louse_data_P$m_f_rat, statistics = "quantiles", quantiles =  
c(0.025,0.5, 0.975))$table #Calculating the quantiles of relative male sizes  
relative_male_size_quantiles_table[1,4:9]=louse_data_P[which(abs(louse_data_P$m_f_rat-  
P_quantiles[1])==min(abs(louse_data_P$m_f_rat-  
P_quantiles[1]))),c("m_f_rat","male_total_body_length","female_total_body_length","host_weigh  
t","louse_species","host_species")][1,] #Finding the closest species to that quantile  
relative_male_size_quantiles_table[2,4:9]=louse_data_P[which(abs(louse_data_P$m_f_rat-  
P_quantiles[2])==min(abs(louse_data_P$m_f_rat-  
P_quantiles[2]))),c("m_f_rat","male_total_body_length","female_total_body_length","host_weigh  
t","louse_species","host_species")][1,] #Finding the closest species to that quantile  
relative_male_size_quantiles_table[3,4:9]=louse_data_P[which(abs(louse_data_P$m_f_rat-  
P_quantiles[3])==min(abs(louse_data_P$m_f_rat-  
P_quantiles[3]))),c("m_f_rat","male_total_body_length","female_total_body_length","host_weigh  
t","louse_species","host_species")][1,] #Finding the closest species to that quantile
```

#Menoponidae

```
louse_data_M$louse_species=as.character(louse_data_M$louse_species)  
louse_data_M$host_species=as.character(louse_data_M$host_species)  
M_quantiles=numSummary(louse_data_M$m_f_rat, statistics = "quantiles", quantiles =  
c(0.025,0.5, 0.975))$table #Calculating the quantiles of relative male sizes  
relative_male_size_quantiles_table[4,4:9]=louse_data_M[which(abs(louse_data_M$m_f_rat-  
M_quantiles[1])==min(abs(louse_data_M$m_f_rat-  
M_quantiles[1]))),c("m_f_rat","male_total_body_length","female_total_body_length","host_weigh  
t","louse_species","host_species")][1,] #Finding the closest species to that quantile  
relative_male_size_quantiles_table[5,4:9]=louse_data_M[which(abs(louse_data_M$m_f_rat-  
M_quantiles[2])==min(abs(louse_data_M$m_f_rat-  
M_quantiles[2]))),c("m_f_rat","male_total_body_length","female_total_body_length","host_weigh  
t","louse_species","host_species")][1,] #Finding the closest species to that quantile  
relative_male_size_quantiles_table[6,4:9]=louse_data_M[which(abs(louse_data_M$m_f_rat-  
M_quantiles[3])==min(abs(louse_data_M$m_f_rat-  
M_quantiles[3]))),c("m_f_rat","male_total_body_length","female_total_body_length","host_weigh  
t","louse_species","host_species")][1,] #Finding the closest species to that quantile
```

#Ricinidae

```
louse_data_R$louse_species=as.character(louse_data_R$louse_species)  
louse_data_R$host_species=as.character(louse_data_R$host_species)  
R_quantiles=numSummary(louse_data_R$m_f_rat, statistics = "quantiles", quantiles =  
c(0.025,0.5, 0.975))$table #Calculating the quantiles of relative male sizes  
relative_male_size_quantiles_table[7,4:9]=louse_data_R[which(abs(louse_data_R$m_f_rat-  
R_quantiles[1])==min(abs(louse_data_R$m_f_rat-  
R_quantiles[1]))),c("m_f_rat","male_total_body_length","female_total_body_length","host_weigh  
t","louse_species","host_species")][1,] #Finding the closest species to that quantile  
relative_male_size_quantiles_table[8,4:9]=louse_data_R[which(abs(louse_data_R$m_f_rat-  
R_quantiles[2])==min(abs(louse_data_R$m_f_rat-  
R_quantiles[2]))),c("m_f_rat","male_total_body_length","female_total_body_length","host_weigh  
t","louse_species","host_species")][1,] #Finding the closest species to that quantile  
relative_male_size_quantiles_table[9,4:9]=louse_data_R[which(abs(louse_data_R$m_f_rat-  
R_quantiles[3])==min(abs(louse_data_R$m_f_rat-  
R_quantiles[3]))),c("m_f_rat","male_total_body_length","female_total_body_length","host_weigh  
t","louse_species","host_species")][1,] #Finding the closest species to that quantile
```

#Philopteridae - Passeriformes

```
louse_data_P_Passeriformes$louse_species=as.character(louse_data_P_Passeriformes$louse_specie  
s)  
louse_data_P_Passeriformes$host_species=as.character(louse_data_P_Passeriformes$host_species)  
P_Passeriformes_quantiles=numSummary(louse_data_P_Passeriformes$m_f_rat, statistics =  
"quantiles", quantiles = c(0.025,0.5, 0.975))$table #Calculating the quantiles of relative  
male sizes  
relative_male_size_quantiles_table[10,4:9]=louse_data_P_Passeriformes[which(abs(louse_data_P_  
Passeriformes$m_f_rat-  
P_Passeriformes_quantiles[1])==min(abs(louse_data_P_Passeriformes$m_f_rat-  
P_Passeriformes_quantiles[1]))),c("m_f_rat","male_total_body_length","female_total_body_lengt  
h","host_weight","louse_species","host_species")][1,] #Finding the closest species to that  
quantile
```



```

_M_Charadriiformes$m_f_rat-
M_Charadriiformes_quantiles[1]) == min(abs(louse_data_M_Charadriiformes$m_f_rat-
M_Charadriiformes_quantiles[1])), c("m_f_rat", "male_total_body_length", "female_total_body_len
gth", "host_weight", "louse_species", "host_species"))][1,] #Finding the closest species to that
quantile
relative_male_size_quantiles_table[20,4:9]=louse_data_M_Charadriiformes[which(abs(louse_data_
M_Charadriiformes$m_f_rat-
M_Charadriiformes_quantiles[2]) == min(abs(louse_data_M_Charadriiformes$m_f_rat-
M_Charadriiformes_quantiles[2])), c("m_f_rat", "male_total_body_length", "female_total_body len
gth", "host_weight", "louse_species", "host_species"))][1,] #Finding the closest species to that
quantile
relative_male_size_quantiles_table[21,4:9]=louse_data_M_Charadriiformes[which(abs(louse_data_
M_Charadriiformes$m_f_rat-
M_Charadriiformes_quantiles[3]) == min(abs(louse_data_M_Charadriiformes$m_f_rat-
M_Charadriiformes_quantiles[3])), c("m_f_rat", "male_total_body_length", "female_total_body len
gth", "host_weight", "louse_species", "host_species"))][1,] #Finding the closest species to that
quantile

#Philopteridae - Galliformes
louse_data_P_Galliformes$louse_species=as.character(louse_data_P_Galliformes$louse_species)
louse_data_P_Galliformes$host_species=as.character(louse_data_P_Galliformes$host_species)
P_Galliformes_quantiles=numSummary(louse_data_P_Galliformes$m_f_rat, statistics =
"quantiles", quantiles = c(0.025,0.5, 0.975))$table #Calculating the quantiles of relative
male sizes
relative_male_size_quantiles_table[22,4:9]=louse_data_P_Galliformes[which(abs(louse_data_P_Ga
lliformes$m_f_rat-P_Galliformes_quantiles[1]) == min(abs(louse_data_P_Galliformes$m_f_rat-
P_Galliformes_quantiles[1])), c("m_f_rat", "male_total_body_length", "female_total_body_length"
, "host_weight", "louse_species", "host_species"))][1,] #Finding the closest species to that
quantile
relative_male_size_quantiles_table[23,4:9]=louse_data_P_Galliformes[which(abs(louse_data_P_Ga
lliformes$m_f_rat-P_Galliformes_quantiles[2]) == min(abs(louse_data_P_Galliformes$m_f_rat-
P_Galliformes_quantiles[2])), c("m_f_rat", "male_total_body_length", "female_total_body_length"
, "host_weight", "louse_species", "host_species"))][1,] #Finding the closest species to that
quantile
relative_male_size_quantiles_table[24,4:9]=louse_data_P_Galliformes[which(abs(louse_data_P_Ga
lliformes$m_f_rat-P_Galliformes_quantiles[3]) == min(abs(louse_data_P_Galliformes$m_f_rat-
P_Galliformes_quantiles[3])), c("m_f_rat", "male_total_body_length", "female_total_body_length"
, "host_weight", "louse_species", "host_species"))][1,] #Finding the closest species to that
quantile

#Menoponidae - Galliformes
louse_data_M_Galliformes$louse_species=as.character(louse_data_M_Galliformes$louse_species)
louse_data_M_Galliformes$host_species=as.character(louse_data_M_Galliformes$host_species)
M_Galliformes_quantiles=numSummary(louse_data_M_Galliformes$m_f_rat, statistics =
"quantiles", quantiles = c(0.025,0.5, 0.975))$table #Calculating the quantiles of relative
male sizes
relative_male_size_quantiles_table[25,4:9]=louse_data_M_Galliformes[which(abs(louse_data_M_Ga
lliformes$m_f_rat-M_Galliformes_quantiles[1]) == min(abs(louse_data_M_Galliformes$m_f_rat-
M_Galliformes_quantiles[1])), c("m_f_rat", "male_total_body_length", "female_total_body_length"
, "host_weight", "louse_species", "host_species"))][1,] #Finding the closest species to that
quantile
relative_male_size_quantiles_table[26,4:9]=louse_data_M_Galliformes[which(abs(louse_data_M_Ga
lliformes$m_f_rat-M_Galliformes_quantiles[2]) == min(abs(louse_data_M_Galliformes$m_f_rat-
M_Galliformes_quantiles[2])), c("m_f_rat", "male_total_body_length", "female_total_body_length"
, "host_weight", "louse_species", "host_species"))][1,] #Finding the closest species to that
quantile
relative_male_size_quantiles_table[27,4:9]=louse_data_M_Galliformes[which(abs(louse_data_M_Ga
lliformes$m_f_rat-M_Galliformes_quantiles[3]) == min(abs(louse_data_M_Galliformes$m_f_rat-
M_Galliformes_quantiles[3])), c("m_f_rat", "male_total_body_length", "female_total_body_length"
, "host_weight", "louse_species", "host_species"))][1,] #Finding the closest species to that
quantile

relative_male_size_quantiles_table
write.csv(relative_male_size_quantiles_table, "Table_3_Relative_male_size_quantiles.csv",
row.names = F)

```

```

##### Table 3: phyl.RMA results and sample sizes #####
table_phyl_RMA_results=rbind(
Philopteridae=c(Intercept=rensch_phyl_RMA_P$RMA.beta[1],Slope=rensch_phyl_RMA_P$RMA.beta[2],r
ensch_phyl_RMA_P$test,lambda=rensch_phyl_RMA_P$lambda,influence=rensch_phyl_RMA_P_influence,
N=length(P_log_female)),
Menoponidae=c(Intercept=rensch_phyl_RMA_M$RMA.beta[1],Slope=rensch_phyl_RMA_M$RMA.beta[2],ren
sch_phyl_RMA_M$test,lambda=rensch_phyl_RMA_M$lambda,influence=rensch_phyl_RMA_M_influence,
N=length(M_log_female)),
Ricinidae=c(Intercept=rensch_phyl_RMA_R$RMA.beta[1],Slope=rensch_phyl_RMA_R$RMA.beta[2],rensc
h_phyl_RMA_R$test,lambda=rensch_phyl_RMA_R$lambda,influence=rensch_phyl_RMA_P_influence,

```

```

P_log_female=c(Intercept=rensch_phyl_RMA_P_Passeriformes$RMA.beta[1],lambda=rensch_phyl_RMA_P_Passeriformes$RMA.beta[2],rensch_phyl_RMA_P_Passeriformes$test,lambda=rensch_phyl_RMA_P_Passeriformes$lambda,influence=rensch_phyl_RMA_P_Passeriformes_influence,
N=length(R_log_female)),
P_Passeriformes=c(Intercept=rensch_phyl_RMA_P_Passeriformes$RMA.beta[1],Slope=rensch_phyl_RMA_P_Passeriformes$RMA.beta[2],rensch_phyl_RMA_P_Passeriformes$test,lambda=rensch_phyl_RMA_P_Passeriformes$lambda,influence=rensch_phyl_RMA_P_Passeriformes_influence,
N=length(P_Passeriformes_log_female)),
M_Passeriformes=c(Intercept=rensch_phyl_RMA_M_Passeriformes$RMA.beta[1],Slope=rensch_phyl_RMA_M_Passeriformes$RMA.beta[2],rensch_phyl_RMA_M_Passeriformes$test,lambda=rensch_phyl_RMA_M_Passeriformes$lambda,influence=rensch_phyl_RMA_M_Passeriformes_influence,
N=length(M_Passeriformes_log_female)),
P_Charadriiformes=c(Intercept=rensch_phyl_RMA_P_Charadriiformes$RMA.beta[1],Slope=rensch_phyl_RMA_P_Charadriiformes$RMA.beta[2],rensch_phyl_RMA_P_Charadriiformes$test,lambda=rensch_phyl_RMA_P_Charadriiformes$lambda,influence=rensch_phyl_RMA_P_Charadriiformes_influence,
N=length(P_Charadriiformes_log_female)),
M_Charadriiformes=c(Intercept=rensch_phyl_RMA_M_Charadriiformes$RMA.beta[1],Slope=rensch_phyl_RMA_M_Charadriiformes$RMA.beta[2],rensch_phyl_RMA_M_Charadriiformes$test,lambda=rensch_phyl_RMA_M_Charadriiformes$lambda,influence=rensch_phyl_RMA_M_Charadriiformes_influence,
N=length(M_Charadriiformes_log_female)),
P_Galliformes=c(Intercept=rensch_phyl_RMA_P_Galliformes$RMA.beta[1],Slope=rensch_phyl_RMA_P_Galliformes$RMA.beta[2],rensch_phyl_RMA_P_Galliformes$test,lambda=rensch_phyl_RMA_P_Galliformes$lambda,influence=rensch_phyl_RMA_P_Galliformes_influence,
N=length(P_Galliformes_log_female)),
M_Galliformes=c(Intercept=rensch_phyl_RMA_M_Galliformes$RMA.beta[1],Slope=rensch_phyl_RMA_M_Galliformes$RMA.beta[2],rensch_phyl_RMA_M_Galliformes$test,lambda=rensch_phyl_RMA_M_Galliformes$lambda,influence=rensch_phyl_RMA_M_Galliformes_influence,
N=length(M_Galliformes_log_female))
)
table_phyl_RMA_results[,c(-9,-6)]=round(table_phyl_RMA_results[,c(-9,-6)],digits = 2)
table_phyl_RMA_results[,6]=round(table_phyl_RMA_results[,6],digits = 4)

table_phyl_RMA_results

write.csv(table_phyl_RMA_results, file = "Table_3_pRMA_results_and_sapmle_sizes.csv")

##### Figure 2: Louse families #####
louse_data_gg=louse_data
levels(louse_data_gg$louse_family)=c("Philopteridae","Menoponidae","Ricinidae")

fam_fitted=data.frame(rbind(
P_f=c(x=min(P_log_female),xend=max(P_log_female),
y=(rensch_phyl_RMA_P$RMA.beta[1]+rensch_phyl_RMA_P$RMA.beta[2]*min(P_log_female)),
yend=(rensch_phyl_RMA_P$RMA.beta[1]+rensch_phyl_RMA_P$RMA.beta[2]*max(P_log_female))),
M_f=c(x=min(M_log_female),xend=max(M_log_female),
y=(rensch_phyl_RMA_M$RMA.beta[1]+rensch_phyl_RMA_M$RMA.beta[2]*min(M_log_female)),
yend=(rensch_phyl_RMA_M$RMA.beta[1]+rensch_phyl_RMA_M$RMA.beta[2]*max(M_log_female))),
R_f=c(x=min(R_log_female),xend=max(R_log_female),
y=(rensch_phyl_RMA_R$RMA.beta[1]+rensch_phyl_RMA_R$RMA.beta[2]*min(R_log_female)),
yend=(rensch_phyl_RMA_R$RMA.beta[1]+rensch_phyl_RMA_R$RMA.beta[2]*max(R_log_female)))
))
fam_fitted$louse_family=relevel(factor(c("Philopteridae","Menoponidae","Ricinidae")),
ref="Philopteridae")

fam_fig=ggplot()+
facet_wrap(~louse_family, ncol=2) +
geom_point(data=louse_data_gg, aes(x=log_female_total_body_length,
y=log_male_total_body_length),alpha=0.4, shape=1, size=1) +
coord_fixed(ratio = 1, xlim = c(6.5,9.2), ylim = c(6.5,9.2), expand = TRUE)+
geom_abline(slope=1,intercept = 0, linetype="dashed")+
geom_segment(data = fam_fitted, aes(x=x,xend=xend,y=y,yend=yend)
,size=1.2 , colour="white",
show.legend = T) +
geom_segment(data = fam_fitted, aes(x=x,xend=xend,y=y,yend=yend)
,size=1 , colour="grey40",
show.legend = T) +
xlab("log(Female body length (Âµm))")+
ylab("log(Male body length (Âµm))")+
theme(
strip.text.x = element_text(size=11),
strip.background = element_rect(fill = "white", colour = "black"),
panel.background = element_blank(),
panel.grid.major = element_line(colour = "gray90"),
panel.grid.minor = element_line(colour = "gray90"),
panel.border = element_rect(colour = "black", size = 0.5, linetype = 1, fill=NA),
legend.position = "right"
)
fam_fig

```

```
##### Figure 3: Louse families by orders #####
louse_host_order_data_gg=droplevels(louse_data_gg[louse_data_gg$order=="Passeriformes" |
                                     louse_data_gg$order=="Charadriiformes" |
                                     louse_data_gg$order=="Galliformes"
                                     ,])
louse_host_order_data_gg=droplevels(louse_host_order_data_gg[louse_host_order_data_gg$louse_f
amily!="Ricinidae",])
levels(louse_host_order_data_gg$louse_family)
louse_host_order_data_gg$order=factor(louse_host_order_data_gg$order,levels(louse_host_order_
data_gg$order)[c(3,1,2)])

fam_host_order_fitted=data.frame(rbind(
P_Passeriformes_f=c(x=min(P_Passeriformes_log_female),xend=max(P_Passeriformes_log_female),
                    y=
                    (rensch_phyl_RMA_P_Passeriformes$RMA.beta[1]+rensch_phyl_RMA_P_Passeriformes$RMA.beta[2]*min(
P_Passeriformes_log_female)),
                    yend=
                    (rensch_phyl_RMA_P_Passeriformes$RMA.beta[1]+rensch_phyl_RMA_P_Passeriformes$RMA.beta[2]*max(
P_Passeriformes_log_female))),
M_Passeriformes_f=c(x=min(M_Passeriformes_log_female),xend=max(M_Passeriformes_log_female),
                    y=
                    (rensch_phyl_RMA_M_Passeriformes$RMA.beta[1]+rensch_phyl_RMA_M_Passeriformes$RMA.beta[2]*min(
M_Passeriformes_log_female)),
                    yend=
                    (rensch_phyl_RMA_M_Passeriformes$RMA.beta[1]+rensch_phyl_RMA_M_Passeriformes$RMA.beta[2]*max(
M_Passeriformes_log_female))),
P_Charadriiformes_f=c(x=min(P_Charadriiformes_log_female),xend=max(P_Charadriiformes_log_fema
le),
                    y=
                    (rensch_phyl_RMA_P_Charadriiformes$RMA.beta[1]+rensch_phyl_RMA_P_Charadriiformes$RMA.beta[2]*
min(P_Charadriiformes_log_female)),
                    yend=
                    (rensch_phyl_RMA_P_Charadriiformes$RMA.beta[1]+rensch_phyl_RMA_P_Charadriiformes$RMA.beta[2]*
max(P_Charadriiformes_log_female))),
M_Charadriiformes_f=c(x=min(M_Charadriiformes_log_female),xend=max(M_Charadriiformes_log_fema
le),
                    y=
                    (rensch_phyl_RMA_M_Charadriiformes$RMA.beta[1]+rensch_phyl_RMA_M_Charadriiformes$RMA.beta[2]*
min(M_Charadriiformes_log_female)),
                    yend=
                    (rensch_phyl_RMA_M_Charadriiformes$RMA.beta[1]+rensch_phyl_RMA_M_Charadriiformes$RMA.beta[2]*
max(M_Charadriiformes_log_female))),
P_Galliformes_f=c(x=min(P_Galliformes_log_female),xend=max(P_Galliformes_log_female),
                    y=
                    (rensch_phyl_RMA_P_Galliformes$RMA.beta[1]+rensch_phyl_RMA_P_Galliformes$RMA.beta[2]*min(P_Ga
lliformes_log_female)),
                    yend=
                    (rensch_phyl_RMA_P_Galliformes$RMA.beta[1]+rensch_phyl_RMA_P_Galliformes$RMA.beta[2]*max(P_Ga
lliformes_log_female))),
M_Galliformes_f=c(x=min(M_Galliformes_log_female),xend=max(M_Galliformes_log_female),
                    y=
                    (rensch_phyl_RMA_M_Galliformes$RMA.beta[1]+rensch_phyl_RMA_M_Galliformes$RMA.beta[2]*min(M_Ga
lliformes_log_female)),
                    yend=
                    (rensch_phyl_RMA_M_Galliformes$RMA.beta[1]+rensch_phyl_RMA_M_Galliformes$RMA.beta[2]*max(M_Ga
lliformes_log_female))))
fam_host_order_fitted$order=factor(c("Passeriformes","Passeriformes","Charadriiformes","Chara
driiformes","Galliformes","Galliformes"))
fam_host_order_fitted$louse_family=factor(rep(c("Philopteridae","Menoponidae"),3))
fam_host_order_fitted$order=factor(fam_host_order_fitted$order,levels(fam_host_order_fitted$o
rder)[c(3,1,2)])
fam_host_order_fitted$louse_family=factor(fam_host_order_fitted$louse_family,levels(fam_host_
order_fitted$louse_family)[c(2,1)])
```

```
fam_host_order_fig=ggplot()+
  facet_grid(order~louse_family) +
  geom_point(data=louse_host_order_data_gg, aes(x=log_female_total_body_length,
y=log_male_total_body_length),alpha=0.4, shape=1, size=1) +
  coord_fixed(ratio = 1, xlim = c(6.5,9.2), ylim = c(6.5,9.2), expand = TRUE)+
  geom_abline(slope=1,intercept = 0, linetype="dashed")+
  geom_segment(data = fam_host_order_fitted, aes(x=x,xend=xend,y=y,yend=yend)
              ,size=1.2 , colour="white",
              show.legend = T) +
```

```

geom_segment(data = fam_host_order_fitted, aes(x=x,xend=xend,y=y,yend=yend)
            ,size=1 , colour="grey40",
            show.legend = T) +
xlab("log(Female body length ( $\hat{\mu}$ m))")+
ylab("log(Male body length ( $\hat{\mu}$ m))")+
theme(
  strip.text.x = element_text(size=11),
  strip.text.y = element_text(size=11),
  strip.background = element_rect(fill = "white", colour = "black"),
  panel.background = element_blank(),
  panel.grid.major = element_line(colour = "gray90"),
  panel.grid.minor = element_line(colour = "gray90"),
  panel.border = element_rect(colour = "black", size = 0.5, linetype = 1, fill=NA),
  legend.position = "right"
)
fam_host_order_fig

##### Things mentioned in the article #####
#FBSSD ratios
#Families
round(prop.table(table(iffelse(louse_data$female_total_body_length>louse_data$male_total_bo
dy_length,"FBSSD","MBSSD"))), digits=3)
#Philopterid ecomorphs
round(prop.table(table(iffelse(ecom_data$female_total_body_length>ecom_data$male_total_body
_length,"FBSSD","MBSSD"))), digits=3)

#Host order frequencies in the dataset
orders=as.matrix(table(louse_data$order,louse_data$louse_family))
orders[order(rowSums(orders[,1:2]), decreasing = T),]

#Observations that change the significance of pRMA slopes
#Menoponidae - Galliformes
summary(rensch_phyl_RMA_M_Galliformes_jk_results[,-1])
rensch_phyl_RMA_M_Galliformes_jk_results[rensch_phyl_RMA_M_Galliformes_jk_results$p<=0.05,
]
names(M_Galliformes_log_female[rensch_phyl_RMA_M_Galliformes_jk_results[rensch_phyl_RMA_M_Gal
liformes_jk_results$p<=0.05,"row_num"]])
length(names(M_Galliformes_log_female[rensch_phyl_RMA_M_Galliformes_jk_results[rensch_phyl_RM
A_M_Galliformes_jk_results$p<=0.05,"row_num"]]))
</pre></body></html>

```