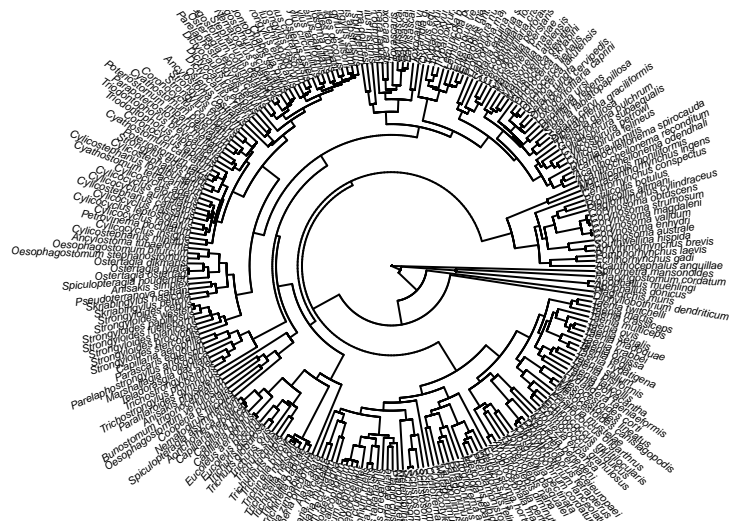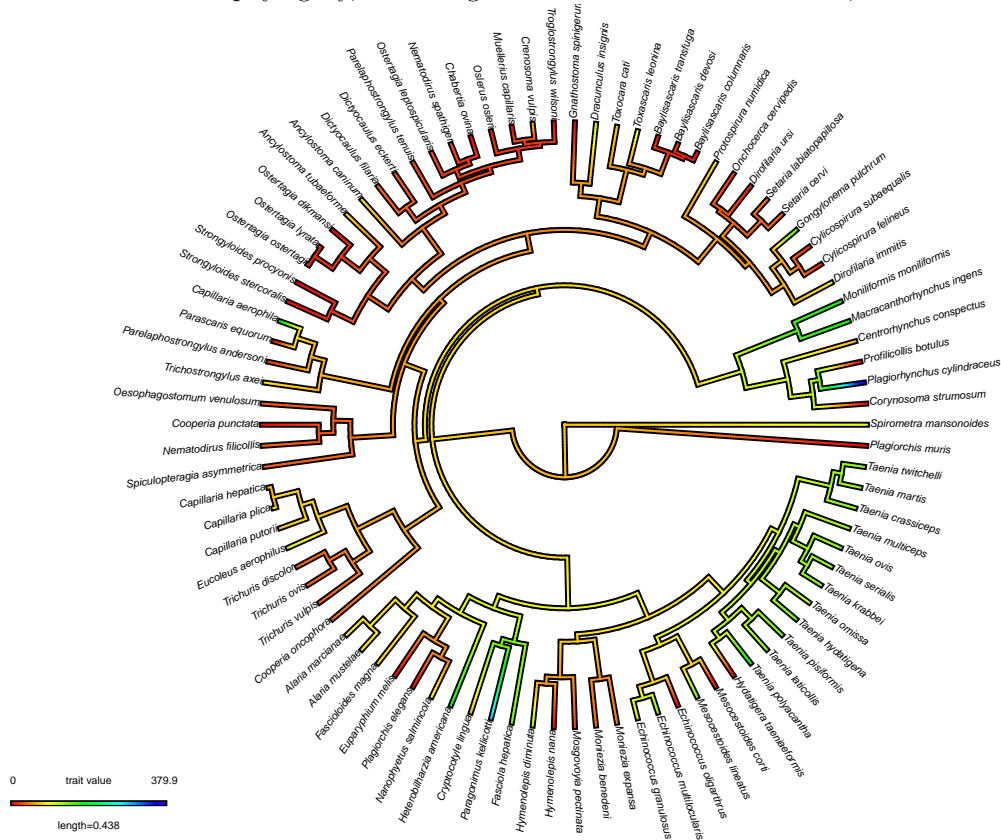# Supplementary

APB

1/8/2021

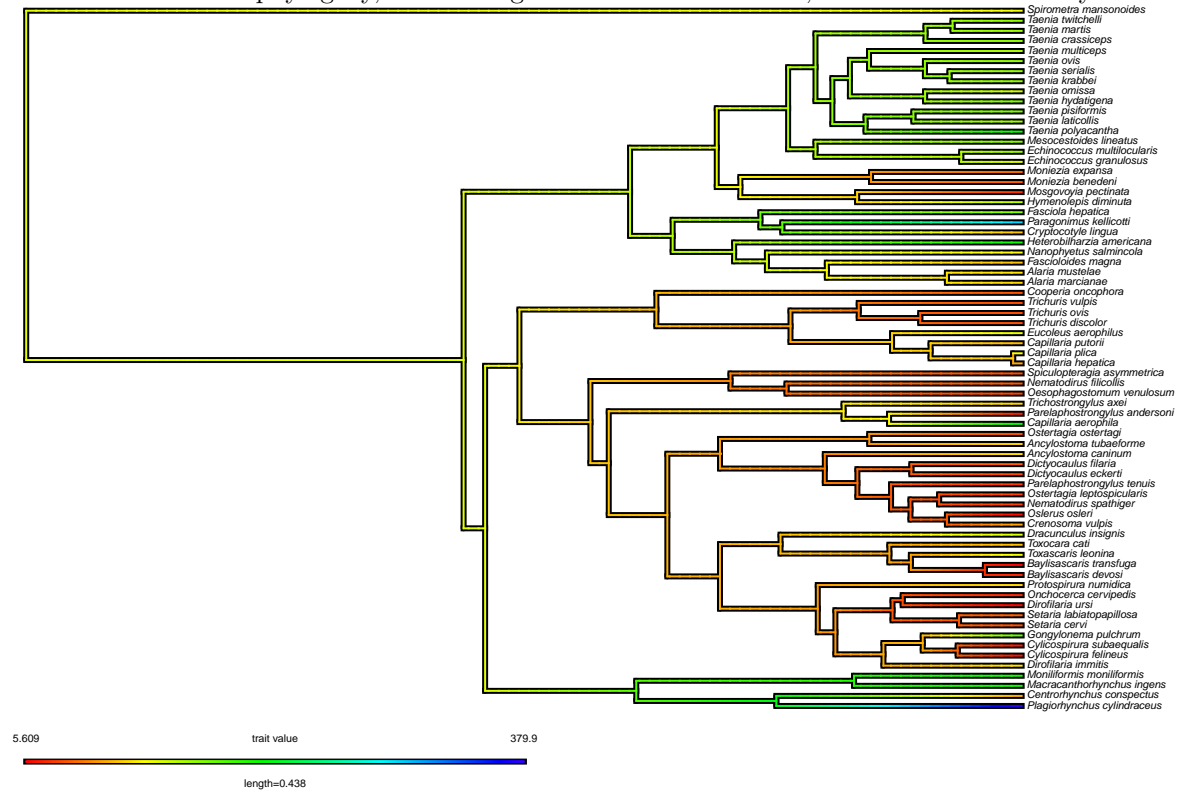Supplmental Figure 1. 249 taxa helminth molecular phylogeny

Nearctic helminth phylogeny, with single host taxa's MPD value = 0, branches colored by MPD value

Test of phylogenetic signal in MPD using the Nearctic helminth phylogeny, with single host taxa's MPD value = 0

```
## # A tibble: 2 x 4
##   model   aicc deltaaicc  waicc
##   <chr>  <dbl>     <dbl>  <dbl>
## 1 lambda 1017.        0  0.953
## 2 star   1023.     6.04 0.0465
```
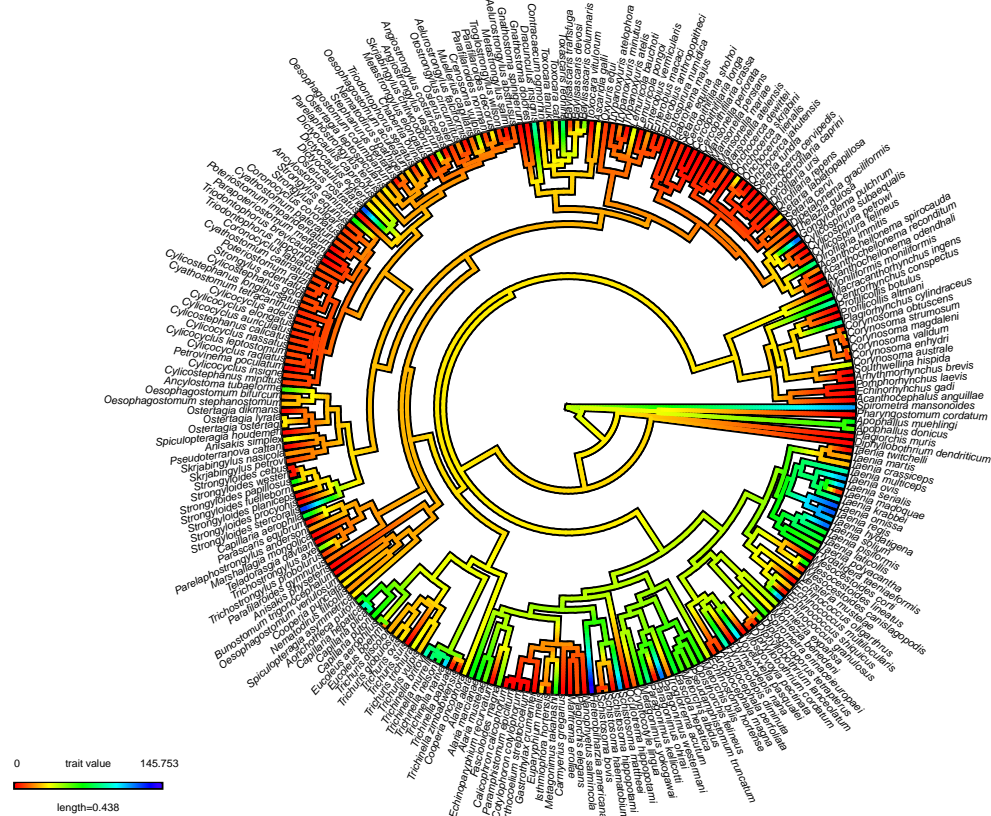
Nearctic helminth phylogney, with single host taxa removed, branches colored by MPD value

Test of phylogenetic signal in MPD using the Nearctic helminth phylogeny,with single host taxa removed

```
## # A tibble: 2 x 4
##   model   aicc deltaaicc    waicc
##   <chr>  <dbl>     <dbl>    <dbl>
## 1 lambda  773.        0   1.000
## 2 star    792.     18.4 0.000104
```
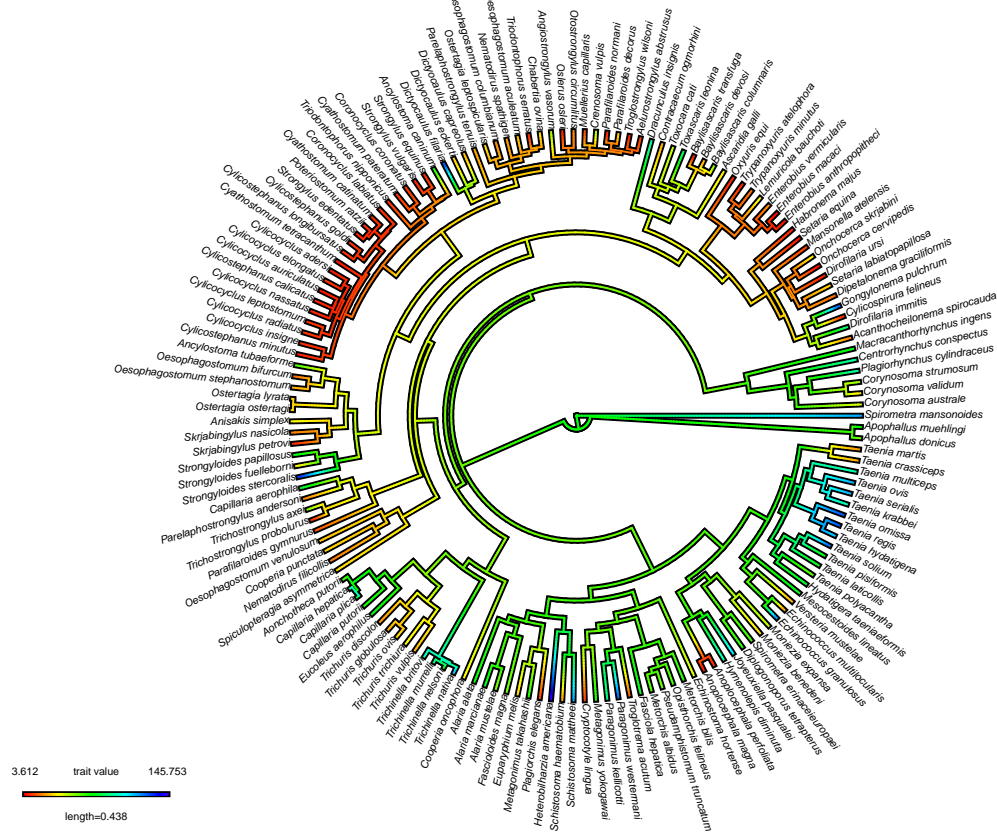
GMPD helminth phylogeny, with single host taxa's MPD value = 0, branches colored by MPD value

Test of phylogenetic signal in MPD using the GMPD helminth phylogeny, with single host taxa's MPD value = 0

```
## # A tibble: 2 x 4
##   model    aicc deltaaicc        waicc
##   <chr>   <dbl>     <dbl>        <dbl>
## 1 lambda 2474.         0  1.000
## 2 star   2509.      35.5 0.0000000197
```

GMPD helminth phylogeny, with single host taxa removed, branches colored by MPD value

Test of phylogenetic signal in MPD using the GMPD helminth phylogeny, with single host taxa removed

```
## # A tibble: 2 x 4
##   model   aicc deltaaicc    waicc
##   <chr>  <dbl>     <dbl>    <dbl>
## 1 lambda 1548.        0  10.00e- 1
## 2 star   1606.     58.6  1.85e-13
```

Test of phylogenetic signal in taxonomic breadth using the Nearctic helminth phylogeny, with single host taxa included

```
## # A tibble: 2 x 4
##   model    aicc deltaaicc waicc
##   <chr>   <dbl>     <dbl> <dbl>
## 1 star    470.          0 0.701
## 2 lambda  471.       1.70 0.299
```

Test of phylogenetic signal in taxonomic breadth using the Nearctic helminth phylogeny, with single host taxa removed

```
## # A tibble: 2 x 4
##   model    aicc deltaaicc waicc
##   <chr>   <dbl>     <dbl> <dbl>
## 1 star    361.          0 0.730
## 2 lambda  363.       1.99 0.270
```

Test of phylogenetic signal in taxonomic breadth using the GMPD helminth phylogeny, with single host taxa included

```
## # A tibble: 2 x 4
##   model    aicc deltaaicc waicc
##   <chr>   <dbl>     <dbl> <dbl>
## 1 star   1157.          0 0.738
## 2 lambda 1159.       2.07 0.262
```

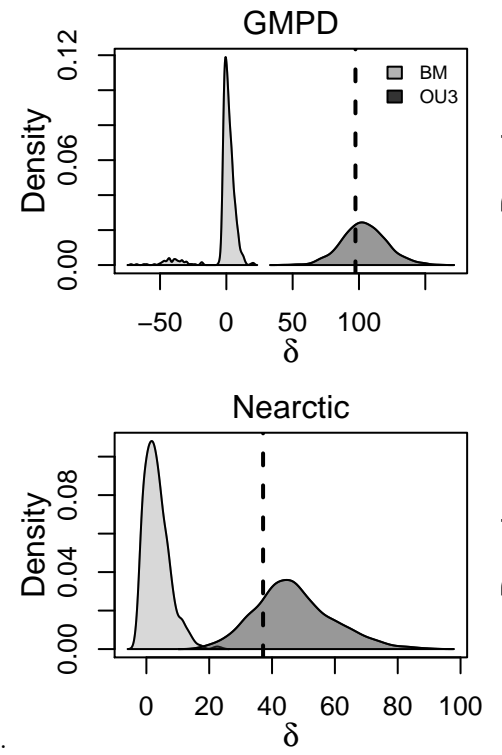Test of phylogenetic signal in taxonomic breadth using the GMPD helminth phylogeny, with single host taxa removed

```
## # A tibble: 2 x 4
##   model    aicc deltaaicc waicc
##   <chr>   <dbl>     <dbl> <dbl>
## 1 star    801.          0 0.740
## 2 lambda  803.       2.09 0.260
```

Supplemental Figure 2. The likelihood ratio distributions for BM versus OU(3).

GMPD
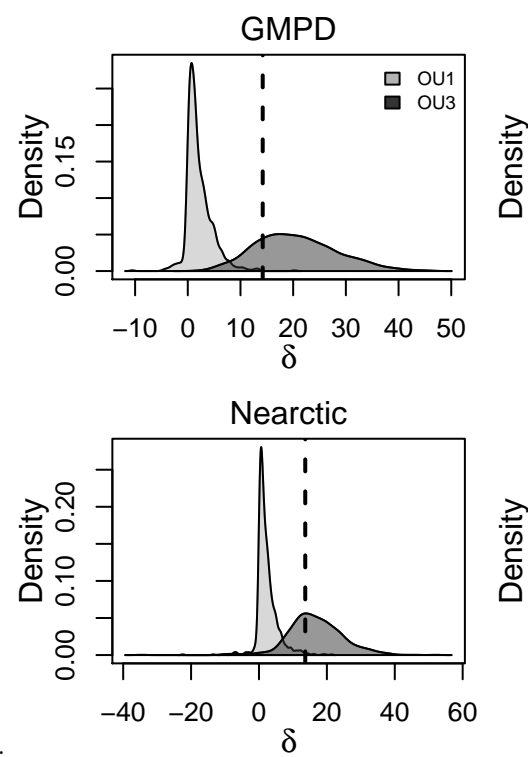
Nearctic

Supplemental Figure 3. The likelihood ratio distributions for OU(1) versus OU(3).

Supplemental Table 1. Summary table for evolutionary models of MPD in the Nearctic dataset with single host taxa = 0

```
## # A tibble: 3 x 4
##   model  aicc deltaaicc        waicc
##   <chr> <dbl>     <dbl>        <dbl>
## 1 OU3   1009.        0   0.990
## 2 OU1   1018.     9.20   0.00996
## 3 BM    1039.     30.6   0.000000228
```

Supplemental Table 2. Summary table for evolutionary models of MPD in the Nearctic dataset with single host taxa removed

```
## # A tibble: 3 x 4
##   model  aicc deltaaicc      waicc
##   <chr> <dbl>     <dbl>      <dbl>
## 1 OU3    763.        0   1.000
## 2 OU1    779.     15.6   0.000414
## 3 BM     783.     19.7   0.0000525
```

Supplemental Table 3. Summary table for evolutionary models of MPD in the GMPD with single host taxa = 0

```
## # A tibble: 3 x 4
##   model  aicc deltaaicc     waicc
##   <chr> <dbl>     <dbl>     <dbl>
## 1 OU3   2480.        0   9.94e- 1
## 2 OU1   2490.     10.1   6.47e- 3
## 3 BM    2571.     91.2   1.60e-20
```

Supplemental Table 4. Summary table for evolutionary models of MPD in the GMPD with single host taxa removed

```
## # A tibble: 3 x 4
##   model  aicc deltaaicc       waicc
##   <chr> <dbl>     <dbl>       <dbl>
## 1 OU3   1540.        0   0.881
## 2 OU1   1544.     4.00   0.119
## 3 BM    1563.     23.8   0.00000586
```

```
#### Load parasite body size data from Benesh, Lafferty, and Kuris 2017 ####
## Length and width measurments are in mm
benesh_data_para<- read_csv("Benesh_et_al_2017/ecy1680-sup-0001-datas1/CLC_database_lifehistory.csv")

## Parsed with column specification:
## cols(
##   .default = col_character(),
##   Host.no = col_double(),
##   Development.time = col_double(),
##   Temp = col_double(),
##   Length = col_double(),
##   Width = col_double(),
##   Max.length = col_double(),
##   Max.width = col_double(),
##   n = col_double(),
##   Asexual = col_logical(),
##   Year = col_double()
## )
```

```
## See spec(...) for full column specifications.

## Warning: 86 parsing failures.
##  row      col               expected actual
## 3346 Asexual 1/0/T/F/TRUE/FALSE clonal 'Benesh_et_al_2017/ecy1680-sup-0001-datas1/CLC_database_lifehi
## 3347 Asexual 1/0/T/F/TRUE/FALSE clonal 'Benesh_et_al_2017/ecy1680-sup-0001-datas1/CLC_database_lifehi
## 3352 Asexual 1/0/T/F/TRUE/FALSE clonal 'Benesh_et_al_2017/ecy1680-sup-0001-datas1/CLC_database_lifehi
## 3353 Asexual 1/0/T/F/TRUE/FALSE clonal 'Benesh_et_al_2017/ecy1680-sup-0001-datas1/CLC_database_lifehi
## 3357 Asexual 1/0/T/F/TRUE/FALSE clonal 'Benesh_et_al_2017/ecy1680-sup-0001-datas1/CLC_database_lifehi
## .... ........ .................. ...... ....................................................................
## See problems(...) for more details.
```

```r
benesh_data_para$Host.species <-gsub(" ", "_", benesh_data_para$Host.species)

## remove parasites from Benesh et al. dataset that don't exist in the phylogeny
setdiff(benesh_data_para$Parasite.species, GMPDsmall$ParasiteCorrectedName)->nothanks
benesh_data_para[-which(benesh_data_para$Parasite.species %in% nothanks) ,] -> b_para_subset

## average the body size for rows that are the same species
subset(b_para_subset, Sex=="f") %>%
  group_by(Parasite.species) %>%
  summarise(mean_l=mean(Length, na.rm = TRUE)) ->data_fem_len

subset(b_para_subset, Sex=="f") %>%
  group_by(Parasite.species) %>%
  summarise(mean_w=mean(Width, na.rm = TRUE)) ->data_fem_wid

## combine length and width to calculate 'body size' (L*W)?
b.size<-left_join(data_fem_len, data_fem_wid, by="Parasite.species")
b.size$ratio<-(b.size$mean_l*b.size$mean_w)

write.csv(b.size, "bodysizepara.csv")


#### Trim the tree to include only those parasite species for which there is body size data ####

##nearctic mpd, single host = 0
setdiff(nearctic_tree$tip.label, b.size$Parasite.species)->no_body_size
nearctic_pgls <- drop.tip(nearctic_tree, nearctic_tree$tip.label[which(nearctic_tree$tip.label%in%no_bod

# make sure body size is in the same order as the parasite phylogeny
nearctic.b.size <- b.size[match(nearctic_pgls$tip.label, b.size$Parasite.species),]


##nearctic mpd, single host removed
setdiff(remove_nearctic_tree$tip.label, b.size$Parasite.species)->no_body_size1
remove_nearctic_pgls <- drop.tip(remove_nearctic_tree, remove_nearctic_tree$tip.label[which(remove_nearc

# make sure body size is in the same order as the parasite phylogeny
remove.nearctic.b.size <- b.size[match(remove_nearctic_pgls$tip.label, b.size$Parasite.species),]


##global mpd, single host = 0
setdiff(global_tree$tip.label, b.size$Parasite.species)->no_body_size2
global_pgls <- drop.tip(global_tree, global_tree$tip.label[which(global_tree$tip.label%in%no_body_size2
```

```r
# make sure body size is in the same order as the parasite phylogeny
global.b.size <- b.size[match(global_pgls$tip.label, b.size$Parasite.species),]

##global mpd, single host removed
setdiff(remove_global_tree$tip.label, b.size$Parasite.species)->no_body_size3
remove_global_pgls <- drop.tip(remove_global_tree, remove_global_tree$tip.label[which(remove_global_tree

# make sure body size is in the same order as the parasite phylogeny
remove.global.b.size <- b.size[match(remove_global_pgls$tip.label, b.size$Parasite.species),]



#### adding in host trait data (mass.g) from PHYLACINE ####
#Faurby, S., Davis, M., Pedersen, R. Ø., Schowanek, S. D., Antonelli, A., & Svenning, J.C. (In Press).
#load mammal data
Trait_data <- read_csv("Trait_data.csv")

## Parsed with column specification:
## cols(
##   .default = col_character(),
##   Terrestrial = col_double(),
##   Marine = col_double(),
##   Freshwater = col_double(),
##   Aerial = col_double(),
##   Mass.g = col_double(),
##   Diet.Plant = col_double(),
##   Diet.Vertebrate = col_double(),
##   Diet.Invertebrate = col_double()
## )
## See spec(...) for full column specifications.
#correct for spaces in the binomial names
Trait_data$Binomial.1.2<-gsub("_", " ", Trait_data$Binomial.1.2)

#make column called "Host" in Trait_data
Trait_data$HostCorrectedName<-Trait_data$Binomial.1.2

#merge
left_join(GMPDsmall, Trait_data, by = "HostCorrectedName")->ss
host_trait_data<-data.frame("Parasite" = ss$ParasiteCorrectedName,
                            "Host" = ss$HostCorrectedName,
                            "Mass.g" = ss$Mass.g)


host_trait_data %>%
  group_by(Parasite) %>%
  summarise(avgMass=mean(Mass.g,na.rm=T)) -> Host_mass


##subset host data for each group

#nearctic with single hosts = 0
setdiff(Host_mass$Parasite, nearctic_pgls$tip.label)-> getout
nearctic_traits<-Host_mass[-which(Host_mass$Parasite %in% getout),]
```

11

```r
#put in tree tip label order
nearctic_traits <- nearctic_traits[match(nearctic_pgls$tip.label, nearctic_traits$Parasite),]


#nearctic with single hosts removed
setdiff(Host_mass$Parasite, remove_nearctic_pgls$tip.label)-> getout1
remove_nearctic_traits<-Host_mass[-which(Host_mass$Parasite %in% getout1),]
#put in tree tip label order
remove_nearctic_traits <- remove_nearctic_traits[match(remove_nearctic_pgls$tip.label, remove_nearctic_


#global with single hosts = 0
global_traits<-Host_mass
#put in tree tip label order
global_traits <- global_traits[match(global_pgls$tip.label, global_traits$Parasite),]


#global with single hosts removed
setdiff(Host_mass$Parasite, remove_global_pgls$tip.label)-> getout2
remove_global_traits<-Host_mass[-which(Host_mass$Parasite %in% getout2),]
#put in tree tip label order
remove_global_traits <- remove_global_traits[match(remove_global_pgls$tip.label, remove_global_traits$Pa


#### clean parasite transmission data ####

#nearctic with single hosts = 0
nearctic_trans<-GMPDparasite[which(GMPDparasite$CorrectName %in% nearctic_pgls$tip.label),]
nearctic_trans<-nearctic_trans[match(nearctic_pgls$tip.label, nearctic_trans$CorrectName),]

#neartic with single species removed
remove_nearctic_trans<-GMPDparasite[which(GMPDparasite$CorrectName %in% remove_nearctic_pgls$tip.label)
remove_nearctic_trans<-remove_nearctic_trans[match(remove_nearctic_pgls$tip.label, remove_nearctic_trans


#global with single hosts = 0
global_trans<-GMPDparasite[which(GMPDparasite$CorrectName %in% global_pgls$tip.label),]
global_trans<-global_trans[match(global_pgls$tip.label, global_trans$CorrectName),]

#global with single species removed
remove_global_trans<-GMPDparasite[which(GMPDparasite$CorrectName %in% remove_global_pgls$tip.label),]
remove_global_trans<-remove_global_trans[match(remove_global_pgls$tip.label, remove_global_trans$Correct

###NEARCTIC DATASET####

##with single host species MPD = 0

#clean nearctic.mam.mpd
pgls.nearctic.para.mpd<-nearctic.para.mpd[match(nearctic_pgls$tip.label, names(nearctic.para.mpd))]

nearctic_dat<-data.frame(taxa=nearctic_pgls$tip.label,
                para.mpd=pgls.nearctic.para.mpd,
                para.l=nearctic.b.size$mean_l,
```

```
                    para.w=nearctic.b.size$mean_w,
                    para.b=nearctic.b.size$ratio,
                    close=as.factor(nearctic_trans$close),
                    nonclose=as.factor(nearctic_trans$nonclose),
                    intermediate=as.factor(nearctic_trans$intermediate),
                    host_mass=nearctic_traits$avgMass)

## constructs the data.frame of the taxa names and data in the order of the tree tips
nearctic_cdat<-comparative.data(data=nearctic_dat, phy=nearctic_pgls, names.col = "taxa")
print(nearctic_cdat)
```

```
## Comparative dataset of 28 taxa:
## Phylogeny: nearctic_pgls
##     28 tips, 27 internal nodes
##     chr [1:28] "Corynosoma strumosum" "Plagiorhynchus cylindraceus" ...
## Data: nearctic_dat
##     $ para.mpd    : num [1:28] 0 380 181 179 155 ...
##     $ para.l      : num [1:28] 4.42 10.4 247.42 141.17 77.05 ...
##     $ para.w      : num [1:28] 1.042 2.258 6.5 2.183 0.301 ...
##     $ para.b      : num [1:28] 4.6 23.5 1608.2 308.2 23.2 ...
##     $ close       : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 2 ...
##     $ nonclose    : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 2 2 2 1 ...
##     $ intermediate: Factor w/ 2 levels "0","1": 2 2 2 2 2 2 2 2 2 1 1 ...
##     $ host_mass   : num [1:28] 79871 5626 10082 3834 59111 ...
## Dropped taxa:
##     nearctic_pgls { 5 ( 28 } 0 ) nearctic_dat
## model testing ##
```

```
#all predictors
nearctic_mod <- pgls(para.mpd~ para.l + close + nonclose + intermediate + host_mass, nearctic_cdat, laml
summary(nearctic_mod)
```

```
##
## Call:
## pgls(formula = para.mpd ~ para.l + close + nonclose + intermediate +
##       host_mass, data = nearctic_cdat, lambda = 0.384)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -175.87   -57.02    -8.12    34.62   328.48
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
## lambda [Fix]  : 0.384
## delta  [Fix]  : 1.000
##
## Coefficients:
##                  Estimate  Std. Error  t value  Pr(>|t|)
## (Intercept)    1.9385e+02  6.6662e+01   2.9080  0.008155 **
## para.l         1.7893e-01  2.3785e-01   0.7523  0.459868
## close1        -1.0649e+02  1.0293e+02  -1.0345  0.312121
## nonclose1     -8.5904e+01  6.1025e+01  -1.4077  0.173199
```

```
## intermediate1 -7.9533e+01  6.3528e+01 -1.2519 0.223740
## host_mass     -4.2292e-04  2.0902e-04 -2.0233 0.055359 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 112.2 on 22 degrees of freedom
## Multiple R-squared:  0.28,   Adjusted R-squared: 0.1164
## F-statistic: 1.711 on 5 and 22 DF,  p-value: 0.1739
```

```
anova(nearctic_mod)
```

```
## Analysis of Variance Table
## Sequential SS for pgls: lambda = 0.38, delta = 1.00, kappa = 1.00
##
## Response: para.mpd
##            Df Sum Sq Mean Sq F value  Pr(>F)
## para.l      1  12430   12430  0.9872 0.33123
## close       1    995     995  0.0791 0.78121
## nonclose    1  27488   27488  2.1831 0.15371
## intermediate 1  15269   15269  1.2126 0.28272
## host_mass   1  51546   51546  4.0937 0.05536 .
## Residuals  22 277014   12592
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#removed parasite length
nearctic_mod2<-pgls(para.mpd ~ close + nonclose + intermediate + host_mass, nearctic_cdat, lambda=.384)
summary(nearctic_mod2)
```

```
##
## Call:
## pgls(formula = para.mpd ~ close + nonclose + intermediate + host_mass,
##     data = nearctic_cdat, lambda = 0.384)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -192.93  -49.35  -12.54   35.88  318.74
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
## lambda [Fix]  : 0.384
## delta  [Fix]  : 1.000
##
## Coefficients:
##                 Estimate  Std. Error t value Pr(>|t|)
## (Intercept)   1.9007e+02  6.5842e+01  2.8868 0.008323 **
## close1       -9.0298e+01  9.9703e+01 -0.9057 0.374501
## nonclose1    -7.1952e+01  5.7588e+01 -1.2494 0.224069
## intermediate1 -6.1500e+01  5.8274e+01 -1.0554 0.302218
## host_mass    -4.5265e-04  2.0331e-04 -2.2264 0.036067 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 111.1 on 23 degrees of freedom
```

```
## Multiple R-squared: 0.2615,   Adjusted R-squared: 0.133
## F-statistic: 2.036 on 4 and 23 DF,   p-value: 0.1227
```

```
anova(nearctic_mod2)
```

```
## Analysis of Variance Table
## Sequential SS for pgls: lambda = 0.38, delta = 1.00, kappa = 1.00
##
## Response: para.mpd
##               Df Sum Sq Mean Sq F value  Pr(>F)
## close          1    692     692  0.0560 0.81505
## nonclose       1  32557   32557  2.6354 0.11813
## intermediate   1   6119    6119  0.4953 0.48865
## host_mass      1  61236   61236  4.9568 0.03607 *
## Residuals     23 284140   12354
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#removed parasite length and close transmission
nearctic_mod3<-pgls(para.mpd ~ nonclose + intermediate + host_mass, nearctic_cdat, lambda=.384)
summary(nearctic_mod3)
```

```
##
## Call:
## pgls(formula = para.mpd ~ nonclose + intermediate + host_mass,
##     data = nearctic_cdat, lambda = 0.384)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -178.27  -70.10   -7.08   35.45  329.88
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
## lambda [Fix]  : 0.384
## delta  [Fix]  : 1.000
##
## Coefficients:
##                  Estimate  Std. Error t value Pr(>|t|)
## (Intercept)    1.4958e+02  4.8158e+01  3.1061 0.004817 **
## nonclose1     -3.6881e+01  4.2463e+01 -0.8685 0.393705
## intermediate1 -2.4615e+01  4.1522e+01 -0.5928 0.558854
## host_mass     -4.2786e-04  2.0070e-04 -2.1318 0.043460 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 110.7 on 24 degrees of freedom
## Multiple R-squared: 0.2351,   Adjusted R-squared: 0.1395
## F-statistic: 2.459 on 3 and 24 DF,   p-value: 0.08723
```

```
anova(nearctic_mod3)
```

```
## Analysis of Variance Table
## Sequential SS for pgls: lambda = 0.38, delta = 1.00, kappa = 1.00
##
## Response: para.mpd
```

```
##              Df Sum Sq Mean Sq F value  Pr(>F)
## nonclose      1  32883   32883  2.6818 0.11455
## intermediate  1   1865    1865  0.1521 0.70001
## host_mass     1  55723   55723  4.5446 0.04346 *
## Residuals    24 294273   12261
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(nearctic_mod2, nearctic_mod3)
```

```
## Analysis of Variance Table
## pgls: lambda = 0.38, delta = 1.00, kappa = 1.00
##
## Model 1: para.mpd ~ close + nonclose + intermediate + host_mass
## Model 2: para.mpd ~ nonclose + intermediate + host_mass
##   Res.Df    RSS Df Sum of Sq      F Pr(>F)
## 1     23 284140
## 2     24 294273 -1    -10133 0.8202 0.3745
```

```
#removed parasite length and close transmission + intermediate ##### BEST MODEL #####
nearctic_mod4<-pgls(para.mpd ~ nonclose + host_mass, nearctic_cdat, lambda=.384)
summary(nearctic_mod4)
```

```
##
## Call:
## pgls(formula = para.mpd ~ nonclose + host_mass, data = nearctic_cdat,
##     lambda = 0.384)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -170.067  -77.056   -4.891   37.990  302.595
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
## lambda [Fix]  : 0.384
## delta  [Fix]  : 1.000
##
## Coefficients:
##               Estimate  Std. Error t value Pr(>|t|)
## (Intercept)  1.2676e+02  2.8548e+01  4.4402 0.000159 ***
## nonclose1   -1.9091e+01  2.9650e+01 -0.6439 0.525525
## host_mass   -4.1644e-04  1.9717e-04 -2.1121 0.044840 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 109.3 on 25 degrees of freedom
## Multiple R-squared: 0.2239,  Adjusted R-squared: 0.1619
## F-statistic: 3.607 on 2 and 25 DF,  p-value: 0.04204
```

```
anova(nearctic_mod4)
```

```
## Analysis of Variance Table
## Sequential SS for pgls: lambda = 0.38, delta = 1.00, kappa = 1.00
##
## Response: para.mpd
```

```
##              Df Sum Sq Mean Sq F value  Pr(>F)
## nonclose    1  32883   32883  2.7532 0.10955
## host_mass   1  53279   53279  4.4610 0.04484 *
## Residuals  25 298582   11943
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
anova(nearctic_mod3, nearctic_mod4)
```

```
## Analysis of Variance Table
## pgls: lambda = 0.38, delta = 1.00, kappa = 1.00
##
## Model 1: para.mpd ~ nonclose + intermediate + host_mass
## Model 2: para.mpd ~ nonclose + host_mass
##   Res.Df    RSS Df Sum of Sq      F Pr(>F)
## 1     24 294273
## 2     25 298582 -1   -4308.9 0.3514 0.5589
```

Best model fit with PGLS for the Nearctic helminth phylogeny, with single host taxa included.

```
##
## Call:
## pgls(formula = para.mpd ~ host_mass, data = nearctic_cdat, lambda = 0.384)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -184.21  -74.97  -18.47   37.89  299.67
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
## lambda [Fix]  : 0.384
## delta  [Fix]  : 1.000
##
## Coefficients:
##                Estimate  Std. Error t value  Pr(>|t|)
## (Intercept)  1.2234e+02  2.7397e+01  4.4654 0.0001378 ***
## host_mass   -4.6865e-04  1.7769e-04 -2.6375 0.0139127 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 108 on 26 degrees of freedom
## Multiple R-squared: 0.2111,  Adjusted R-squared: 0.1807
## F-statistic: 6.956 on 1 and 26 DF,  p-value: 0.01391
```

Best model fit with PGLS for the Nearctic helminth phylogeny, without single host taxa.

```
##
## Call:
## pgls(formula = para.mpd ~ para.l + close + nonclose + intermediate,
##     data = remove_nearctic_cdat, lambda = 0.926)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -149.81  -49.58  -11.09   60.42  125.36
##
## Branch length transformations:
```

```
##
## kappa  [Fix]  : 1.000
## lambda [Fix]  : 0.926
## delta  [Fix]  : 1.000
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -23.28819   39.99328 -0.5823  0.56759
## para.l         -0.27584    0.15170 -1.8183  0.08570 .
## close1         69.46682   57.81292  1.2016  0.24510
## nonclose1      64.80921   35.44612  1.8284  0.08411 .
## intermediate1  61.25735   34.95243  1.7526  0.09669 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 78.94 on 18 degrees of freedom
## Multiple R-squared: 0.2377,  Adjusted R-squared: 0.06833
## F-statistic: 1.403 on 4 and 18 DF,  p-value: 0.2728

## Analysis of Variance Table
## Sequential SS for pgls: lambda = 0.93, delta = 1.00, kappa = 1.00
##
## Response: para.mpd
##            Df Sum Sq Mean Sq F value  Pr(>F)
## para.l      1  12027 12026.7  1.9298 0.18173
## close       1   1315  1315.3  0.2111 0.65144
## nonclose    1   2499  2498.9  0.4010 0.53455
## intermediate 1 19142 19142.2  3.0716 0.09669 .
## Residuals  18 112177  6232.0
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Best model fit with PGLS for the GMPD helminth phylogeny, with single host taxa included.

```
##
## Call:
## pgls(formula = para.mpd ~ close, data = global_cdat, lambda = 0.607)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -145.81  -48.54  -11.06   20.29  102.52
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
## lambda [Fix]  : 0.607
## delta  [Fix]  : 1.000
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   30.123     13.253  2.2730  0.02688 *
## close1       -19.752     16.638 -1.1872  0.24016
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Residual standard error: 58.15 on 56 degrees of freedom
## Multiple R-squared: 0.02455, Adjusted R-squared: 0.007132
## F-statistic: 1.409 on 1 and 56 DF,  p-value: 0.2402

## Analysis of Variance Table
## Sequential SS for pgls: lambda = 0.61, delta = 1.00, kappa = 1.00
##
## Response: para.mpd
##           Df Sum Sq Mean Sq F value Pr(>F)
## close      1   4765  4765.5  1.4094 0.2402
## Residuals 56 189344  3381.1
```

Best model fit with PGLS for the GMPD helminth phylogeny, without single host taxa.

```
##
## Call:
## pgls(formula = para.mpd ~ close, data = remove_global_cdat, lambda = 0.895)
##
## Residuals:
##      Min      1Q   Median      3Q      Max
## -126.542  -20.638   -3.945   19.786  106.102
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
## lambda [Fix]  : 0.895
## delta  [Fix]  : 1.000
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   16.280     10.253  1.5879  0.12019
## close1        23.425     13.451  1.7415  0.08927 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 37.61 on 40 degrees of freedom
## Multiple R-squared: 0.07048, Adjusted R-squared: 0.04724
## F-statistic: 3.033 on 1 and 40 DF,  p-value: 0.08927

## Analysis of Variance Table
## Sequential SS for pgls: lambda = 0.90, delta = 1.00, kappa = 1.00
##
## Response: para.mpd
##           Df Sum Sq Mean Sq F value  Pr(>F)
## close      1   4290  4290.4   3.033 0.08927 .
## Residuals 40  56584  1414.6
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```