Supplementary analysis for Pace of ecology drives temporal perception across the Animal Kingdom

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Introduction

This document outlines the supplementary analysis used for the publication Haarlem et al (Pace of ecology drives temporal perception across the Animal Kingdom). The only difference with the main analysis is that the species Black fire beetle (Melanophila acuminata) is dropped in this analysis as it has an unusally high CFF that is not likely linked to temporal perception in the same manner as other species. The script comprises of a phylogeny comparative analysis testing if different trophic strategies, volancy, body size and light level affect the critical flicker fusion of animals in marine and non-marine habitats. The analysis comprises a phylogentic comparative approach in a Bayesian framework using the `MCMCglmm` package and the `mulTree` package to incorporate uncerrtainly in the phylogeny itself.

Please see main document for details on methods and data collection.

Loading packages

The main packages used are `MCMCglmm` for the Bayesian comparative analysis as this package can allow for correcting for phylogeny using the animal term. More details on the package can be found here (https://www.jstatsoft.org/article/view/v033i02)

To upload the phylogeny and for other functions associated with handling the phylogeny we used the `phytools` and `caper` packages.

To incorporate the uncertainty associated with building phylogenies we used the `mulTree` package which is downloaded from github. This packages is a wrapper that loops the MCMCglmm function across a given distribution of phylogenies. It automatically writes the model outputs outside the R environment to avoid issues with RAM available in the R environment. For more details see (https://github.com/TGuillerme/mulTree)

package and `Multree` package

```
#If you need to install any of these packages run this line
#install.packages("phytools","caper","MCMCglmm","hdrcde")
library(phytools)
library(caper)
library(MCMCglmm)
library(hdrcde)

#If you need to install mulTree run these lines
#if(!require(devtools)) install.packages("devtools")
#library(devtools)
#install_github("TGuillerme/mulTree", ref = "release")
library(mulTree)
```

Data

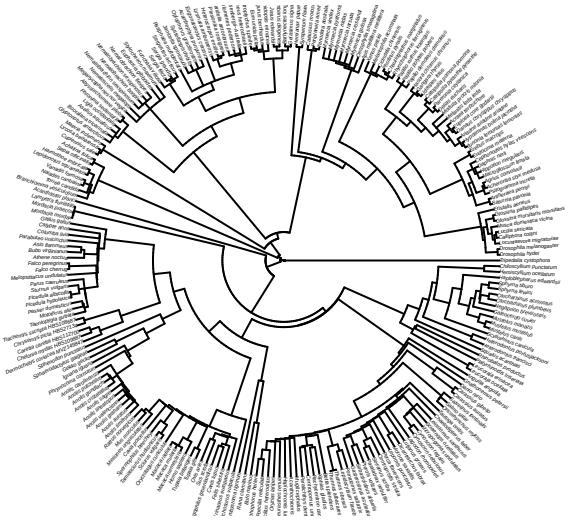
Next we load in the dataset Haarlem_et_al_cff_dataset_21_10_2025.csv.

We will also add a column for log10 of CFF which will be the response variable and set sessile_food as the baseline category for the mode_of_life variable and terrestrial as the baseline for the habitat variable.

Phylogeny

Read in the phylogeny Haarlem_et_al_tree.tre which is a supertree constructed by combining various published phylogeny. For more details see the supplementary S1.

```
cff_tree <- read.tree("cff_tree_test2.tree")

plot(cff_tree[[1]],
     type = "fan",
     cex = 0.15)
```



Main models

For the main analysis we will both marine and terrestrial species into one model. First we set up a multree object which will contain the data and the distribution of 100 phylogenies. We will also set what the random terms which will include the animal term for the phylogentic effect and a term for speies level variation we will call Species_phylo.

Next we set the number of iterations (nitt) the thinning (thin) and the burnin (burnin) and save them as the vector parameters. These parameters were set based on previous runs and inspection to ensure that the MCMC chains are long enough to converge and have an effective samples size > 1000.

```
nitt <- 240000
thin <- 100
burnin <- 40000

parameters <- c(nitt,
                thin,
                burnin)
```

Next we set the priors to be non informative based on the recommendation of Hadfield, J. D. & Nakagawa (2010).

```
prior <-list(R = list(V = 1, nu=0.002),
             G = list(G1=list(V = 1,n = 2,
                              nu=0.002),
                      G2=list(V = 1,n = 2,
                              nu=0.002)
                      ))
```

Finally we set the mulTree model to run. Note that here we will not set it to run here due to the long run time. Instead we will read in a previous model below. If you wish to run the model simply run the block of code below.

```
mulTree(mulTree.data = cff_mul,
        formula = CFF_log ~ log10(body_mass)*forage_light_level
                                  + mode_of_life
                                  + habitat
                                  + Method,
        parameters = parameters,
        chains = 3,
        priors = prior,
        convergence = 1.1,
        ESS = 1000,
        verbose = TRUE,
        output = "mulTree_supp_models",
        warn = FALSE,
        ask = TRUE)
```

After the models have run (or in this case using the models we previously ran) we can read them in. In this case we will read in the fixed terms as the Main_models and the random terms as the Main_models_sp

```
Main_models <-   read.mulTree(mulTree.chain = "mulTree_supp_models",
                              convergence = FALSE,
                              model = FALSE)

Main_models_sp <-   read.mulTree(mulTree.chain = "mulTree_supp_models",
                              convergence = FALSE,
                              model = FALSE,
                              extract = c("VCV"))
```

We can now simply use summary to see the model output for the combined postior distributions across the full set of 100 trees

```
print(summary(Main_models)[,c(1,2,5)],
      digits = 2)
```

```
##                                          Estimates(mode hdr) lower.CI(2.5)
## (Intercept)                                           1.1950        0.8319
## log10(body_mass)                                     -0.0200       -0.0566
## forage_light_levellow                                -0.3125       -0.3954
## mode_of_lifeballistic                                 0.1244        0.0310
## mode_of_lifepursuit                                   0.1957        0.0392
## habitatnektonic                                       0.2216       -0.0281
## habitatdemersal                                       0.1985       -0.0502
## habitatvolant                                         0.2514        0.0495
## MethodElectrophysiology                               0.0723        0.0044
## log10(body_mass):forage_light_levellow               -0.0031       -0.0373
## phylogenetic.variance                                 0.1336        0.0752
```

```
## residual.variance                                    0.0204        0.0070
##                                       upper.CI(97.5)
## (Intercept)                                    1.528
## log10(body_mass)                               0.016
## forage_light_levellow                         -0.226
## mode_of_lifeballistic                          0.216
## mode_of_lifepursuit                            0.353
## habitatnektonic                                0.486
## habitatdemersal                                0.467
## habitatvolant                                  0.451
## MethodElectrophysiology                        0.139
## log10(body_mass):forage_light_levellow         0.033
## phylogenetic.variance                          0.224
## residual.variance                              0.034
```

We can see from this output that the 95% CI does not cross zero for light levels, with species in lower light environments having lower CFF, for ballistic and pursuit foraging,with both these groups having higher CFF values compared to species which feed on sessile food sources, for volant species, with volant species having a higher CFF compared to non-volant species and for CFF values with Electrophysiology methods compared to behavioral approaches.

We can also look at the varaince terms in more detail.

```
#phylo term
phylo_animal <- list()
for(i in 1:length(Main_models_sp)){
phylo_animal[[i]] <- Main_models_sp[[1]][,"animal"]
}
phylo_animal <- unlist(phylo_animal)


#species term
sp_rand <- list()
for(i in 1:length(Main_models_sp)){
sp_rand[[i]] <- Main_models_sp[[1]][,"Species_phylo"]
}
sp_rand <- unlist(sp_rand)


#resids term

resids_rand <- list()
for(i in 1:length(Main_models_sp)){
resids_rand[[i]] <- Main_models_sp[[1]][,"units"]
}
resids_rand <- unlist(resids_rand)

random_main_terms_summary <- data.frame(phylo_animal,
                                        sp_rand,
                                        resids_rand)
summary(random_main_terms_summary)
```

```
##   phylo_animal        sp_rand           resids_rand
##  Min.   :0.05996   Min.   :0.0007462   Min.   :0.007105
##  1st Qu.:0.11856   1st Qu.:0.0161185   1st Qu.:0.012039
##  Median :0.14219   Median :0.0207082   Median :0.014013
```

```
##  Mean   :0.14593   Mean   :0.0205064   Mean   :0.014677
##  3rd Qu.:0.16987   3rd Qu.:0.0249070   3rd Qu.:0.016538
##  Max.   :0.35718   Max.   :0.0497796   Max.   :0.033552
```

lets also look at the H2 value for the model which will tell use the level of phylogeny signal in our model.

```
# Calculate H2
H_main <- phylo_animal/c(phylo_animal + sp_rand + resids_rand)
H_out <- list(mode = hdr(H_main)$mode,
              CI_95 = hdr(H_main)$hdr[2,1:2])
H_out
```

```
## $mode
## [1] 0.833168
##
## $CI_95
## [1] 0.6621950 0.6687198
```

In this case the mode H2 value is 0.79 with a 95% CI of 0.63-0.88 indicating an overall high level of phylogentic signal in the data.

If we want we can check each individual model separately. Lets look at the model for two chains of the first tree. Doing this will give all the standard output from a MCMCglmm object. To do so we read them in with model = T and the specific model named.

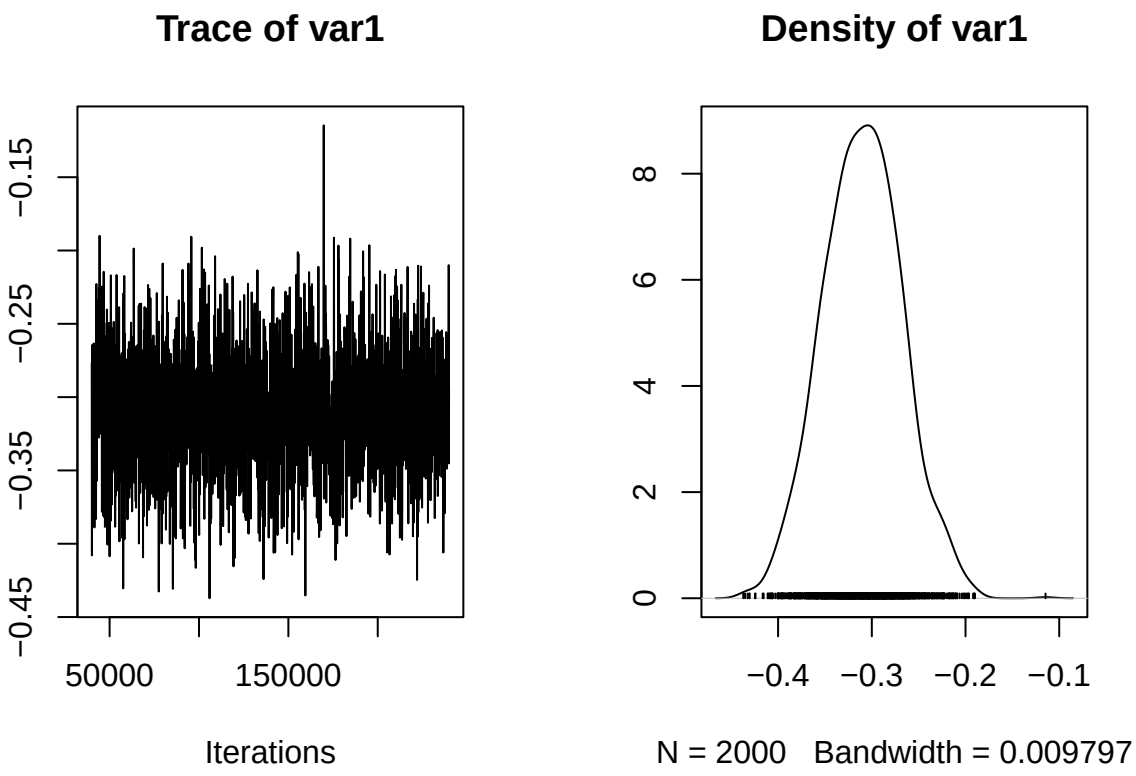
```
Main_models_c1 <-   read.mulTree(mulTree.chain = "mulTree_supp_models-tree1_chain1",
                                 convergence = FALSE,
                                 model = T)

Main_models_c2 <-   read.mulTree(mulTree.chain = "mulTree_supp_models-tree1_chain2",
                                 convergence = FALSE,
                                 model = T)


summary(Main_models_c1)
```

```
##
##  Iterations = 40001:239901
##  Thinning interval  = 100
##  Sample size  = 2000
##
##  DIC: -222.6399
##
##  G-structure:  ~animal
##
##        post.mean l-95% CI u-95% CI eff.samp
## animal    0.1459  0.07403   0.2163     2000
##
##                ~Species_phylo
##
##               post.mean l-95% CI u-95% CI eff.samp
## Species_phylo   0.02051 0.006943  0.03388     1760
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units   0.01468 0.008424  0.02269     1839
```

```
##
##  Location effects: CFF_log ~ log10(body_mass) * forage_light_level + mode_of_life + habitat + Method
##
##                                       post.mean  l-95% CI  u-95% CI eff.samp
## (Intercept)                            1.184212  0.849059  1.516168     2000
## log10(body_mass)                      -0.019549 -0.053726  0.015840     2000
## forage_light_levellow                 -0.309656 -0.388061 -0.222550     1865
## mode_of_lifeballistic                  0.124992  0.030716  0.206738     2000
## mode_of_lifepursuit                    0.194611  0.042664  0.352878     2000
## habitatnektonic                        0.235111 -0.009639  0.504443     1682
## habitatdemersal                        0.214755 -0.045798  0.465908     1971
## habitatvolant                          0.244465  0.046457  0.438278     2789
## MethodElectrophysiology                0.071227  0.001203  0.136024     2151
## log10(body_mass):forage_light_levellow -0.002591 -0.039960  0.029213     2000
##                                        pMCMC
## (Intercept)                           <5e-04 ***
## log10(body_mass)                       0.281
## forage_light_levellow                 <5e-04 ***
## mode_of_lifeballistic                  0.009 **
## mode_of_lifepursuit                    0.015 *
## habitatnektonic                        0.074 .
## habitatdemersal                        0.096 .
## habitatvolant                          0.021 *
## MethodElectrophysiology                0.039 *
## log10(body_mass):forage_light_levellow  0.874
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

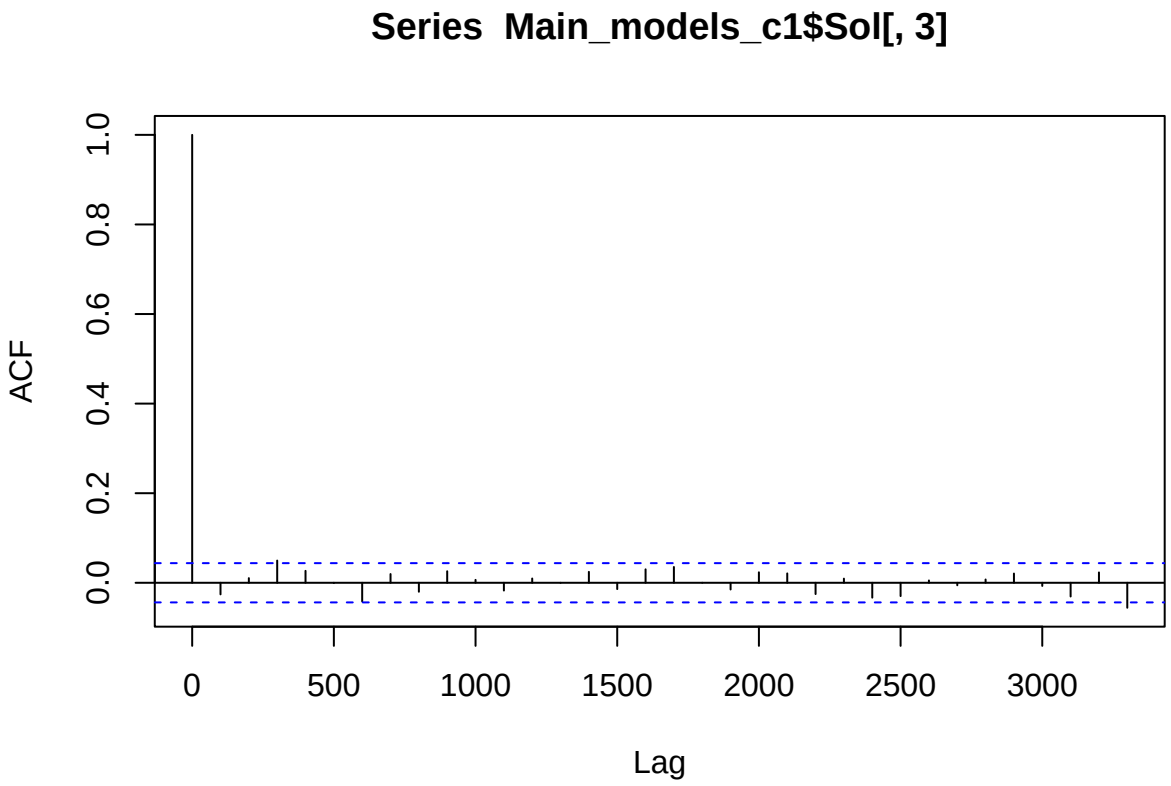
We can also plot the output from the first model. For example, we can look at the trace of the posterior distribution for light levels.

```
plot(Main_models_c1$Sol[,3])
```



We can also check out the auto-corrolation using the `acf()` function

```
acf(Main_models_c1$Sol[,3])
```



We next want to check the convergence for our models. We can check convergence between two chains for single models like below.

```
gelman.diag(mcmc.list(Main_models_c1$Sol,
            Main_models_c2$Sol))
```

```
## Potential scale reduction factors:
##
##                                         Point est. Upper C.I.
## (Intercept)                                      1          1
## log10(body_mass)                                 1          1
## forage_light_levellow                            1          1
## mode_of_lifeballistic                            1          1
## mode_of_lifepursuit                              1          1
## habitatnektonic                                  1          1
## habitatdemersal                                  1          1
## habitatvolant                                    1          1
## MethodElectrophysiology                          1          1
## log10(body_mass):forage_light_levellow           1          1
##
## Multivariate psrf
##
## 1
```

We see that the values are less than 1.1 which indicates convergance. However, mulTree checks for convergance while running and will send a flag if either convergence fails or the ESS is below 1000 for any set of chain across the 100 trees, hence this has all been checked while running the models. However, we can pull the convergence checks across all models as a list by reading them in using read.mulTree and ask if any of the Rubin Gelman values are greater than 1.1.

```
convergance_check <-  read.mulTree(mulTree.chain = "mulTree_supp_models",
                                   convergence = T,
                                   model = F)

any(unlist(convergance_check) >1.1)
```

```
## [1] FALSE
```

We can see that there is no model with a value greater than 1.1 so its clear the chains have converged.

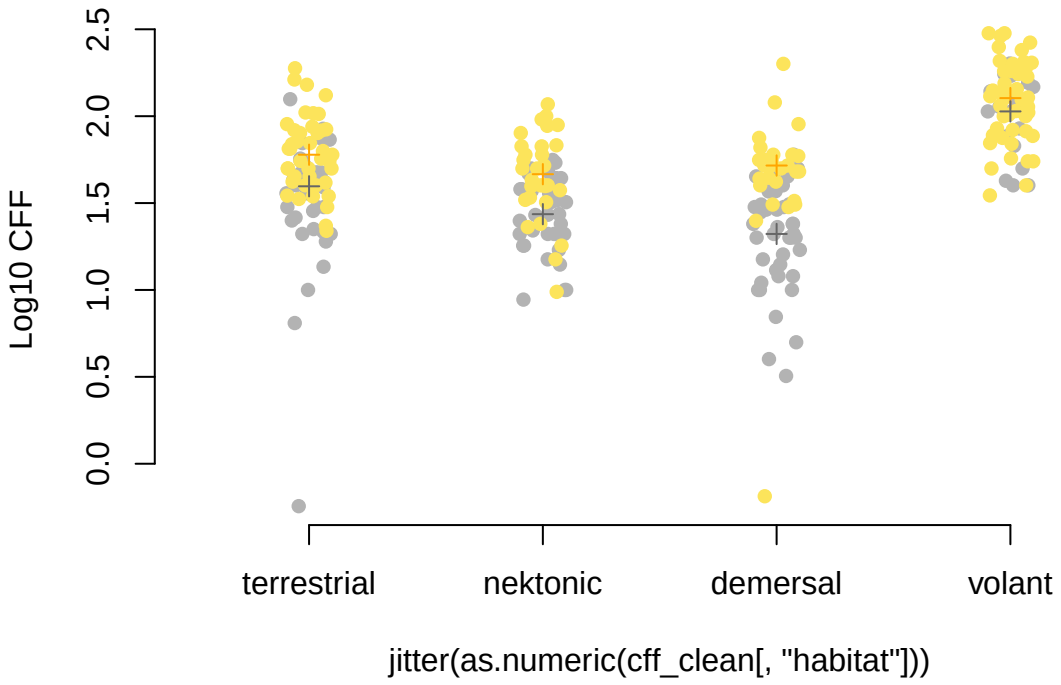
Main plots

We can now do the plots for the main analysis. These are the raw versions here with silhouettes added in inkscape. The first plot is for figure 3 which compares habitat type of terrestrial, nektonic, demersal and volant.

```
plot(log10(cff_clean[, "CFF"]) ~ jitter(as.numeric(cff_clean[, "habitat"])),
       col = "white",
       pch= 16,
     bty = "n",
     xlim = c(0.5,4.5),
      xaxt = "n",
     ylab = "Log10 CFF",
     )

axis(1, at=1:4, labels= c("terrestrial",
                          "nektonic",
                          "demersal",
```

```
                          "volant"))


#For ease we will save the estimates for each of the parameters here.
inter_main_p <-  hdr(Main_models$`(Intercept)`)
mass_log10_main_p <-  hdr(Main_models$`log10(body_mass)`)
lit_low_main_p <-  hdr(Main_models$forage_light_levellow)
ballistic_main_p <-  hdr(Main_models$mode_of_lifeballistic)
pur_main_p <-  hdr(Main_models$mode_of_lifepursuit)
nek_main_p <-  hdr(Main_models$habitatnektonic)
dem_main_p <-  hdr(Main_models$habitatdemersal)
vol_main_p <-  hdr(Main_models$habitatvolant)
body_lit_inter_main_p <-  hdr(Main_models$`log10(body_mass):forage_light_levellow`)



points(log10(cff_clean[cff_clean$forage_light_level == "low", "CFF"]) ~
         jitter(as.numeric(cff_clean[cff_clean$forage_light_level == "low", "habitat"]),
                0.5),
       col = "grey70",
       pch= 16)

points(log10(cff_clean[cff_clean$forage_light_level == "high", "CFF"])
       ~ jitter(as.numeric(cff_clean[cff_clean$forage_light_level == "high",
                                     "habitat"]), 0.5),
       col = rgb(247/250,224/250,89/250),
       pch= 16)



points(1,median(log10(cff_clean[cff_clean$forage_light_level == "high"
                                & cff_clean$habitat == "terrestrial", "CFF"])),
       col = "orange",
       pch= 3)

points(1,median(log10(cff_clean[cff_clean$forage_light_level == "low"
                                & cff_clean$habitat == "terrestrial", "CFF"])),
       col = "grey40",
       pch= 3)



points(2,median(log10(cff_clean[cff_clean$forage_light_level == "high"
                                & cff_clean$habitat == "nektonic", "CFF"])),
       col = "orange",
       pch= 3)

points(2,median(log10(cff_clean[cff_clean$forage_light_level == "low"
                                & cff_clean$habitat == "nektonic", "CFF"])),
       col = "grey40",
       pch= 3)
```

```
points(3,median(log10(cff_clean[cff_clean$forage_light_level == "high"
                                & cff_clean$habitat == "demersal", "CFF"])),
       col = "orange",
       pch= 3)

points(3,median(log10(cff_clean[cff_clean$forage_light_level == "low"
                                & cff_clean$habitat == "demersal", "CFF"])),
       col = "grey40",
       pch= 3)


points(4,median(log10(cff_clean[cff_clean$forage_light_level == "high"
                                & cff_clean$habitat == "volant", "CFF"])),
       col = "orange",
       pch= 3)

points(4,median(log10(cff_clean[cff_clean$forage_light_level == "low"
                                & cff_clean$habitat == "volant", "CFF"])),
       col = "grey40",
       pch= 3)
```



Terrestrial model

As before we need to set the data and phylogeny into a Multree object. First we need to subset to just the non-marine species.

```
#Subset to just volant and terrestrial sepcies
cff_t <- cff_clean[cff_clean$habitat %in% c("volant",
                                            "terrestrial"
                                            ),]

#reset the habitat factors to have just two levels of terrestrial and volant
cff_t$habitat <- factor(cff_t$habitat,
                                      levels = c("terrestrial",
                                                 "volant"
                                                 ))
#Put it in a Multree object.
cff_mul_terr <- as.mulTree(cff_t,
                           cff_tree,
                           taxa = "animal",
                           rand.terms = ~animal + Species_phylo,
                           clean.data = FALSE)
```

As before we can run these models but given they take some time we can upload the model that have been run previously.

```
mulTree(mulTree.data = cff_mul_terr,
        formula = CFF_log ~ log10(body_mass)*forage_light_level
                                      + mode_of_life
                                      + habitat
                                      + Method,
        parameters = parameters,
        chains = 3,
        priors = prior,
        convergence = 1.1,
        ESS = 1000,
        verbose = TRUE,
        output = "cff_supp_terr_models",
        warn = FALSE,
        ask = TRUE)
```

We can now read in the model results for the terrestrial models

```
ter_models <-   read.mulTree(mulTree.chain = "cff_supp_terr_models",
                             convergence = FALSE,
                             model = FALSE,
                             extract = NULL)


ter_models_sp <-   read.mulTree(mulTree.chain = "cff_supp_terr_models",
                             convergence = FALSE,
                             model = FALSE,
                             extract = "VCV")

print(summary(ter_models)[,c(1,2,5)], digits = 2)
```

```
##                                      Estimates(mode hdr) lower.CI(2.5)
## (Intercept)                                        1.355        0.9331
```

```
## log10(body_mass)                                    0.007       -0.0462
## forage_light_levellow                              -0.200       -0.3011
## mode_of_lifeballistic                              -0.039       -0.2519
## mode_of_lifepursuit                                 0.127       -0.0520
## habitatvolant                                       0.247        0.0482
## MethodElectrophysiology                             0.081       -0.0022
## log10(body_mass):forage_light_levellow             -0.017       -0.0722
## phylogenetic.variance                               0.144        0.0720
## residual.variance                                   0.011        0.0003
##                                          upper.CI(97.5)
## (Intercept)                                       1.754
## log10(body_mass)                                  0.061
## forage_light_levellow                            -0.100
## mode_of_lifeballistic                             0.176
## mode_of_lifepursuit                               0.306
## habitatvolant                                     0.448
## MethodElectrophysiology                           0.163
## log10(body_mass):forage_light_levellow            0.038
## phylogenetic.variance                             0.280
## residual.variance                                 0.025
```

Like in the main model the factors with high support as indicated by the 95% CI not crossing zero includes light level, with low light species having lower CFF and volancy, with volant species having higher CFF values. We also see strong support for a negative interaction term for body size and light levels. However, body size was not strongly support as a factor and in this model the support for a posative effect associated with pursuit predators is lower which there is now a negative relationship, although it is only weakly supported, for ballistic species.

Like before we can also look at the phylogentic signal in more detail.

```
H_terr <- phylo_t_animal/c(phylo_t_animal + sp_t_rand + resids_t_rand)
hdr(H_terr)
```

```
## $hdr
##          [,1]      [,2]      [,3]      [,4]      [,5]      [,6]      [,7]
## 99% 0.6166072 0.6241041 0.6367763 0.6383034 0.6574737 0.6727832 0.6774514
## 95% 0.7087009 0.9358417        NA        NA        NA        NA        NA
## 50% 0.8189858 0.8273099 0.8318004 0.8991814        NA        NA        NA
##         [,8]
## 99% 0.949785
## 95%       NA
## 50%       NA
##
## $mode
## [1] 0.8635778
##
## $falpha
##        1%        5%       50%
## 0.2825770 0.8684114 5.4879744
```

Similar to the main model the H2 value is 0.86 indicating a strong phylogentic effect.

We can also plot the output from the first model

```
terr_models_c1 <-   read.mulTree(mulTree.chain = "cff_supp_terr_models-tree1_chain1",
                                 convergence = FALSE,
                                 model = T)
```

```
terr_models_c2 <-   read.mulTree(mulTree.chain = "cff_supp_terr_models-tree1_chain2",
                                 convergence = FALSE,
                                 model = T)
summary(terr_models_c1)
```

```
##
##  Iterations = 40001:239901
##  Thinning interval  = 100
##  Sample size  = 2000
##
##  DIC: -108.7193
##
##  G-structure:  ~animal
##
##        post.mean l-95% CI u-95% CI eff.samp
## animal    0.1648   0.0704   0.2652     1791
##
##                ~Species_phylo
##
##               post.mean  l-95% CI u-95% CI eff.samp
## Species_phylo   0.01255 0.0003099  0.02536     1585
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units   0.01688 0.008639   0.0255     1819
##
##  Location effects: CFF_log ~ log10(body_mass) * forage_light_level + mode_of_life + habitat + Method
##
##                                       post.mean  l-95% CI  u-95% CI eff.samp
## (Intercept)                            1.346728  0.948939  1.730030     2000
## log10(body_mass)                       0.007003 -0.048734  0.057027     2241
## forage_light_levellow                 -0.199798 -0.301277 -0.104903     2195
## mode_of_lifeballistic                 -0.036708 -0.240529  0.171498     2000
## mode_of_lifepursuit                    0.127858 -0.053446  0.301663     2000
## habitatvolant                          0.248913  0.053215  0.439555     2000
## MethodElectrophysiology                0.081275  0.001012  0.163711     1829
## log10(body_mass):forage_light_levellow -0.018244 -0.068880  0.039293     2000
##                                        pMCMC
## (Intercept)                           <5e-04 ***
## log10(body_mass)                       0.784
## forage_light_levellow                 <5e-04 ***
## mode_of_lifeballistic                  0.730
## mode_of_lifepursuit                    0.174
## habitatvolant                          0.016 *
## MethodElectrophysiology                0.052 .
## log10(body_mass):forage_light_levellow  0.502
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

and check convergence between the first two chains

```
gelman.diag(mcmc.list(terr_models_c1$Sol,
           terr_models_c2$Sol))
```

```
## Potential scale reduction factors:
##
##                                          Point est. Upper C.I.
## (Intercept)                                       1       1.00
## log10(body_mass)                                  1       1.00
## forage_light_levellow                             1       1.00
## mode_of_lifeballistic                             1       1.01
## mode_of_lifepursuit                               1       1.00
## habitatvolant                                     1       1.00
## MethodElectrophysiology                           1       1.00
## log10(body_mass):forage_light_levellow            1       1.01
##
## Multivariate psrf
##
## 1
```

However, mulTree checks for convergance while running and will send flag if either convergence fails or the ESS is below 1000 so this has all been checked. We can pull the convergance checks across all models as a list by reading them in using read.mulTree and ask if any of the Rubin Gelman values are greater than 1.1.

```
convergance_terr_check <-  read.mulTree(mulTree.chain = "cff_supp_terr_models",
                              convergence = T,
                              model = F)

any(unlist(convergance_terr_check) >1.1)
```

```
## [1] FALSE
```