Pace of ecology drives temporal perception across the Animal Kingdom

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Introduction

This document outlines the analysis used for the publication Haarlem et al (Pace of ecology drives temporal perception across the Animal Kingdom). 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 uncertainly 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`, `plotrix` and `caper` packages.

To incorporate the uncertinty associated with building phylogenies we used the `mulTree` package which is downladed 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 availble in the R envirnment. 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)
library(plotrix)

#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

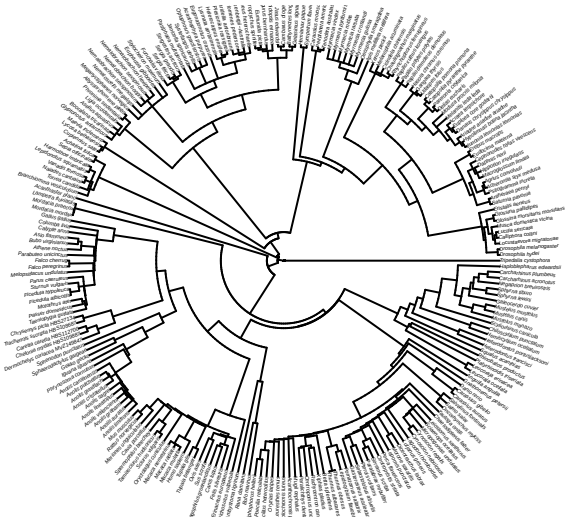
Next we load in the dataset Haarlem_et_al_cff_dataset_21_10_2025.csv.

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. We can plot out one of the phylogenies.

```
cff_tree <- read.tree("Haarlem_et_al_tree.tre")

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



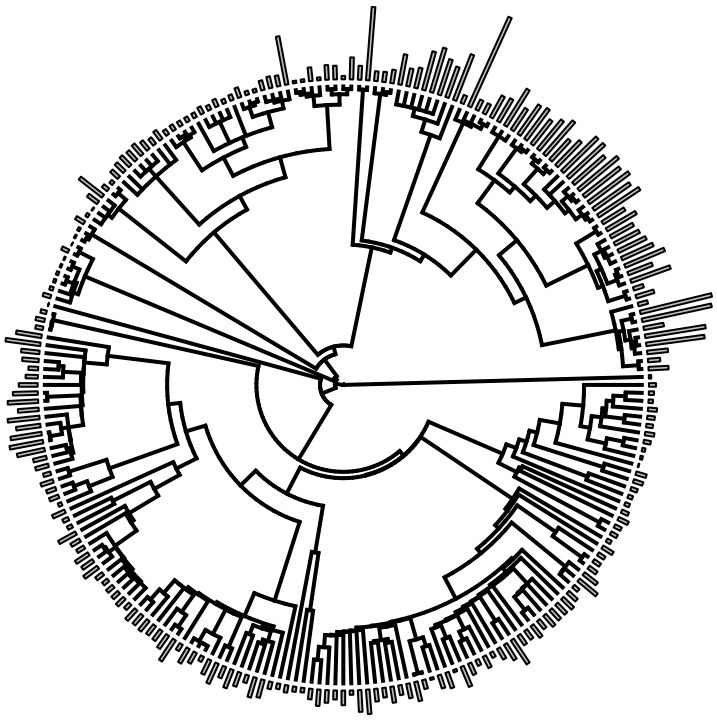
We can also plot the phylogeny with cff values indicated by bars. I combine the normal plot with the barplot in inkscape to create figure 2.

```
cff_phylo_plot_cff <- c()
cff_phylo_plot_light <- c()
cff_phylo_plot_species <- c()

for(i in 1:length(unique(cff_clean$Species_phylo))){

 cff_phylo_plot_species[i] <-  unique(cff_clean$Species_phylo)[i]
 cff_phylo_plot_light[i] <-  cff_clean[cff_clean$Species_phylo ==
                                       unique(cff_clean$Species_phylo)[i],
                                     "forage_light_level"][1]
 cff_phylo_plot_cff[i] <-  max(cff_clean[cff_clean$Species_phylo ==
                                         unique(cff_clean$Species_phylo)[i],
                                       "CFF"])

}


cff_phylo_plot <- data.frame(cff_phylo_plot_species,
```

```
                              cff_phylo_plot_light,
                              cff_phylo_plot_cff)


#create data with rownames for p
rownames(cff_phylo_plot) <- cff_phylo_plot$cff_phylo_plot_species

plots_v <- fastBM(cff_tree[[1]],bounds=c(0,Inf))

for(i in 1:length(cff_phylo_plot$cff_phylo_plot_species)){

  plots_v[i] <- cff_phylo_plot[cff_phylo_plot$cff_phylo_plot_species == names(plots_v)[i],
                               "cff_phylo_plot_cff"]
}
```

```
## Warning in plots_v[i] <- cff_phylo_plot[cff_phylo_plot$cff_phylo_plot_species
## == : number of items to replace is not a multiple of replacement length
```

```
CFF_plot_val <-setNames(cff_phylo_plot$cff_phylo_plot_cff,
              rownames(cff_phylo_plot))

par(mar=c(4.1,4.1,4.1,2.1))

plotTree.wBars(cff_tree[[1]],
               CFF_plot_val,
     type = "fan",
     scale = 0.5,
     tip.labels = F)
```



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_us)*forage_light_level
                                  + mode_of_life
                                  + habitat
                                  + Method,
        parameters = parameters,
        chains = 3,
        priors = prior,
        convergence = 1.1,
        ESS = 1000,
        verbose = TRUE,
        output = "mulTree_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_models",
                              convergence = FALSE,
                              model = FALSE)

Main_models_sp <-   read.mulTree(mulTree.chain = "mulTree_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)                                              1.2207        0.8665
## log10(body_mass_us)                                     -0.0140       -0.0519
## forage_light_levellow                                   -0.3091       -0.3972
## mode_of_lifeballistic                                    0.1164        0.0210
## mode_of_lifepursuit                                      0.1856        0.0233
## habitatpelagic                                           0.1881       -0.0530
## habitatdemersal                                          0.1643       -0.0810
## habitatvolant                                            0.3362        0.1299
## MethodElectrophysiology                                  0.0731        0.0039
## log10(body_mass_us):forage_light_levellow               -0.0034       -0.0409
## phylogenetic.variance                                    0.1167        0.0636
## residual.variance                                        0.0252        0.0118
##                                           upper.CI(97.5)
## (Intercept)                                        1.538
## log10(body_mass_us)                                0.022
## forage_light_levellow                             -0.217
## mode_of_lifeballistic                              0.209
## mode_of_lifepursuit                                0.346
## habitatpelagic                                     0.457
## habitatdemersal                                    0.433
## habitatvolant                                      0.547
## MethodElectrophysiology                            0.140
## log10(body_mass_us):forage_light_levellow          0.033
## phylogenetic.variance                              0.206
## residual.variance                                  0.040
```

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.   :0.04236   Min.   :0.0007215   Min.   :0.006842
##  1st Qu.:0.10561   1st Qu.:0.0205978   1st Qu.:0.011994
##  Median :0.12713   Median :0.0250356   Median :0.014068
##  Mean   :0.13118   Mean   :0.0251008   Mean   :0.014604
##  3rd Qu.:0.15343   3rd Qu.:0.0296787   3rd Qu.:0.016630
##  Max.   :0.29284   Max.   :0.0495493   Max.   :0.039406
```

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] 0.7870918
##
## $CI_95
## [1] 0.6254163 0.8816590
```

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.

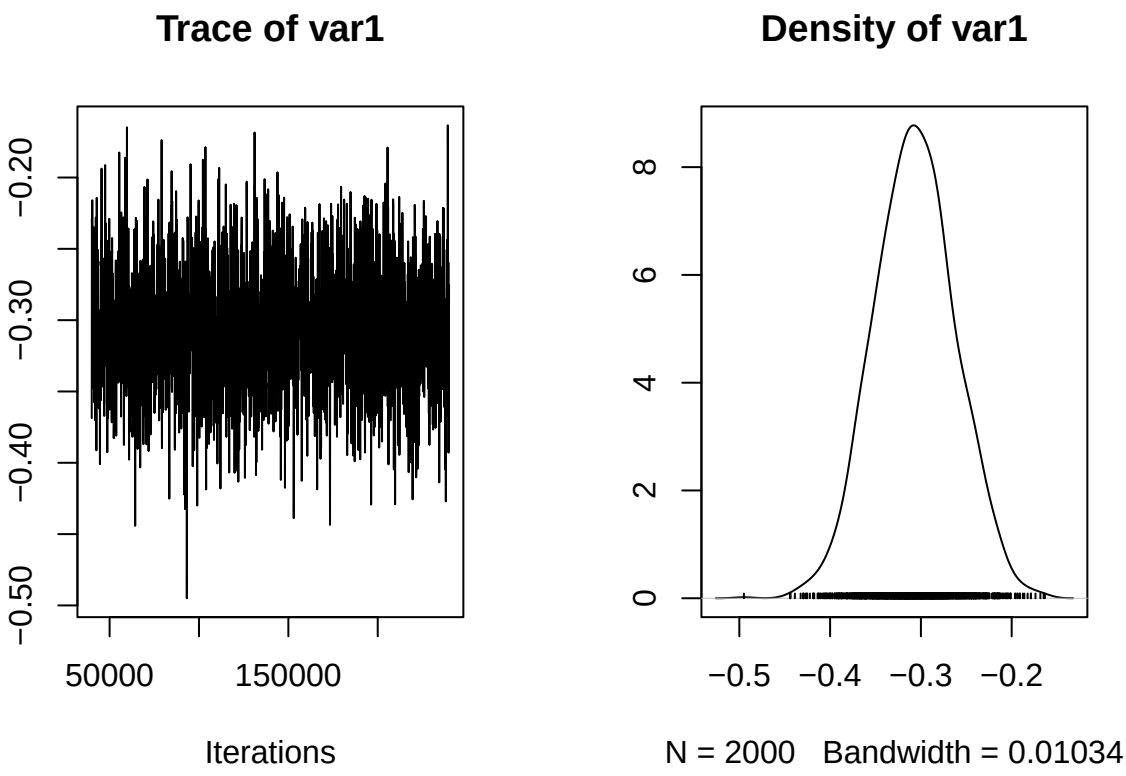
```
Main_models_c1 <-   read.mulTree(mulTree.chain = "mulTree_models-tree1_chain1",
                                 convergence = FALSE,
                                 model = T)

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


summary(Main_models_c1)
```

```
##
```

```
##  Iterations = 40001:239901
##  Thinning interval  = 100
##  Sample size  = 2000
##
##  DIC: -222.0482
##
##  G-structure:  ~animal
##
##        post.mean l-95% CI u-95% CI eff.samp
## animal    0.1312  0.06708    0.202     1813
##
##                ~Species_phylo
##
##               post.mean l-95% CI u-95% CI eff.samp
## Species_phylo    0.0251  0.01274  0.03953     2309
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units    0.0146 0.008354  0.02187     2000
##
##  Location effects: CFF_log ~ log10(body_mass_us) * forage_light_level + mode_of_life + habitat + Meth
##
##                                           post.mean  l-95% CI  u-95% CI
## (Intercept)                                1.193863  0.872300  1.530689
## log10(body_mass_us)                       -0.016760 -0.051462  0.022106
## forage_light_levellow                     -0.306629 -0.391301 -0.218340
## mode_of_lifeballistic                      0.113399  0.024183  0.208461
## mode_of_lifepursuit                        0.184232  0.021771  0.342687
## habitatpelagic                             0.211490 -0.050004  0.470405
## habitatdemersal                            0.184997 -0.075063  0.452844
## habitatvolant                              0.350423  0.149239  0.567594
## MethodElectrophysiology                    0.072724  0.004808  0.135936
## log10(body_mass_us):forage_light_levellow -0.004099 -0.038802  0.033966
##                                           eff.samp  pMCMC
## (Intercept)                                   2000 <5e-04 ***
## log10(body_mass_us)                           2000  0.366
## forage_light_levellow                         2000 <5e-04 ***
## mode_of_lifeballistic                         2000  0.015 *
## mode_of_lifepursuit                           2000  0.025 *
## habitatpelagic                                1827  0.098 .
## habitatdemersal                               1858  0.167
## habitatvolant                                 2000  0.001 ***
## MethodElectrophysiology                       2000  0.028 *
## log10(body_mass_us):forage_light_levellow     2000  0.829
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

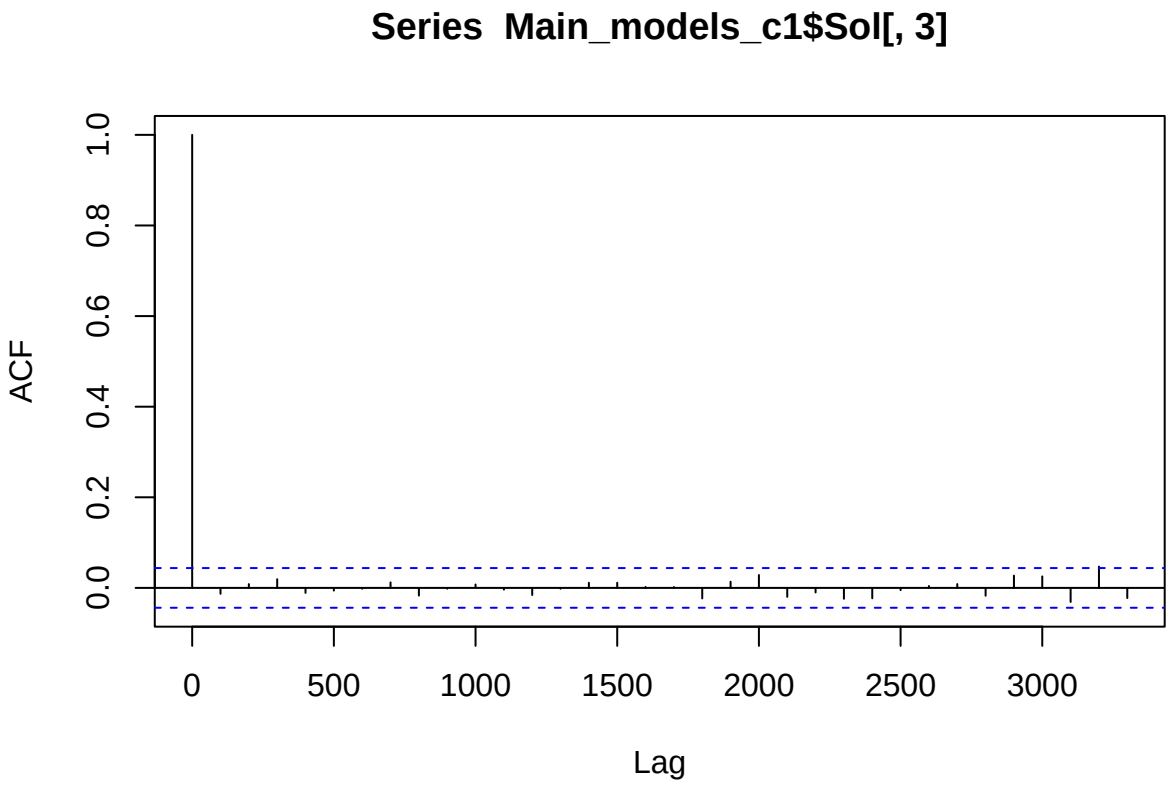
We can also plot the output from the first model. For example, we can look at the trace of the posterior distribution for light levels.

```
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       1.01
## log10(body_mass_us)                                1       1.00
## forage_light_levellow                              1       1.00
## mode_of_lifeballistic                              1       1.00
## mode_of_lifepursuit                                1       1.00
## habitatpelagic                                     1       1.01
## habitatdemersal                                    1       1.00
## habitatvolant                                      1       1.00
## MethodElectrophysiology                            1       1.00
## log10(body_mass_us):forage_light_levellow          1       1.00
##
## 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_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.

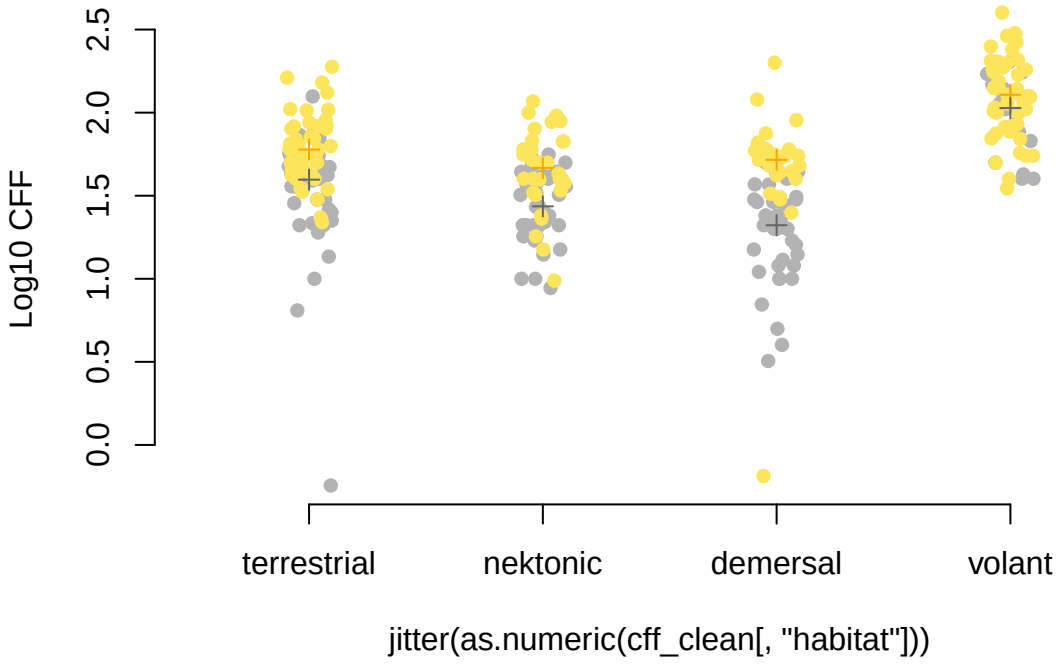
Main plots

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_us)`)
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$mode_of_lifepursuit)
nek_main_p <-  hdr(Main_models$habitatpelagic)
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_us):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_us)*forage_light_level
                                      + mode_of_life
                                      + habitat
                                      + Method,
        parameters = parameters,
        chains = 3,
        priors = prior,
        convergence = 1.1,
        ESS = 1000,
        verbose = TRUE,
        output = "cff_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_terr_models",
                             convergence = FALSE,
                             model = FALSE,
                             extract = NULL)


ter_models_sp <-   read.mulTree(mulTree.chain = "cff_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)                                           1.3529       0.93784
```

```
## log10(body_mass_us)                                    0.0073      -0.04712
## forage_light_levellow                                 -0.1799      -0.28607
## mode_of_lifeballistic                                 -0.0340      -0.24849
## mode_of_lifepursuit                                    0.1389      -0.04682
## habitatvolant                                          0.2829       0.07683
## MethodElectrophysiology                                0.0845      -0.00150
## log10(body_mass_us):forage_light_levellow             -0.0266      -0.08346
## phylogenetic.variance                                  0.1379       0.06760
## residual.variance                                      0.0125       0.00033
##                                          upper.CI(97.5)
## (Intercept)                                       1.737
## log10(body_mass_us)                               0.060
## forage_light_levellow                            -0.074
## mode_of_lifeballistic                             0.179
## mode_of_lifepursuit                               0.316
## habitatvolant                                     0.499
## MethodElectrophysiology                           0.165
## log10(body_mass_us):forage_light_levellow         0.031
## phylogenetic.variance                             0.267
## residual.variance                                 0.027
```

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% 0.6254689 0.6335364 0.6418199 0.6568609 0.6628273 0.6814439 0.6852013
## 95% 0.6914095 0.7007325 0.7156791 0.9399663        NA        NA        NA
## 50% 0.8153008 0.8919179        NA        NA        NA        NA        NA
##          [,8]
## 99% 0.9517021
## 95%        NA
## 50%        NA
##
## $mode
## [1] 0.8550741
##
## $falpha
##        1%        5%       50%
## 0.3621734 0.8921353 5.2507973
```

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_terr_models-tree1_chain1",
                                 convergence = FALSE,
                                 model = T)
```

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

```
##
##  Iterations = 40001:239901
##  Thinning interval  = 100
##  Sample size  = 2000
##
##  DIC: -107.3754
##
##  G-structure:  ~animal
##
##        post.mean l-95% CI u-95% CI eff.samp
## animal     0.159   0.0577   0.2565     1860
##
##                ~Species_phylo
##
##               post.mean  l-95% CI u-95% CI eff.samp
## Species_phylo   0.01322 0.0003027    0.026     1587
##
##  R-structure:  ~units
##
##       post.mean l-95% CI u-95% CI eff.samp
## units   0.01695 0.008874  0.02702     1811
##
##  Location effects: CFF_log ~ log10(body_mass_us) * forage_light_level + mode_of_life + habitat + Met
##
##                                            post.mean   l-95% CI   u-95% CI
## (Intercept)                                 1.3272143  0.9032724  1.7040448
## log10(body_mass_us)                         0.0052310 -0.0456526  0.0621071
## forage_light_levellow                      -0.1809804 -0.2900806 -0.0781279
## mode_of_lifeballistic                      -0.0292650 -0.2437748  0.1811541
## mode_of_lifepursuit                         0.1359146 -0.0509179  0.3128357
## habitatvolant                               0.3047472  0.0898872  0.5317528
## MethodElectrophysiology                     0.0827747 -0.0003069  0.1624846
## log10(body_mass_us):forage_light_levellow -0.0260627 -0.0889308  0.0288671
##                                            eff.samp  pMCMC
## (Intercept)                                    2000 <5e-04 ***
## log10(body_mass_us)                            2000  0.829
## forage_light_levellow                          2000 <5e-04 ***
## mode_of_lifeballistic                          2000  0.790
## mode_of_lifepursuit                            2000  0.142
## habitatvolant                                  2000  0.008 **
## MethodElectrophysiology                        2000  0.043 *
## log10(body_mass_us):forage_light_levellow      2000  0.363
## ---
## 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_us)                                1       1.00
## forage_light_levellow                              1       1.00
## mode_of_lifeballistic                              1       1.00
## mode_of_lifepursuit                                1       1.00
## habitatvolant                                      1       1.01
## MethodElectrophysiology                            1       1.01
## log10(body_mass_us):forage_light_levellow          1       1.00
##
## Multivariate psrf
##
## 1
```

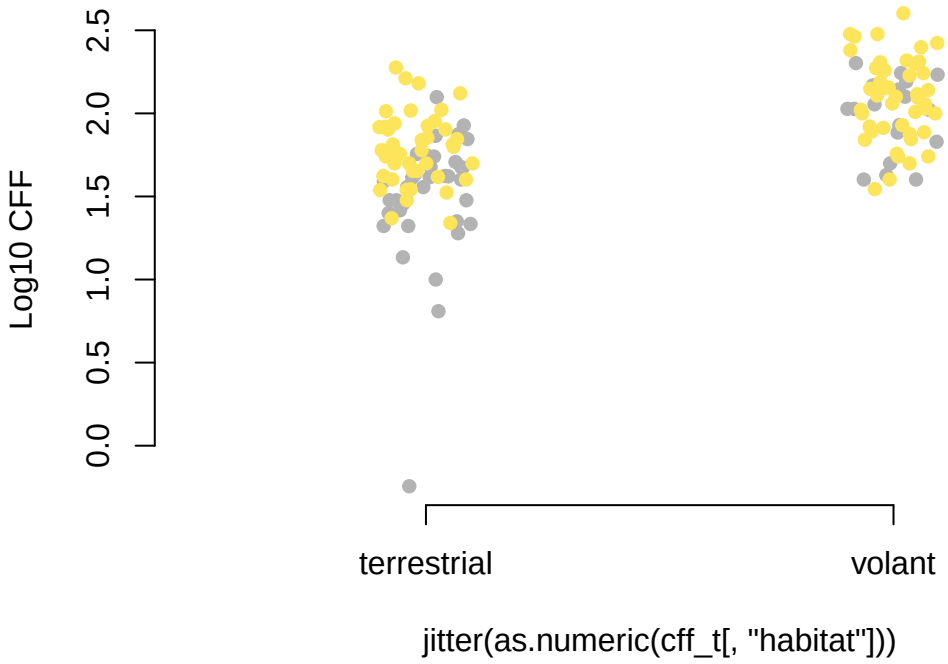
However, mulTree checks for convergance while running and will send flag if either convergence fails or the ESS is below 1000 so this has all been checked. We can pull the convergance checks across all models as a list by reading them in using read.mulTree and ask if any of the Rubin Gelman values are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

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

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

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

Finally, we can plot the volant versus nonvolant.

```
plot(log10(cff_t[, "CFF"]) ~ jitter(as.numeric(cff_t[, "habitat"])),
       col = "white",
       pch= 16,
     bty = "n",
     xlim = c(0.5,2.5),
      xaxt = "n",
     ylab = "Log10 CFF",
     )

axis(1, at=1:2, labels= c("terrestrial",
                          "volant"))

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

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


Log10 CFF
0.0
0.5
1.0
1.5
2.0
2.5
terrestrial
volant
jitter(as.numeric(cff_t[, "habitat"]))

Marine models

The final models focus on the just marine species so first we need to subset and make a Multree object.

```
cff_m <- cff_clean[cff_clean$habitat %in% c("nektonic",
                                            "demersal"
                                            ),]

cff_m$habitat <- factor(cff_m$habitat,
                                    levels = c("demersal",
                                               "nektonic"
                                    ))


cff_mul_mar <- as.mulTree(cff_m,
                          cff_tree,
                          taxa = "animal",
                          rand.terms = ~animal + Species_phylo,
                          clean.data = FALSE)
```

As in the other models if you wish to rerun the models across all 100 tree the code below will do it and export the output to the current working directory folder. However, to avoid long run times here we will skip this step and upload the model results from a previous run.

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

Read in the multiple marine models and get an overall summary of the results.

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

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

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

```
##                                          Estimates(mode hdr) lower.CI(2.5)
## (Intercept)                                           1.3696       0.94950
## log10(body_mass_us)                                  -0.0468      -0.09539
```

```
## forage_light_levellow                                -0.6004      -0.73337
## mode_of_lifeballistic                                 0.1444       0.04235
## mode_of_lifepursuit                                   0.3000      -0.00787
## habitatpelagic                                        0.0474      -0.04742
## MethodElectrophysiology                               0.0375      -0.07886
## log10(body_mass_us):forage_light_levellow             0.0861       0.03722
## phylogenetic.variance                                 0.2145       0.11873
## residual.variance                                     0.0012       0.00017
##                                          upper.CI(97.5)
## (Intercept)                                      1.7859
## log10(body_mass_us)                              0.0044
## forage_light_levellow                           -0.4643
## mode_of_lifeballistic                            0.2468
## mode_of_lifepursuit                              0.6139
## habitatpelagic                                   0.1433
## MethodElectrophysiology                          0.1535
## log10(body_mass_us):forage_light_levellow        0.1369
## phylogenetic.variance                            0.3577
## residual.variance                                0.0187
```

Similar to the main overall model and the terrestrial model light levels are strongly supported, with species in low light environments associated with lower CFF values. The is strong support for ballistic predators having higher CFF values compared to species that forage on sessile food items and while slightly weaker, as the 95% CI crosses zero, there is some support for pursuit predators also having higher CFF values. Notable, an effect for body size is strongly supported in marine species with larger species having a lower CFF value and there is also strong support for for a negative interaction term between body mass and light levels. While still a positive effect the associated with Electrophysiology methods is not strongly supported in this model.

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

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


#resids term

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

marine_rand <- data.frame(phylo_m_animal,
                          sp_m_rand,
                          resids_m_rand)
```

```
summary(marine_rand)
```

```
##  phylo_m_animal     sp_m_rand         resids_m_rand
##  Min.   :0.0713   Min.   :0.0001942   Min.   :0.003419
##  1st Qu.:0.1847   1st Qu.:0.0031213   1st Qu.:0.009035
##  Median :0.2225   Median :0.0066019   Median :0.011537
##  Mean   :0.2270   Mean   :0.0078985   Mean   :0.012136
##  3rd Qu.:0.2625   3rd Qu.:0.0112206   3rd Qu.:0.014470
##  Max.   :0.5095   Max.   :0.0378134   Max.   :0.030814
```

We can also calculate the H2 value for the marine model

```
m_terr <- phylo_m_animal/c(phylo_m_animal + sp_m_rand + resids_m_rand)
hdr(m_terr)
```

```
## $hdr
##          [,1]      [,2]      [,3]      [,4]      [,5]      [,6]
## 99% 0.7849948 0.7888769 0.7913944 0.8037895 0.8049211 0.9774483
## 95% 0.8272116 0.8313791 0.8393337 0.9757380        NA        NA
## 50% 0.9052914 0.9168884 0.9200536 0.9542766        NA        NA
##
## $mode
## [1] 0.9321022
##
## $falpha
##        1%        5%       50%
## 0.3739766 1.4534298 9.3856192
```

Like in the previous models the H2 value is high, at 0.93, indicating a strong phylogentic signal.

We can no also plot the relationship between the foraging stratagy,

```
plot(log10(cff_m[, "CFF"]) ~ jitter(as.numeric(cff_m[, "mode_of_life"])),
       col = "white",
       pch= 16,
     bty = "n",
     xlim = c(0.5,3.5),
      xaxt = "n",
     ylab = "Log10 CFF",
     )

axis(1, at=1:3, labels= c("forage",
                          "ballistic",
                          "pursuit"))

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

points(log10(cff_m[cff_m$forage_light_level == "high", "CFF"])
       ~ jitter(as.numeric(cff_m[cff_m$forage_light_level == "high",
                                 "mode_of_life"]),
                0.5),
```

```
        col = rgb(247/250,224/250,89/250),
        pch= 16)
```