

# Olfactory camouflage and communication in birds

## R code for the comparative analysis on seasonal differences in preen oil composition

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Required packages

```
library(ape)
library(MCMCglmm)
library(coda)
library(plotMCMC)
```

# 1 Data

## 1.1 Data on seasonal differences

Import data on seasonal differences

```
df <- read.csv("data_season.csv")
# Remove rows where sex is undefined (NA) as this information is needed for the analysis
df <- df[!is.na(df$sex),]
```

Sample size = number of occurrences (1 occurrence = 1 sex within a species)

```
nrow(df)
```

```
## [1] 91
```

Number of occurrences in each category of each variable

```
ss.seas <- data.frame(table(df$seasonalchange)["0"], table(df$seasonalchange)["1"])
colnames(ss.seas) <- c("no", "yes")
rownames(ss.seas) <- c("seasonal difference")
ss.seas
```

```
##                no yes
## seasonal difference 14  77
```

```
ss.inc <- data.frame(table(df$incubation)["0"], table(df$incubation)["1"])
colnames(ss.inc) <- c("no", "yes")
rownames(ss.inc) <- c("incubation")
ss.inc
```

```
##                no yes
## incubation 28  63
```

```
ss.nest <- data.frame(table(df$nest)["0"], table(df$nest)["1"])
colnames(ss.nest) <- c("nonground", "ground")
rownames(ss.nest) <- c("nest ecology")
ss.nest
```

```
##                nonground ground
## nest ecology      46      45
```

```
ss.timesc <- data.frame(table(df$timescale)[0],table(df$timescale)[1])
colnames(ss.timesc) <- c("within breeding","across breeding and nonbreeding")
rownames(ss.timesc) <- c("time scale")
ss.timesc
```

```
##                within breeding across breeding and nonbreeding
## time scale              19              72
```

Number of species

```
length(unique(df$species))
```

```
## [1] 43
```

Number of studies

```
length(unique(df$study))
```

```
## [1] 25
```

## 1.2 Phylogenetic data

Import phylogenetic data

```
# birdtree.org, 1000 trees, from source: Stage2 MayrAll Hackett
tree <- read.nexus("data_phylo.nex")
# this tree contains all species included in the review
class(tree)
```

Build consensus tree

```
# Consensus tree: given a series of trees, this function returns the consensus tree.
# By default, the strict-consensus tree is computed.
# To get the majority-rule consensus tree, use p = 0.5.
# Any value between 0.5 and 1 can be used.
consensustree <- consensus(tree, p = 0.5, check.labels = TRUE)
class(consensustree)

# Check that the tree covers all the species
species <- df$phylo
setdiff(species, as.character(consensustree$tip.label))
# 0 species listed in our data but not in the tree
setdiff(as.character(consensustree$tip.label),species)
# species listed in the tree but not in our data (df = data with seasonal differences)

# Trim tree to have only species where seasonal differences are known
subtree <- drop.tip(consensustree, tip=setdiff(consensustree$tip.label,df$phylo))
```

```

# Check that the tree covers all the species
setdiff(species, as.character(subtree$tip.label))
# 0 species listed in our data but not in the tree
setdiff(as.character(subtree$tip.label), species)
# 0 species listed in the tree but not in our data

# Dealing with polytomies
is.binary.tree(subtree) # FALSE > there are some polytomies
subtree_random <- multi2di(subtree, random=TRUE)
# randomization approach to take care of the polytomies
is.binary.tree(subtree_random) # TRUE > no more polytomies

```

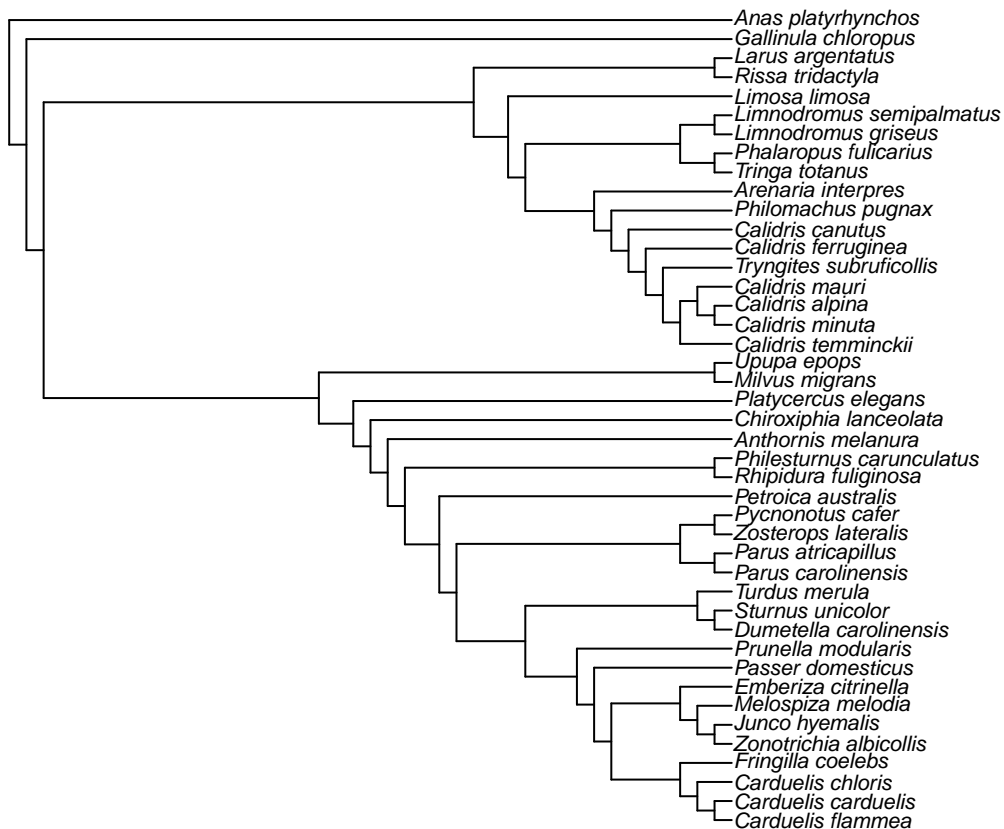
Some name synonyms had to be fixed to match the list of bird tree: Poecile > Parus, Chlorus > Carduelis, Acanthis > Carduelis NB: Cory's shearwater (*Calonectris borealis*) is considered a subspecies of Scopoli's shearwater (*C. diomedea*) by some authors. In birdtree.org Cory's shearwater (*Calonectris borealis*) is absent, so we used the name of Scopoli's shearwater (i.e. *Calonectris diomedea*) as they are phylogenetically close/equivalent

Plot tree

```

# Plot tree
plot(subtree_random, cex=.7, label.offset =.1, no.margin = TRUE)

```



Get phylogenetic matrix

```

# Compute branch lengths of tree
phylo_branch <- compute.brlen(subtree_random, method = "Grafen", power = 1)

# Check tree is ultrametric
is.ultrametric(phylo_branch)

# Calculate the inverse of the matrix of phylogenetic relatedness (to be used in MCMCglmm)
inv.phylo <- inverseA(phylo_branch,nodes="TIPS",scale=TRUE)

```

## 2 MCMCglmm

### 2.1 Prior

Because we have no a priori belief on the value of the parameter, we set a weakly informative prior (inverse-gamma)

```

prior2 <- list(G = list(G1 = list(V = 1, n = 0.002),
                          G2 = list(V = 1, n = 0.002)),
               R = list(V = 1, n = 0.002))

```

### 2.2 Model

Model parameters: burnin and thin should be big enough to get rid of autocorrelation and ensure convergence, nitt should be big enough to have sufficient sample size (nitt-burnin/thin  $\geq 1000$ ).

```

# Model 1
mcmc1 <- MCMCglmm(seasonalchange ~ incubation * nest + timescale,
                  random = ~ phylo + species,
                  family = "categorical",
                  data = df,
                  prior = prior2,
                  ginverse = list(phylo = inv.phylo$Ainv),
                  nitt=13000000,burnin=10000,thin=3500,
                  verbose = FALSE)

```

## 3 Model verifications

Diagnostics

```

raftery.diag(mcmc1) # tells you how many MCMC iterations you need to run for convergence

```

```

##
## Quantile (q) = 0.025
## Accuracy (r) = +/- 0.005
## Probability (s) = 0.95
##
## You need a sample size of at least 3746 with these values of q, r and s

```

### 3.1 Check autocorrelation

Check that autocorrelation is low

```
autocorr(mcmc1$Sol[,1])
```

```
## , , 1
##
##      [,1]
## Lag 0      1.00000000
## Lag 3500    0.37958901
## Lag 17500   0.21236079
## Lag 35000   0.12392560
## Lag 175000  0.04046309
```

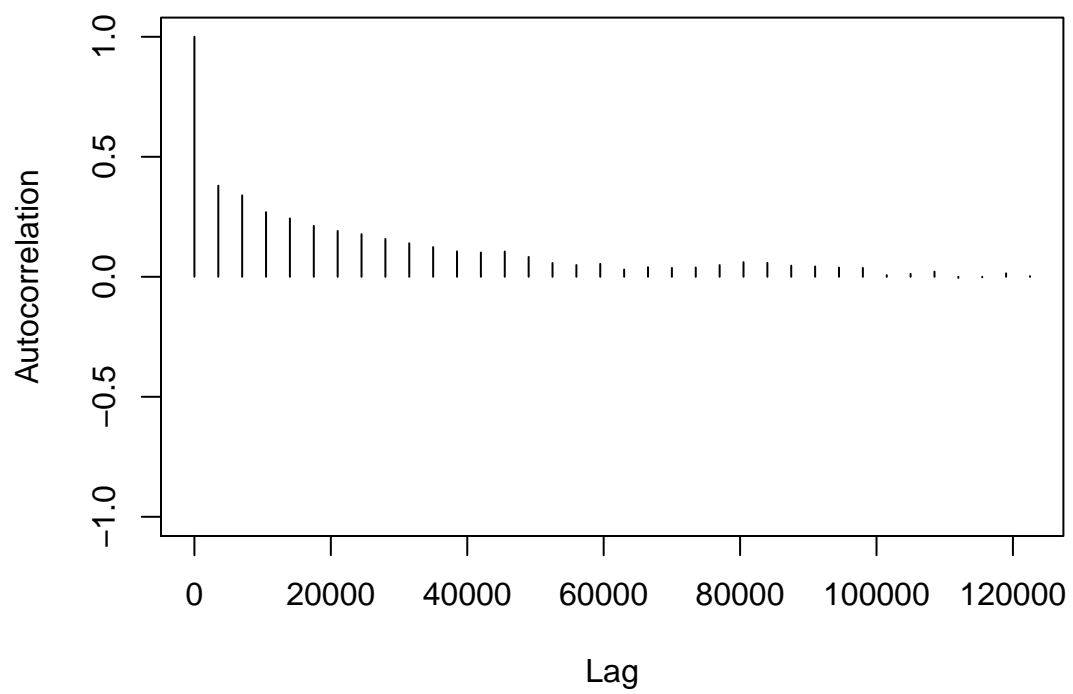
```
autocorr(mcmc1$VCV)
```

```
## , , phylo
##
##      phylo      species      units
## Lag 0      1.00000000 -0.04939853 -0.071542361
## Lag 3500    0.36924961  0.06046334 -0.006768565
## Lag 17500   0.13427923  0.12383975  0.035734097
## Lag 35000   0.06273137  0.05576325  0.054913188
## Lag 175000 -0.03154558 -0.01101676  0.026003653
##
## , , species
##
##      phylo      species      units
## Lag 0     -0.049398530  1.000000000 -0.15455297
## Lag 3500    0.063402629  0.419611201 -0.04511764
## Lag 17500   0.043444400  0.084456223  0.04264906
## Lag 35000   0.032239064 -0.004639062  0.06501596
## Lag 175000  0.002815193  0.006781332  0.04419779
##
## , , units
##
##      phylo      species      units
## Lag 0     -0.071542361 -0.15455297  1.00000000
## Lag 3500   -0.007851831 -0.05790042  0.7307936
## Lag 17500    0.041673906 -0.01539563  0.5522284
## Lag 35000    0.047964673  0.03161814  0.4467288
## Lag 175000   0.024765614  0.01548655  0.1944505
```

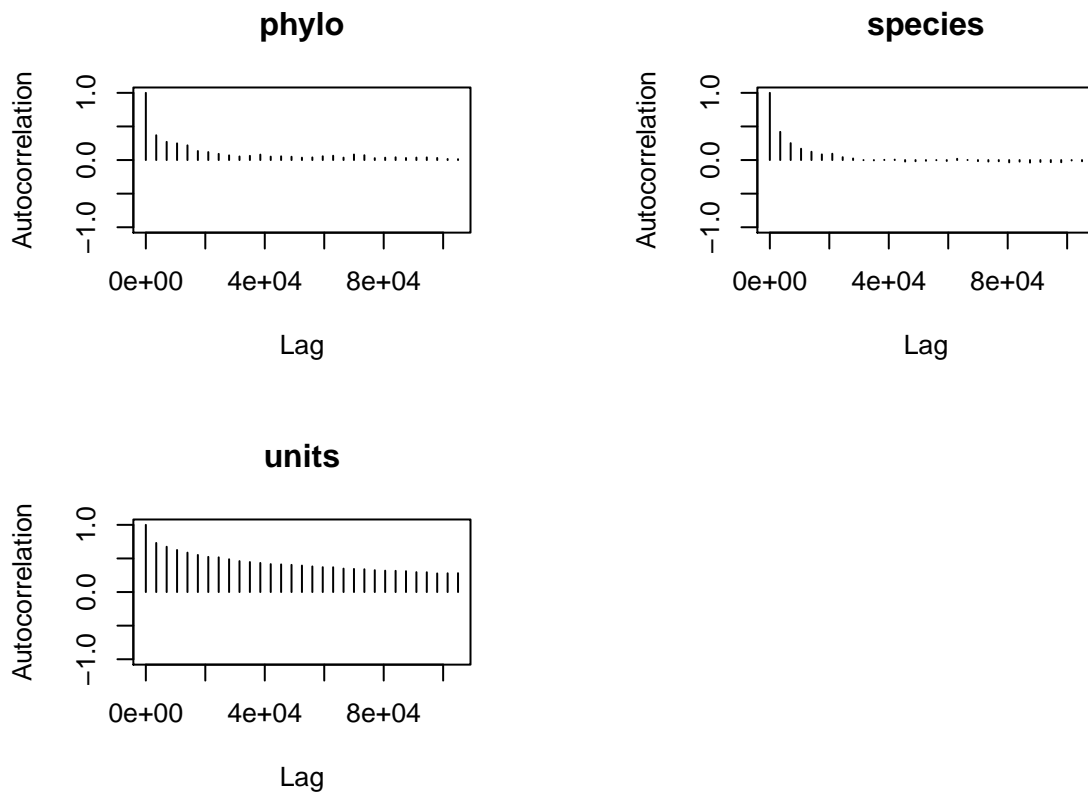
<.05 after Lag 10000 = low autocorrelation

Visualize autocorrelation

```
par(mar=c(5,5,4,4))
autocorr.plot(mcmc1$Sol[,1])
```



```
autocorr.plot(mcmc1$VCV)
```

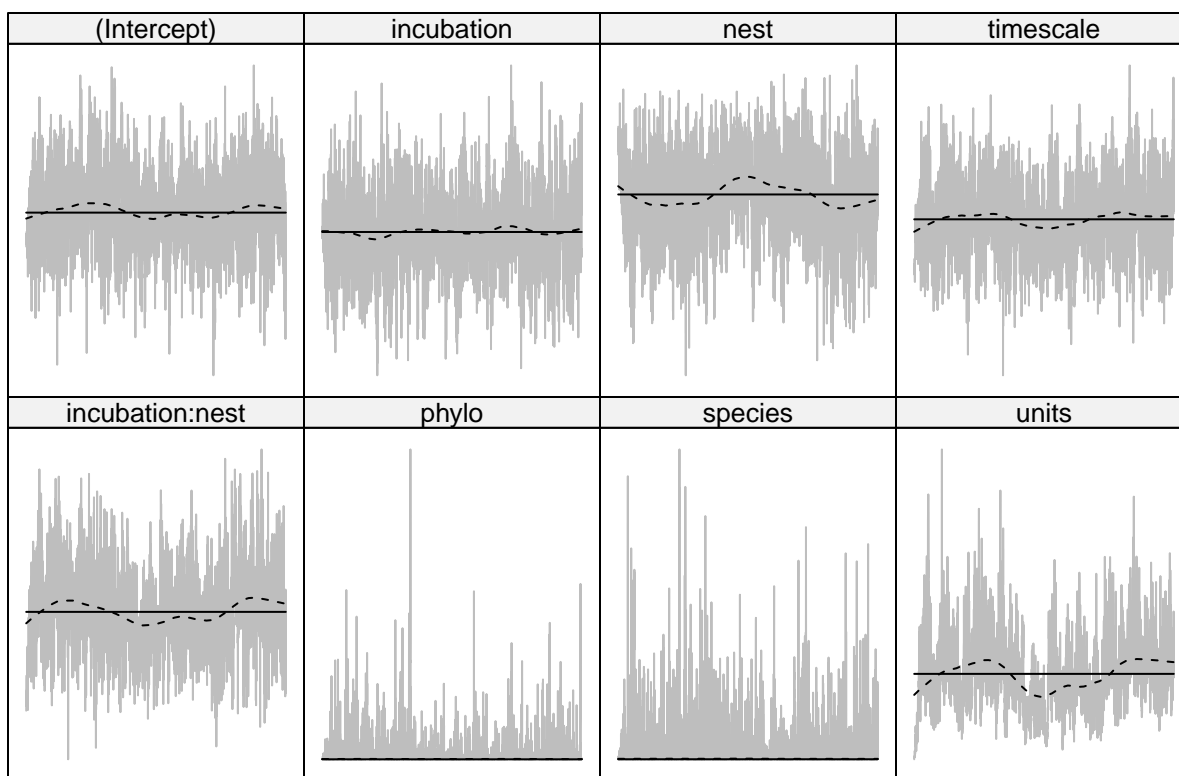


No pattern of autocorrelation, as it curves quickly to 0.

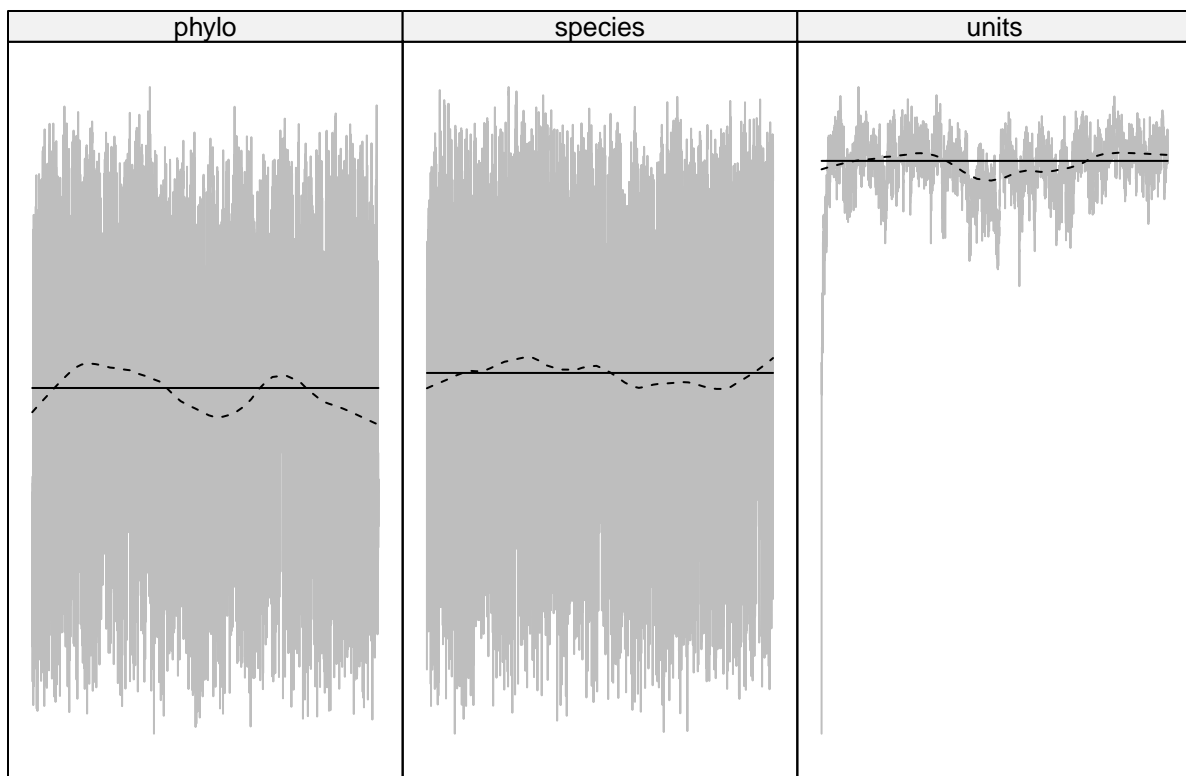
View traces to make sure there are no patterns or autocorrelation

```
allChains <- as.mcmc(cbind(mcmc1$Sol,mcmc1$VCV))
plotTrace(allChains)
```





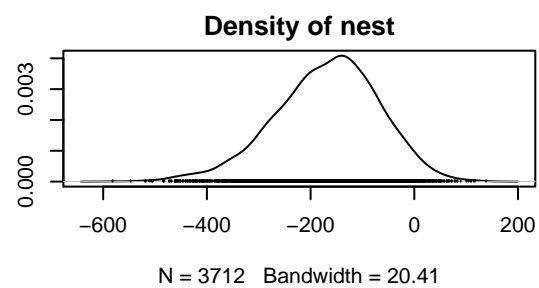
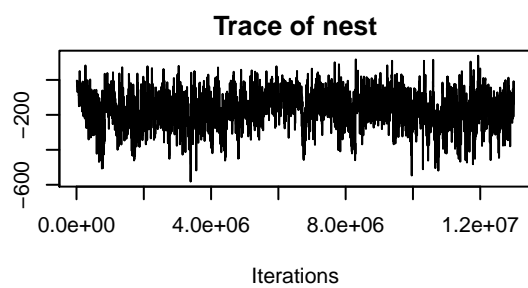
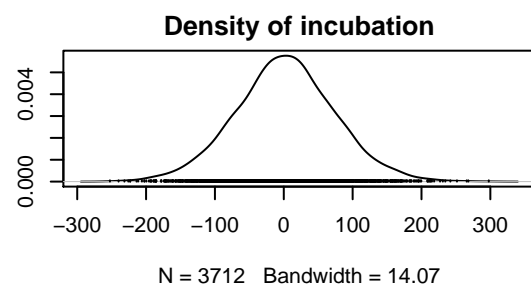
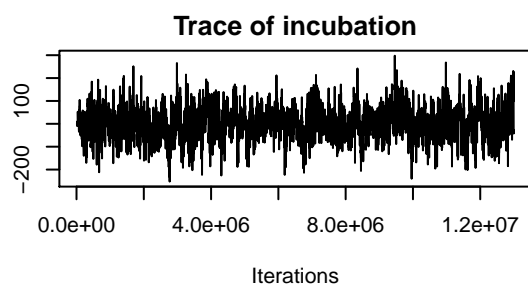
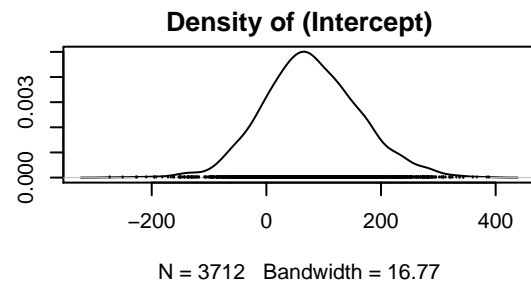
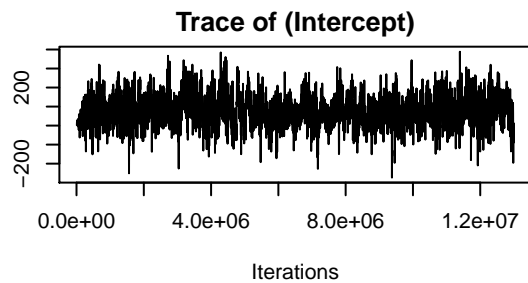
```
logChain<-log10(mcmc1$VCV)
plotTrace(logChain)
```

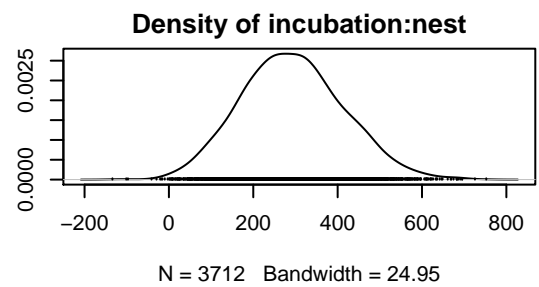
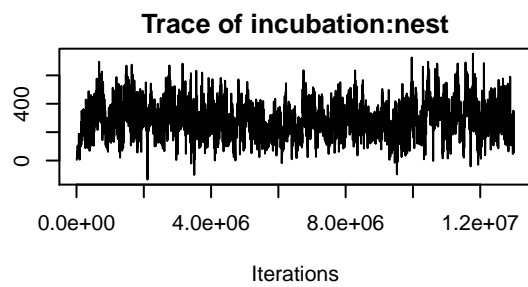
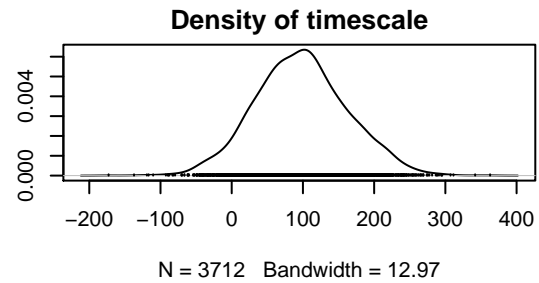
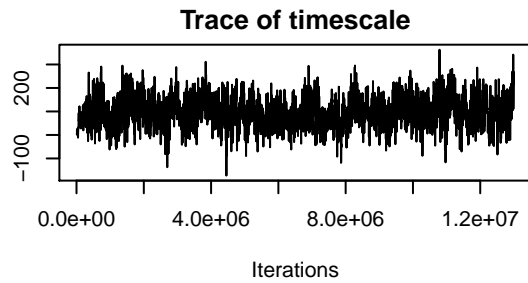


### 3.2 Check convergence

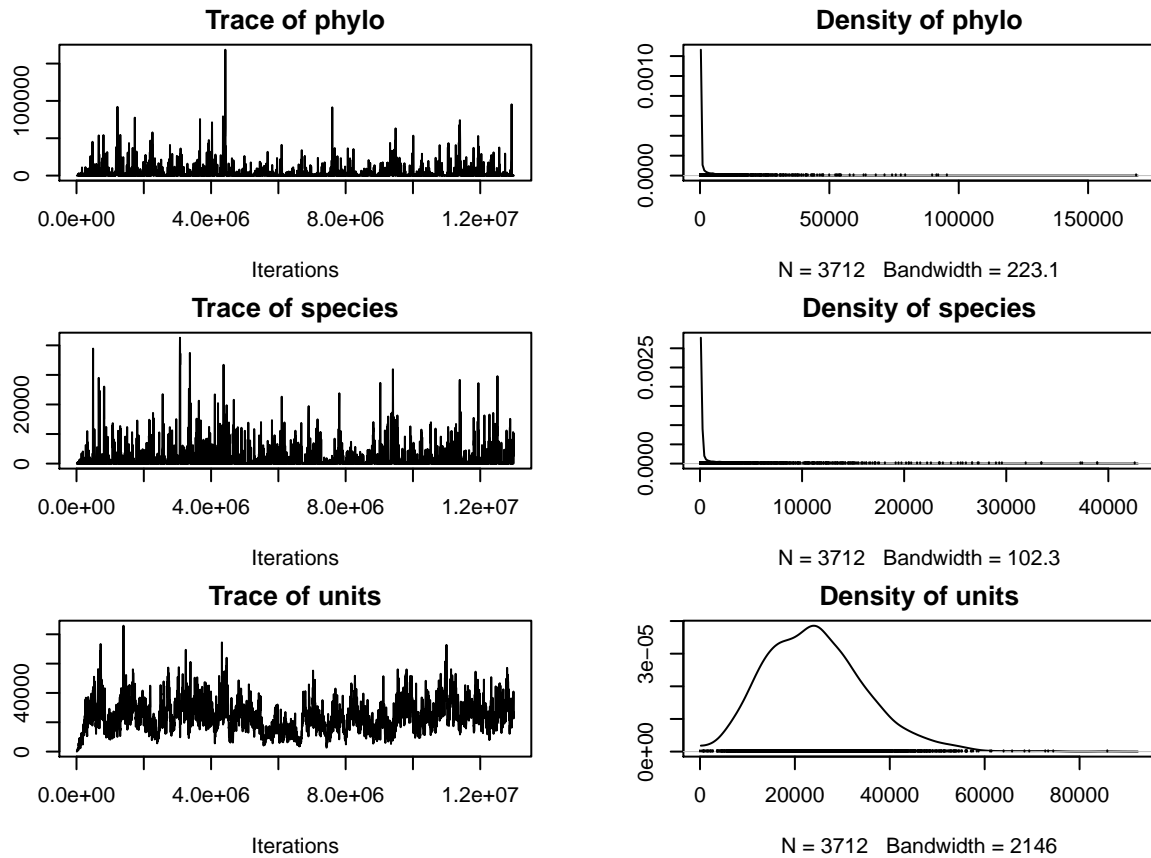
Plot the trace and density of the inferred intercepts and variances

```
par(mar=c(4,4,2,2))
plot(mcmc1$Sol) # intercept
```





```
plot(mcmc1$VCV) # variance
```



Looks like a "hairy caterpillar, suggesting good convergence.

### 3.3 Gelman-Rubin Statistics

Comparison of the same model run multiple times

Run the same model two more times

```
# Model 2
mcmc2 <- MCMCglmm(seasonalchange ~ incubation * nest + timescale,
  random = ~ phylo + species,
  family = "categorical",
  data = df,
  prior = prior2,
  ginverse = list(phylo = inv.phylo$Ainv),
  nitt=13000000, burnin=10000, thin=3500,
  verbose = FALSE)

# Model 3
mcmc3 <- MCMCglmm(seasonalchange ~ incubation * nest + timescale,
  random = ~ phylo + species,
  family = "categorical",
  data = df,
  prior = prior2,
  ginverse = list(phylo = inv.phylo$Ainv),
```

```
nitt=13000000,burnin=10000,thin=3500,
verbose = FALSE)
```

Compare posterior mode and mean for the three different runs (mean and posterior mode of each model should be similar)

```
m1 <- mean(mcmc1$Sol[,1])
pm1 <- posterior.mode(mcmc1$Sol[,1])
m2 <- mean(mcmc2$Sol[,1])
pm2 <- posterior.mode(mcmc2$Sol[,1])
m3 <- mean(mcmc3$Sol[,1])
pm3 <-posterior.mode(mcmc3$Sol[,1])
stat <- c("mean","post.mode")
mcmc.1 <- c(m1,pm1)
mcmc.2 <- c(m2,pm2)
mcmc.3 <- c(m3,pm3)
data.frame(stat,mcmc.1,mcmc.2,mcmc.3)
```

```
##          stat  mcmc.1  mcmc.2  mcmc.3
##          mean 78.32662 77.85107 76.93800
## var1 post.mode 72.61910 39.11786 85.50209
```

Posterior modes and means are similar across runs

Gelman-Rubin statistics: the potential scale reduction factor (PSRF) should be less than 1.1 among chains

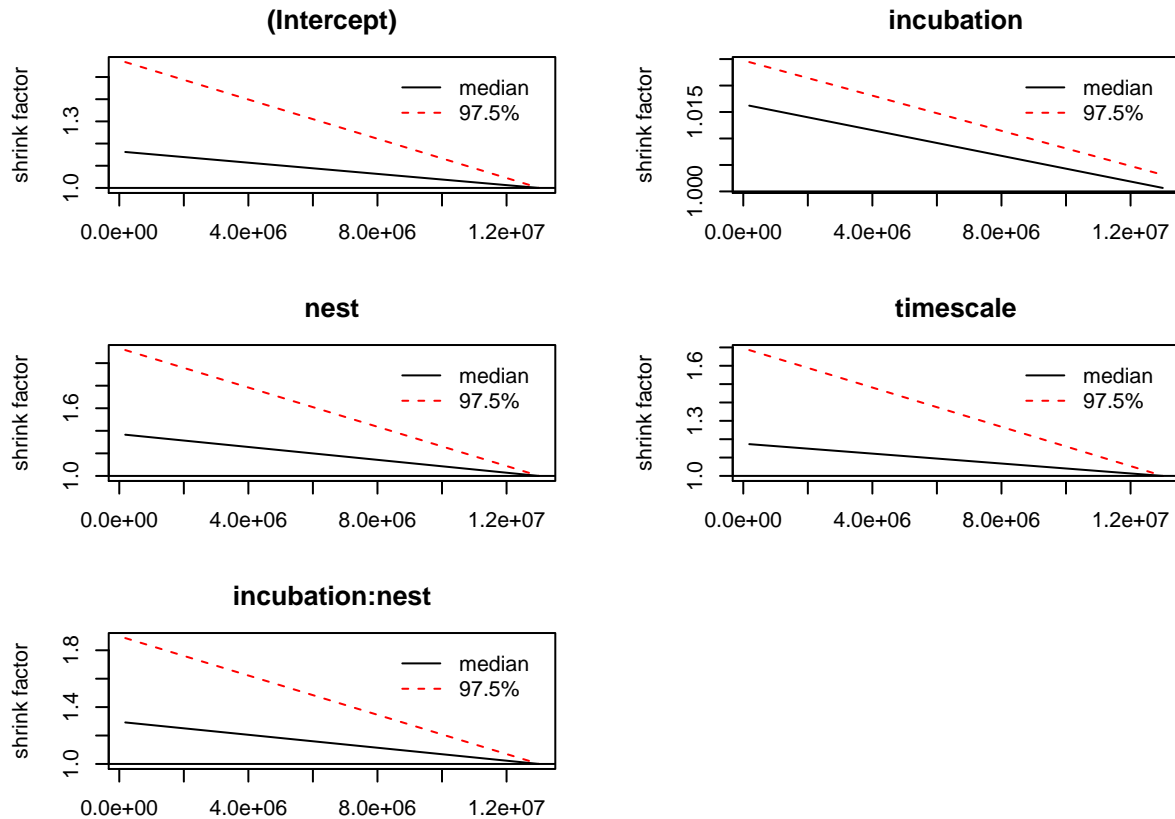
```
# To check for independent chain posterior convergence
model.all <- mcmc.list(mcmc1$Sol,mcmc2$Sol,mcmc3$Sol)
gelman.diag(model.all, confidence = 0.95, transform=FALSE, autoburnin=TRUE)
```

```
## Potential scale reduction factors:
##
##          Point est. Upper C.I.
## (Intercept)          1          1
## incubation           1          1
## nest                 1          1
## timescale            1          1
## incubation:nest      1          1
##
## Multivariate psrf
##
## 1
```

We can see that these are very close to 1, suggesting good convergence.

Gelman plots

```
par(mar=c(3,5,3,2))
gelman.plot(model.all)
```



This is also evident when looking at the plot of the values generation per generation as the mixing is very good.

## 4 Results

Summary of the three models

```
summary(mcmc1)
```

```
##
## Iterations = 10001:12998501
## Thinning interval = 3500
## Sample size = 3712
##
## DIC: 1.557043
##
## G-structure: ~phylo
##
##      post.mean  1-95% CI u-95% CI eff.samp
## phylo      3177 0.0003263   18275    586.5
##
##      ~species
##
##      post.mean  1-95% CI u-95% CI eff.samp
```

```

## species      1512 0.0002442      9214      1038
##
## R-structure: ~units
##
##      post.mean l-95% CI u-95% CI eff.samp
## units      24348      5619      45080      100.7
##
## Location effects: seasonalchange ~ incubation * nest + timescale
##
##      post.mean l-95% CI u-95% CI eff.samp      pMCMC
## (Intercept)      78.327  -81.533   245.014      560.3 0.32920
## incubation      2.065  -147.534   141.753      476.5 0.97737
## nest      -169.020  -369.106    19.311      374.2 0.06573 .
## timescale      97.736  -25.892   226.346      397.1 0.11584
## incubation:nest  292.581    64.195   533.173      317.4 0.00539 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```
summary(mcmc2)
```

```

##
## Iterations = 10001:12998501
## Thinning interval = 3500
## Sample size = 3712
##
## DIC: 1.563587
##
## G-structure: ~phylo
##
##      post.mean l-95% CI u-95% CI eff.samp
## phylo      2653 0.0002265    16205      3712
##
##      ~species
##
##      post.mean l-95% CI u-95% CI eff.samp
## species      1585 0.0002954      9932      3712
##
## R-structure: ~units
##
##      post.mean l-95% CI u-95% CI eff.samp
## units      23579      4298      43148      3712
##
## Location effects: seasonalchange ~ incubation * nest + timescale
##
##      post.mean l-95% CI u-95% CI eff.samp      pMCMC
## (Intercept)      77.851  -80.702   249.835      3712 0.32112
## incubation      -1.104  -146.047   147.458      3712 0.99677
## nest      -165.874  -352.363    27.980      3712 0.06627 .
## timescale      97.781  -15.986   231.931      3712 0.10884
## incubation:nest  292.488    43.720   520.924      3712 0.00862 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```



```
summary(mcmc3)
```

```
##
## Iterations = 10001:12998501
## Thinning interval = 3500
## Sample size = 3712
##
## DIC: 1.563786
##
## G-structure: ~phylo
##
##      post.mean  l-95% CI u-95% CI eff.samp
## phylo      3052 0.0002712   18357    3119
##
##      ~species
##
##      post.mean  l-95% CI u-95% CI eff.samp
## species      1386 0.0002861    8838    3712
##
## R-structure: ~units
##
##      post.mean l-95% CI u-95% CI eff.samp
## units      23642    5673   44218    3712
##
## Location effects: seasonalchange ~ incubation * nest + timescale
##
##      post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept)    76.938  -85.105   241.114    3712 0.3222
## incubation     -1.363 -152.116   147.533    3712 0.9962
## nest          -168.033 -374.114    21.384    3448 0.0630 .
## timescale      97.847  -21.227   228.832    3712 0.1169
## incubation:nest 294.940   71.690   543.743    3458 0.0113 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

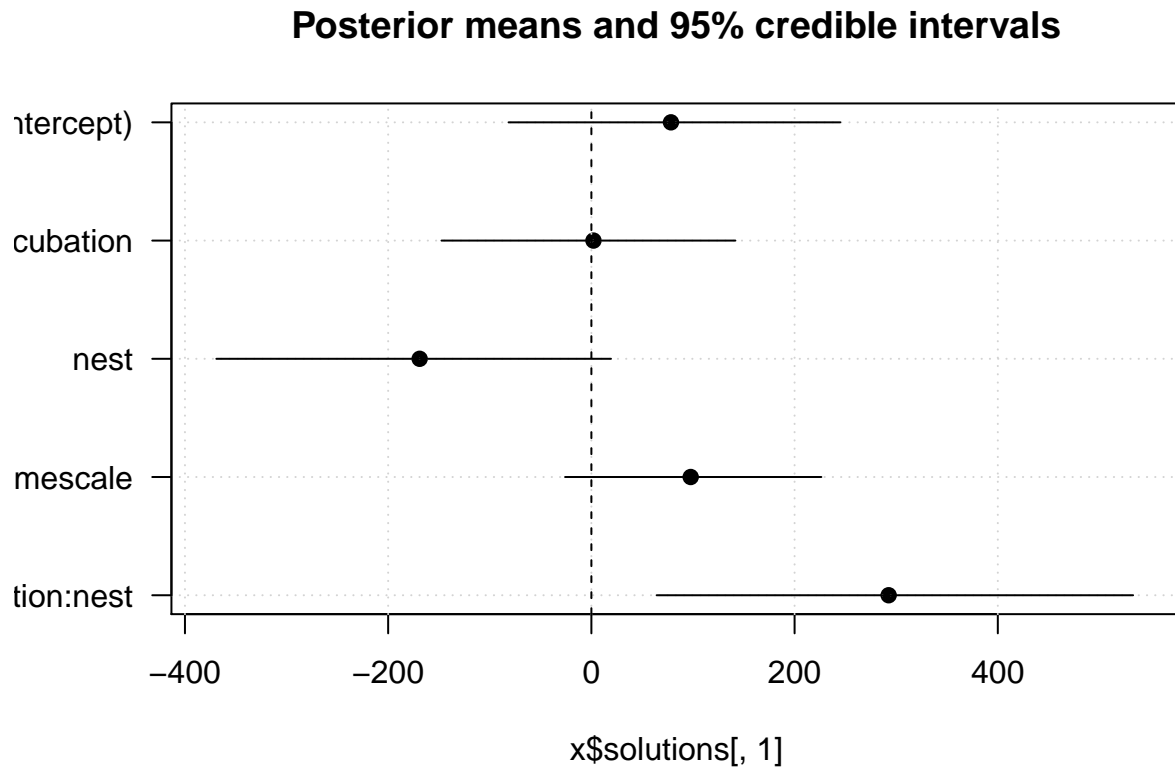
The effective sample sizes are all relatively good (higher than the value recommended by the function `raftery.diag`), both for random and fixed effects.

The three runs give the same results but values differ slightly. The second and third models were run only for verification purposes (Gelman-Rubin statistics). We report only the results of the first model (i.e. `mcmc1`).

## 4.1 Fixed effects

Plot the parameter estimates and 95% CIs

```
plot.estimates(mcmc1)
```



## 4.2 Random effects

See below.

## 5 Random effects

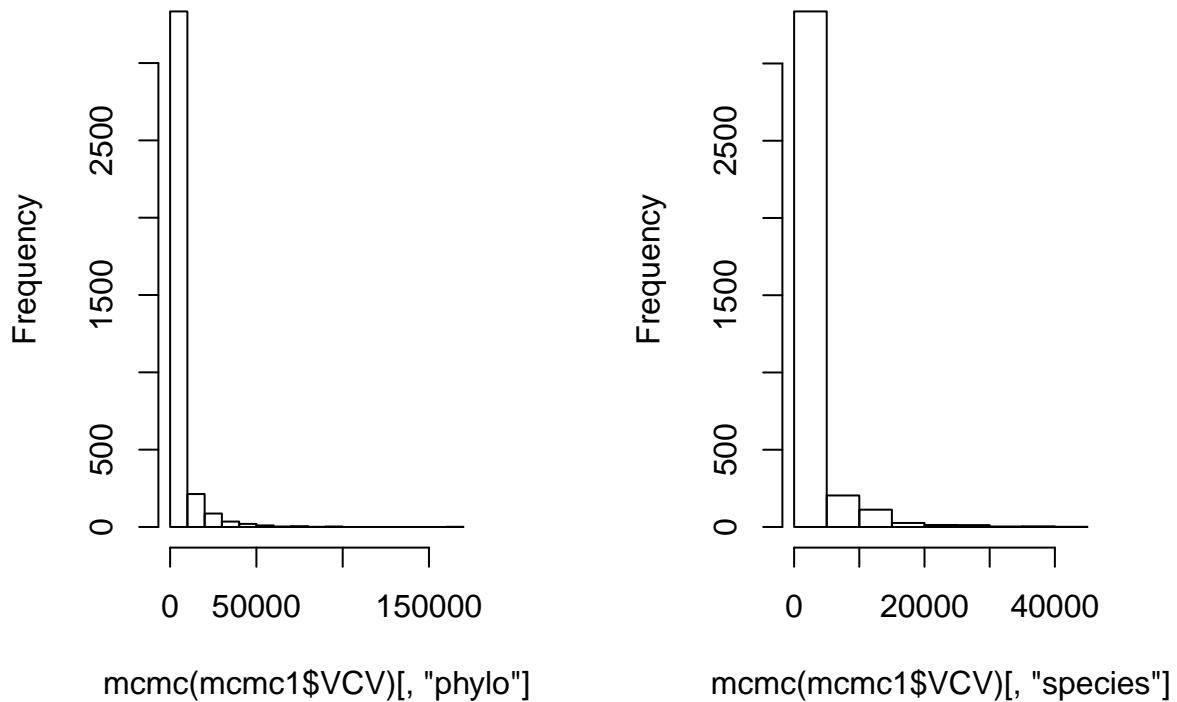
We included phylogeny and species as random effects. Let's see if they have an effect on the probability to detect seasonal differences in preen oil composition.

### 5.1 Posterior distribution

Plot the posterior distribution as a histogram to check for significance and whether it's been well estimated or not.

```
par(mfrow = c(1,2),mar = c(6, 6, 2, 2)) # plot panel
hist(mcmc(mcmc1$VCV)[,"phylo"]) # non-significant
hist(mcmc(mcmc1$VCV)[,"species"]) # non-significant
```

## Histogram of `mcmc(mcmc1$VCV)[, "phylo"]`, histogram of `mcmc(mcmc1$VCV)[, "species"]`



Posterior distribution is pushed up against 0 for both random effects (phylogenetic relatedness and species), which therefore seem to have little effect on seasonal variation in preen oil composition. Indeed, because variance cannot be zero, if the mean value is pushed up against zero, it reflects a non-significant effect. The large spread of the histogram indicate that the distribution is not well estimated (poor precision).

## 5.2 Proportion of the total variance explained by the random effects

To evaluate variance explained by the random effects, it is useful to look at the relative proportion of the variance explained by each effect and by the residuals (units).

```
# Proportion of variance explained by random factors
rand <- mcmc1$VCV/apply(mcmc1$VCV,1,sum)
# Get median values (50%) and 95% quantiles
apply(rand,2,function(c) quantile(c,probs = c(0.025,0.5,0.975)))
```

```
##           phylo           species      units
## 2.5%  7.275274e-08 5.956063e-08 0.3485261
## 50%   6.386695e-04 3.836737e-04 0.9756401
## 97.5% 5.888437e-01 4.636505e-01 0.9999983
```

```
# Get the mean value
apply(rand,2,mean)
```

```
##      phylo      species      units
## 0.07941296 0.05301837 0.86756867
```

The large confidence intervals confirm the poor precision of the estimates.

### 5.3 Inclusion of random effects and fit of the model

Run the different models (phylo only, species only, no random effect) to check if their inclusion in the model improves its fit. Note that a specific prior is built for each model.

Model phylo only

```
prior1 <- list(R=list(V=1,nu=0.002),G=list(G1=list(V=1,nu=0.002)))

mcmc.phylo <- MCMCglmm(seasonalchange ~ incubation * nest + timescale,
  random = ~phylo,
  family = "categorical",
  data = df,
  prior = prior1,
  ginverse = list(phylo = inv.phylo$Ainv),
  nitt=13000000,burnin=10000,thin=3500,
  verbose = FALSE)

summary(mcmc.phylo)
```

```
##
## Iterations = 10001:12998501
## Thinning interval = 3500
## Sample size = 3712
##
## DIC: 1.573732
##
## G-structure: ~phylo
##
##      post.mean  l-95% CI u-95% CI eff.samp
## phylo      3145 0.0001892   18542    3712
##
## R-structure: ~units
##
##      post.mean l-95% CI u-95% CI eff.samp
## units      24375    4419   43657    3712
##
## Location effects: seasonalchange ~ incubation * nest + timescale
##
##      post.mean l-95% CI u-95% CI eff.samp  pMCMC
## (Intercept)    74.973  -69.379  257.028    3712 0.33944
## incubation    -1.355 -143.616  137.782    3712 0.97198
## nest        -167.736 -371.250    9.751    3712 0.05873 .
## timescale     97.125  -19.982  227.234    3611 0.11692
## incubation:nest 296.074   70.979  542.763    3941 0.00916 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model species only

```

mcmc.species <- MCMCglmm(seasonalchange ~ incubation * nest + timescale,
  random = ~species,
  family = "categorical",
  data = df,
  prior = prior1,
  ginverse = list(phylo = inv.phylo$Ainv),
  nitt=13000000,burnin=10000,thin=3500,
  verbose = FALSE)
summary(mcmc.species)

```

```

##
## Iterations = 10001:12998501
## Thinning interval = 3500
## Sample size = 3712
##
## DIC: 1.585432
##
## G-structure: ~species
##
##      post.mean l-95% CI u-95% CI eff.samp
## species      1766 0.000303    10781    3531
##
## R-structure: ~units
##
##      post.mean l-95% CI u-95% CI eff.samp
## units      23835    5374    43354    3712
##
## Location effects: seasonalchange ~ incubation * nest + timescale
##
##      post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept)    80.457  -58.191  238.554    3712 0.27748
## incubation     -1.864 -144.673  139.280    3712 0.98976
## nest          -168.669 -355.406    3.447    3712 0.04580 *
## timescale       98.481  -16.224  232.339    3712 0.10237
## incubation:nest 292.878   64.722  519.452    3405 0.00485 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Model no random effect

```

prior0 <- list(R=list(V=1,nu=0.002))

mcmc.norandom <- MCMCglmm(seasonalchange ~ incubation * nest + timescale,
  family = "categorical",
  data = df,
  prior = prior0,
  ginverse = list(phylo = inv.phylo$Ainv),
  nitt=13000000,burnin=10000,thin=3500,
  verbose = FALSE)

summary(mcmc.norandom)

```

```
##
```

```
## Iterations = 10001:12998501
## Thinning interval = 3500
## Sample size = 3712
##
## DIC: 1.599972
##
## R-structure: ~units
##
##      post.mean l-95% CI u-95% CI eff.samp
## units      25229      7055      47027      3712
##
## Location effects: seasonalchange ~ incubation * nest + timescale
##
##      post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept)      79.024  -64.887  225.308    3712 0.26562
## incubation      -4.963 -148.269   134.308    3712 0.93373
## nest          -169.477 -351.273    3.817    3712 0.04041 *
## timescale       98.505  -15.704   223.259    3712 0.09052 .
## incubation:nest  298.306   75.073   533.265    3712 0.00808 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Compare the different models using the Deviance Information Criterion (DIC; lower values are best).

```
# Compare fit of the models (DIC)
data.frame(models=c("mcmc.norandom", "mcmc.phylo", "mcmc.species", "mcmc1"),
            random.effects=c("NA", "phylo", "species", "phylo+species"),
            DIC=c(mcmc.norandom$DIC, mcmc.phylo$DIC, mcmc.species$DIC, mcmc1$DIC))
```

```
##      models random.effects      DIC
## 1 mcmc.norandom      NA 1.599972
## 2 mcmc.phylo      phylo 1.573732
## 3 mcmc.species      species 1.585432
## 4 mcmc1 phylo+species 1.557043
```

Inclusion of both phylogeny and species increases the fit of the model (lower DIC).

## 6 Focus on the interaction nest:incubation

Split the data into nonground-nesting and ground-nesting species and run separate analyses for the effect of incubation.

Split the data

```
# Data with only ground nesting species
df_g <- df[which(df$nest==1),]

# Data with only nonground nesting species
df_ng <- df[which(df$nest==0),]
```

Prepare phylogenetic matrices corresponding to both data sets

```

# Trim consensus tree
subtree_g <- drop.tip(consensustree, tip=setdiff(consensustree$tip.label,df_g$phylo)) # ground nesting
subtree_ng <- drop.tip(consensustree, tip=setdiff(consensustree$tip.label,df_ng$phylo)) # nonground nes

# Check that the trees cover all the species
# Ground nesting species
species_g <- df_g$phylo
setdiff(species_g, as.character(subtree_g$tip.label))
setdiff(as.character(subtree_g$tip.label),species_g)
# Nonground nesting speices
species_ng <- df_ng$phylo
setdiff(species_ng, as.character(subtree_ng$tip.label))
setdiff(as.character(subtree_ng$tip.label),species_ng)

# Dealing with polytomies
# Ground nesting species
is.binary.tree(subtree_g) # FALSE > there are some polytomies
subtree_g_random <- multi2di(subtree_g,random=TRUE) # randomization to take care of the polytomies
is.binary.tree(subtree_g_random) # TRUE > no more polytomies
# Nonground nesting speices
is.binary.tree(subtree_ng) # FALSE > there are some polytomies
subtree_ng_random <- multi2di(subtree_ng,random=TRUE) # randomization to take care of the polytomies
is.binary.tree(subtree_ng_random) # TRUE > no more polytomies

# Compute branch lengths of tree
phylo_branch_g <- compute.brlen(subtree_g_random, method = "Grafen", power = 1)
phylo_branch_ng <- compute.brlen(subtree_ng_random, method = "Grafen", power = 1)

# Calculate the inverse of the matrix of phylogenetic relatedness (to be used in MCMCglmm)
inv.phylo_g <- inverseA(phylo_branch_g,nodes="TIPS",scale=TRUE)
inv.phylo_ng <- inverseA(phylo_branch_ng,nodes="TIPS",scale=TRUE)

```

Model on ground nesting species

```

mcmc_g <- MCMCglmm(seasonalchange ~ incubation + timescale,
                  random = ~ phylo + species,
                  family = "categorical",
                  data = df_g,
                  prior = prior2,
                  ginverse = list(phylo = inv.phylo_g$Ainv),
                  nitt=13000000,burnin=10000,thin=3500,
                  verbose = FALSE)
summary(mcmc_g)

```

```

##
## Iterations = 10001:12998501
## Thinning interval = 3500
## Sample size = 3712
##
## DIC: 0.6735118
##
## G-structure: ~phylo
##

```

```
##           post.mean 1-95% CI u-95% CI eff.samp
## phylo           637 0.0001809      3069      3712
##
##           ~species
##
##           post.mean 1-95% CI u-95% CI eff.samp
## species          607.1 0.0002212      3032      3712
##
## R-structure: ~units
##
##           post.mean 1-95% CI u-95% CI eff.samp
## units           21260      771    43030      3712
##
## Location effects: seasonalchange ~ incubation + timescale
##
##           post.mean 1-95% CI u-95% CI eff.samp pMCMC
## (Intercept)   -20.097 -209.251  159.003      3712  0.846
## incubation    283.038   96.254  485.362      3712 <3e-04 ***
## timescale      2.202 -185.864  187.613      3712  0.987
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model on nonground nesting species

```
mcmc_ng <- MCMCglmm(seasonalchange ~ incubation + timescale,
  random = ~ phylo + species,
  family = "categorical",
  data = df_ng,
  prior = prior2,
  ginverse = list(phylo = inv.phylo_ng$Ainv),
  nitt=13000000, burnin=10000, thin=3500,
  verbose = FALSE)
summary(mcmc_ng)
```

```
##
## Iterations = 10001:12998501
## Thinning interval = 3500
## Sample size = 3712
##
## DIC: 2.018305
##
## G-structure: ~phylo
##
##           post.mean 1-95% CI u-95% CI eff.samp
## phylo           31783 0.0002383   124494    1456
##
##           ~species
##
##           post.mean 1-95% CI u-95% CI eff.samp
## species          15373 0.0002658    58078    1445
##
## R-structure: ~units
##
```



```

##           post.mean 1-95% CI u-95% CI eff.samp
## units          4376 0.0002082    19605      2160
##
## Location effects: seasonalchange ~ incubation + timescale
##
##           post.mean 1-95% CI u-95% CI eff.samp pMCMC
## (Intercept)   -37.68 -276.77   192.05     3319 0.748
## incubation     53.57  -57.61   186.29     2489 0.286
## timescale     225.01   45.99   456.47     1362 0.007 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```