

# The influence of phylogeny and life history strategies on adult telomere lengths among bird species - supp1 - TEL

09/03/2020

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## Load required packages

```
library(ape)
library(apTreeshape)
library(caper)
library(MCMCglmm)
library(phytools)
library(sjPlot)
library(stargazer)
library(dplyr)
library(ggplot2)
```

## Set working directory and Load the phylogenetic trees (n=100)

### Load the consensus tree (n=1 out of 100)

```
library(ape)
Bird.phylo<-read.tree("/home/quentin/Documents/disque D/collab/FC/meta-analyse-review/2020-06-12/consensus.tre")
Bird.phylo
```

```
##
## Phylogenetic tree with 53 tips and 48 internal nodes.
##
## Tip labels:
## Macronectes_halli, Macronectes_giganteus, Fulmarus_glacialis, Calonectris_diomedea, Diomedea_exulans
##
## Rooted; includes branch lengths.
```

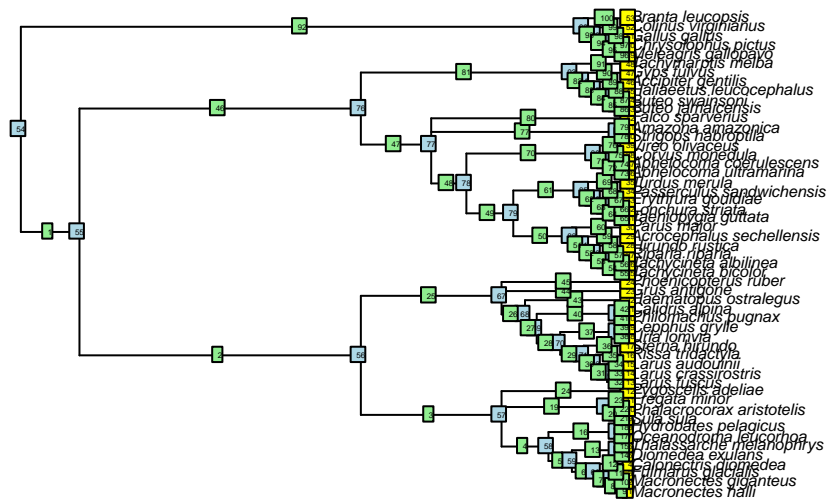
```
str(Bird.phylo)

## List of 4
## $ edge      : int [1:100, 1:2] 54 55 56 57 58 59 60 61 62 62 ...
## $ edge.length: num [1:100] 0.0962 0.4615 0.2308 0.0769 0.0385 ...
## $ Nnode     : int 48
## $ tip.label  : chr [1:53] "Macronectes_halli" "Macronectes_giganteus" "Fulmarus_glacialis" "Calonectris_diomedea" "Diomedea_exulans"
## - attr(*, "class")= chr "phylo"
## - attr(*, "order")= chr "cladewise"
```

```
names(Bird.phylo)
```

```
## [1] "edge"          "edge.length" "Nnode"       "tip.label"
```

```
plot(Bird.phylo,cex=0.5)  
tiplabels(cex=0.25)  
nodelabels(cex=0.25)  
edgelabels(cex=0.25)
```



```
summary(Bird.phylo)
```

```
##  
## Phylogenetic tree: Bird.phylo  
##  
## Number of tips: 53  
## Number of nodes: 48  
## Branch lengths:  
## mean: 0.07980769  
## variance: 0.01540834  
## distribution summary:  
## Min. 1st Qu. Median 3rd Qu. Max.  
## 0.01923077 0.01923077 0.03846154 0.07692308 0.92307692  
## No root edge.  
## First ten tip labels: Macronectes_halli
```

```
##           Macronectes_giganteus
##           Fulmarus_glacialis
##           Calonectris_diomedea
##           Diomedea_exulans
##           Thalassarche_melanophrys
##           Oceanodroma_leucorhoa
##           Hydrobates_pelagicus
##           Sula_sula
##           Phalacrocorax_aristotelis
## No node labels.
```

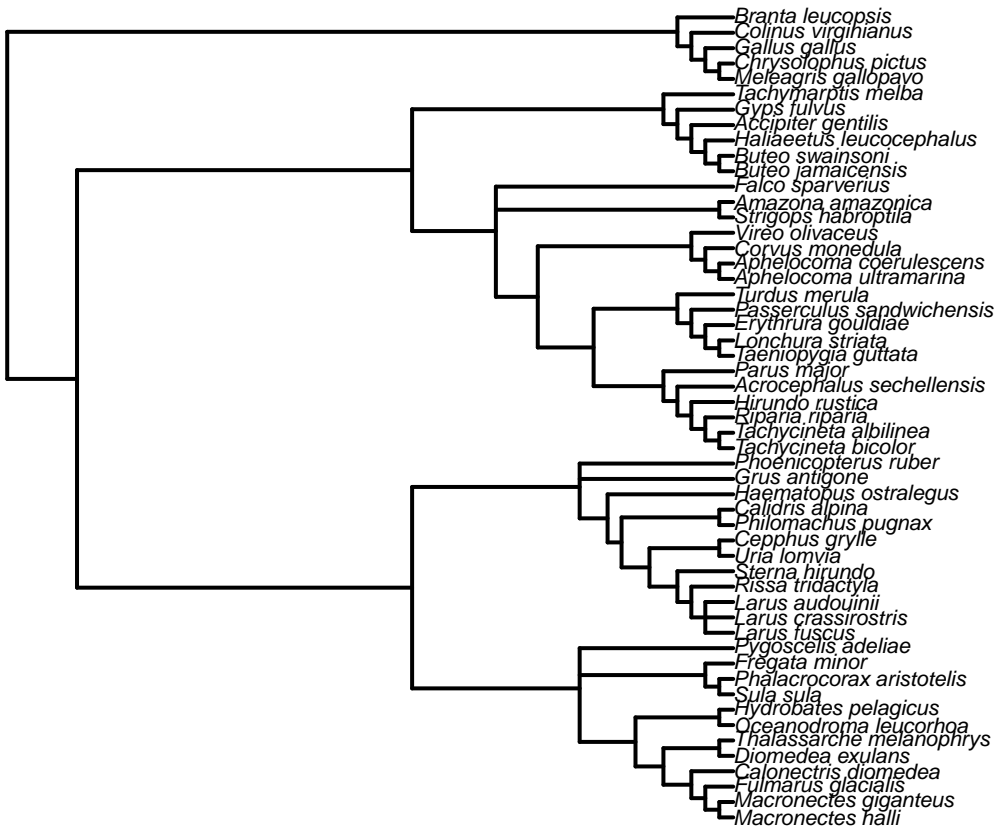
```
check.species <- function(x) {any(x==Bird.phylo$tip.label)}
print(check.species)
```

```
## function(x) {any(x==Bird.phylo$tip.label)}
```

```
is.ultrametric(Bird.phylo)
```

```
## [1] TRUE
```

```
plot(Bird.phylo,no.margin=TRUE,edge.width=2,cex=0.7)
```



```
str(Bird.phylo)
```

```
## List of 4
## $ edge      : int [1:100, 1:2] 54 55 56 57 58 59 60 61 62 62 ...
## $ edge.length: num [1:100] 0.0962 0.4615 0.2308 0.0769 0.0385 ...
## $ Nnode     : int 48
## $ tip.label  : chr [1:53] "Macronectes_halli" "Macronectes_giganteus" "Fulmarus_glacialis" "Calonec
## - attr(*, "class")= chr "phylo"
## - attr(*, "order")= chr "cladewise"
```

```
summary(Bird.phylo)
```

```
##
## Phylogenetic tree: Bird.phylo
##
## Number of tips: 53
## Number of nodes: 48
## Branch lengths:
## mean: 0.07980769
## variance: 0.01540834
## distribution summary:
## Min. 1st Qu. Median 3rd Qu. Max.
## 0.01923077 0.01923077 0.03846154 0.07692308 0.92307692
## No root edge.
## First ten tip labels: Macronectes_halli
##                        Macronectes_giganteus
##                        Fulmarus_glacialis
##                        Calonectris_diomedea
##                        Diomedea_exulans
##                        Thalassarche_melanophrys
##                        Oceanodroma_leucorhoa
##                        Hydrobates_pelagicus
##                        Sula_sula
##                        Phalacrocorax_aristotelis
## No node labels.
```

```
IA <- inverseA(Bird.phylo, nodes = "TIPS")
IAasreml <- sm2asreml(IA$Ainv, IA$node.names)
summary(IAasreml)
```

```
##      Row      Column      Ainverse
## Min.   : 1.00   Min.   : 1.00   Min.   : -25.367524
## 1st Qu.:24.00   1st Qu.: 7.00   1st Qu.: -0.026630
## Median :35.00   Median :15.00   Median : -0.000968
## Mean   :32.58   Mean   :17.09   Mean    : 0.441079
## 3rd Qu.:42.00   3rd Qu.:25.00   3rd Qu.: -0.000160
## Max.   :53.00   Max.   :53.00   Max.    : 30.973672
```

## Load the dataset

```
Bird.data <- read.csv("/home/quentin/Documents/disque D/collab/FC/meta-analyse-review/2020-06-12/2020-1  
Bird.data$animal<-Bird.data$Latin  
Bird.data$Latin %in% Bird.phylo$tip.label
```

```
## [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE  
## [16] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE  
## [31] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE  
## [46] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
```

```
dim(Bird.data)
```

```
## [1] 53 64
```

## set.seed

```
set.seed(36849)
```

## Mean telomere length in adult and the historical relationships among the species, as reflected by the phylogeny

```
p.var1=var(Bird.data$Mean.telomere.adult)  
prior1 <-list(G=list(G1=list(V=(diag(1)*0.2*p.var1),n=1)),  
              R=list(V=(0.8*p.var1),n=2))  
set.seed(1)  
m11.mcmc <- MCMCgllmm(Mean.telomere.adult ~1, random = ~animal, mev=Bird.data$mev ,  
                     data = Bird.data, prior=prior1,  
                     pedigree = Bird.phylo, nitt = 105000, thin = 50, burnin = 5000,  
                     pr = TRUE, pl = TRUE, verbose = TRUE, DIC = TRUE)
```

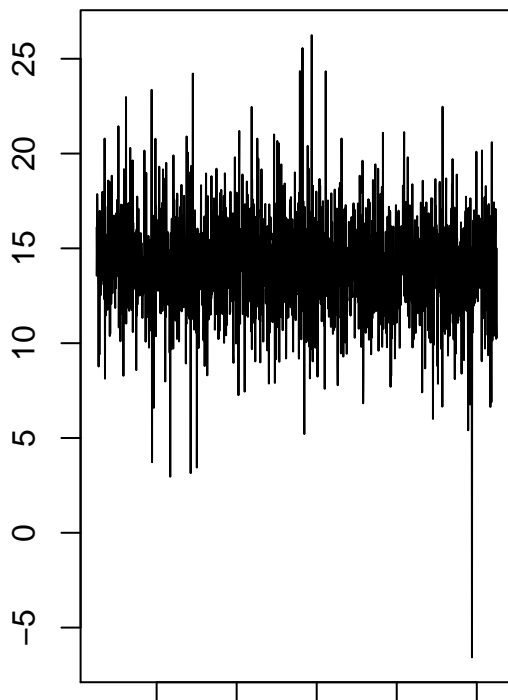
```
summary(m11.mcmc)
```

```
##  
## Iterations = 5001:104951  
## Thinning interval = 50  
## Sample size = 2000  
##  
## DIC: 393.327  
##  
## G-structure: ~animal  
##  
##          post.mean l-95% CI u-95% CI eff.samp  
## animal      15.91    0.8529    49.39     1398
```

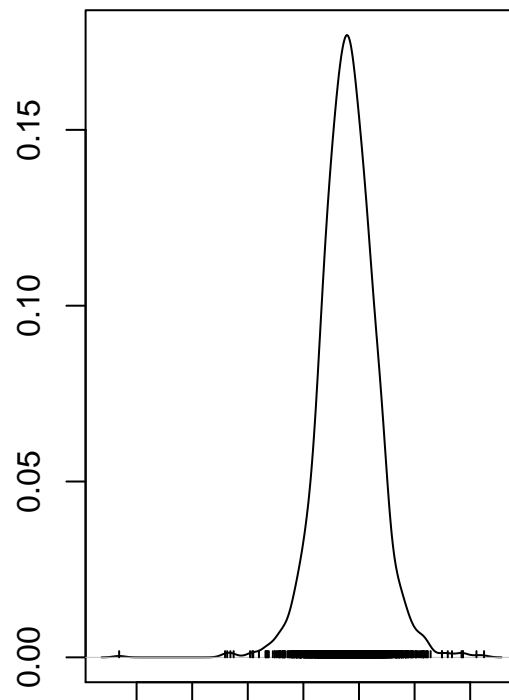
```
##
## R-structure: ~units
##
##      post.mean l-95% CI u-95% CI eff.samp
## units    90.35   58.14   128.1    2000
##
## Location effects: Mean.telomere.adult ~ 1
##
##      post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept)  14.030   8.928  18.690    2000 0.001 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

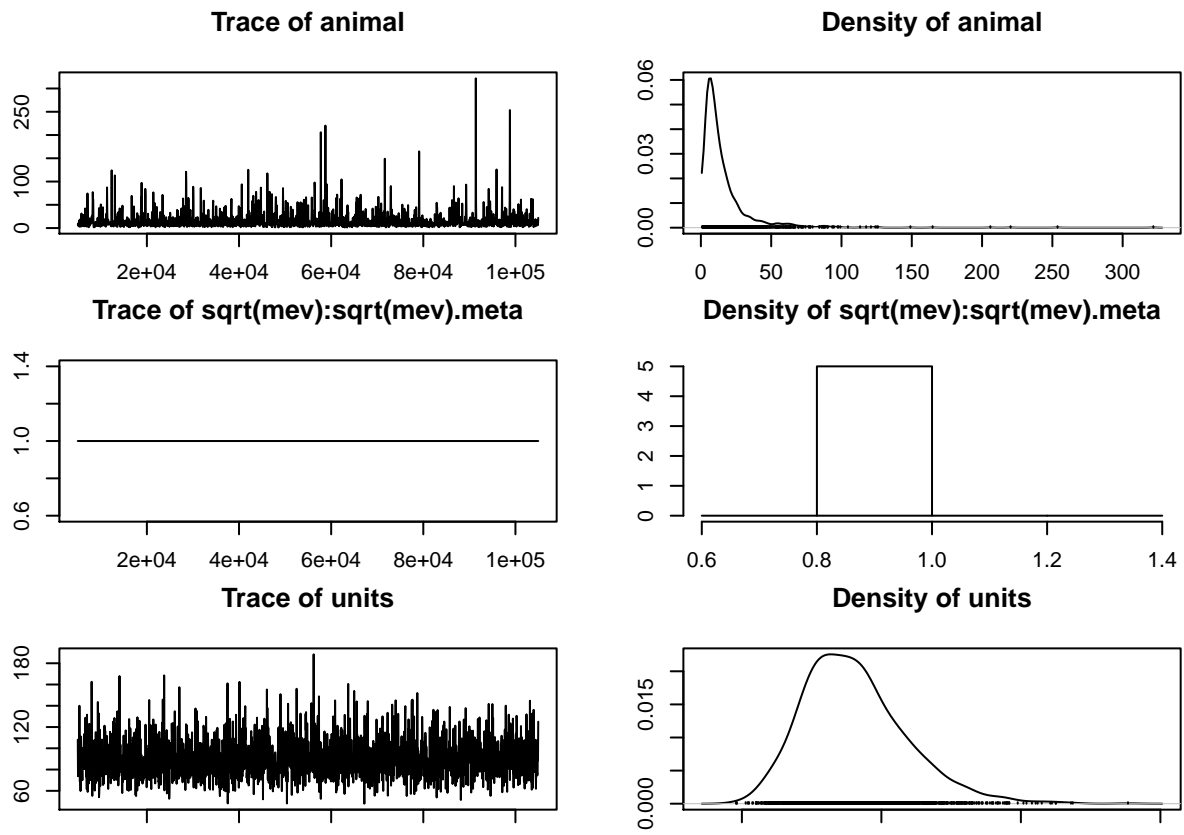
```
par(mar=c(1,4,4,1))
plot(m11.mcmc)
```

**Trace of (Intercept)**



**Density of (Intercept)**





### Proportion of Variance explained by phylogeny in Adult mean TL

```
TL_phylogeny<-m11.mcmc$VCV['animal']/(m11.mcmc$VCV['animal']+m11.mcmc$VCV['units']+m11.mcmc$VCV["sq
posterior.mode(TL_phylogeny)
```

```
##      var1
## 0.07397586
```

```
effectiveSize(TL_phylogeny)
```

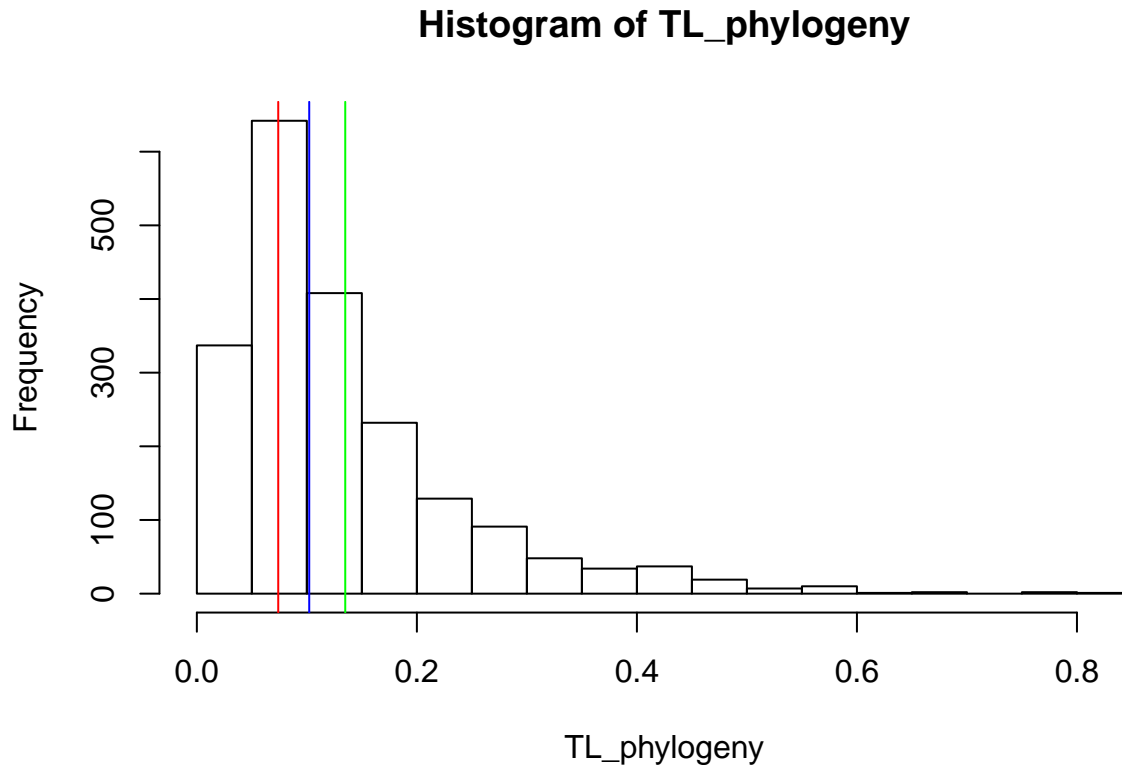
```
##      var1
## 1310.431
```

```
HPDinterval(TL_phylogeny)
```

```
##          lower      upper
## var1 0.01350046 0.3744376
## attr("Probability")
## [1] 0.95
```



```
hist(TL_phylogeny, breaks=15)
abline(v=posterior.mode((TL_phylogeny)), col="red")
abline(v=median((TL_phylogeny)), col="blue")
abline(v=mean((TL_phylogeny)), col="green")
```



## PCA1 and the historical relationships among the species, as reflected by the phylogeny

#defining priors This first line specifies the dependent variable, `cbind(PCA1, PCA2)`, and the fixed effects, `-1 + trait + Modality`. The term `trait` is not part of the original data set—rather, it's a reserved term in the `MCMCglmm` package. `trait` comes from phylogenetics, where the dependent variable is some observed trait in an organism. For our purposes, including the `trait` term tells the model to estimate an intercept for each of the observed outcomes. We follow the advice from the tutorial and enter this as `-1 + trait`. This guarantees an intercept for each non-baseline level of the outcome, rather than an overall intercept term with an offset for  $k-2$  levels.

```
p.var1=var(Bird.data$PCA1)
prior1 <-list(G=list(G1=list(V=(diag(1)*0.2*p.var1),n=1)),
              R=list(V=(0.8*p.var1),n=2))
```

The above specifies uninformative priors where most weight is divided such that 20% of the variance in each trait is placed on the between-subject level and the remaining on the residual variance. Those are non-informative priors, but still we expect that there is more variation between individual/species, than within.

As always in Bayesian analysis, one needs to verify that prior specifications do not determine the result by evaluating the sensitivity of inferences to different priors.

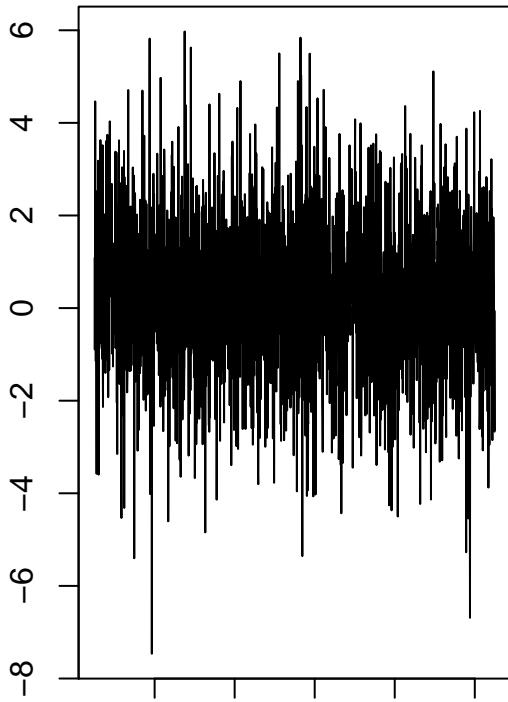
```
set.seed(1)
m22.mcmc <-MCMCglmm(PCA1 ~ 1, random = ~animal, mev=Bird.data$mev , data = Bird.data, prior=prior1 ,fam
```

```
summary(m22.mcmc)
```

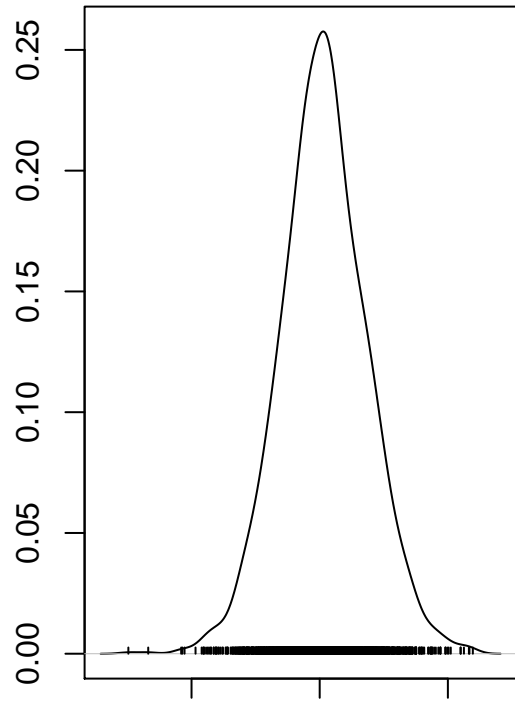
```
##
## Iterations = 5001:104951
## Thinning interval = 50
## Sample size = 2000
##
## DIC: 206.9867
##
## G-structure: ~animal
##
##      post.mean l-95% CI u-95% CI eff.samp
## animal    10.37   1.644    21.4    1942
##
## R-structure: ~units
##
##      post.mean l-95% CI u-95% CI eff.samp
## units        2.3   0.9158   3.945    1978
##
## Location effects: PCA1 ~ 1
##
##      post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept)  0.1518  -3.0162   3.5963    2000 0.925
```

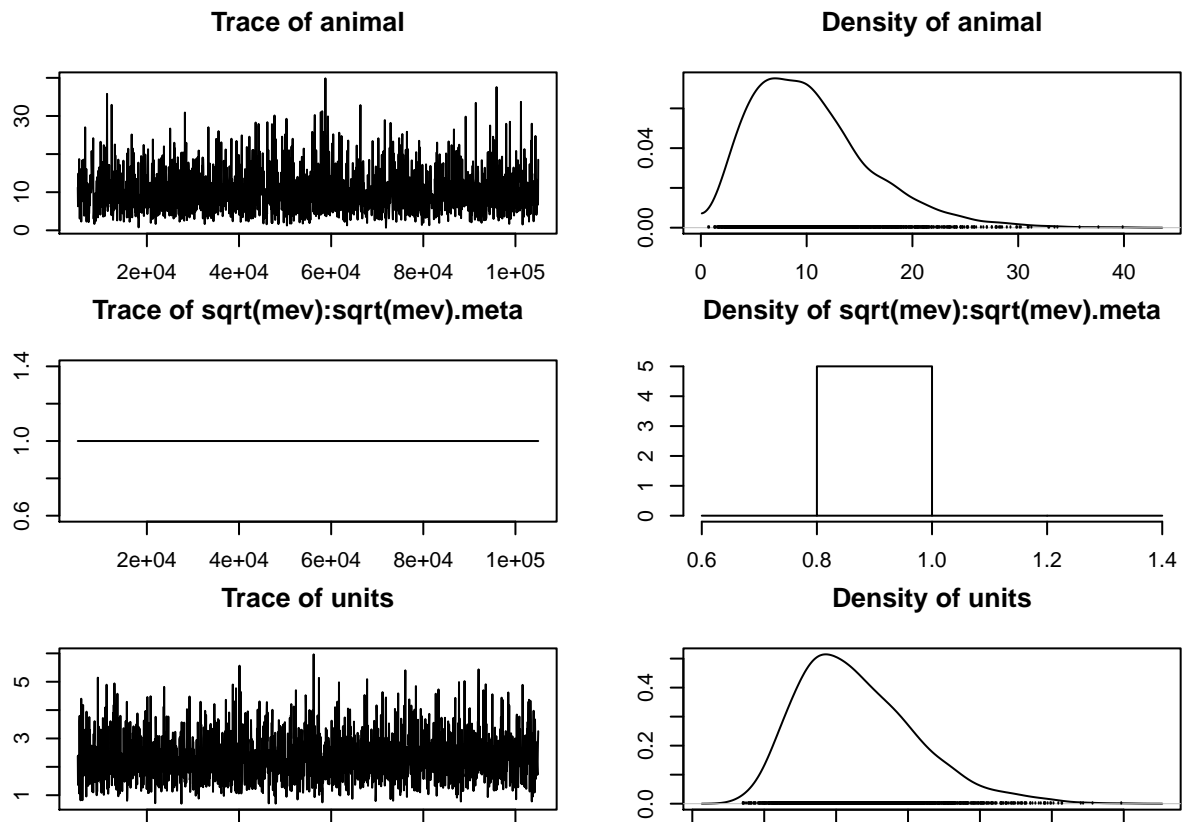
```
par(mar=c(1,4,4,1))
plot(m22.mcmc)
```

**Trace of (Intercept)**



**Density of (Intercept)**





## Proportion of Variance explained by phylogeny in PCA1

```
PCA1_phylogeny<-m22.mcmc$VCV[, 'animal']/(m22.mcmc$VCV[, 'animal']+m22.mcmc$VCV[, 'units']+m22.mcmc$VCV[, ''])
posterior.mode(PCA1_phylogeny)
```

```
##      var1
## 0.8032231
```

```
effectiveSize(PCA1_phylogeny)
```

```
##      var1
## 1833.804
```

```
HPDinterval(PCA1_phylogeny)
```

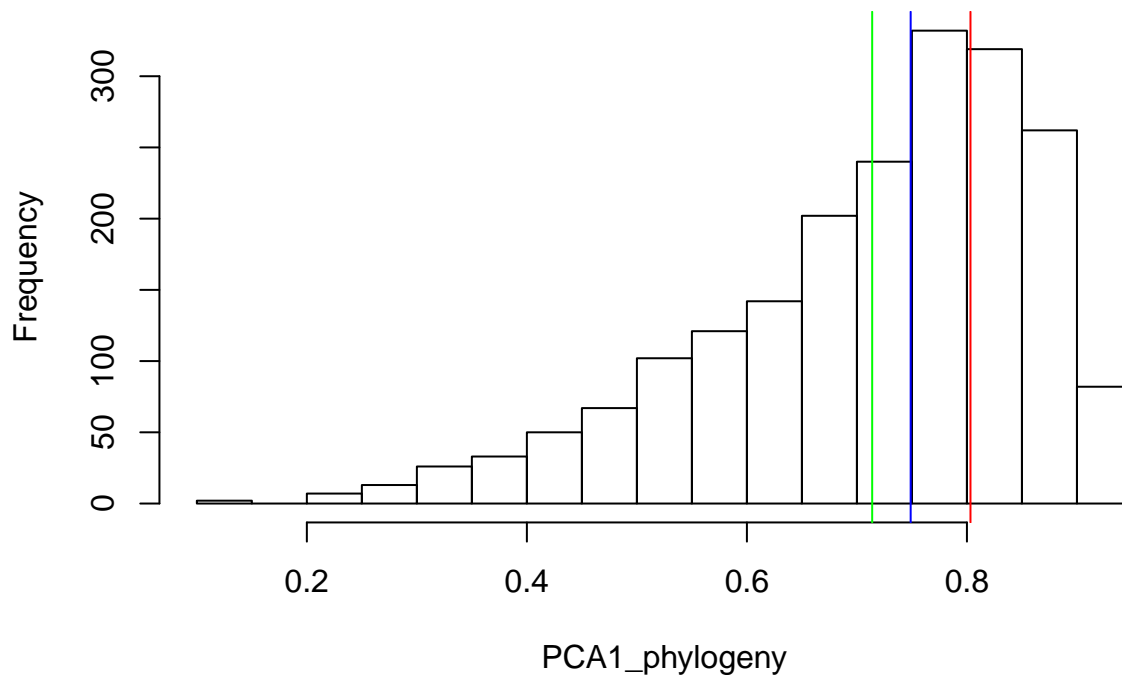
```
##           lower      upper
## var1 0.3990639 0.9202694
## attr(,"Probability")
## [1] 0.95
```

```

hist(PCA1_phylogeny, breaks=15)
abline(v=posterior.mode((PCA1_phylogeny)), col="red")
abline(v=median((PCA1_phylogeny)), col="blue")
abline(v=mean((PCA1_phylogeny)), col="green")

```

**Histogram of PCA1\_phylogeny**



**PCA2 and the historical relationships among the species, as reflected by the phylogeny**

```

p.var1=var(Bird.data$PCA2)
prior1 <-list(G=list(G1=list(V=(diag(1)*0.2*p.var1),n=1)),
              R=list(V=(0.8*p.var1),n=2))
set.seed(1)
m33.mcmc <- MCMCglmm(PCA2 ~ 1, random = ~animal , mev=Bird.data$mev , data = Bird.data,
                    family=c("gaussian"), prior=prior1, pedigree = Bird.phylo, nitt = 105000, thin = 50,
                    burnin = 5000, pr = TRUE, pl = TRUE, verbose = TRUE, DIC = TRUE)

```

```
summary(m33.mcmc)
```

```

##
## Iterations = 5001:104951
## Thinning interval = 50

```

```

## Sample size = 2000
##
## DIC: 117.4362
##
## G-structure: ~animal
##
##      post.mean l-95% CI u-95% CI eff.samp
## animal    1.439    0.251    3.033    2000
##
## R-structure: ~units
##
##      post.mean l-95% CI u-95% CI eff.samp
## units    0.3931    0.1797    0.6661    2000
##
## Location effects: PCA2 ~ 1
##
##      post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept)  0.4437  -0.8149   1.6801   3583 0.458

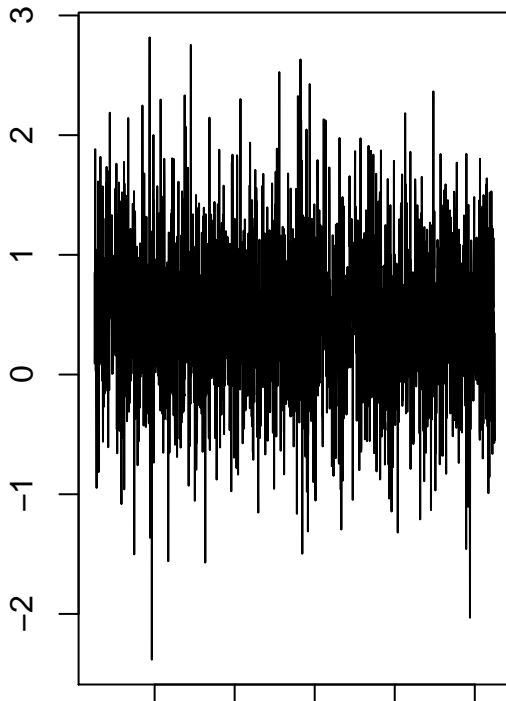
```

```

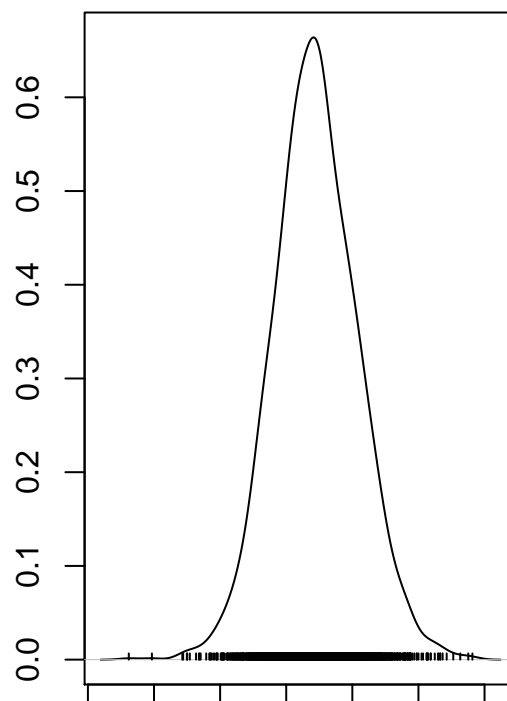
par(mar=c(1,4,4,1))
plot(m33.mcmc)

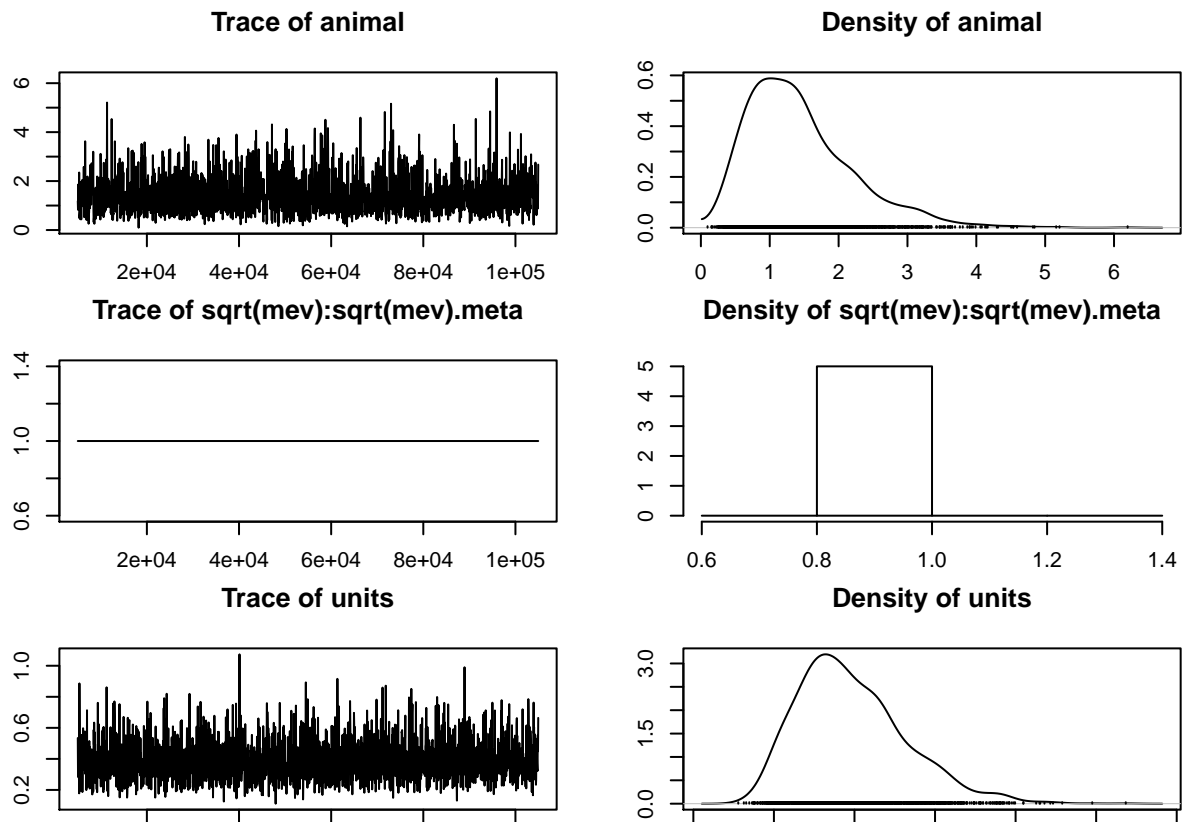
```

**Trace of (Intercept)**



**Density of (Intercept)**





## Proportion of Variance explained by phylogeny in PCA2

```
PCA2_phylogeny<-m33.mcmc$VCV[, 'animal']/(m33.mcmc$VCV[, 'animal']+m33.mcmc$VCV[, 'units']+m33.mcmc$VCV[, '
posterior.mode(PCA2_phylogeny)
```

```
##      var1
## 0.4623099
```

```
effectiveSize(PCA2_phylogeny)
```

```
## var1
## 2000
```

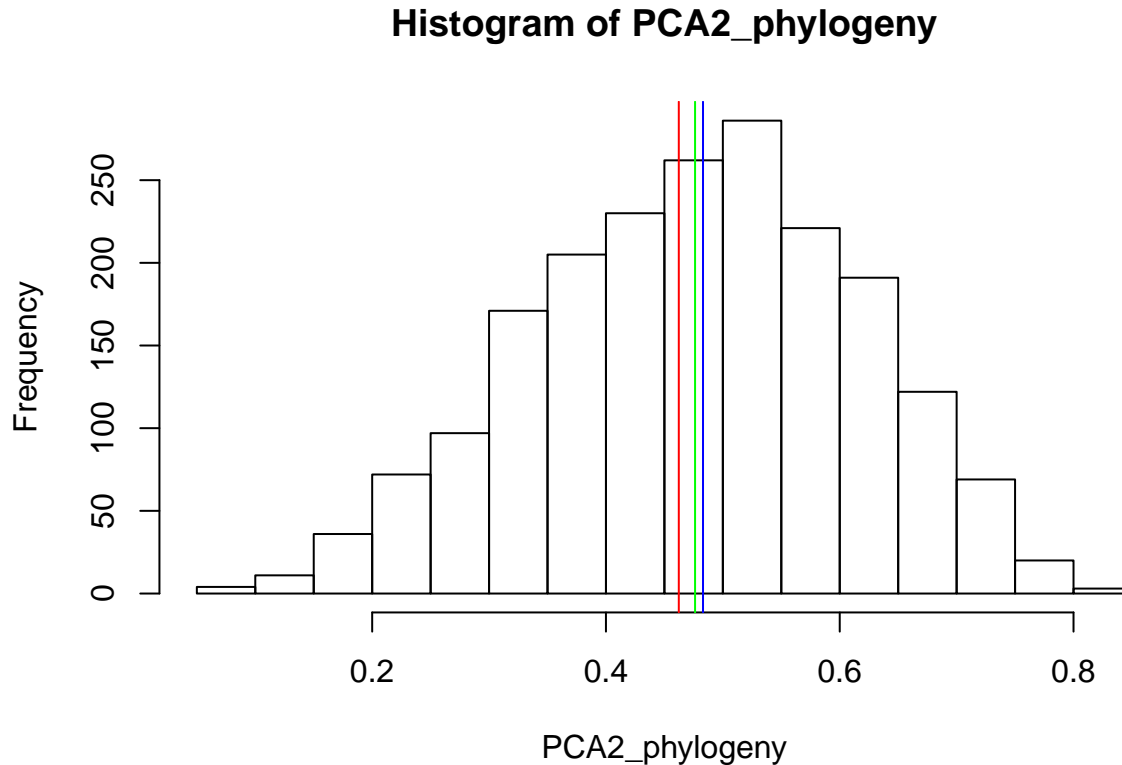
```
HPDinterval(PCA2_phylogeny)
```

```
##      lower      upper
## var1 0.2038243 0.7227777
## attr(,"Probability")
## [1] 0.95
```

```

hist(PCA2_phylogeny, breaks=15)
abline(v=posterior.mode((PCA2_phylogeny)), col="red")
abline(v=median((PCA2_phylogeny)), col="blue")
abline(v=mean((PCA2_phylogeny)), col="green")

```



PCA3 and the historical relationships among the species, as reflected by the phylogeny

```

p.var1=var(Bird.data$PCA3)
prior1 <-list(G=list(G1=list(V=(diag(1)*0.2*p.var1),n=1)),
              R=list(V=(0.8*p.var1),n=2))

set.seed(1)
m44.mcmc <- MCMCglmm(PCA3 ~ 1, random = ~animal, mev=Bird.data$mev, data = Bird.data,
                    prior=prior1,
                    family=c("gaussian"), pedigree = Bird.phylo, nitt = 105000, thin = 50,
                    burnin = 5000, pr = TRUE, pl = TRUE, verbose = TRUE, DIC = TRUE)

```

```
summary(m44.mcmc)
```

```
##
```



```

## Iterations = 5001:104951
## Thinning interval = 50
## Sample size = 2000
##
## DIC: 153.7216
##
## G-structure: ~animal
##
##      post.mean l-95% CI u-95% CI eff.samp
## animal    0.3952  0.01604   1.411    1144
##
## R-structure: ~units
##
##      post.mean l-95% CI u-95% CI eff.samp
## units     0.8621   0.4621   1.286    1777
##
## Location effects: PCA3 ~ 1
##
##      post.mean l-95% CI u-95% CI eff.samp pMCMC
## (Intercept)  0.03394 -0.65944  0.77686    2000 0.941

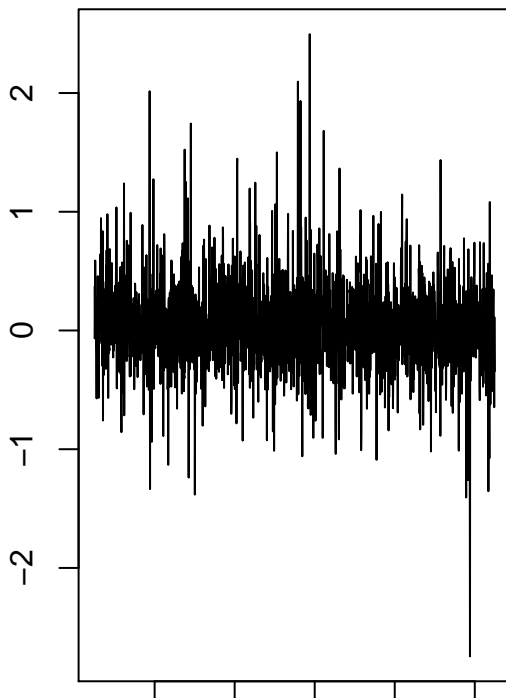
```

```

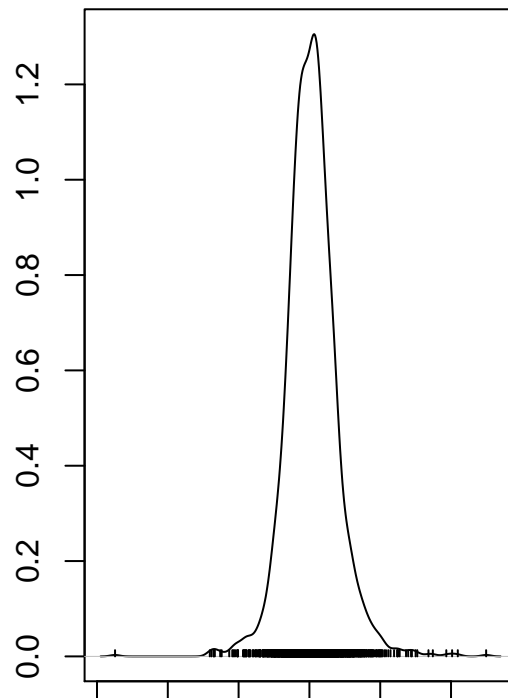
par(mar=c(1,4,4,1))
plot(m44.mcmc)

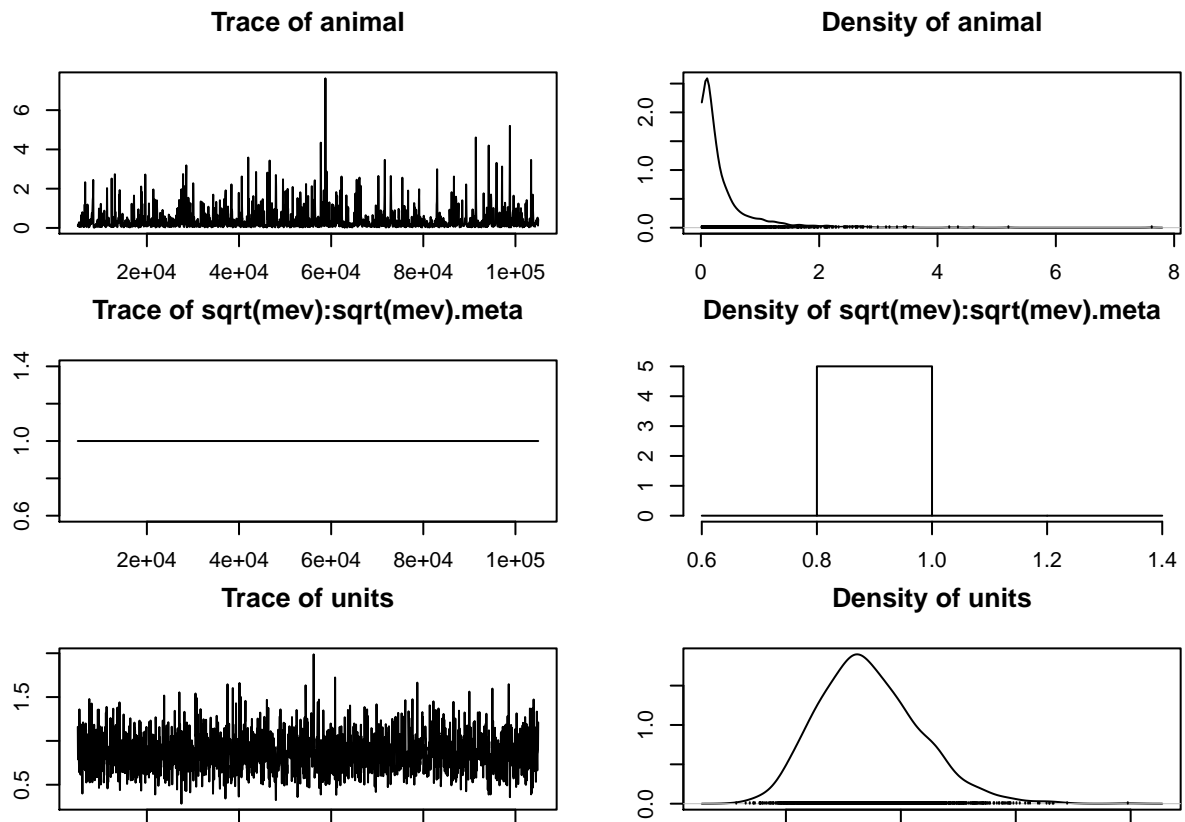
```

**Trace of (Intercept)**



**Density of (Intercept)**





## Proportion of Variance explained by phylogeny in PCA3

```
PCA3_phylogeny<-m44.mcmc$VCV[, 'animal']/(m44.mcmc$VCV[, 'animal']+m44.mcmc$VCV[, 'units']+m44.mcmc$VCV[, 'units'])
posterior.mode(PCA3_phylogeny)
```

```
##      var1
## 0.04244583
```

```
effectiveSize(PCA3_phylogeny)
```

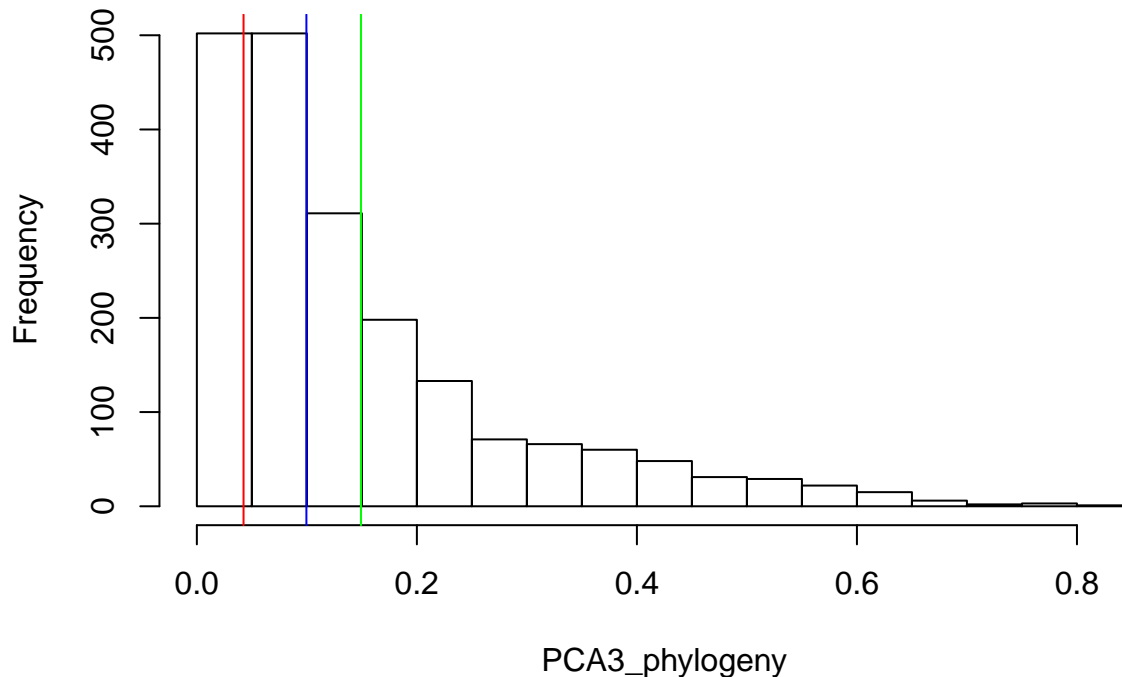
```
##      var1
## 945.583
```

```
HPDinterval(PCA3_phylogeny)
```

```
##           lower      upper
## var1 0.00757482 0.464313
## attr(,"Probability")
## [1] 0.95
```

```
hist(PCA3_phylogeny, breaks=15)
abline(v=posterior.mode((PCA3_phylogeny)), col="red")
abline(v=median((PCA3_phylogeny)), col="blue")
abline(v=mean((PCA3_phylogeny)), col="green")
```

**Histogram of PCA3\_phylogeny**



**PCA1 + PCA2 + PCA3 and the historical relationships among the species, as reflected by the phylogeny**

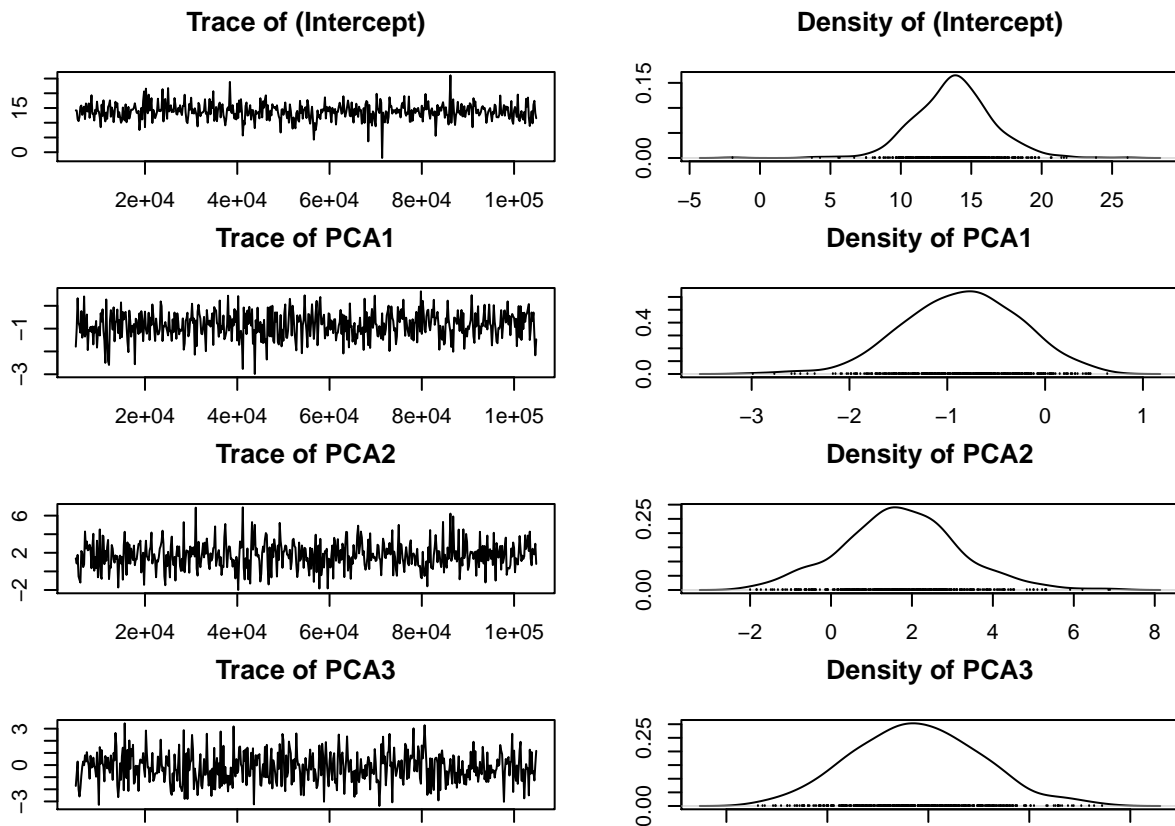
```
p.var1=var(Bird.data$Mean.telomere.adult)
prior1 <-list(G=list(G1=list(V=(diag(1)*0.2*p.var1),n=1)),
              R=list(V=(0.8*p.var1),n=2))

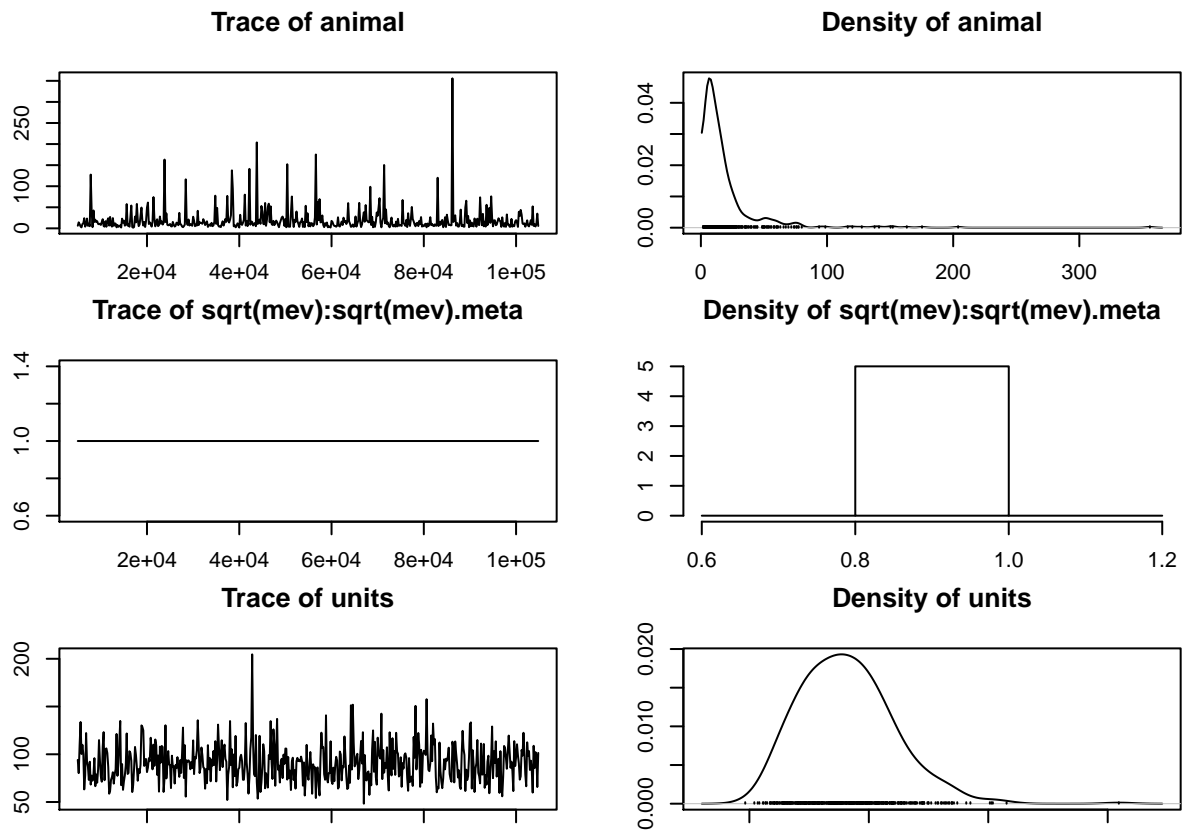
m55.mcmc <- MCMCglmm(Mean.telomere.adult ~PCA1+PCA2+PCA3, random = ~animal , mev=Bird.data$mev,
                    data = Bird.data, prior=prior1,
                    pedigree = Bird.phylo, nitt = 105000, thin = 200, burnin = 5000,
                    pr = TRUE, pl = TRUE, verbose = TRUE, DIC = TRUE)
```

```
oneModel <- clean.MCMC(m55.mcmc) # get all the info from summary(modelName)
oneModel$modelName <- getName.MCMC(m55.mcmc) # add the model's name in a new column
oneModel<-oneModel[,-c(5)]
stargazer(oneModel, type = "text", summary = FALSE)
```

```
##
## =====
##          variable      post.mean 1.95..CI u.95..CI pMCMC  effect  modelName
## -----
## 1      (Intercept)      13.756   8.803   19.559  0.004  fixed   m55.mcmc
## 2         PCA1         -0.849  -1.953   0.310  0.140  fixed   m55.mcmc
## 3         PCA2          1.714  -1.132   4.524  0.224  fixed   m55.mcmc
## 4         PCA3         -0.225  -2.795   2.093  0.848  fixed   m55.mcmc
## 5         animal      19.823   1.634  62.932          random m55.mcmc
## 6 sqrt(mev):sqrt(mev).meta  1         1         1          random m55.mcmc
## 7         units      90.783  55.658 129.069          residual m55.mcmc
## -----
```

```
par(mar=c(1,4,4,1))
plot(m55.mcmc)
```





## Posterior distribution of PCs fixed effect

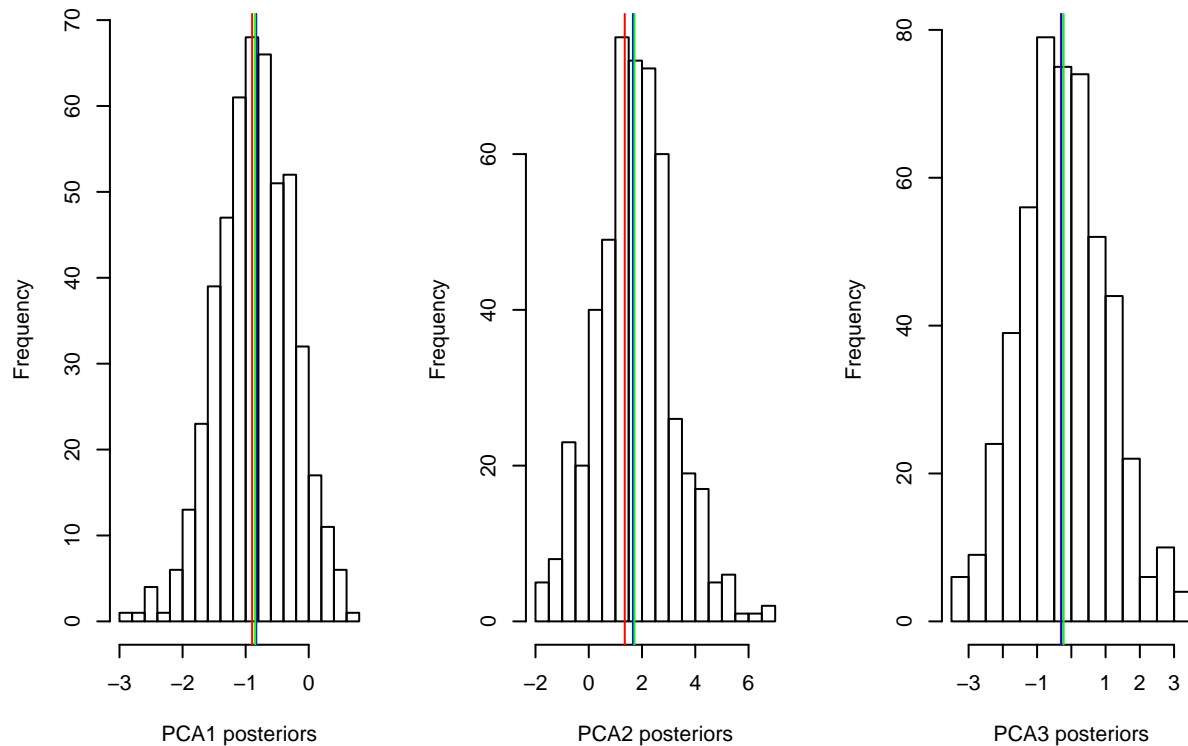
```

par(mfrow=c(1,3))
hist(m55.mcmc$Sol[,2], breaks=15, xlab="PCA1 posteriors", main="")
abline(v=posterior.mode((m55.mcmc$Sol[,2])), col="red")
abline(v=median((m55.mcmc$Sol[,2])), col="blue")
abline(v=mean((m55.mcmc$Sol[,2])), col="green")

hist(m55.mcmc$Sol[,3], breaks=15, xlab="PCA2 posteriors", main="")
abline(v=posterior.mode((m55.mcmc$Sol[,3])), col="red")
abline(v=median((m55.mcmc$Sol[,3])), col="blue")
abline(v=mean((m55.mcmc$Sol[,3])), col="green")

hist(m55.mcmc$Sol[,4], breaks=15, xlab="PCA3 posteriors", main="")
abline(v=posterior.mode((m55.mcmc$Sol[,4])), col="red")
abline(v=median((m55.mcmc$Sol[,4])), col="blue")
abline(v=mean((m55.mcmc$Sol[,4])), col="green")

```



### Proportion of Variance explained by phylogeny in Telomeres considering PCA1-2-3 as fixed factors

```
TL_phylogeny<-m55.mcmc$VCV['animal']/(m55.mcmc$VCV['animal']+m55.mcmc$VCV['units']+m55.mcmc$VCV["sq
posterior.mode(TL_phylogeny)
```

```
## var1
## 0.050027
```

```
effectiveSize(TL_phylogeny)
```

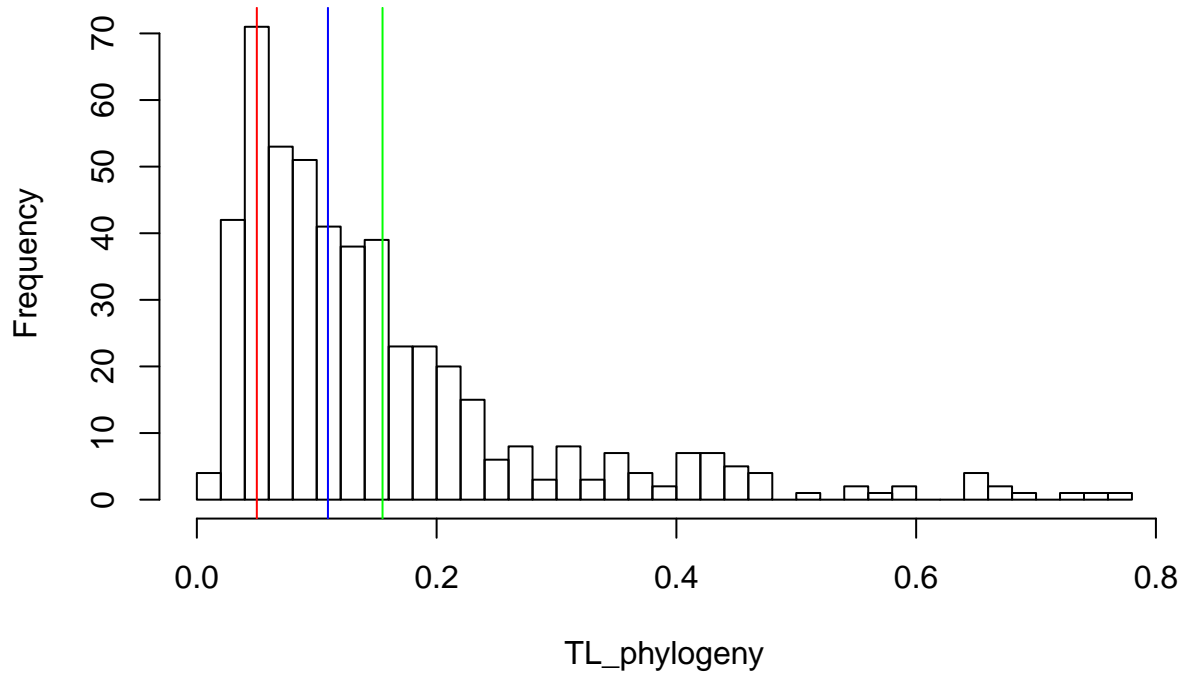
```
## var1
## 500
```

```
HPDinterval(TL_phylogeny)
```

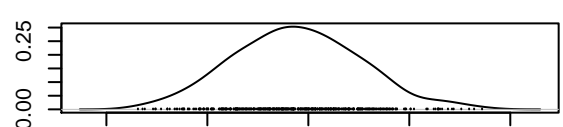
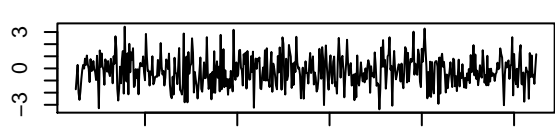
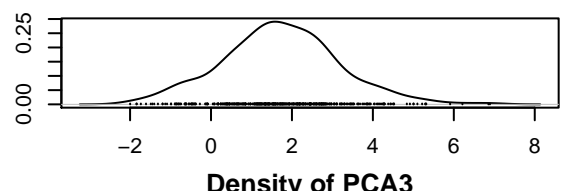
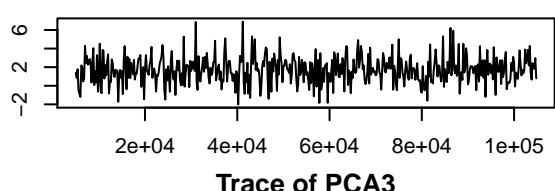
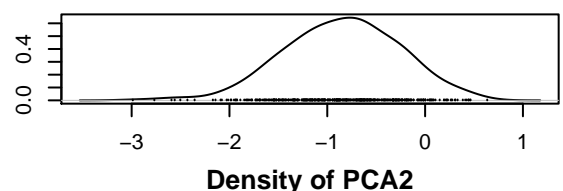
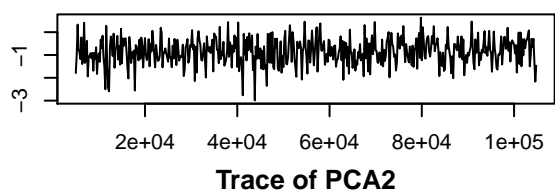
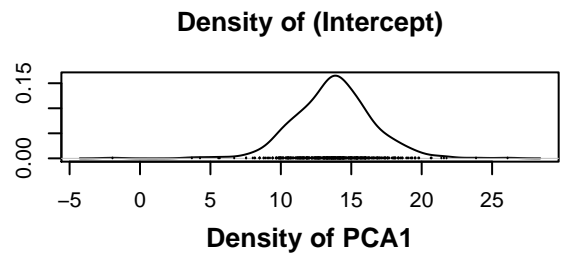
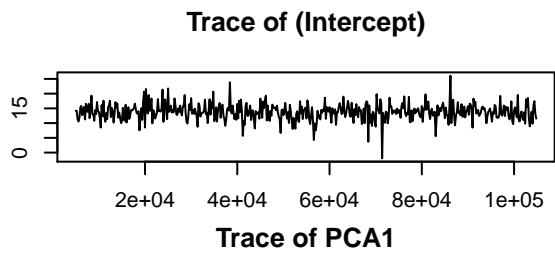
```
## lower upper
## var1 0.01601154 0.440403
## attr("Probability")
## [1] 0.95
```

```
hist(TL_phylogeny, breaks=30)
abline(v=posterior.mode((TL_phylogeny)), col="red")
abline(v=median((TL_phylogeny)), col="blue")
abline(v=mean((TL_phylogeny)), col="green")
```

## Histogram of TL\_phylogeny

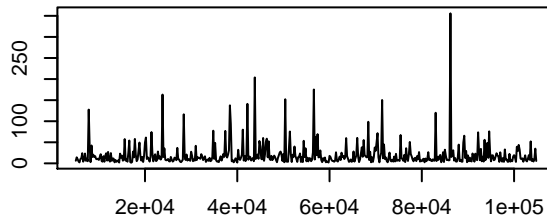


```
par(mar=c(1,4,4,1))
plot(m55.mcmc)
```

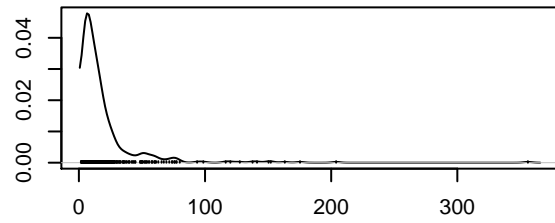




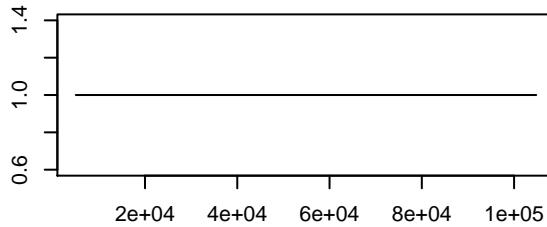
**Trace of animal**



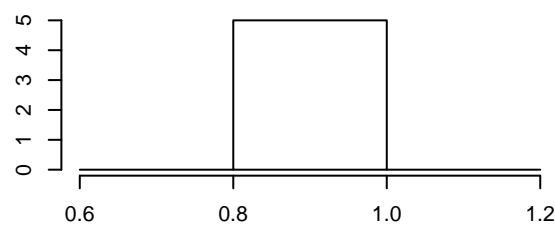
**Density of animal**



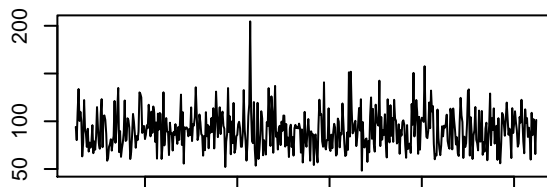
**Trace of sqrt(mev):sqrt(mev).meta**



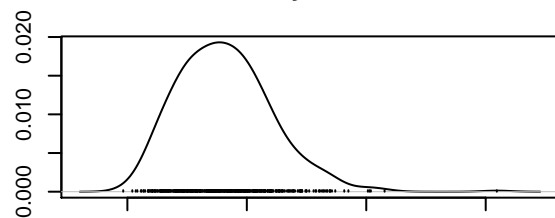
**Density of sqrt(mev):sqrt(mev).meta**



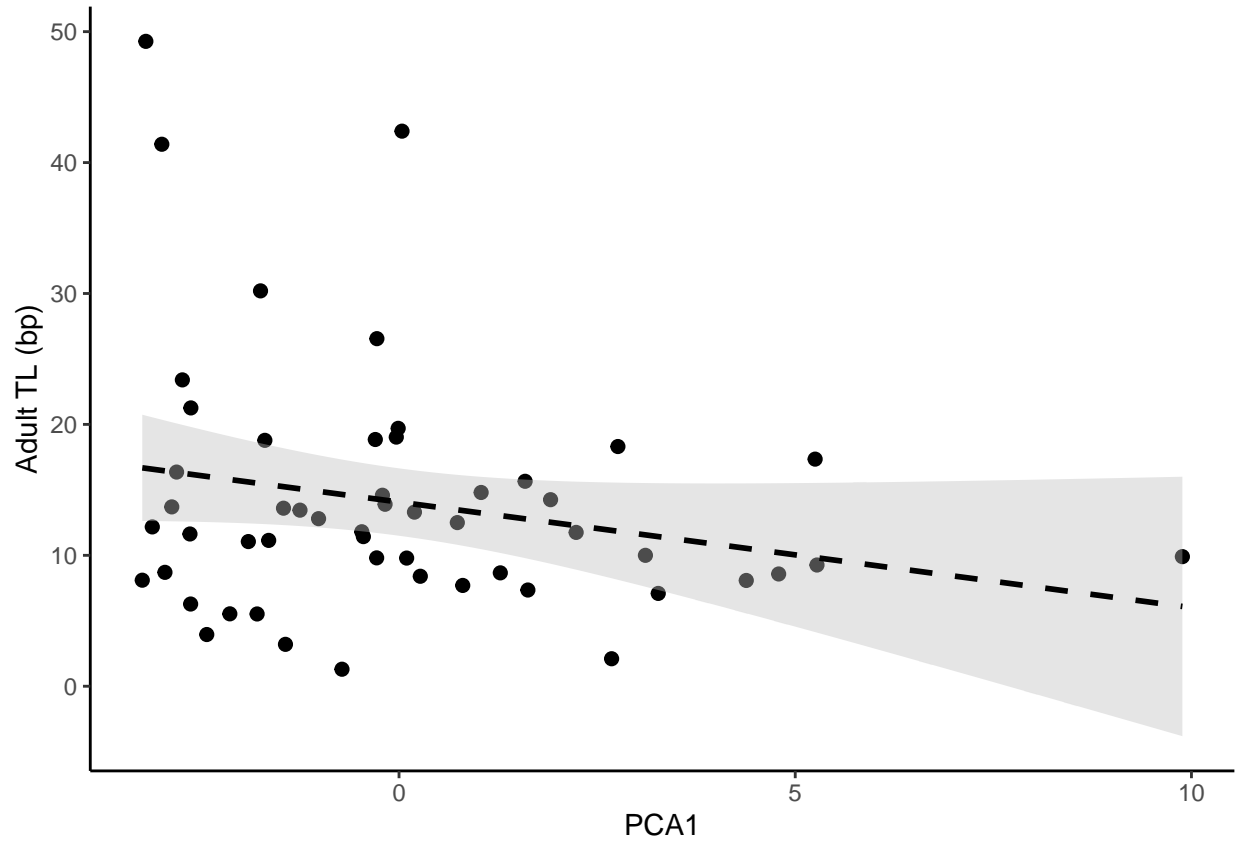
**Trace of units**



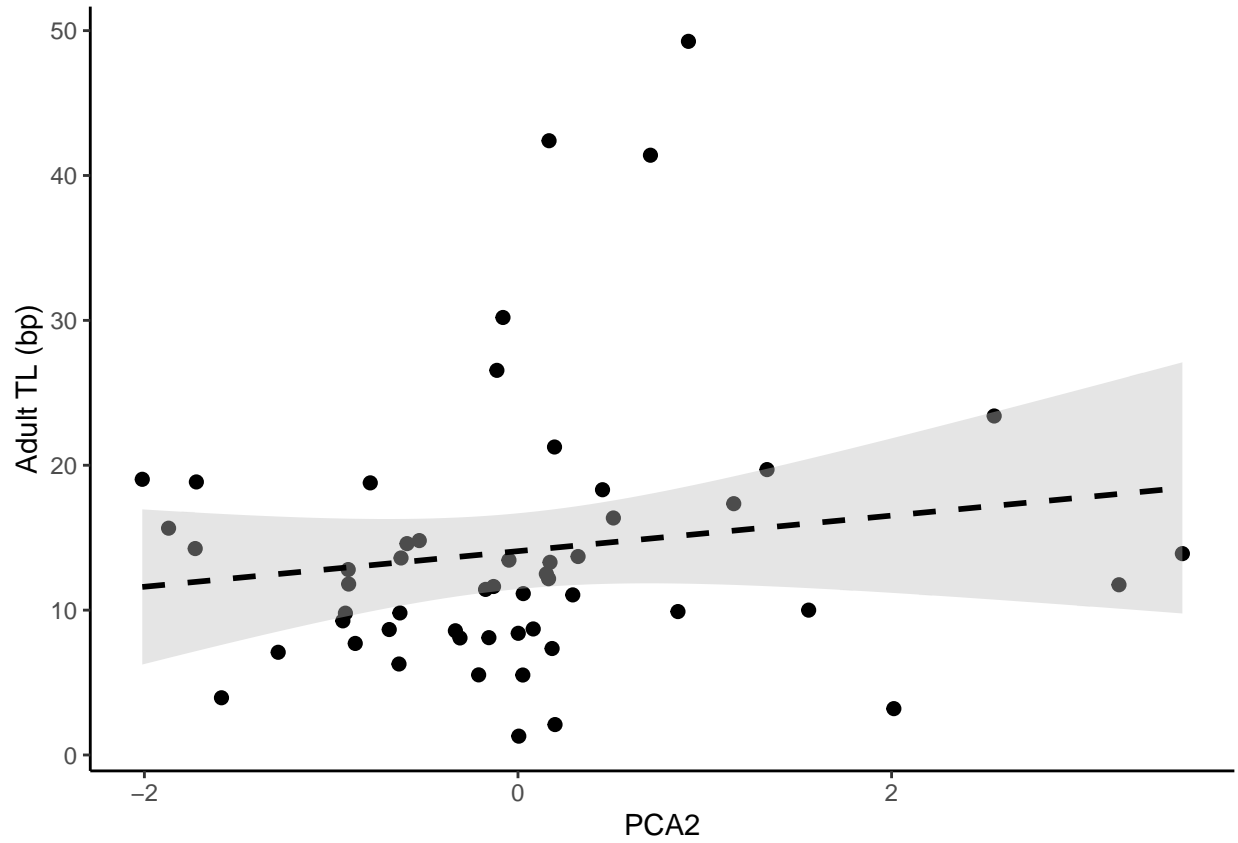
**Density of units**



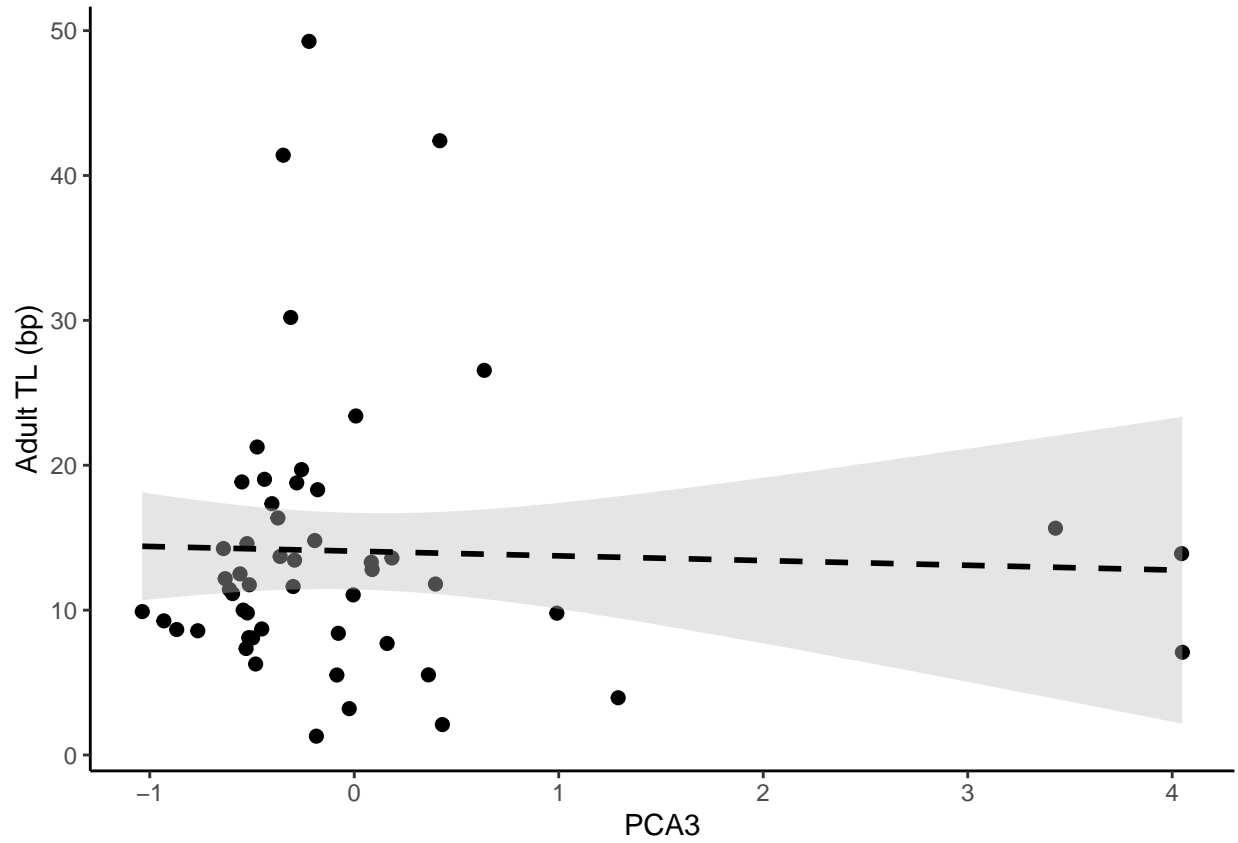
```
p<-ggplot(Bird.data, aes(x=Bird.data$PCA1, y=Bird.data$Mean.telomere.adult)) +  
  geom_point(size=2)+scale_color_grey()+  
  theme_classic()+  
  geom_smooth(method=lm,linetype="dashed",color="black",fill="grey")  
p+labs(x="PCA1",y="Adult TL (bp)")
```



```
p<-ggplot(Bird.data, aes(x=Bird.data$PCA2, y=Bird.data$Mean.telomere.adult))+
  geom_point(size=2)+scale_color_grey()+
  theme_classic()+
  geom_smooth(method=lm,linetype="dashed",color="black",fill="grey")
p+labs(x="PCA2",y="Adult TL (bp)")
```

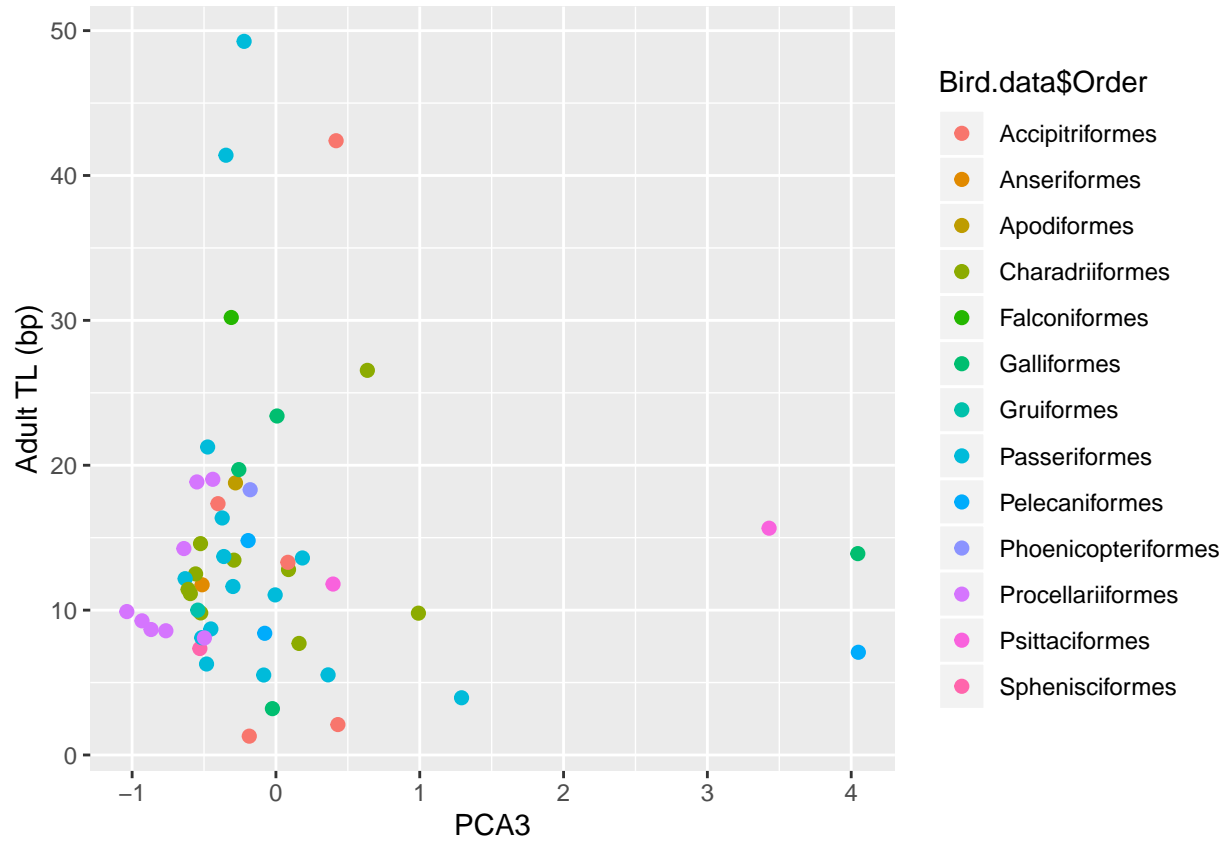


```
p<-ggplot(Bird.data, aes(x=Bird.data$PCA3, y=Bird.data$Mean.telomere.adult))+
  geom_point(size=2)+scale_color_grey()+
  theme_classic()+
  geom_smooth(method=lm,linetype="dashed",color="black",fill="grey")
p+labs(x="PCA3",y="Adult TL (bp)")
```

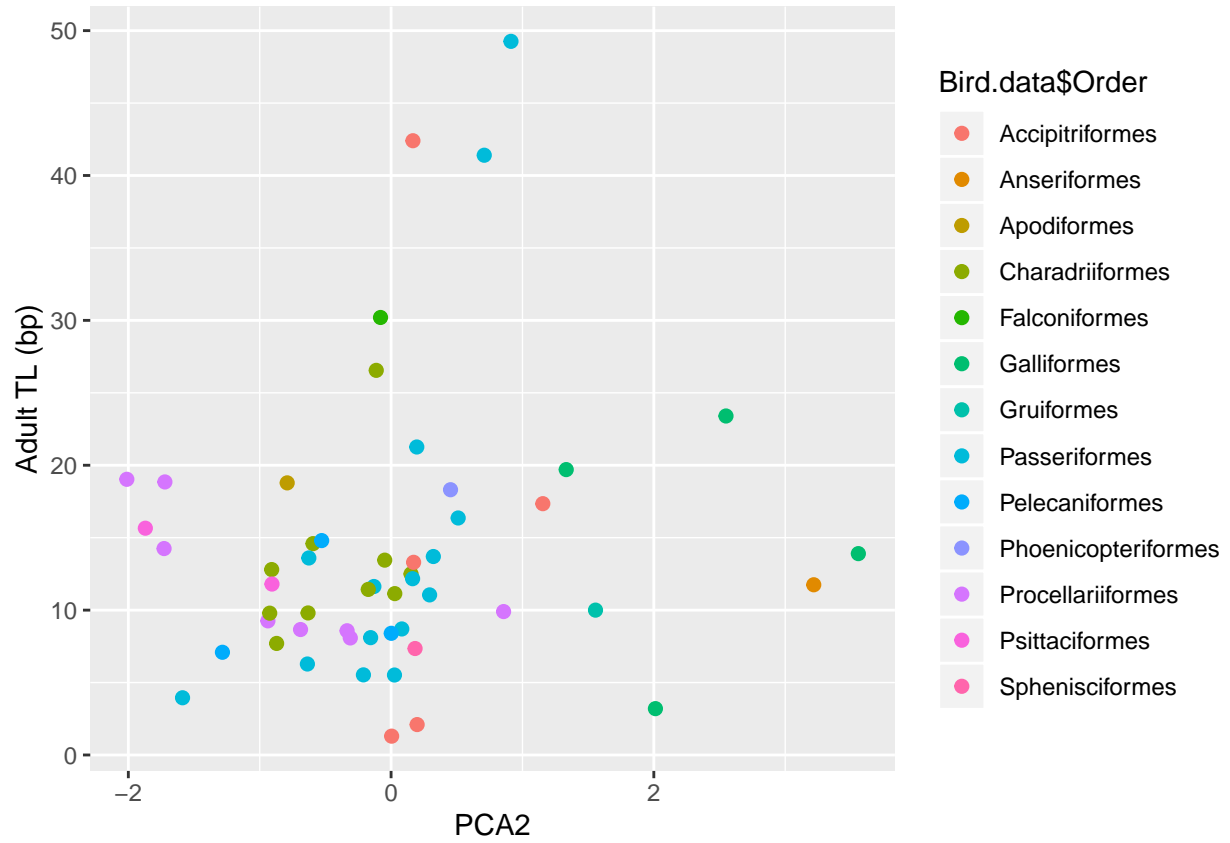


#By orders

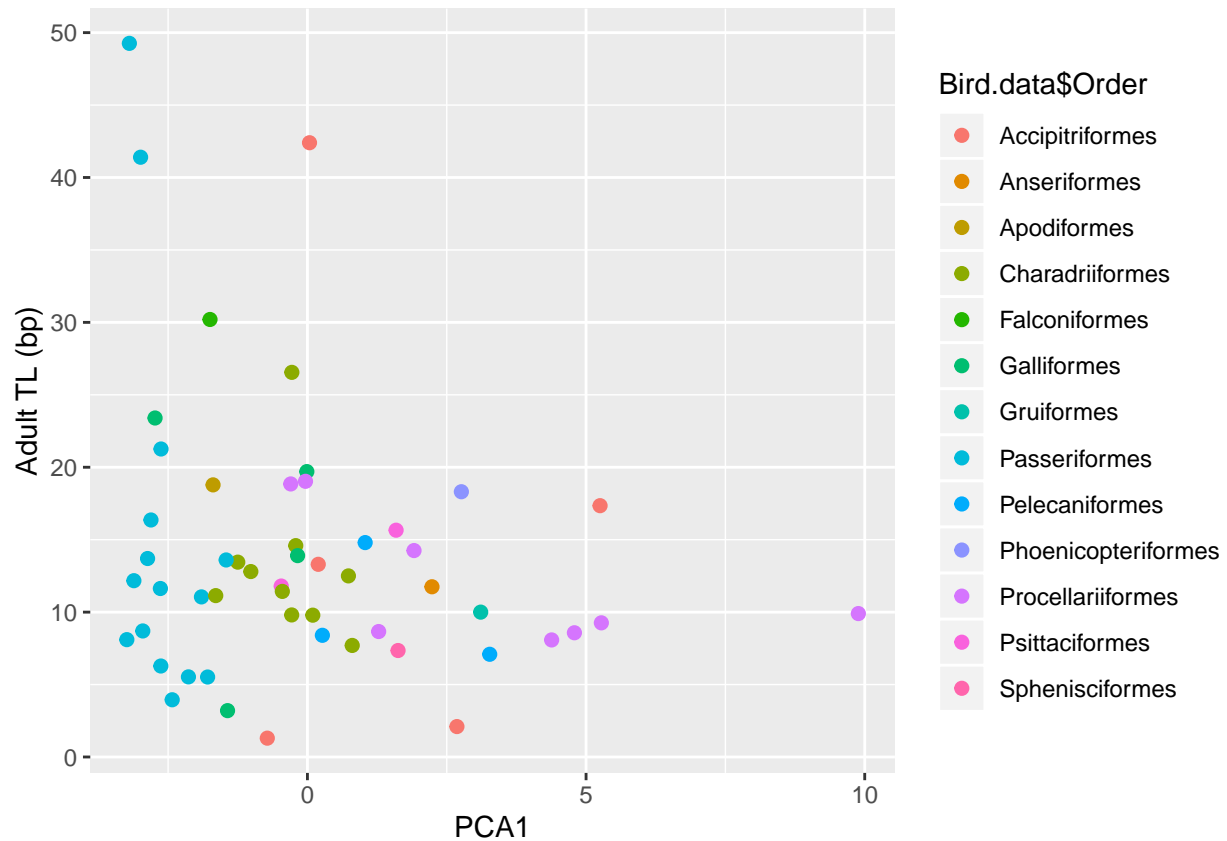
```
p<-ggplot(Bird.data, aes(x=Bird.data$PCA3, y=Bird.data$Mean.telomere.adult, color=Bird.data$Order))+  
  geom_point(size=2)  
p+labs(x="PCA3",y="Adult TL (bp)")
```



```
p<-ggplot(Bird.data, aes(x=Bird.data$PCA2, y=Bird.data$Mean.telomere.adult, color=Bird.data$Order))+
  geom_point(size=2)
p+labs(x="PCA2",y="Adult TL (bp)")
```



```
p<-ggplot(Bird.data, aes(x=Bird.data$PCA1, y=Bird.data$Mean.telomere.adult, color=Bird.data$Order))+
  geom_point(size=2)
p+labs(x="PCA1",y="Adult TL (bp)")
```



## Unadjusted Pearson's correlation

```
cor.test(Bird.data$Mean.telomere.adult, Bird.data$PCA1, alternative = c("two.sided"), method = c("pearson"))
```

```
##
## Pearson's product-moment correlation
##
## data: Bird.data$Mean.telomere.adult and Bird.data$PCA1
## t = -1.6733, df = 51, p-value = 0.1004
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.4694718 0.0449387
## sample estimates:
## cor
## -0.2281261
```

```
cor.test(Bird.data$Mean.telomere.adult, Bird.data$PCA2, alternative = c("two.sided"), method = c("pearson"))
```

```
##
## Pearson's product-moment correlation
##
## data: Bird.data$Mean.telomere.adult and Bird.data$PCA2
```

```
## t = 1.061, df = 51, p-value = 0.2937
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.1284398 0.4013091
## sample estimates:
##      cor
## 0.1469558
```

```
cor.test(Bird.data$Mean.telomere.adult, Bird.data$PCA3, alternative = c("two.sided"), method = c("pearson"))
```

```
##
## Pearson's product-moment correlation
##
## data: Bird.data$Mean.telomere.adult and Bird.data$PCA3
## t = -0.25744, df = 51, p-value = 0.7979
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.3033649 0.2365723
## sample estimates:
##      cor
## -0.03602509
```

```
#By orders #Procellariiformes
```

```
proc<-Bird.data[Bird.data$Order=="Procellariiformes",]
cor.test(proc$Mean.telomere.adult, proc$PCA1, alternative = c("two.sided"), method = c("pearson"))
```

```
##
## Pearson's product-moment correlation
##
## data: proc$Mean.telomere.adult and proc$PCA1
## t = -2.1593, df = 6, p-value = 0.07415
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.93176162 0.08127514
## sample estimates:
##      cor
## -0.6612703
```

```
cor.test(proc$Mean.telomere.adult, proc$PCA2, alternative = c("two.sided"), method = c("pearson"))
```

```
##
## Pearson's product-moment correlation
##
## data: proc$Mean.telomere.adult and proc$PCA2
## t = -2.933, df = 6, p-value = 0.02619
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.9554447 -0.1369107
## sample estimates:
##      cor
## -0.767534
```



```
cor.test(proc$Mean.telomere.adult, proc$PCA3, alternative = c("two.sided"), method = c("pearson"))
```

```
##  
## Pearson's product-moment correlation  
##  
## data: proc$Mean.telomere.adult and proc$PCA3  
## t = 1.8923, df = 6, p-value = 0.1073  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## -0.1639607 0.9197791  
## sample estimates:  
## cor  
## 0.6113464
```

```
#Charadriiformes
```

```
cha<-Bird.data[Bird.data$Order=="Charadriiformes",]  
cor.test(cha$Mean.telomere.adult, cha$PCA1, alternative = c("two.sided"), method = c("pearson"))
```

```
##  
## Pearson's product-moment correlation  
##  
## data: cha$Mean.telomere.adult and cha$PCA1  
## t = -0.37244, df = 8, p-value = 0.7192  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## -0.7024379 0.5437728  
## sample estimates:  
## cor  
## -0.1305506
```

```
cor.test(cha$Mean.telomere.adult, cha$PCA2, alternative = c("two.sided"), method = c("pearson"))
```

```
##  
## Pearson's product-moment correlation  
##  
## data: cha$Mean.telomere.adult and cha$PCA2  
## t = 1.1414, df = 8, p-value = 0.2867  
## alternative hypothesis: true correlation is not equal to 0  
## 95 percent confidence interval:  
## -0.3341408 0.8124216  
## sample estimates:  
## cor  
## 0.3742141
```

```
cor.test(cha$Mean.telomere.adult, cha$PCA3, alternative = c("two.sided"), method = c("pearson"))
```

```
##  
## Pearson's product-moment correlation  
##
```

```

## data: cha$Mean.telomere.adult and cha$PCA3
## t = 0.84052, df = 8, p-value = 0.425
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.4201188 0.7754109
## sample estimates:
##      cor
## 0.2848573

#Passeriformes

pas<-Bird.data[Bird.data$Order=="Passeriformes",]
cor.test(pas$Mean.telomere.adult, pas$PCA1, alternative = c("two.sided"), method = c("pearson"))

##
## Pearson's product-moment correlation
##
## data: pas$Mean.telomere.adult and pas$PCA1
## t = -1.6166, df = 13, p-value = 0.13
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.7617435 0.1304818
## sample estimates:
##      cor
## -0.4091275

cor.test(pas$Mean.telomere.adult, pas$PCA2, alternative = c("two.sided"), method = c("pearson"))

##
## Pearson's product-moment correlation
##
## data: pas$Mean.telomere.adult and pas$PCA2
## t = 3.3425, df = 13, p-value = 0.005297
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## 0.2571296 0.8841828
## sample estimates:
##      cor
## 0.6798447

cor.test(pas$Mean.telomere.adult, pas$PCA3, alternative = c("two.sided"), method = c("pearson"))

##
## Pearson's product-moment correlation
##
## data: pas$Mean.telomere.adult and pas$PCA3
## t = -0.95629, df = 13, p-value = 0.3564
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.6794033 0.2945861
## sample estimates:
##      cor
## -0.2563634

```

```
#Multivariate phylogenetic analysis
```

```
### defininf priors
phen.var<-apply(Bird.data[,c("Mean.telomere.adult","PCA1","PCA2", "PCA3")],2,function(m)
  var(m,na.rm=T))

#phenotypic variance divided 80% residual and 20% between-subject as prior, uninformative
prior3 <- list(R=list(V=diag(4)*phen.var*0.8, nu=2),
  G=list(G1=list(V=diag(4)*0.2*phen.var, nu=2)))

## Multivariate Models
m112.mcmc <- MCMCglmm(cbind(Mean.telomere.adult,PCA1,PCA2,PCA3) ~ trait-1,

  random = ~us(trait):animal,
  rcov = ~us(trait):units,
  mev=Bird.data$mev,
  data = Bird.data,
  family=c("gaussian", "gaussian", "gaussian", "gaussian"),
  pedigree = Bird.phylo,
  verbose=T,
  prior=prior3,
  nitt=105000,
  thin = 50, burnin = 10000, pr = TRUE, pl = TRUE, DIC = TRUE)
```

```
summary(m112.mcmc)
```

```
##
## Iterations = 10001:104951
## Thinning interval = 50
## Sample size = 1900
##
## DIC: 838.8021
##
## G-structure: ~us(trait):animal
##
##
##
## traitMean.telomere.adult:traitMean.telomere.adult.animal    post.mean  1-95% CI
## traitPCA1:traitMean.telomere.adult.animal                   -6.4779  -31.98775
## traitPCA2:traitMean.telomere.adult.animal                    0.1728   -8.73642
## traitPCA3:traitMean.telomere.adult.animal                   -0.1311  -6.57440
## traitMean.telomere.adult:traitPCA1.animal                   -6.4779  -31.98775
## traitPCA1:traitPCA1.animal                                   11.0561   1.92590
## traitPCA2:traitPCA1.animal                                   1.0666   -2.19796
## traitPCA3:traitPCA1.animal                                   -0.5104  -3.44715
## traitMean.telomere.adult:traitPCA2.animal                   0.1728   -8.73642
## traitPCA1:traitPCA2.animal                                   1.0666   -2.19796
## traitPCA2:traitPCA2.animal                                   1.3687    0.20596
## traitPCA3:traitPCA2.animal                                   -0.2359  -1.48830
## traitMean.telomere.adult:traitPCA3.animal                   -0.1311  -6.57440
## traitPCA1:traitPCA3.animal                                   -0.5104  -3.44715
## traitPCA2:traitPCA3.animal                                   -0.2359  -1.48830
## traitPCA3:traitPCA3.animal                                   0.6539   0.03702
##
##
## u-95% CI eff.samp
```

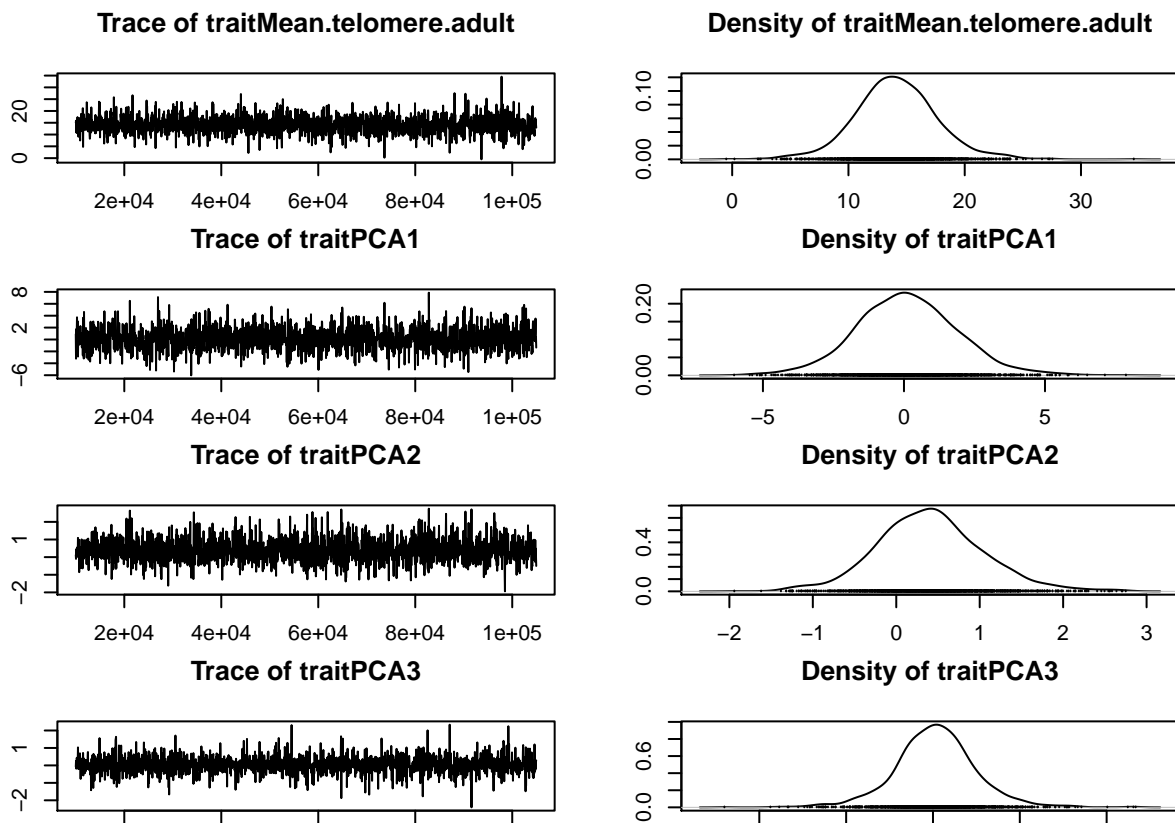
```

## traitMean.telomere.adult:traitMean.telomere.adult.animal 100.3564 1121.3
## traitPCA1:traitMean.telomere.adult.animal 17.5844 962.9
## traitPCA2:traitMean.telomere.adult.animal 8.2066 957.7
## traitPCA3:traitMean.telomere.adult.animal 5.8417 788.8
## traitMean.telomere.adult:traitPCA1.animal 17.5844 962.9
## traitPCA1:traitPCA1.animal 23.0722 1556.5
## traitPCA2:traitPCA1.animal 5.0851 1103.6
## traitPCA3:traitPCA1.animal 2.3544 825.4
## traitMean.telomere.adult:traitPCA2.animal 8.2066 957.7
## traitPCA1:traitPCA2.animal 5.0851 1103.6
## traitPCA2:traitPCA2.animal 3.0404 1133.9
## traitPCA3:traitPCA2.animal 0.7919 736.7
## traitMean.telomere.adult:traitPCA3.animal 5.8417 788.8
## traitPCA1:traitPCA3.animal 2.3544 825.4
## traitPCA2:traitPCA3.animal 0.7919 736.7
## traitPCA3:traitPCA3.animal 1.9617 902.0
##
## R-structure: ~us(trait):units
##
##
## post.mean 1-95% CI
## traitMean.telomere.adult:traitMean.telomere.adult.units 95.7379 57.1744
## traitPCA1:traitMean.telomere.adult.units -2.1016 -8.7489
## traitPCA2:traitMean.telomere.adult.units 1.3876 -1.1701
## traitPCA3:traitMean.telomere.adult.units -0.6477 -4.0537
## traitMean.telomere.adult:traitPCA1.units -2.1016 -8.7489
## traitPCA1:traitPCA1.units 2.6126 0.9060
## traitPCA2:traitPCA1.units 0.3567 -0.1998
## traitPCA3:traitPCA1.units 0.3339 -0.2749
## traitMean.telomere.adult:traitPCA2.units 1.3876 -1.1701
## traitPCA1:traitPCA2.units 0.3567 -0.1998
## traitPCA2:traitPCA2.units 0.4909 0.1852
## traitPCA3:traitPCA2.units -0.2816 -0.5935
## traitMean.telomere.adult:traitPCA3.units -0.6477 -4.0537
## traitPCA1:traitPCA3.units 0.3339 -0.2749
## traitPCA2:traitPCA3.units -0.2816 -0.5935
## traitPCA3:traitPCA3.units 0.9012 0.4485
##
## u-95% CI eff. samp
## traitMean.telomere.adult:traitMean.telomere.adult.units 137.223264 1739
## traitPCA1:traitMean.telomere.adult.units 3.374676 1900
## traitPCA2:traitMean.telomere.adult.units 4.247047 2010
## traitPCA3:traitMean.telomere.adult.units 2.543228 1786
## traitMean.telomere.adult:traitPCA1.units 3.374676 1900
## traitPCA1:traitPCA1.units 4.335664 1746
## traitPCA2:traitPCA1.units 0.988975 1484
## traitPCA3:traitPCA1.units 1.007569 1604
## traitMean.telomere.adult:traitPCA2.units 4.247047 2010
## traitPCA1:traitPCA2.units 0.988975 1484
## traitPCA2:traitPCA2.units 0.796190 1656
## traitPCA3:traitPCA2.units -0.007427 1286
## traitMean.telomere.adult:traitPCA3.units 2.543228 1786
## traitPCA1:traitPCA3.units 1.007569 1604
## traitPCA2:traitPCA3.units -0.007427 1286
## traitPCA3:traitPCA3.units 1.383284 1588
##

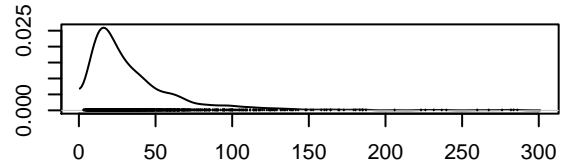
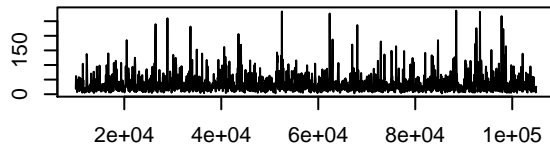
```

```
## Location effects: cbind(Mean.telomere.adult, PCA1, PCA2, PCA3) ~ trait - 1
##
##
##          post.mean l-95% CI u-95% CI eff.samp  pMCMC
## traitMean.telomere.adult 14.10248  7.16382 21.78657    1900 0.00105 **
## traitPCA1                0.11689 -3.30092  3.90086    1900 0.96000
## traitPCA2                0.40532 -0.82111  1.77839    1900 0.51579
## traitPCA3                0.02954 -0.92711  0.99422    1900 0.94421
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

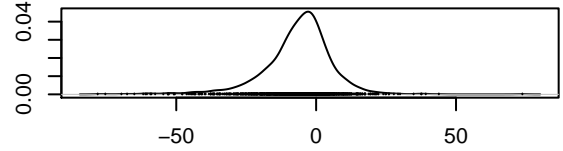
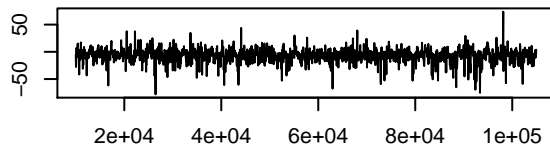
```
par(mar=c(1,4,4,1))
plot(m112.mcmc)
```



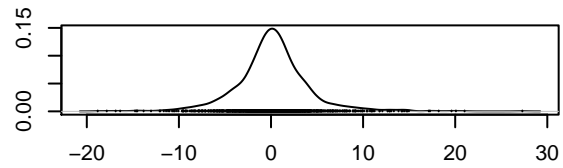
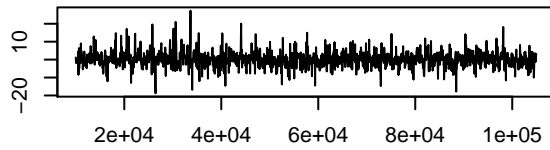
Trace of traitMean.telomere.adult:traitMean.telomere.adult.y of traitMean.telomere.adult:traitMean.telomere.adult.y



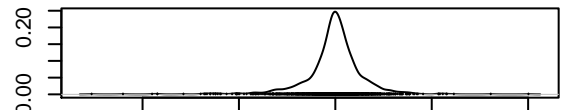
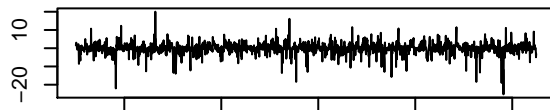
Trace of traitPCA1:traitMean.telomere.adult.y Density of traitPCA1:traitMean.telomere.adult.y



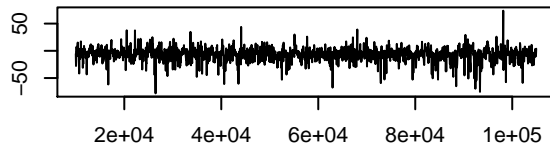
Trace of traitPCA2:traitMean.telomere.adult.y Density of traitPCA2:traitMean.telomere.adult.y



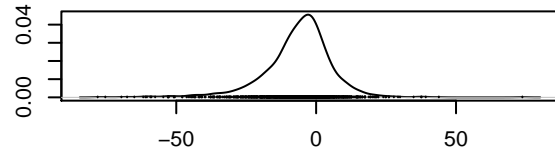
Trace of traitPCA3:traitMean.telomere.adult.y Density of traitPCA3:traitMean.telomere.adult.y



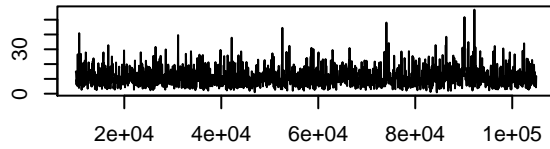
Trace of traitMean.telomere.adult:traitPCA1.ani    Density of traitMean.telomere.adult:traitPCA1.ar



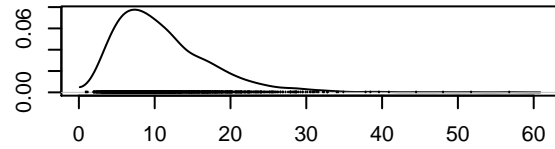
Trace of traitPCA1:traitPCA1.animal



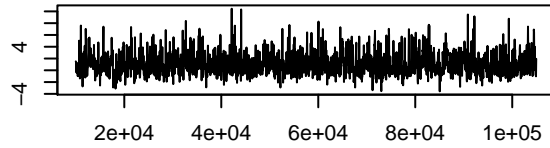
Density of traitPCA1:traitPCA1.animal



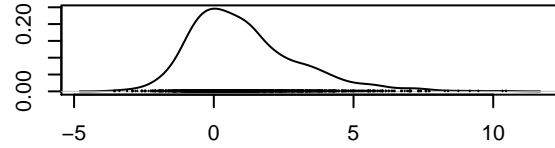
Trace of traitPCA2:traitPCA1.animal



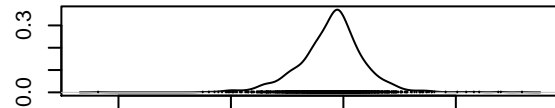
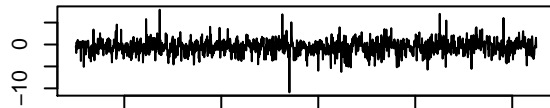
Density of traitPCA2:traitPCA1.animal



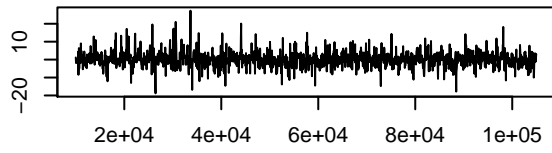
Trace of traitPCA3:traitPCA1.animal



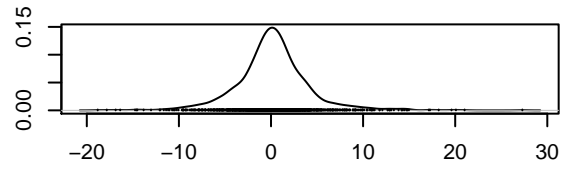
Density of traitPCA3:traitPCA1.animal



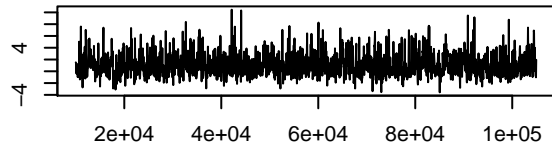
Trace of traitMean.telomere.adult:traitPCA2.ani    Density of traitMean.telomere.adult:traitPCA2.ar



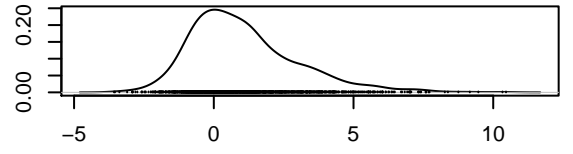
Trace of traitPCA1:traitPCA2.animal



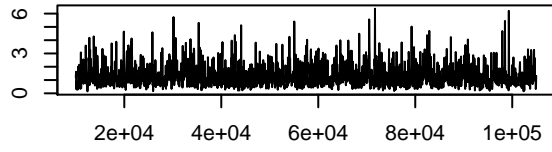
Density of traitPCA1:traitPCA2.animal



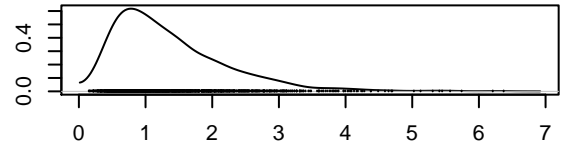
Trace of traitPCA2:traitPCA2.animal



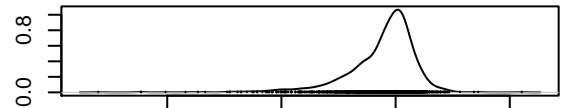
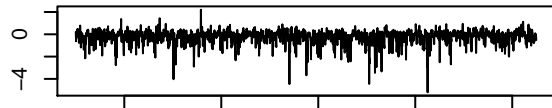
Density of traitPCA2:traitPCA2.animal



Trace of traitPCA3:traitPCA2.animal

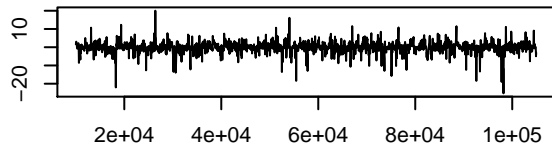


Density of traitPCA3:traitPCA2.animal

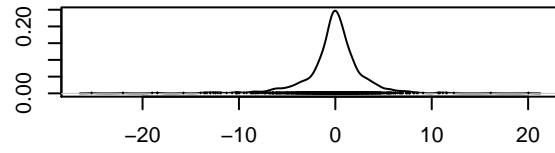




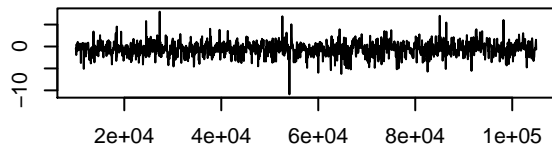
Trace of traitMean.telomere.adult:traitPCA3.ani    Density of traitMean.telomere.adult:traitPCA3.ar



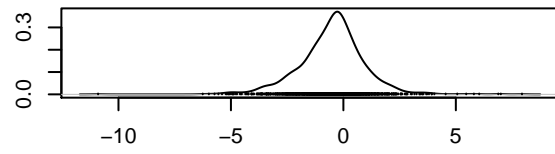
Trace of traitPCA1:traitPCA3.animal



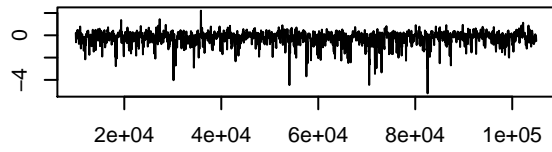
Density of traitPCA1:traitPCA3.animal



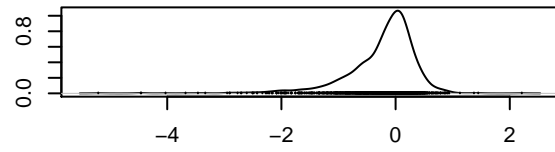
Trace of traitPCA2:traitPCA3.animal



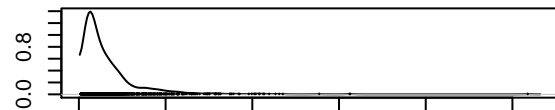
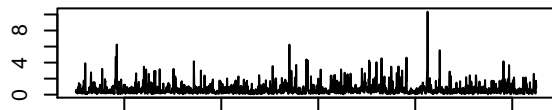
Density of traitPCA2:traitPCA3.animal



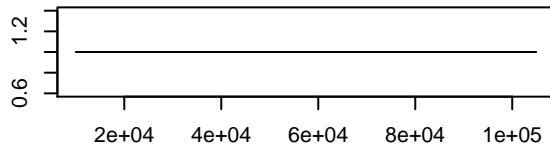
Trace of traitPCA3:traitPCA3.animal



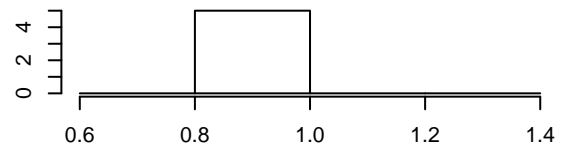
Density of traitPCA3:traitPCA3.animal



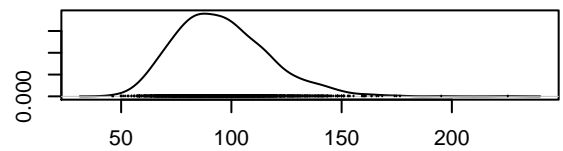
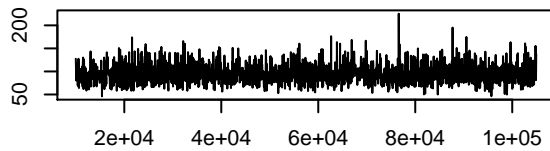
Trace of sqrt(mev):sqrt(mev).meta



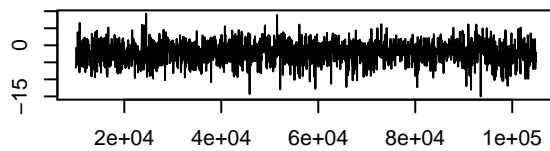
Density of sqrt(mev):sqrt(mev).meta



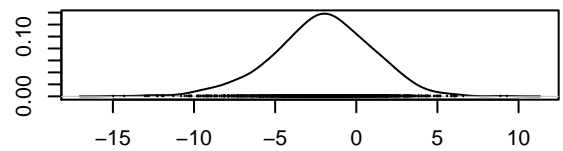
Trace of traitMean.telomere.adult:traitMean.telomere.adult



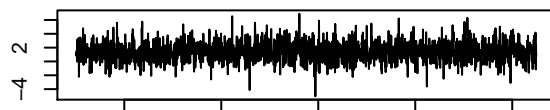
Trace of traitPCA1:traitMean.telomere.adult.un



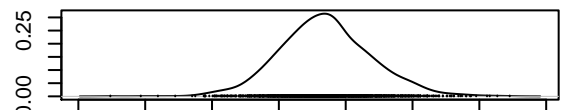
Density of traitPCA1:traitMean.telomere.adult.u



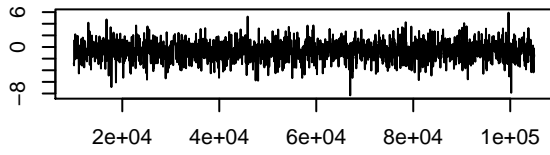
Trace of traitPCA2:traitMean.telomere.adult.un



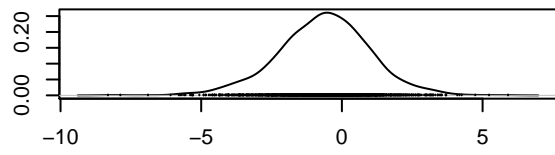
Density of traitPCA2:traitMean.telomere.adult.u



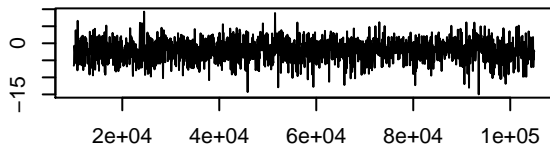
**Trace of traitPCA3:traitMean.telomere.adult.un**



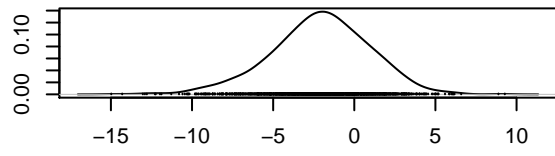
**Density of traitPCA3:traitMean.telomere.adult.u**



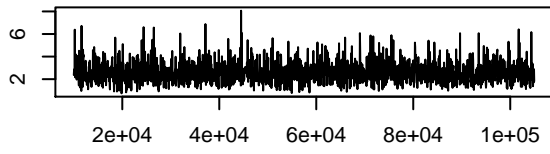
**Trace of traitMean.telomere.adult:traitPCA1.un**



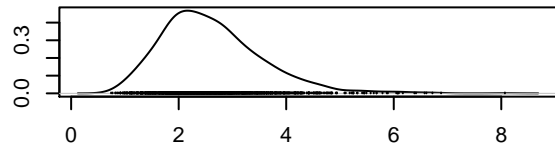
**Density of traitMean.telomere.adult:traitPCA1.u**



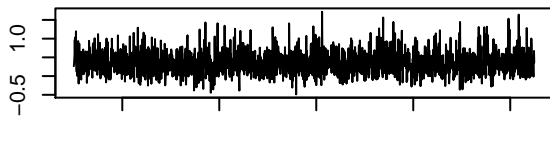
**Trace of traitPCA1:traitPCA1.units**



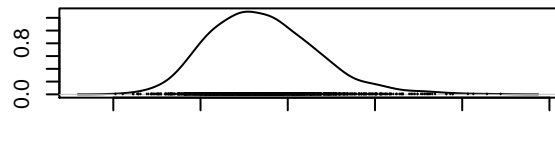
**Density of traitPCA1:traitPCA1.units**



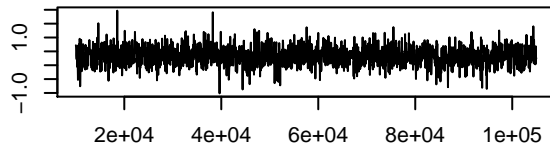
**Trace of traitPCA2:traitPCA1.units**



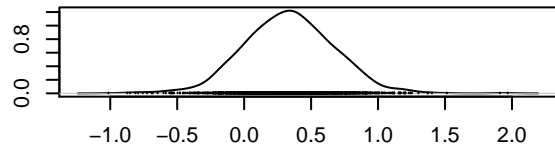
**Density of traitPCA2:traitPCA1.units**



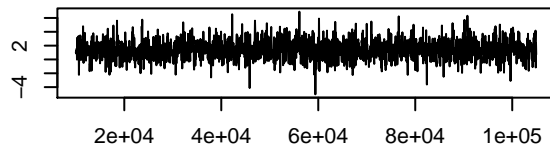
**Trace of traitPCA3:traitPCA1.units**



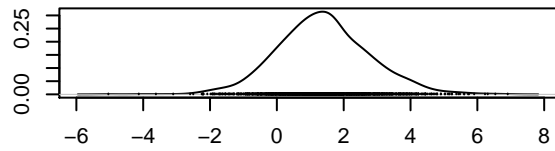
**Density of traitPCA3:traitPCA1.units**



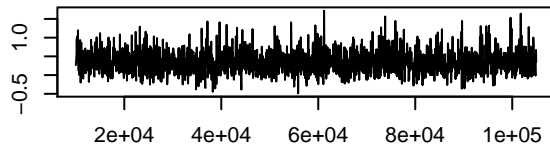
**Trace of traitMean.telomere.adult:traitPCA2.un**



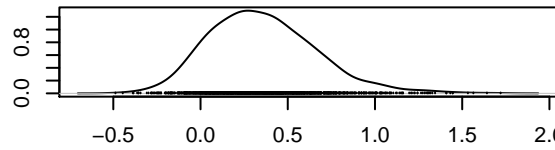
**Density of traitMean.telomere.adult:traitPCA2.u**



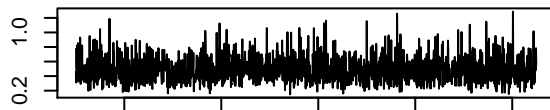
**Trace of traitPCA1:traitPCA2.units**



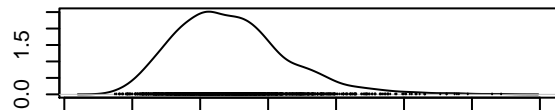
**Density of traitPCA1:traitPCA2.units**



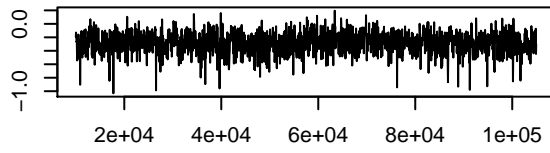
**Trace of traitPCA2:traitPCA2.units**



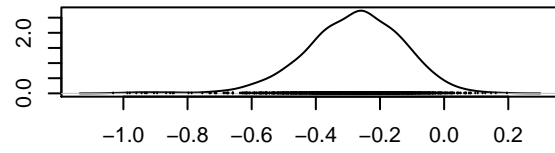
**Density of traitPCA2:traitPCA2.units**



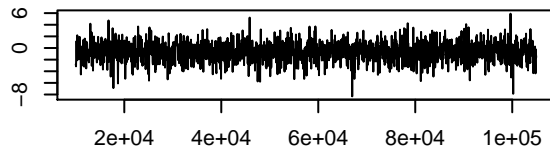
**Trace of traitPCA3:traitPCA2.units**



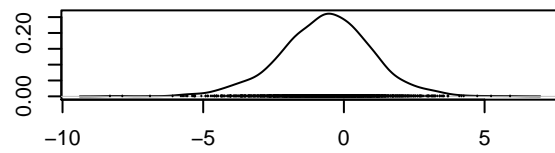
**Density of traitPCA3:traitPCA2.units**



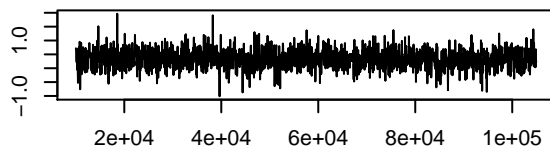
**Trace of traitMean.telomere.adult:traitPCA3.un**



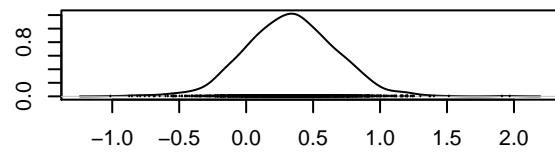
**Density of traitMean.telomere.adult:traitPCA3.u**



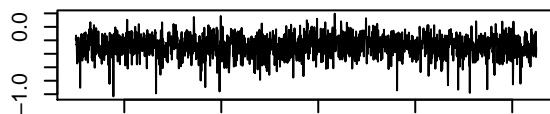
**Trace of traitPCA1:traitPCA3.units**



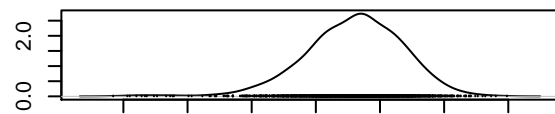
**Density of traitPCA1:traitPCA3.units**

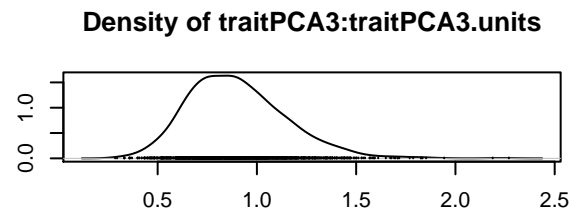
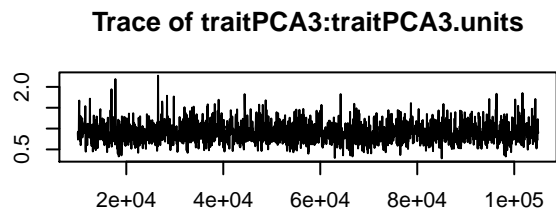


**Trace of traitPCA2:traitPCA3.units**

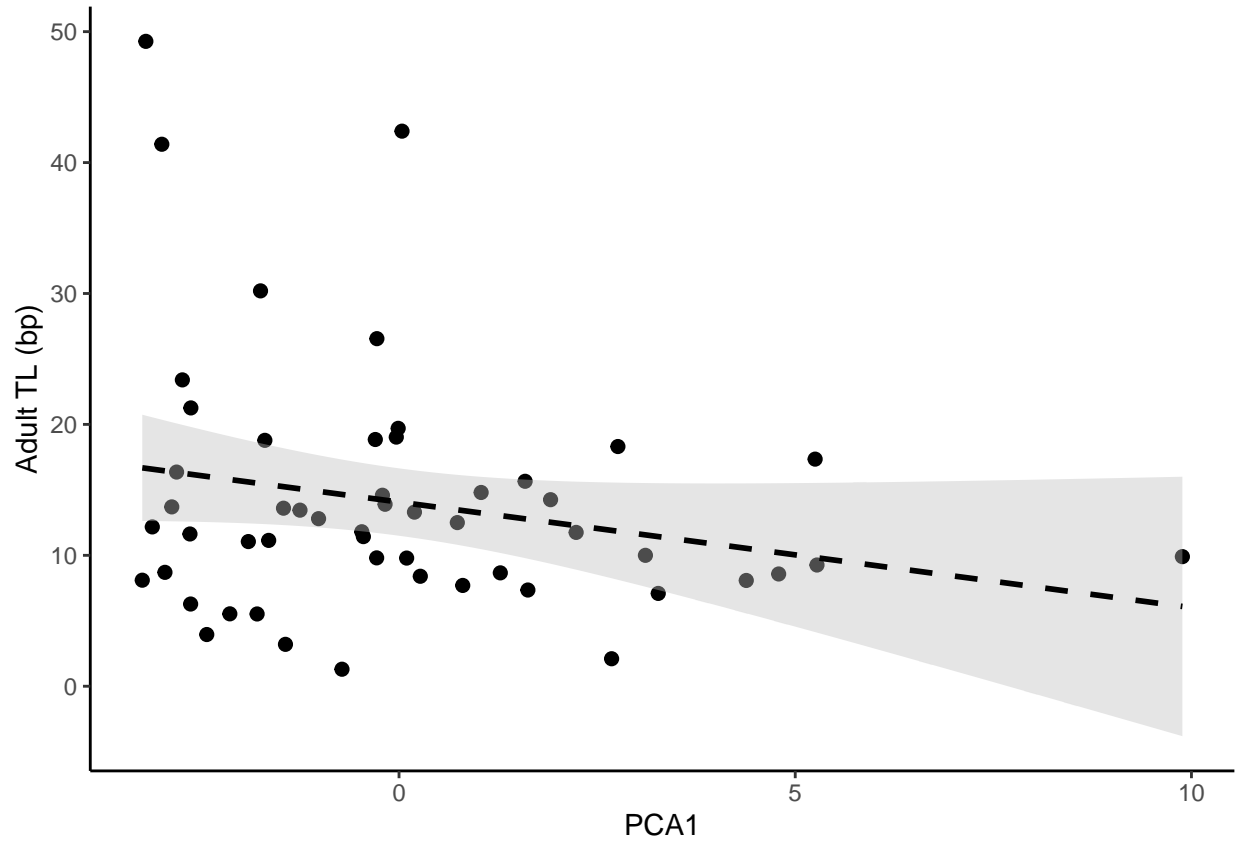


**Density of traitPCA2:traitPCA3.units**

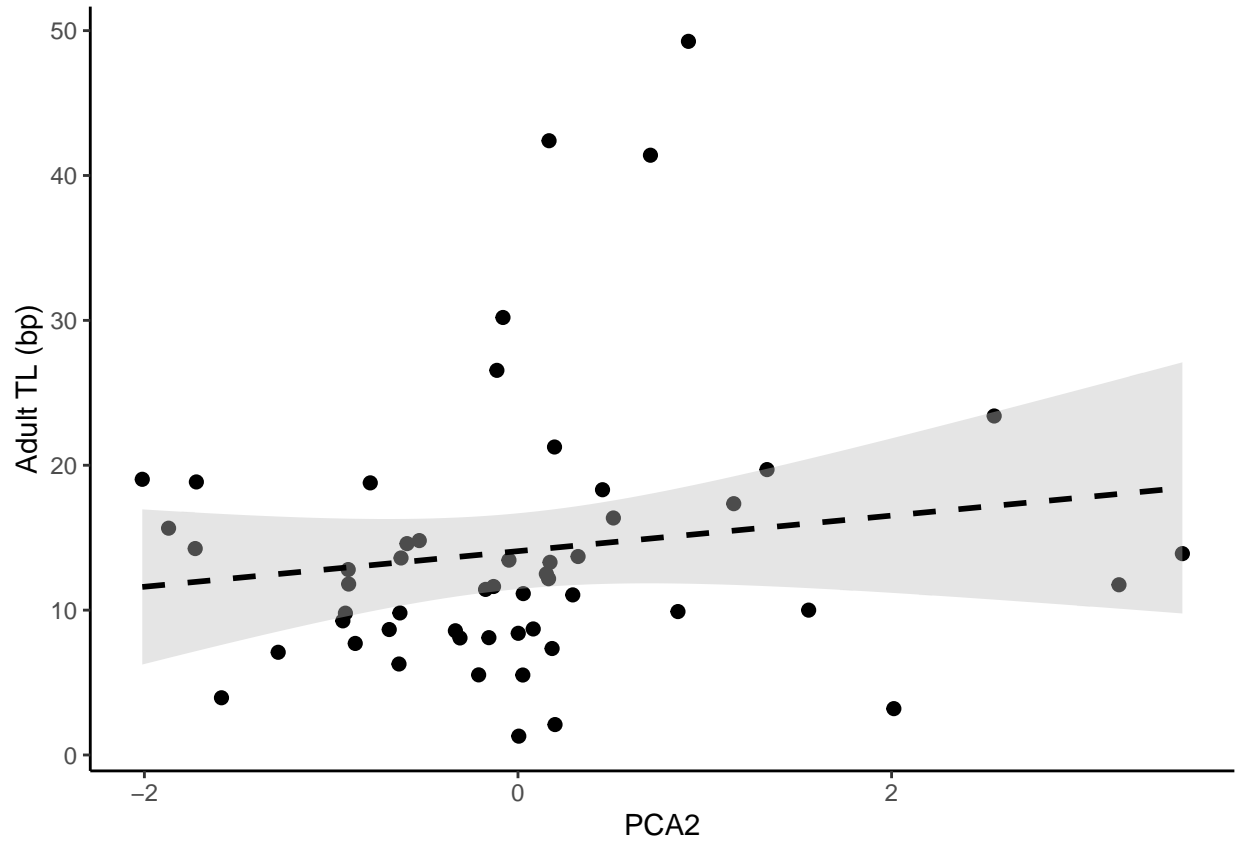




```
p<-ggplot(Bird.data, aes(x=Bird.data$PCA1, y=Bird.data$Mean.telomere.adult)) +
  geom_point(size=2)+scale_color_grey()+
  theme_classic()+geom_smooth(method=lm,linetype="dashed",color="black",fill="grey")
p+labs(x="PCA1",y="Adult TL (bp)")
```

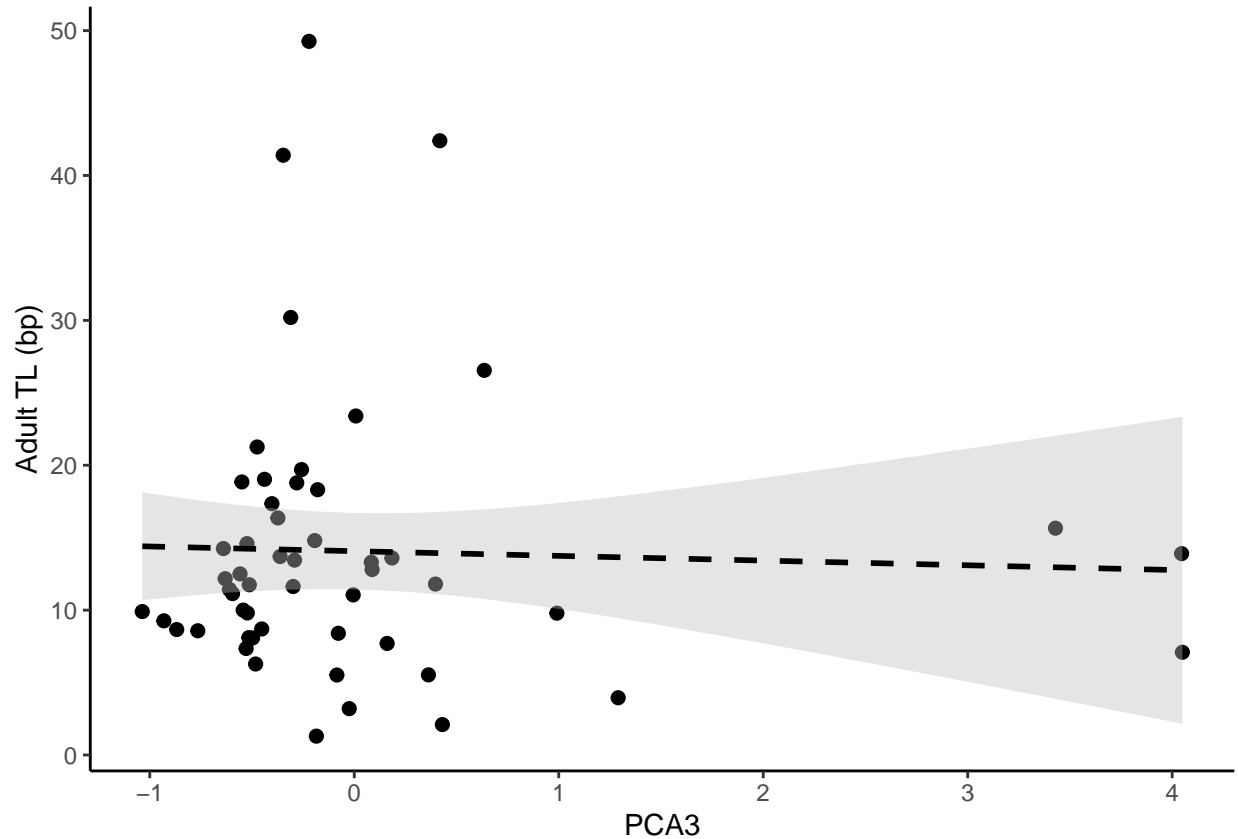


```
p<-ggplot(Bird.data, aes(x=Bird.data$PCA2, y=Bird.data$Mean.telomere.adult)) +
  geom_point(size=2)+
  scale_color_grey()+
  theme_classic()+
  geom_smooth(method=lm,linetype="dashed",color="black",fill="grey")
p+labs(x="PCA2",y="Adult TL (bp)")
```



```
p<-ggplot(Bird.data, aes(x=Bird.data$PCA3, y=Bird.data$Mean.telomere.adult)) +
  geom_point(size=2)+
  scale_color_grey()+theme_classic()+
  geom_smooth(method=lm,linetype="dashed",color="black",fill="grey")
p+labs(x="PCA3",y="Adult TL (bp)")
```





We can use the MCMCglmm function `posterior.cor()` to convert the posterior (co)variance components to posteriors of the correlation. To this end, we need to identify the columns holding the posteriors (`varX`, `covXY`, `covYX`, `varY`). The following output illustrates the principle:

### Variance and covariance explained by phylogeny (animal)

```
#colnames(m112.mcmc$VCV) #to see where the VCV matrix elements are
```

```
#MeanTL + PCA1
```

```
posterior.mode((m112.mcmc$VCV[,c('traitMean.telomere.adult:traitMean.telomere.adult.animal', "traitPCA1:tra
```

```
## traitMean.telomere.adult:traitMean.telomere.adult.animal
##                                16.206317
##          traitPCA1:traitMean.telomere.adult.animal
##                                -1.740873
##          traitMean.telomere.adult:traitPCA1.animal
##                                -1.740873
##                                traitPCA1:traitPCA1.animal
##                                8.307329
```

```
HPDinterval((m112.mcmc$VCV[,c('traitMean.telomere.adult:traitMean.telomere.adult.animal', "traitPCA1:tra
```

```
##                                lower    upper
```

```
## traitMean.telomere.adult:traitMean.telomere.adult.animal 4.031578 100.35637
## traitPCA1:traitMean.telomere.adult.animal -31.987751 17.58439
## traitMean.telomere.adult:traitPCA1.animal -31.987751 17.58439
## traitPCA1:traitPCA1.animal 1.925901 23.07216
## attr("Probability")
## [1] 0.95
```

*#MeanTL + PCA2*

```
posterior.mode((m112.mcmc$VCV[,c(1,3,9,11)]))
```

```
## traitMean.telomere.adult:traitMean.telomere.adult.animal
## 16.2063173
## traitPCA2:traitMean.telomere.adult.animal
## -0.4444579
## traitMean.telomere.adult:traitPCA2.animal
## -0.4444579
## traitPCA2:traitPCA2.animal
## 0.6586806
```

```
HPDinterval((m112.mcmc$VCV[,c(1,3,9,11)]))
```

```
## lower upper
## traitMean.telomere.adult:traitMean.telomere.adult.animal 4.0315776 100.356369
## traitPCA2:traitMean.telomere.adult.animal -8.7364171 8.206627
## traitMean.telomere.adult:traitPCA2.animal -8.7364171 8.206627
## traitPCA2:traitPCA2.animal 0.2059591 3.040411
## attr("Probability")
## [1] 0.95
```

*#MeanTL + PCA3*

```
posterior.mode((m112.mcmc$VCV[,c(1,4,13,16)]))
```

```
## traitMean.telomere.adult:traitMean.telomere.adult.animal
## 16.20631733
## traitPCA3:traitMean.telomere.adult.animal
## -0.08836524
## traitMean.telomere.adult:traitPCA3.animal
## -0.08836524
## traitPCA3:traitPCA3.animal
## 0.27611395
```

```
HPDinterval((m112.mcmc$VCV[,c(1,4,13,16)]))
```

```
## lower upper
## traitMean.telomere.adult:traitMean.telomere.adult.animal 4.03157756 100.356369
## traitPCA3:traitMean.telomere.adult.animal -6.57440140 5.841732
## traitMean.telomere.adult:traitPCA3.animal -6.57440140 5.841732
## traitPCA3:traitPCA3.animal 0.03701813 1.961709
## attr("Probability")
## [1] 0.95
```

## Proportion of variance explained by phylogeny

```
#For telomeres
```

```
TL_phylogeny<-m112.mcmc$VCV[, 'traitMean.telomere.adult:traitMean.telomere.adult.animal']/(m112.mcmc$VCV  
posterior.mode(TL_phylogeny)
```

```
##      var1  
## 0.1343779
```

```
median(TL_phylogeny)
```

```
## [1] 0.2112206
```

```
mean(TL_phylogeny)
```

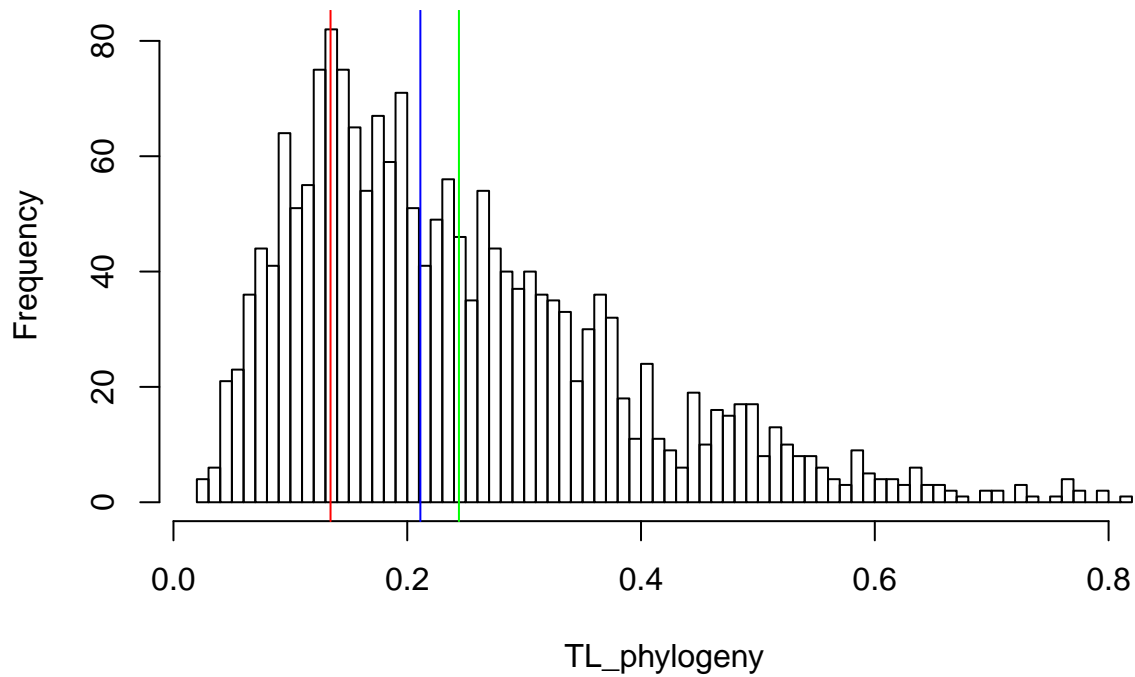
```
## [1] 0.244221
```

```
HPDinterval(TL_phylogeny)
```

```
##           lower      upper  
## var1 0.04174255 0.532838  
## attr(,"Probability")  
## [1] 0.95
```

```
hist(TL_phylogeny, breaks=100)  
abline(v=posterior.mode((TL_phylogeny)), col="red")  
abline(v=median((TL_phylogeny)), col="blue")  
abline(v=mean((TL_phylogeny)), col="green")
```

## Histogram of TL\_phylogeny



```
#For PC1
```

```
PC1_phylogeny<-m112.mcmc$VCV[, 'traitPCA1:traitPCA1.animal']/(m112.mcmc$VCV[, 'traitPCA1:traitPCA1.animal'
```

```
mean(PC1_phylogeny)
```

```
## [1] 0.7666461
```

```
median(PC1_phylogeny)
```

```
## [1] 0.7957121
```

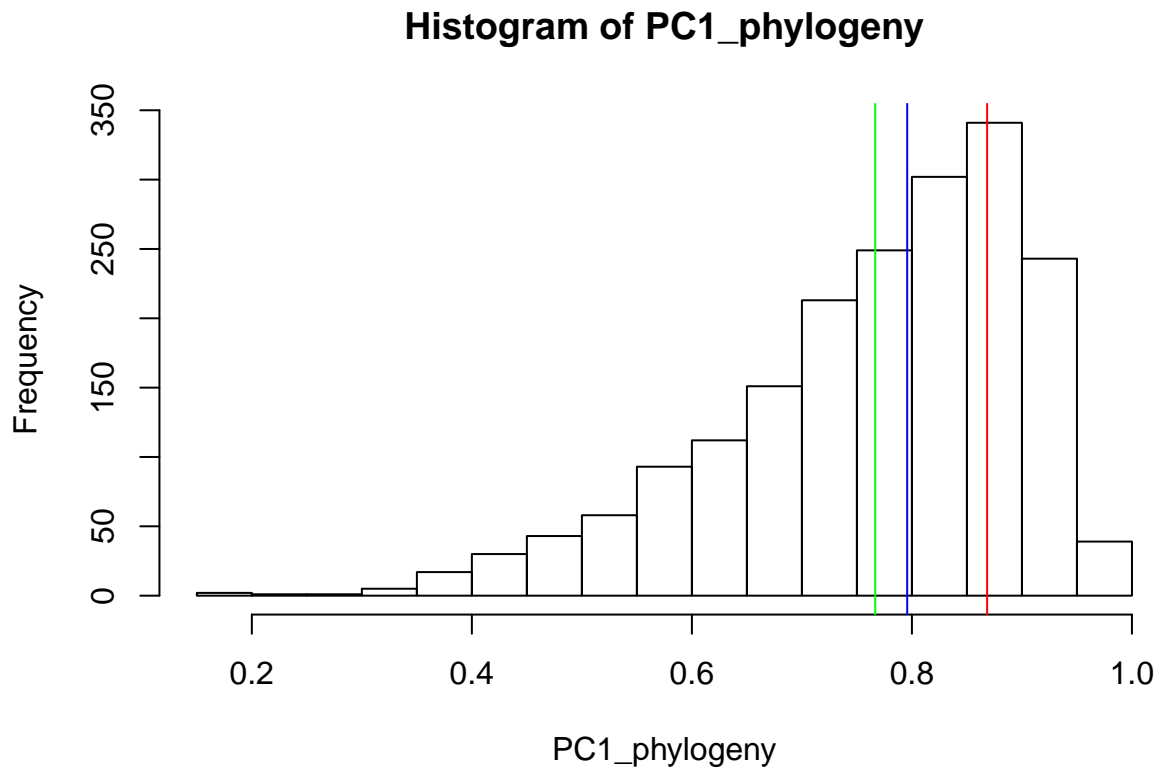
```
posterior.mode(PC1_phylogeny)
```

```
##      var1  
## 0.8683733
```

```
HPDinterval(PC1_phylogeny)
```

```
##      lower      upper  
## var1 0.4915267 0.9636186  
## attr("Probability")  
## [1] 0.95
```

```
hist(PC1_phylogeny, breaks=15)
abline(v=posterior.mode(PC1_phylogeny), col="red")
abline(v=median(PC1_phylogeny), col="blue")
abline(v=mean(PC1_phylogeny), col="green")
```



```
#For PC2
PC2_phylogeny<-m112.mcmc$VCV[, 'traitPCA2:traitPCA2.animal']/(m112.mcmc$VCV[, 'traitPCA2:traitPCA2.animal'
mean(PC2_phylogeny)
```

```
## [1] 0.6861445
```

```
median(PC2_phylogeny)
```

```
## [1] 0.7080719
```

```
posterior.mode(PC2_phylogeny)
```

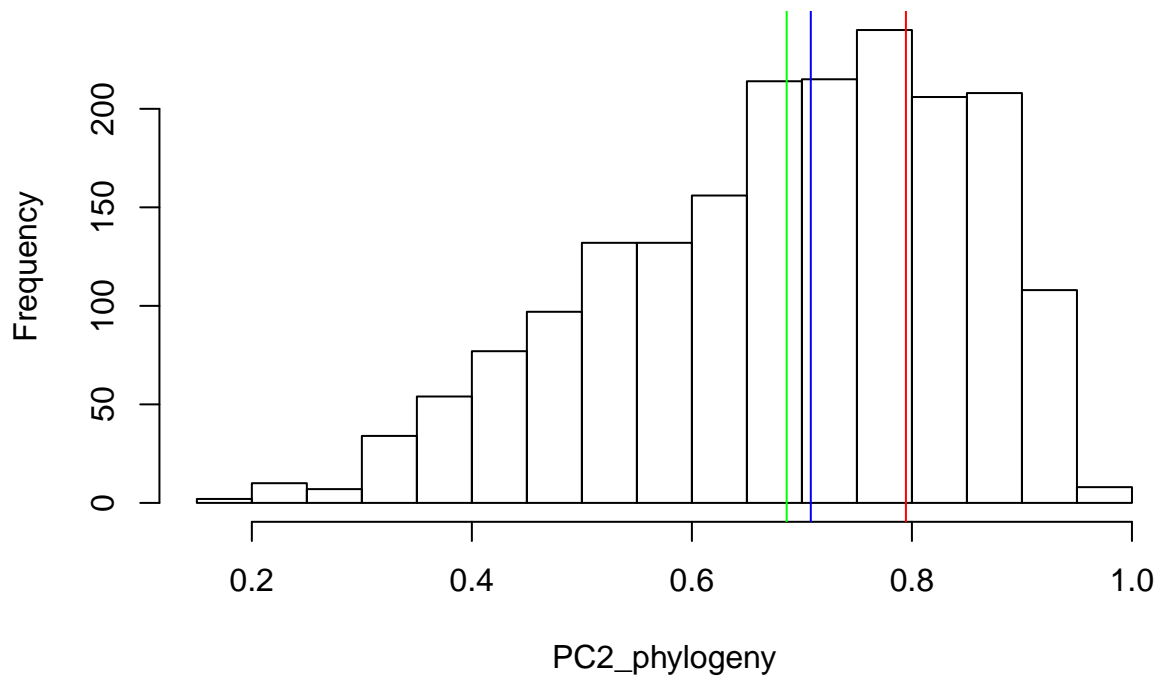
```
##      var1
## 0.7945383
```

```
HPDinterval(PC2_phylogeny)
```

```
##           lower      upper  
## var1 0.3892549 0.9443612  
## attr("Probability")  
## [1] 0.95
```

```
hist(PC2_phylogeny, breaks=15)  
abline(v=posterior.mode((PC2_phylogeny)), col="red")  
abline(v=median((PC2_phylogeny)), col="blue")  
abline(v=mean((PC2_phylogeny)), col="green")
```

## Histogram of PC2\_phylogeny



```
#For PC3
```

```
PC3_phylogeny<-m112.mcmc$VCV[, 'traitPCA3:traitPCA3.animal']/(m112.mcmc$VCV[, 'traitPCA3:traitPCA3.animal
```

```
mean(PC3_phylogeny)
```

```
## [1] 0.3619078
```

```
median(PC3_phylogeny)
```

```
## [1] 0.3250123
```

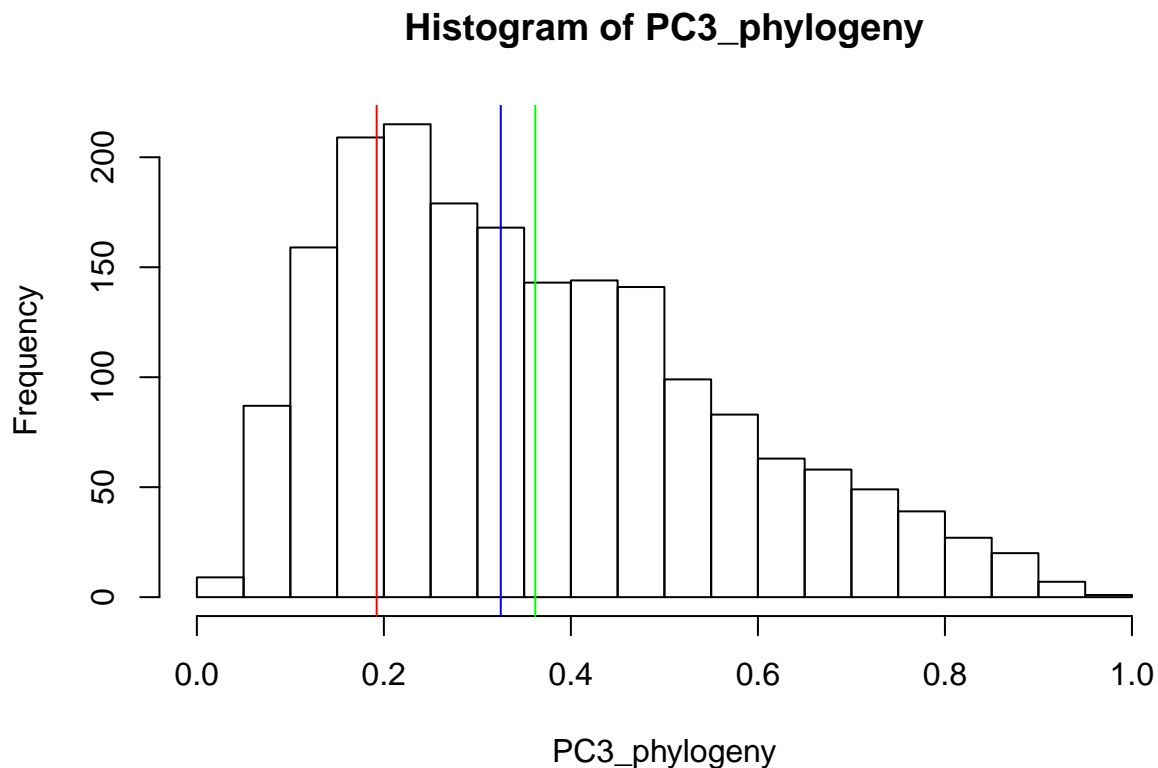
```
posterior.mode(PC3_phylogeny)
```

```
##      var1  
## 0.1923041
```

```
HPDinterval(PC3_phylogeny)
```

```
##          lower      upper  
## var1 0.04538315 0.7515136  
## attr("Probability")  
## [1] 0.95
```

```
hist(PC3_phylogeny, breaks=15)  
abline(v=posterior.mode((PC3_phylogeny)), col="red")  
abline(v=median((PC3_phylogeny)), col="blue")  
abline(v=mean((PC3_phylogeny)), col="green")
```



### Phylogeny correlation, mode, and 95% CRI (correlation between MeanTL and PCs, explained by phylogeny)

#We can use the MCMCglmm function posterior.cor() to convert the posterior (co)variance components to posteriors of the correlation. #To this end, we need to identify the columns holding the posteriors (varX covXY, covYX, varY). #The following output illustrates the principle: # Phylogeny correlation, mode, and 95% CRI

```
#MeanTL + PCA1
PCa1cor<-posterior.cor(m112.mcmc$VCV[,c('traitMean.telomere.adult:traitMean.telomere.adult.animal',"tra
posterior.mode(PCa1cor[,2])
```

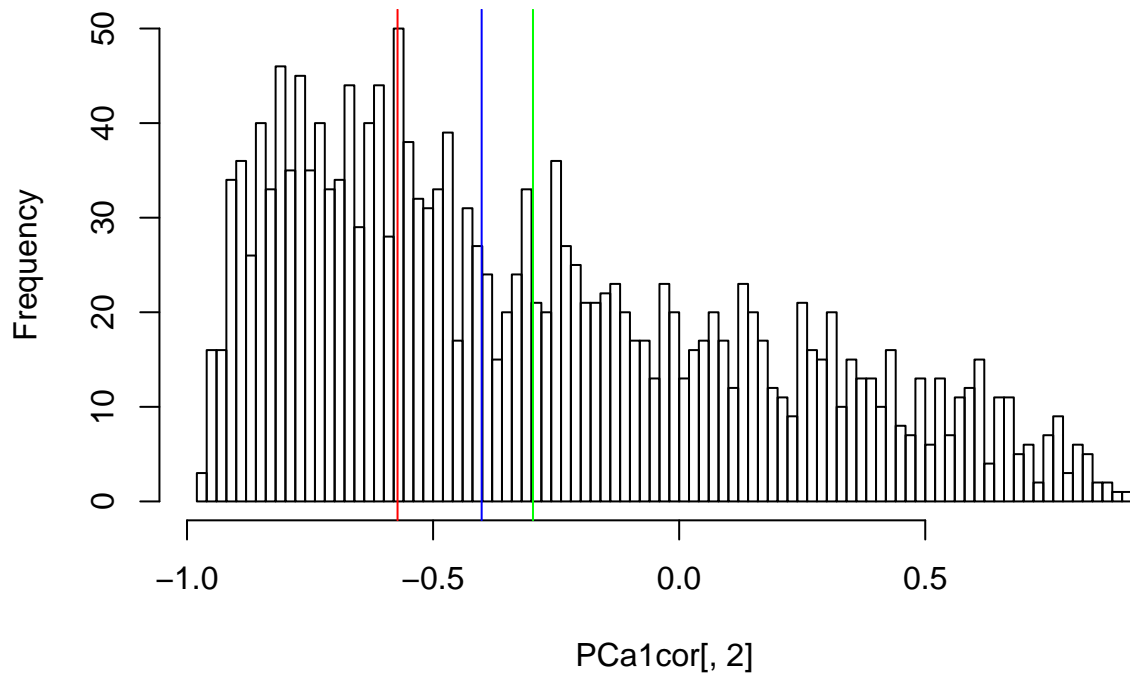
```
##      var1
## -0.5721795
```

```
HPDinterval(PCa1cor[,2])
```

```
##      lower      upper
## var1 -0.9451916 0.6062939
## attr("Probability")
## [1] 0.95
```

```
hist(PCa1cor[,2], breaks=100)
abline(v=posterior.mode((PCa1cor[,2])), col="red")
abline(v=median((PCa1cor[,2])), col="blue")
abline(v=mean((PCa1cor[,2])), col="green")
```

**Histogram of PCa1cor[, 2]**



```
#MeanTL + PCA2
PCa2cor<-posterior.cor(m112.mcmc$VCV[,c('traitMean.telomere.adult:traitMean.telomere.adult.animal',"tra
posterior.mode(PCa2cor[,2])
```

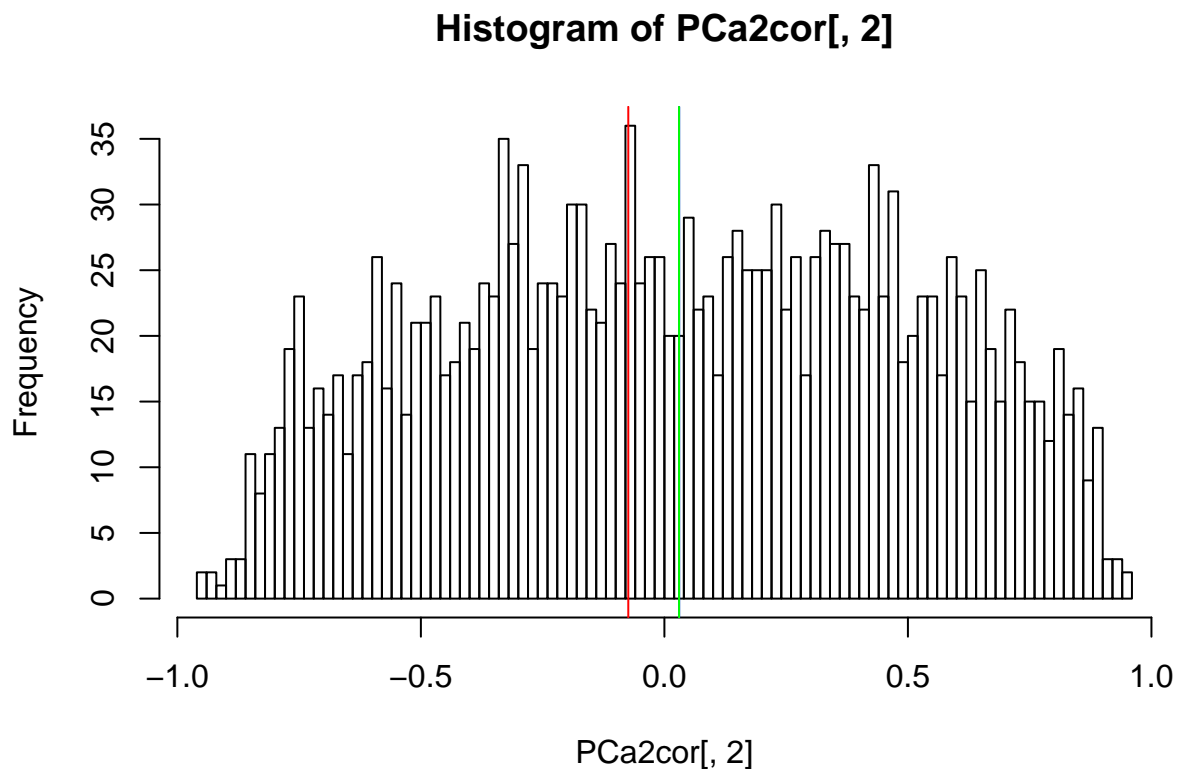


```
##      var1
## -0.0741601
```

```
HPDinterval(PCa2cor[,2])
```

```
##      lower      upper
## var1 -0.77643 0.8431683
## attr("Probability")
## [1] 0.95
```

```
hist(PCa2cor[,2], breaks=100)
abline(v=posterior.mode((PCa2cor[,2])), col="red")
abline(v=median((PCa2cor[,2])), col="blue")
abline(v=mean((PCa2cor[,2])), col="green")
```



```
#MeanTL + PCA3
```

```
PCa3cor<-posterior.cor(m112.mcmc$VCV[,c('traitMean.telomere.adult:traitMean.telomere.adult.animal',"tra
posterior.mode(PCa3cor[,2])
```

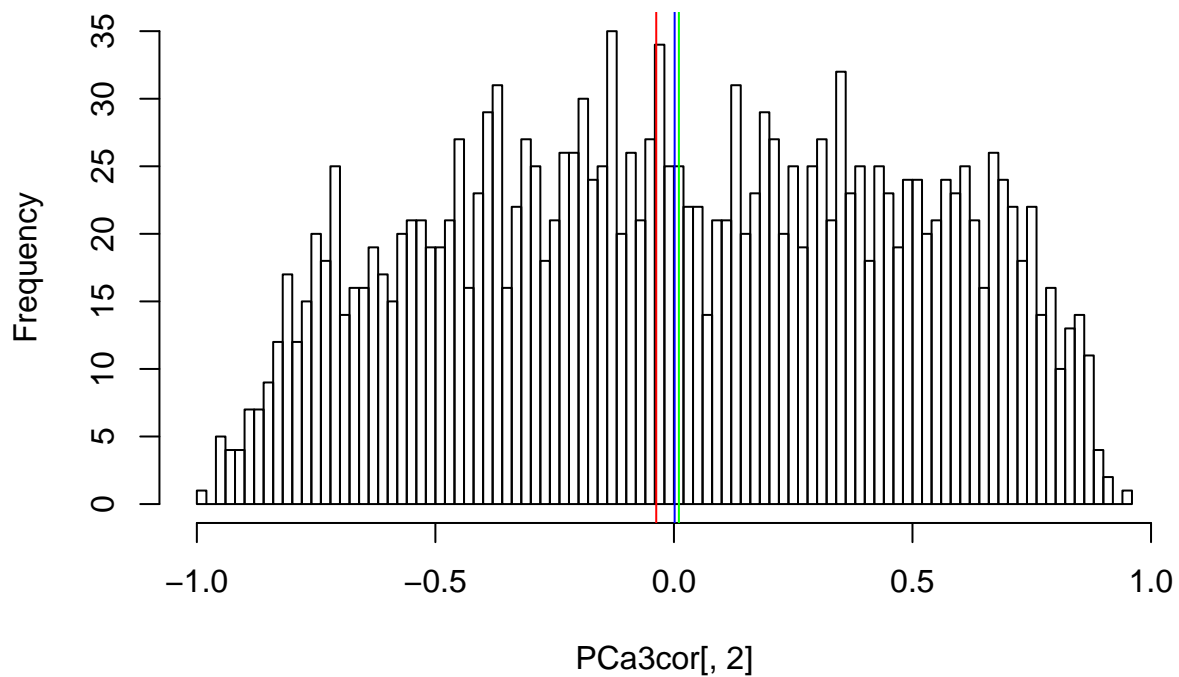
```
##      var1
## -0.03712005
```

```
HPDinterval(PCa3cor[,2])
```

```
##           lower      upper  
## var1 -0.8287246 0.8014177  
## attr("Probability")  
## [1] 0.95
```

```
hist(PCa3cor[,2], breaks=100)  
abline(v=posterior.mode((PCa3cor[,2])), col="red")  
abline(v=median((PCa3cor[,2])), col="blue")  
abline(v=mean((PCa3cor[,2])), col="green")
```

**Histogram of PCa3cor[, 2]**



Residual correlations (Correlation between MeanTL and PCs, not explained by phylogeny), mode and 95% CRI

```
#MeanTL + PCA1  
PCa1corres<-posterior.cor(m112.mcmc$VCV[,c("traitMean.telomere.adult:traitMean.telomere.adult.units", "t  
posterior.mode(PCa1corres[,2])
```

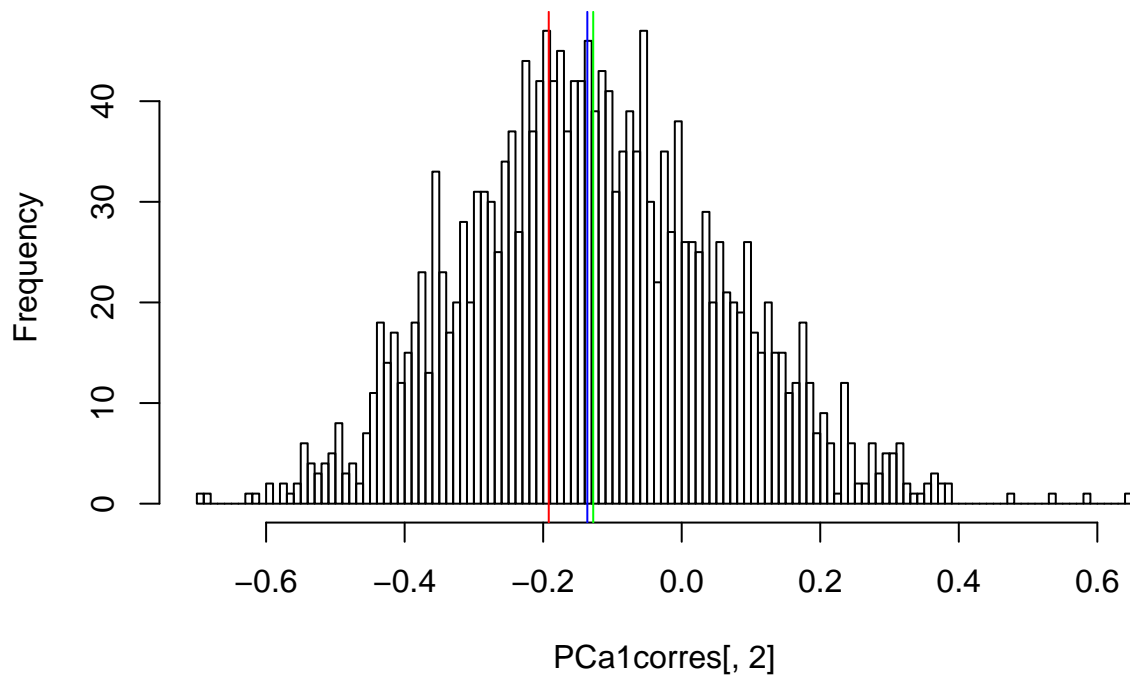
```
##           var1  
## -0.1919689
```

```
HPDinterval(PCa1corres[,2])
```

```
##           lower      upper  
## var1 -0.4653528 0.2488882  
## attr(,"Probability")  
## [1] 0.95
```

```
hist(PCa1corres[,2], breaks=100)  
abline(v=posterior.mode((PCa1corres[,2])), col="red")  
abline(v=median((PCa1corres[,2])), col="blue")  
abline(v=mean((PCa1corres[,2])), col="green")
```

## Histogram of PCa1corres[, 2]



```
#MeanTL + PCA2
```

```
PCa2corres<-posterior.cor(m112.mcmc$VCV[,c("traitMean.telomere.adult:traitMean.telomere.adult.units", "t  
posterior.mode(PCa2corres[,2])
```

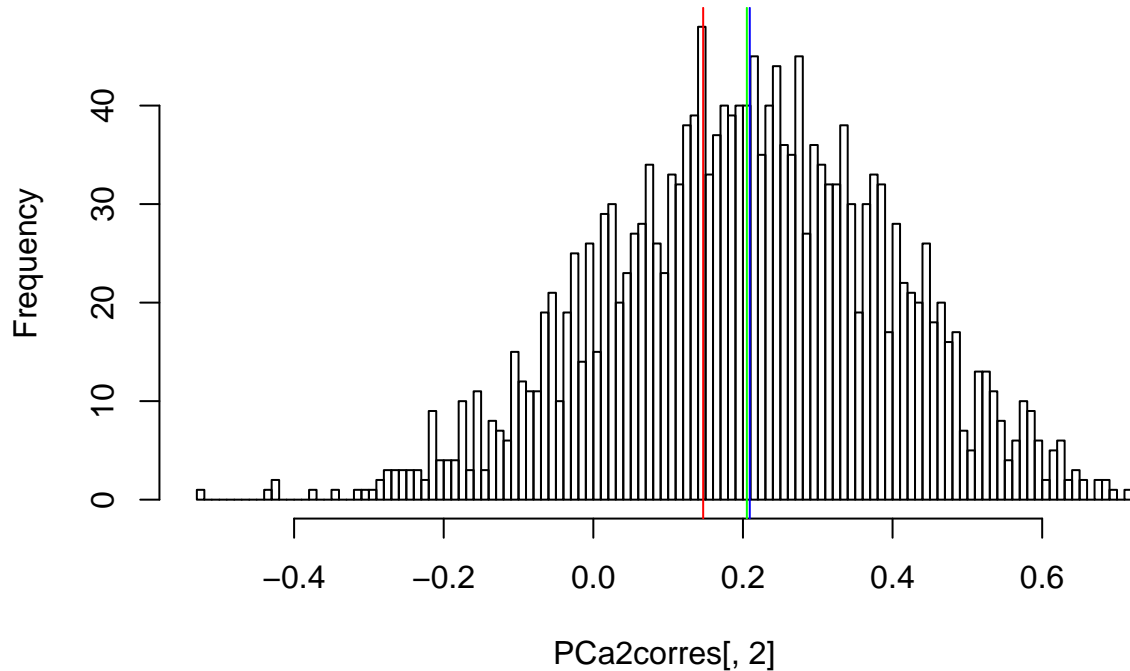
```
##      var1  
## 0.1468357
```

```
HPDinterval(PCa2corres[,2])
```

```
##           lower      upper  
## var1 -0.1596638 0.5889144  
## attr(,"Probability")  
## [1] 0.95
```

```
hist(PCa2corres[,2], breaks=100)
abline(v=posterior.mode((PCa2corres[,2])), col="red")
abline(v=median((PCa2corres[,2])), col="blue")
abline(v=mean((PCa2corres[,2])), col="green")
```

## Histogram of PCa2corres[, 2]



```
#MeanTL + PCA3
```

```
PCa3corres<-posterior.cor(m112.mcmc$VCV[,c("traitMean.telomere.adult:traitMean.telomere.adult.units", "t
posterior.mode(PCa3corres[,2])
```

```
##          var1
## -0.05467054
```

```
HPDinterval(PCa3corres[,2])
```

```
##          lower  upper
## var1 -0.3966478 0.271099
## attr("Probability")
## [1] 0.95
```

```
hist(PCa3corres[,2], breaks=100)
abline(v=posterior.mode((PCa3corres[,2])), col="red")
abline(v=median((PCa3corres[,2])), col="blue")
abline(v=mean((PCa3corres[,2])), col="green")
```

**Histogram of PCa3corres[, 2]**

