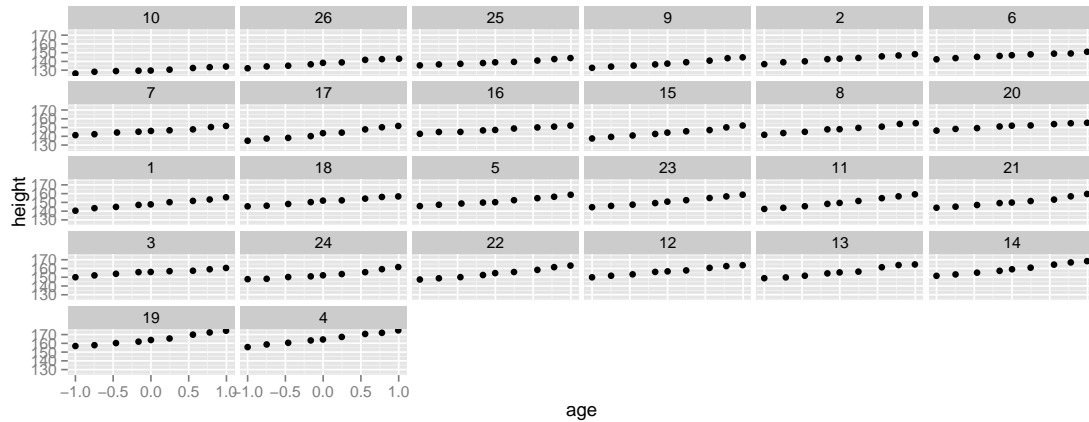


Stat 506 Assignment 7

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1. Revisit the Oxboys data from HW6.

(a) Refit the random intercept and slope model using a correlation between intercept and slope as in Gelmans code on p 376.

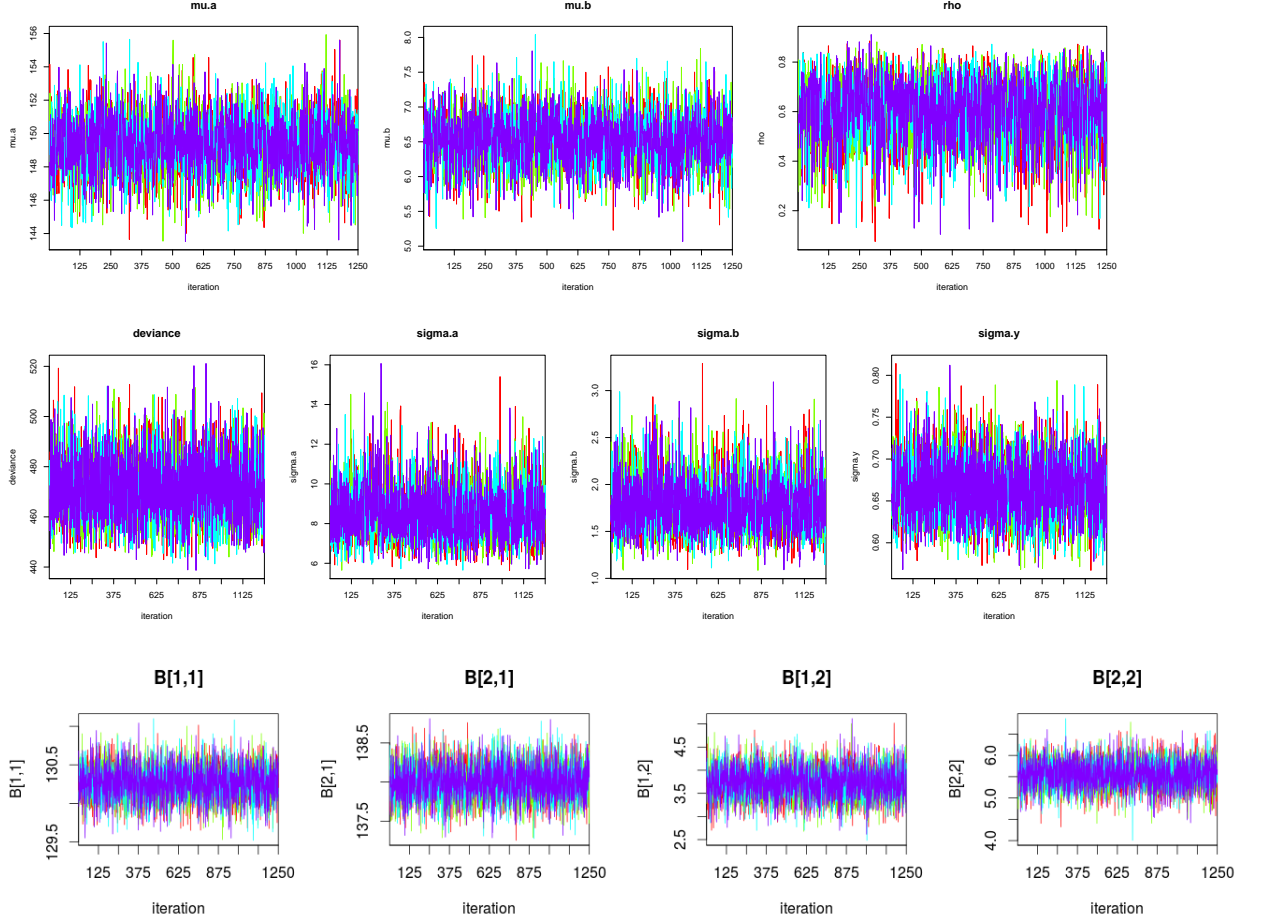


```
#Random slope and intercept with correlation a priori

setwd("~/Documents/Stat506/Homework/HW7")

cat("
model {
  for(i in 1:n){
    y[i] ~ dnorm (y.hat[i], tau.y)
    y.hat[i] <- B[subject[i], 1] + B[subject[i],2] * x[i]
  }
  tau.y <- pow(sigma.y, -2)
  sigma.y ~ dunif (0, 100)
  for(j in 1:J){
    B[j, 1:2] ~ dmnorm(B.hat[j, ], Tau.B[,])
    B.hat[j,1] <- mu.a
    B.hat[j,2] <- mu.b
  }
  mu.a ~ dnorm (0, .0001)
  mu.b ~ dnorm (0, .0001)
  Tau.B[1:2,1:2] <- inverse(Sigma.B[,])
  Sigma.B[1,1] <- pow(sigma.a, 2)
  sigma.a ~ dunif (0, 100)
  Sigma.B[2,2] <- pow(sigma.b, 2)
  sigma.b ~ dunif (0, 100)
  Sigma.B[1,2] <- rho*sigma.a*sigma.b
  Sigma.B[2,1] <- Sigma.B[1,2]
  rho ~ dunif (-1, 1)}", file="CorrSlopInt.jags")
```

(b) Give appropriate plots and summaries.



	mean	sd	2.5%	97.5%	Rhat	n.eff
B[1,1]	130.27	0.22	129.84	130.69	1.00	5000.00
B[10,1]	144.29	0.22	143.85	144.72	1.00	5000.00
B[1,2]	3.73	0.34	3.08	4.38	1.00	5000.00
B[10,2]	7.04	0.34	6.38	7.71	1.00	5000.00
deviance	471.24	11.88	449.67	496.46	1.00	2700.00
mu.a	149.35	1.68	145.93	152.64	1.00	5000.00
mu.b	6.52	0.36	5.80	7.24	1.00	5000.00
rho	0.60	0.13	0.30	0.81	1.00	1300.00
sigma.a	8.54	1.29	6.46	11.49	1.00	3300.00
sigma.b	1.78	0.28	1.33	2.42	1.00	5000.00
sigma.y	0.66	0.04	0.60	0.74	1.00	3000.00

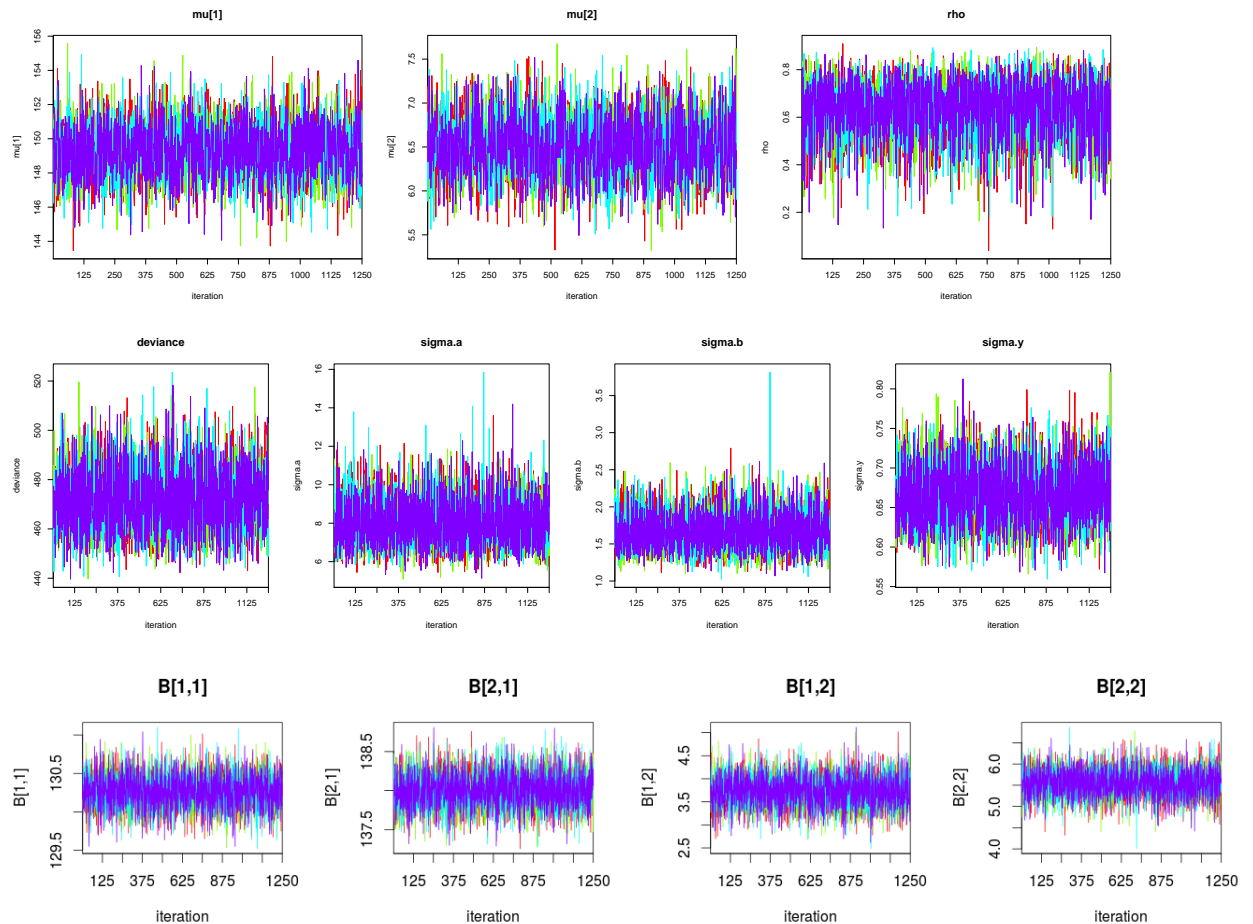
The parameters all converged nicely, with all \hat{R} 's less than 1.005 and all effective sample sizes greater than 1300. The overall y-intercept, averaged over all boys, is estimated to be 149.35 (1.675), and the overall slope is estimated at 6.520 (1.675). The estimated random intercepts and slopes for boys 1 and 10 are shown in the table (the other boys are not displayed). The estimates of the slopes and variance parameters are similar to the estimates before correlation was added to the model a priori. The estimate of ρ is 0.602 (0.131), which is fairly close to the lmer estimate of 0.641.

Traceplots are shown for the fixed effects, ρ , variance parameters, and the deviance. Traceplots are also shown for the random slopes and intercepts for boys 1 and 2. I looked at the traceplots not shown (all the other boys), and all of the traceplots look good.

- (c) Do the same using the Inverse Wishart distribution as in his code on p 3767. Deviances should match, right?

```
cat("
model {
  for(i in 1:n){
    y[i] ~ dnorm (y.hat[i], tau.y)
    y.hat[i] <- B[subject[i], 1] + B[subject[i], 2] * x[i]
  }
  tau.y <- pow(sigma.y, -2)
  sigma.y ~ dunif (0, 100)

  for(j in 1:J){
    B[j, 1:2] ~ dmnorm(mu, Tau.B[,])
  }
  mu[1] ~ dnorm (0, .0001)
  mu[2] ~ dnorm (0, .0001)
  Tau.B[1:2,1:2] ~ dwish(W[,], 3)
  Sigma.B[1:2,1:2] <- inverse(Tau.B[,])
  sigma.a <- sqrt(Sigma.B[1,1])
  sigma.b <- sqrt(Sigma.B[2,2])
  rho <- Sigma.B[1,2]/sqrt(Sigma.B[1,1]*Sigma.B[2,2])}",
file="wishart.jags")
```



	mean	sd	2.5%	97.5%	Rhat	n.eff
B[1,1]	130.28	0.23	129.82	130.72	1.00	5000.00
B[10,1]	144.28	0.22	143.85	144.72	1.00	5000.00
B[1,2]	3.74	0.34	3.06	4.40	1.00	3100.00
B[10,2]	7.03	0.33	6.37	7.69	1.00	3700.00
deviance	471.90	12.02	450.58	497.89	1.00	5000.00
mu[1]	149.33	1.59	146.29	152.46	1.00	2800.00
mu[2]	6.51	0.34	5.86	7.19	1.00	2600.00
rho	0.63	0.12	0.36	0.82	1.00	5000.00
sigma.a	8.00	1.14	6.13	10.56	1.00	5000.00
sigma.b	1.67	0.25	1.27	2.22	1.00	5000.00
sigma.y	0.67	0.04	0.60	0.74	1.00	5000.00

Again, the parameters converged nicely. The estimates and standard errors are all very similar to the estimates from the previous model. I checked all the traceplots, and although the traceplots for the variance parameters showed a few spikes, (see the plot for σ_b), I'm not worried because there is good overlap otherwise.

2. In the Chapter 15 notes we fit the following model to the owls data.

(a) Translate the model to jags code.

```
cat("
model
{
  for(i in 1:n){
    y[i] ~ dpois(lambda[i])
    log(lambda[i]) <- offset[i]+inprod(b.0[, X.0[i,]]+a[nest[i]]+b[nest[i]]*x[i]
  }
  for(k in 1:K){
    b.0[k]~dnorm(0,0.0001)
  }
  for(j in 1:J) {
    a[j] ~ dnorm(0, tau.a)
    b[j] ~ dnorm(0, tau.b)
  }
  tau.a <- pow(sigma.a, -2)
  sigma.a~dunif(0,1000)
  tau.b <- pow(sigma.b, -2)
  sigma.b~dunif(0,1000)
}", file="poisson4.jags")
```

(b) Run the model to convergence and compare to the glmer output.

I didn't have convergence issues, so I didn't include an `a.adj` term or a `b.adj` term because it wasn't necessary. All of the \hat{R} 's were less than 1.01 and the effective sample sizes were all greater than 230. The summary below shows the `favstats` for the \hat{R} values and the effective sample sizes.

	min	Q1	median	Q3	max	mean	sd	n	missing
	1.00	1.00	1.00	1.00	1.01	1.00	0.00	71	0

	min	Q1	median	Q3	max	mean	sd	n	missing
	300.00	1300.00	2700.00	5000.00	5000.00	2985.92	1792.47	71	0

In the summary below, I show the estimated variance parameters for the JAGs model and then the lmer model. The variances of the random intercept and the random slope were estimated to be slightly larger in the JAGs model

	mean	sd
deviance	4484.27	13.65
sigma.a	0.50	0.09
sigma.b	0.24	0.04

	grp	var1	var2	vcov	sdcov
1	Nest	(Intercept)		0.20	0.45
2	Nest	cTime		0.04	0.21
3	Nest	(Intercept)	cTime	-0.02	-0.19

The estimated fixed effects are shown in detail in the table below. I created indicator variables, **foodsat** and **sexmale** that I used when creating the model matrix. The JAGs estimates are compared to the glmer estimates.

In the JAGs model, a satiated owl with a female parent is estimated to give 0.57 fewer calls than a food deprived owl with a female parent ($se=0.06$). In the lmer model, a satiated owl with a female parent is estimated to give 0.60 fewer calls than a food deprived owl with a female parent ($se=0.06$).

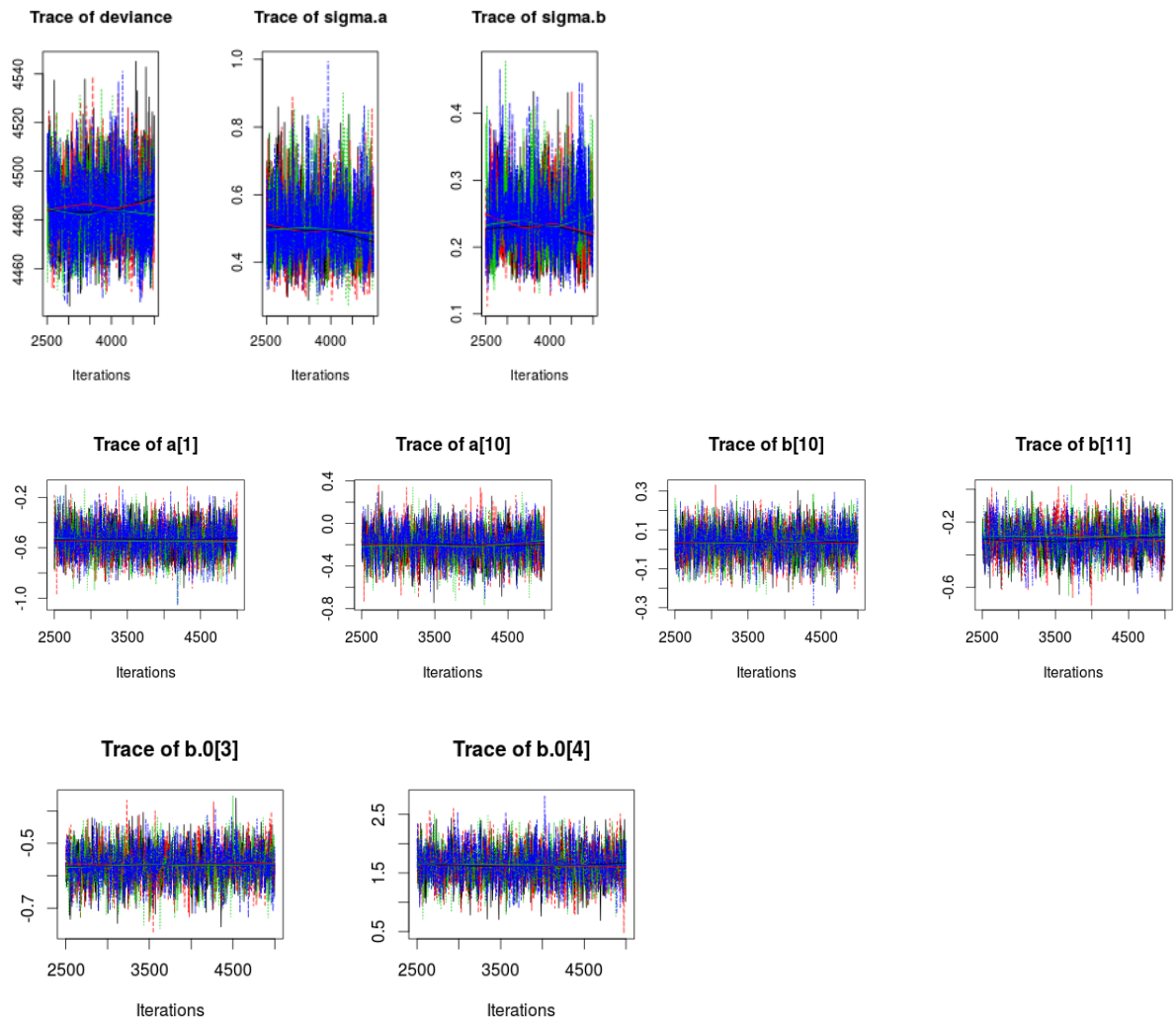
In the JAGs model, a satiated owl with a female parent is estimated to give 0.53 fewer calls than a satiated owl with a male parent ($se=0.32$). In the lmer model, a satiated owl with a female parent is estimated to give 0.57 fewer calls than a satiatedz owl with a male parent ($se=0.32$).

	name	est-JAGS	se-JAGS	est-glmer	se-glmer
b.0[1]	(Intercept)	0.24	0.24	0.30	0.24
b.0[2]	foodsat	-0.57	0.06	-0.60	0.06
b.0[3]	sexmale	-0.53	0.32	-0.57	0.32
b.0[4]	bs1	1.63	0.29	1.50	0.29
b.0[5]	bs2	-0.56	0.21	-0.57	0.21
b.0[6]	bs3	0.60	0.38	0.55	0.37
b.0[7]	bs4	-0.01	0.42	-0.04	0.39
b.0[8]	bs5	-0.59	0.50	-0.58	0.47
b.0[9]	sexmale:foodsat	0.07	0.07	0.07	0.07
b.0[10]	sexmale:bs1	0.70	0.46	0.81	0.46
b.0[11]	sexmale:bs2	0.29	0.30	0.30	0.30
b.0[12]	sexmale:bs3	1.74	0.46	1.65	0.46
b.0[13]	sexmale:bs4	-1.69	0.41	-1.48	0.41
b.0[14]	sexmale:bs5	1.73	0.44	1.71	0.45

Next I compare the random slopes and intercepts in the JAGs model to the lmer model. Only the first five nests are shown. The estimates are fairly similar.

	int-glmer	slope-glmer	int-jags	sd(int)-jags	slope-jags	sd(slope)-jags
AutavauxTV	-0.56	0.24	-0.54	0.13	0.25	0.06
Bochet	-0.02	-0.55	-0.05	0.15	-0.59	0.13
Champmartin	-0.07	-0.04	-0.06	0.14	-0.03	0.07
ChEsard	0.59	-0.01	0.62	0.12	0.02	0.07
Chevroux	-0.21	0.40	-0.24	0.24	0.42	0.10

Lastly I looked at the traceplots. I looked at all the traceplots for the random effects and fixed effects. Only some are shown, but they all looked good. The traceplots of the deviance and the variance parameters are also shown.



Rcode Appendix

```
require(ggplot2)
require(nlme)
data(Oxboys)
ggplot(Oxboys, aes(age, height))+geom_point()+facet_wrap(~Subject)
```

```
#Random slope and intercept with correlation a priori
```

```
setwd("~/Documents/Stat506/Homework/HW7")

cat("
model {
  for(i in 1:n){
    y[i] ~ dnorm (y.hat[i], tau.y)
    y.hat[i] <- B[subject[i], 1] + B[subject[i],2] * x[i]
  }
  tau.y <- pow(sigma.y, -2)
  sigma.y ~ dunif (0, 100)
  for(j in 1:J){
    B[j, 1:2] ~ dmnorm(B.hat[j, ], Tau.B[,])
    B.hat[j,1] <- mu.a
    B.hat[j,2] <- mu.b
  }
  mu.a ~ dnorm (0, .0001)
  mu.b ~ dnorm (0, .0001)
  Tau.B[1:2,1:2] <- inverse(Sigma.B[,])
  Sigma.B[1,1] <- pow(sigma.a, 2)
  sigma.a ~ dunif (0, 100)
  Sigma.B[2,2] <- pow(sigma.b, 2)
  sigma.b ~ dunif (0, 100)
  Sigma.B[1,2] <- rho*sigma.a*sigma.b
  Sigma.B[2,1] <- Sigma.B[1,2]
  rho ~ dunif (-1, 1)}", file="CorrSlopInt.jags")
```

```
##jags call
library(R2jags)
set.seed(52)

oxboys.data <-with(Oxboys, list(n=nrow(Oxboys), J=length(unique(Subject)),
                               subject=as.integer(Subject),
                               y= height, x=age))

oxboys.init2 <- function (){
  list (mu.a=rnorm(1), mu.b=rnorm(1), rho = runif(1, -1, 1),
        sigma.y=runif(1), sigma.a=runif(1) )
}
oxboys.param2 <- c ("B", "mu.a", "mu.b", "sigma.y", "sigma.a", "sigma.b", "rho")

withCorM2 <- jags(data = oxboys.data, inits = oxboys.init2, oxboys.param2,
                  model.file = "CorrSlopInt.jags", n.chains=4, n.iter=5000)
```

```
traceplot(withCorM2, mfrow=c(1,3), varname=c("mu.a", "mu.b", "rho"))
#traceplot(withCorM2, mfrow=c(1,2), varname=c("B"))
traceplot(withCorM2, mfrow=c(1,4), varname=c("deviance", "sigma.a", "sigma.b", "sigma.y"))
```

```
require(xtable)
print(xtable(withCorM2$BUGSoutput$summary[c(1,10,27,36,53:59),c(1:3,7:9)]), table.placement = getOption("xtable.table.placement"))
```

```
cat("
model {
  for(i in 1:n){
    y[i] ~ dnorm (y.hat[i], tau.y)
    y.hat[i] <- B[subject[i], 1] + B[subject[i], 2] * x[i]
  }
  tau.y <- pow(sigma.y, -2)
  sigma.y ~ dunif (0, 100)

  for(j in 1:J){
```

```

      B[j, 1:2] ~ dmnorm(mu, Tau.B[,])
    }
    mu[1] ~ dnorm (0, .0001)
    mu[2] ~ dnorm (0, .0001)
    Tau.B[1:2,1:2] ~ dwish(W[,], 3)
    Sigma.B[1:2,1:2] <- inverse(Tau.B[,])
    sigma.a <- sqrt(Sigma.B[1,1])
    sigma.b <- sqrt(Sigma.B[2,2])
    rho <- Sigma.B[1,2]/sqrt(Sigma.B[1,1]*Sigma.B[2,2])}",
file="wishart.jags")

```

```

#oxboys.data <- list ("n"=n, "J"=J, "x"=x, "y"=y, "county"=county, "W"= diag(2))

```

```

oxboys.data.wish <-with(Oxboys, list(n=nrow(Oxboys), J=length(unique(Subject)),
                                   subject=as.integer(Subject),
                                   y= height, x=age, W=diag(2)))

```

```

oxboys.param3 <- c ("B", "mu", "sigma.y", "sigma.a", "sigma.b", "rho")

```

```

wishart <- jags(data = oxboys.data.wish, parameters.to.save=oxboys.param3,
               model.file = "wishart.jags", n.chains=4, n.iter=5000)

```

```

traceplot(wishart, mfrow=c(1,3), varname=c("mu", "rho"))
#traceplot(withCorM2, mfrow=c(1,2), varname=c("B"))
traceplot(wishart, mfrow=c(1,4), varname=c("deviance", "sigma.a", "sigma.b", "sigma.y"))

```

```

require(xtable)
print(xtable(wishart$BUGSoutput$summary[c(1,10,27,36,53:59),c(1:3,7:9)]), table.placement = getOption("xtable.table.placement",

```

```

owls <- read.table("http://www.math.montana.edu/~jimrc/classes/stat506/data/Owls.txt", head=T)
owls$cTime <- owls$ArrvTime-24
owls$foodsats <- with(owls, ifelse(FoodTrt=="Satiated",1,0))
owls$sexmale <- with(owls, ifelse(SexParent=="Male",1,0))

```

```

require(lme4)
require(splines)
owl.fit3 <- glmer(Ncalls ~ offset(log(BroodSize)) + FoodTrt*SexParent +
                  SexParent*bs(cTime, df=5) +(1 + cTime|Nest), data=owls,
                  family=poisson)

```

```

cat("
model
{
for(i in 1:n){
  y[i] ~ dpois(lambda[i])
  log(lambda[i]) <- offset[i]+inprod(b.0[, X.0[i,])+a[nest[i]]+b[nest[i]]*x[i]
}
for(k in 1:K){
  b.0[k]~dnorm(0,0.0001)
}
for(j in 1:J) {
a[j] ~ dnorm(0, tau.a)
b[j] ~ dnorm(0, tau.b)
}
tau.a <- pow(sigma.a, -2)
sigma.a~dunif(0,1000)
tau.b <- pow(sigma.b, -2)
sigma.b~dunif(0,1000)
}", file="poisson4.jags")

```



```

library(R2jags)
set.seed(52)

owls.data4 <-with(owls,
  list(n=nrow(owls), J=length(unique(Nest)), K=14,
    nest=as.integer(Nest), y=Ncalls, x=cTime,
    offset=log(BroodSize),
    X.0=model.matrix(~foodsat*sexmale+sexmale*bs(cTime,5))))

owls.param4 <- c("b.0","a","b", "sigma.a", "sigma.b")

owls.model4 <- jags(data = owls.data4, parameters.to.save=owls.param4,
  model.file = "poisson4.jags", n.chains=4, n.iter=5000)

```

```

require(mosaic)
xtable(favstats(owls.model4$BUGSoutput$summary[,8]))
xtable(favstats(owls.model4$BUGSoutput$summary[,9]))

```

```

require(xtable)
print(xtable(owls.model4$BUGSoutput$summary[c(69:71), 1:2]), table.placement = getOption("xtable.table.placement", "H"))
print(xtable(data.frame(VarCorr(owl.fit3))), table.placement = getOption("xtable.table.placement", "H"))

```

```

jags.est <- owls.model4$BUGSoutput$summary[c(55:68), 1:2]
names <- c("(Intercept)", "foodsat", "sexmale", "bs1", "bs2", "bs3", "bs4", "bs5", "sexmale:foodsat", "sexmale:bs1", "sexmale:bs2")
glmer.coef <- as.numeric(fixef(owl.fit3))
require(arm)
glmer.se <- as.numeric(se.fixef(owl.fit3))
table <- cbind.data.frame(names, jags.est, glmer.coef, glmer.se)
names(table) <- c("name", "est-JAGS", "se-JAGS", "est-glmer", "se-glmer")
xtable(table)

```

```

ran.efs <- cbind.data.frame(ranef(owl.fit3)$Nest, owls.model4$BUGSoutput$summary[c(1:27), 1:2], owls.model4$BUGSoutput$summary[c(28:54), 1:2])
names(ran.efs) <- c("int-glmer", "slope-glmer", "int-jags", "sd(int)-jags", "slope-jags", "sd(slope)-jags")
print(xtable(ran.efs), table.placement = getOption("xtable.table.placement", "H"))

```

```

traceplot(as.mcmc(owls.model4))

```