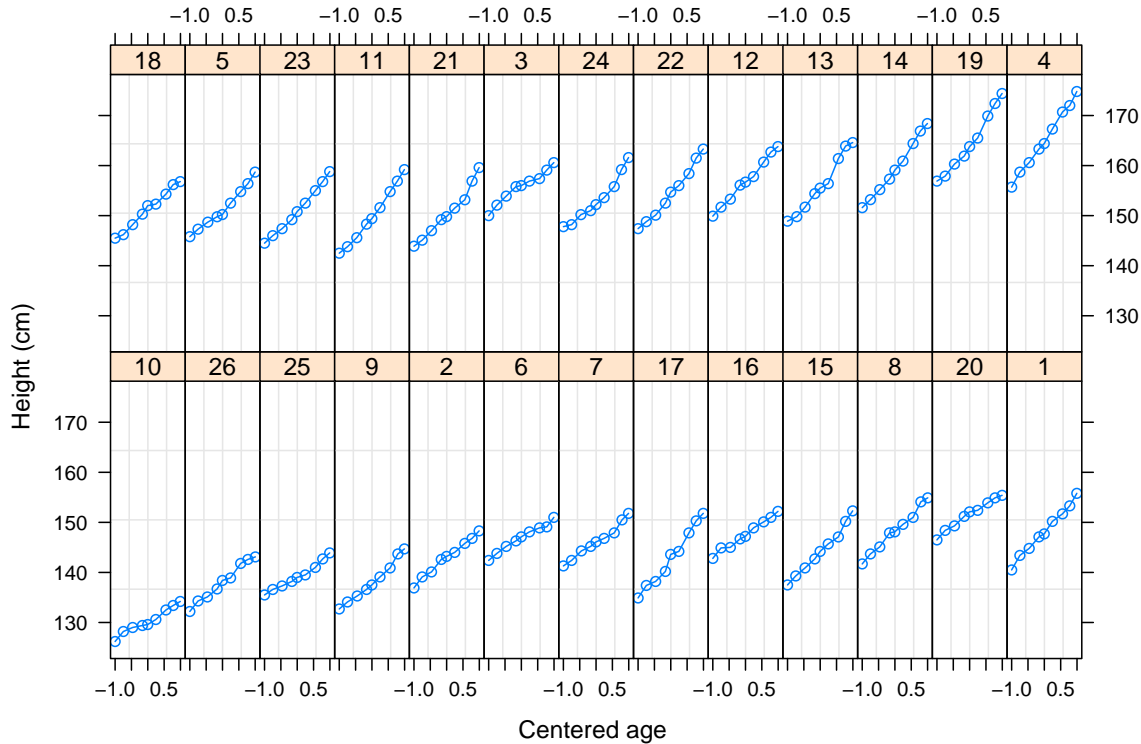


# Stat 506 HW6 Solutions

Spring 2015

Build and run a `jags` model for the “Oxboys” data in the `nlme` package.

1. Plot the data using panel or facet for each boy.



Because this is an ‘nlme’ data set with class ‘grouped Data’, there is a defined method for plotting it.

2. Write out the full mixed model (random slope and intercept) with Greek letters and describe all distributions. Does the plot make it look like both random effects are needed?

$$y_{ij} = \beta_0 + \beta_1 x_{ij} + b_{0j[i]} + b_{1j[i]} x_{ij} + \epsilon_{ij}$$

$$\epsilon_{ij} \sim N(0, \sigma_y^2) \text{ (iid)}$$

$$\begin{pmatrix} b_0 \\ b_1 \end{pmatrix} \sim MVN(0, \Psi) \text{ (iid across boys, independent of } \epsilon \text{'s) } x \text{ is centered age } y \text{ is height.}$$

I see generally linear relationships. Intercepts definitely vary from boy to boy, and I see different slopes as well.

3. To start out with a simple model, use no random effects – just one intercept and one slope.

(a) Show the model description you feed into 'jags'. Use noninformative priors.

```
cat("model {
  for(i in 1:n){
    y[i] ~ dnorm(y.hat[i], tau.y)
    y.hat[i] <- b0 + b1 * x[i]
  }
  tau.y <- pow(sigma.y, -2)
  sigma.y ~ dunif(0, 100)

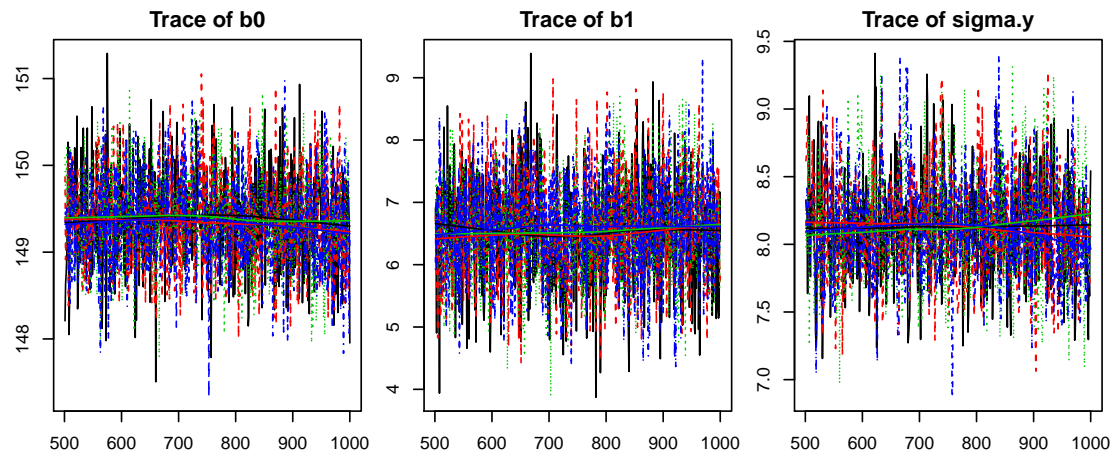
  b0 ~ dnorm(0, .0001)
  b1 ~ dnorm(0, .0001)
}", file="SLR.jags")
```

(b) Run jags with 4 or more chains starting at different parts of the parameter space.

- Plot the traceplots for intercept, slope, residual SD, SE's of intercept and slope.
- Examine the summary of the output including confidence intervals and Rhat and effective sample size. Discuss any convergence issues.
- Compare estimates and SE's to those from an `lm` fit.

Compiling model graph Resolving undeclared variables Allocating nodes Graph Size: 510

Initializing model



	Mean	SD	Naive SE	Time-series SE
b0	149.37	0.54	0.01	0.01
b1	6.54	0.84	0.02	0.02
sigma.y	8.13	0.40	0.01	0.01

Table 1: MCMC Output

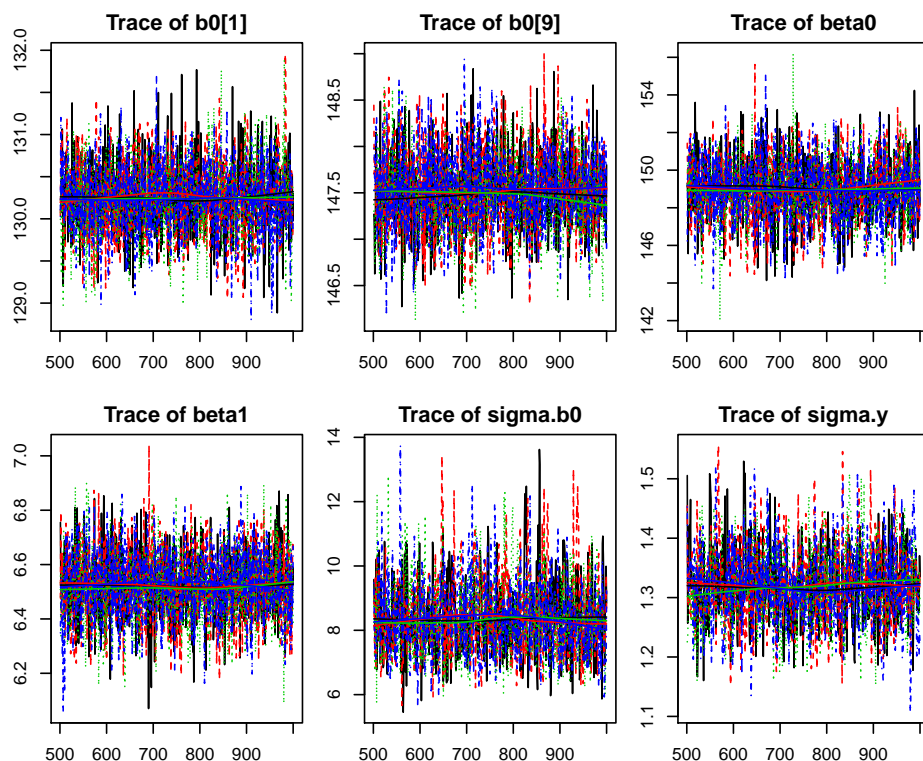
*All parameters converged nicely to estimated intercept 149.37 (SE = 0.535)cm [at centered age zero], slope 6.49 (0.837) cm/year, and median residual standard deviation of 8.134. All  $\hat{R}$ 's are under as 1.005, with effective  $n$ 's of over 690 or more, so there is no sign of convergence problems. The `lm` function gives estimated intercept of 149.37*

	Estimate	Std. Error	t value
(Intercept)	149.37	0.53	282.60
age	6.52	0.82	7.98

Table 2:  $n = 234$  rank = 2 resid sd = 8.0805363 R-Squared = 0.2154451

(0.53), slope of 6.52 (0.817), with residual standard deviation of 8.081 so this is very close agreement.

4. Add a random intercept for each boy. Show the model and summarize output as in 3a and 3b above. No need to plot all 26 individual traceplots, but you should look at them and show me a typical one. Compare to ‘lmer’ output.



	Mean	SD	Naive SE	Time-series SE
b0[1]	130.25	0.45	0.01	0.01
b0[9]	147.51	0.43	0.01	0.01
beta0	148.98	1.67	0.04	0.04
beta1	6.52	0.13	0.00	0.00
sigma.b0	8.42	1.23	0.03	0.04
sigma.y	1.32	0.07	0.00	0.00

Table 3: MCMC Output 2

Excellent convergence, maximum psrf is 1.0036443, and only the intercept is off by 1/3 of a SE.

5. Add a random slope for each boy. Do not worry about setting up a MVN prior for the (inter-

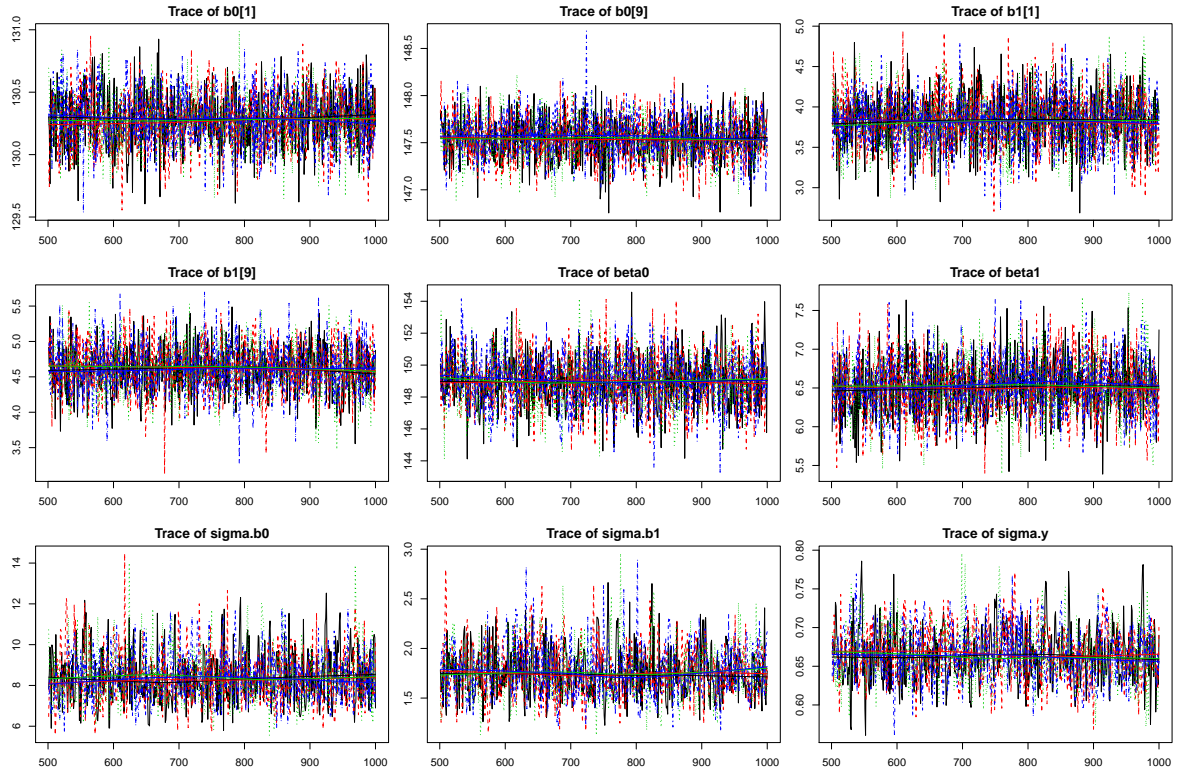
	Std.Dev
Subject	8.10
Residual	1.31

Table 4: lmer StdDevs (2)

	Estimate	Std. Error	t value
(Intercept)	149.37	1.59	93.93
age	6.52	0.13	49.23

Table 5: lmer coefficients (2)

cept, slope) pair, just treat slope as unrelated to intercept. Show the model and summarize output as in 3a and 3b above. Use saved MCMC draws to compute the correlation between the slopes and intercepts random draws across all boys. Fit in lmer using `(1 + age | Subject)` as random effects. How close is the correlation from MCMC draws to the correlation you get from `VarCorr(lmer_model)`?



Again, jags converges well, with  $\max \hat{R} = 1.0034698$ , lmer and jags outputs agree well. The correlation between slope and intercept is only  $-0.004$  at the "fixed" level, and at the "random" level is  $0.616$ , which is close to the lmer output.

	Mean	SD	Naive SE	Time-series SE
b0[1]	130.28	0.22	0.00	0.00
b0[9]	147.55	0.23	0.01	0.00
b1[1]	3.82	0.34	0.01	0.01
b1[9]	4.62	0.34	0.01	0.01
beta0	148.99	1.64	0.04	0.04
beta1	6.52	0.37	0.01	0.01
sigma.b0	8.41	1.25	0.03	0.04
sigma.b1	1.76	0.26	0.01	0.01
sigma.y	0.66	0.03	0.00	0.00

Table 6: MCMC Output 3

	Std.Dev	Correlation
Intercept	8.081	
Slope	1.681	0.641
Residual	0.660	

Table 7: lmer StdDevs (3)

	Estimate	Std. Error	t value
(Intercept)	149.37	1.59	94.22
age	6.53	0.34	19.40

Table 8: lmer Output (3)

## R Code

3.

```
cat("model {  
  for(i in 1:n){  
    y[i] ~ dnorm(y.hat[i], tau.y)  
    y.hat[i] <- b0 + b1 * x[i]  
  }  
  tau.y <- pow(sigma.y, -2)  
  sigma.y ~ dunif (0, 100)  
  
  b0 ~ dnorm(0, .0001)  
  b1 ~ dnorm(0, .0001)  
}", file="SLR.jags")
```

```
require(R2jags, quietly=TRUE)  
jags1.data = with(Oxboys, list("n" = 234, "y" = height, "x" = age))  
oxboys.inits <- function () {  
  list (b0=rnorm(1, 0, 4), b1 = rnorm(1, 0, 4), sigma.y = runif(1))  
}  
OB1.params <- c ("b0", "b1", "sigma.y")  
  
slr.jags <- jags(data = jags1.data, inits = oxboys.inits, OB1.params,  
  model.file = "SLR.jags", n.chains=4, n.iter=1000,  
  progress.bar = "none" )  
  
## slr.jags  
slr.mcmc <- as.mcmc(slr.jags)  
dev.num <- which(colnames(slr.mcmc[[1]]) == "deviance")  
for(ndx in 1:length(slr.mcmc)){  
  slr.mcmc[[ndx]] <- slr.mcmc[[ndx]][,-dev.num]  
}  
par(mfrow=c(1,3), mar=c(3,2,1))  
traceplot(slr.mcmc)  
xtable( summary( slr.mcmc)[[1]], caption = "MCMC Output")  
display.xtable(lm(height ~ age, Oxboys))
```

4.

```
cat("model {  
  for(i in 1:n){  
    y[i] ~ dnorm(y.hat[i], tau.y)  
    y.hat[i] <- b0[Subject[i]] + beta1 * x[i]  
  }  
  tau.y <- pow(sigma.y, -2)  
  sigma.y ~ dunif (0, 100)  
  for (j in 1:J){  
    b0[j] ~ dnorm(beta0, tau.b0)  
  }  
  beta0 ~ dnorm(0, .001)  
  beta1 ~ dnorm(0, .0001)  
  tau.b0 <- pow(sigma.b0, -2)  
  sigma.b0 ~ dunif (0, 100)  
}",  
  file="OB-randInt.jags")  
  
jags2.data = with(Oxboys, list("n" = 234, "J" = 26, "y" = height, "x" = age, "Subject" = Subject))
```

```

oxboys.inits <- function (){
  list (beta0=rnorm(1, 0, 4), beta1 = rnorm(1, 0, 4), sigma.y = runif(1)*10, sigma.b0 = runif(1)*10)
}
OB2.params <- c ("b0", "beta1","beta0", "sigma.y", "sigma.b0")

OBBrandInt.jags <- jags(data = jags2.data, inits = oxboys.inits, OB2.params,
  model.file = "OB-randInt.jags", n.chains=4, n.iter=1000,
  progress.bar = "none")
##OBBrandInt.jags

```

```

OB2.mcmc <- as.mcmc(OBBrandInt.jags)
##colnames(OB2.mcmc[[1]])
for(ndx in 1:length(OB2.mcmc)){
  OB2.mcmc[[ndx]] <- OB2.mcmc[[ndx]][,c(1,26:28,30,31)]
}
par(mfrow=c(2,3), mar = c(3,2,2,1))
traceplot(OB2.mcmc)
xtable( summary( OB2.mcmc)[[1]], caption = "MCMC Output 2")

require(lme4, quietly=TRUE)
lmer2 <- lmer(height ~ age + (1|Subject), Oxboys)
## lmer Random Effects:
vc <- VarCorr(lmer2)
vc <- as.matrix(c(sqrt(vc[[1]][1]), attr(vc,"sc")), ncol=1)
dimnames(vc) = list(c("Subject","Residual"), c("Std.Dev"))
xtable(vc, caption = "lmer StdDevs (2)")

## lmer Fixed Effects:
xtable(summary(lmer2)$coefficients,caption = "lmer coefficients (2)")

```

5.

```

cat("model {
  for(i in 1:n){
    y[i] ~ dnorm(y.hat[i], tau.y)
    y.hat[i] <- b0[Subject[i]] + b1[Subject[i]] * x[i]
  }
  tau.y <- pow(sigma.y, -2)
  sigma.y ~ dunif (0, 100)
  for (j in 1:J){
    b0[j] ~ dnorm(beta0, tau.b0)
    b1[j] ~ dnorm(beta1, tau.b1)
  }
  beta0 ~ dnorm(0, .001)
  beta1 ~ dnorm(0, .0001)
  tau.b0 <- pow(sigma.b0, -2)
  sigma.b0 ~ dunif (0, 100)
  tau.b1 <- pow(sigma.b1, -2)
  sigma.b1 ~ dunif (0, 100)
}",
  file="OB-randIntSlp.jags")

jags2.data = with(Oxboys, list("n" = 234,"J" = 26, "y" = height, "x" = age, "Subject" = Subject))
oxboys.inits <- function (){
  list (beta0=rnorm(1, 0, 4), beta1 = rnorm(1, 0, 4), sigma.y = runif(1)*10, sigma.b0 = runif(1)*10, sigma.b1 = run
}
OB3.params <- c ("b0", "b1","beta0", "beta1", "sigma.y", "sigma.b0", "sigma.b1")

```

```
OB3.jags <- jags(data = jags2.data, inits = oxboys.inits, OB3.params,
  model.file = "OB-randIntSlp.jags", n.chains=4, n.iter=1000,
  progress.bar = "none" )
```

```
OB3.mcmc <- as.mcmc(OB3.jags)
##colnames(OB3.mcmc[[1]])
for(ndx in 1:length(OB3.mcmc)){
  OB3.mcmc[[ndx]] <- OB3.mcmc[[ndx]][,c(1,26:27,52:54,56:58)]
}
par(mfrow=c(3,3), mar = c(3,2,2,1))
traceplot(OB3.mcmc)
xtable( summary( OB3.mcmc)[[1]], caption = "MCMC Output 3")

lmer3 <- lmer(height ~ age + (1 + age|Subject), Oxboys)
## lmer Random Effects:
vc <- VarCorr(lmer3)[[1]]
sigma <- summary(lmer3)$sigma
vc <- matrix(c(attr(vc, "stddev"), sigma,NA,attr(vc, "correlation")[2,1], NA), ncol=2, nrow=3)
dimnames(vc) = list(c("Intercept","Slope","Residual"), c("Std.Dev", "Correlation"))
xtable(vc, digits = 3, caption = "lmer StdDevs (3)")

## lmer Fixed Effects:
xtable(summary(lmer3)$coefficients, caption = "lmer Output (3)")
attach.jags(OB3.jags)
b00 <- b0;dim(b00)<-NULL
b11 <- b1;dim(b11)<-NULL
## cor(b00,b11)      ## similar to lmer correlation
beta0b <- beta0
beta1b <- beta1      ## cor(beta0b, beta1b) is near 0
detach()
```