Linear mixed model for the jaw data

Chapter 4.4: Random effects

Let Y_{ij} be the j^{th} measurement of jaw bone density for patient i. In this model we allow bone density to increase linearly in time and each patient has their own slope and intercept. The random slope model is

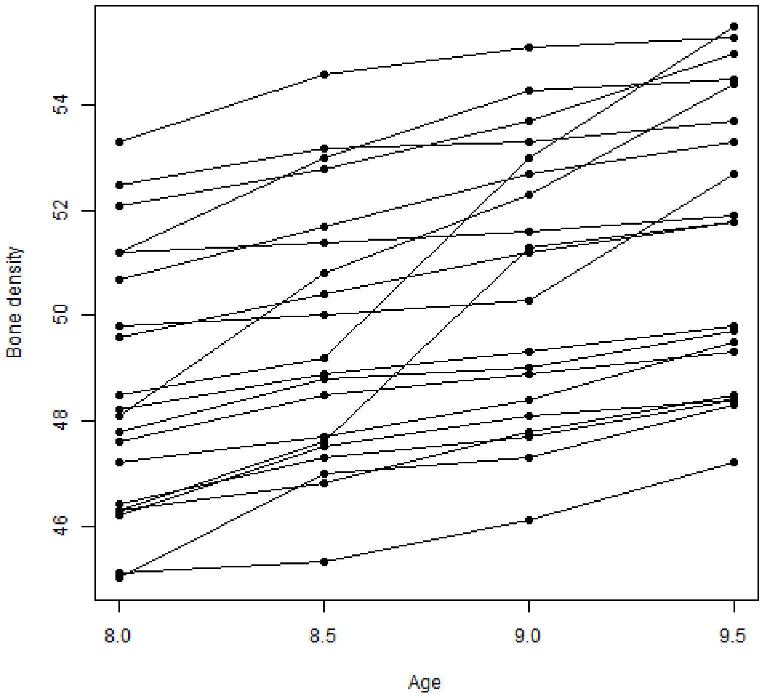
$$Y_{ij}|\alpha_{i1},\alpha_{i2} \sim \text{Normal}(\alpha_{i1} + age_j\alpha_{i2}, \sigma^2) \text{ where } (\alpha_{1i},\alpha_{2i})^T \sim \text{Normal}(\mu,\Sigma).$$

The random effects α_{i1} and α_{i2} are the subject-specific intercept and slope, respectively. The population of intercepts and slopes is assumed to be bivariate normal with mean vector μ and covariance matrix Σ.

The objectives are to borrow strength across patients to estimate each patient's linear trend and then predict future jaw bone density.

Load and plot the data

```
library(rjags)

m   <- 4
n   <- 20
age <- c(8.0, 8.5, 9.0, 9.5)
Y   <- c(47.8, 48.8, 49.0, 49.7,
         46.4, 47.3, 47.7, 48.4,
         46.3, 46.8, 47.8, 48.5,
         45.1, 45.3, 46.1, 47.2,
         47.6, 48.5, 48.9, 49.3,
         52.5, 53.2, 53.3, 53.7,
         51.2, 53.0, 54.3, 54.5,
         49.8, 50.0, 50.3, 52.7,
         48.1, 50.8, 52.3, 54.4,
         45.0, 47.0, 47.3, 48.3,
         51.2, 51.4, 51.6, 51.9,
         48.5, 49.2, 53.0, 55.5,
         52.1, 52.8, 53.7, 55.0,
         48.2, 48.9, 49.3, 49.8,
         49.6, 50.4, 51.2, 51.8,
         50.7, 51.7, 52.7, 53.3,
         47.2, 47.7, 48.4, 49.5,
         53.3, 54.6, 55.1, 55.3,
         46.2, 47.5, 48.1, 48.4,
         46.3, 47.6, 51.3, 51.8)

Y <- matrix(Y,20,4,byrow=TRUE)

plot(NA,xlim=range(age),ylim=range(Y),xlab="Age",ylab="Bone density")
for(i in 1:n){
  lines(age,Y[i,])
  points(age,Y[i,],pch=19)
}
```

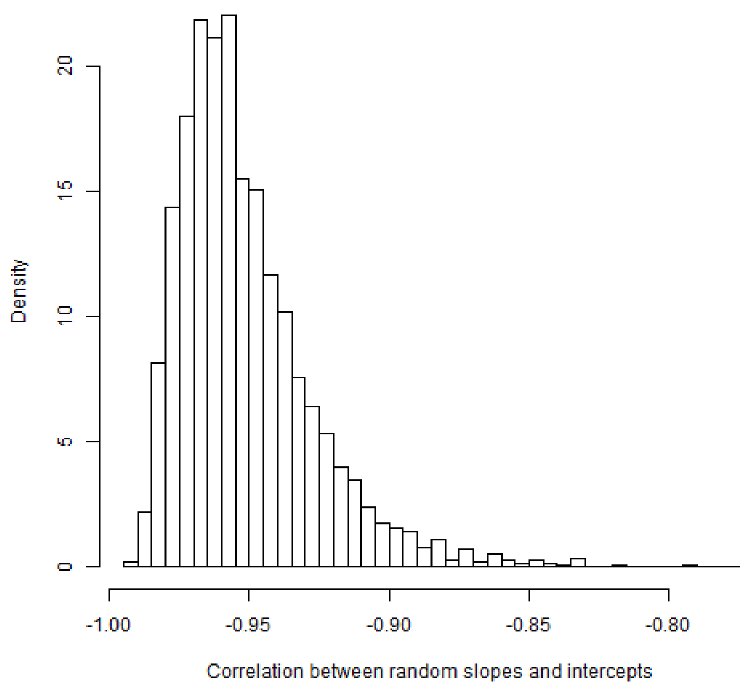


Put the data in JAGS format

```
data      <- list(Y=Y,age=age,n=n,m=m)
burn      <- 10000
n.iter    <- 20000
thin      <- 10
n.chains <- 2
```

Fit the random slopes model

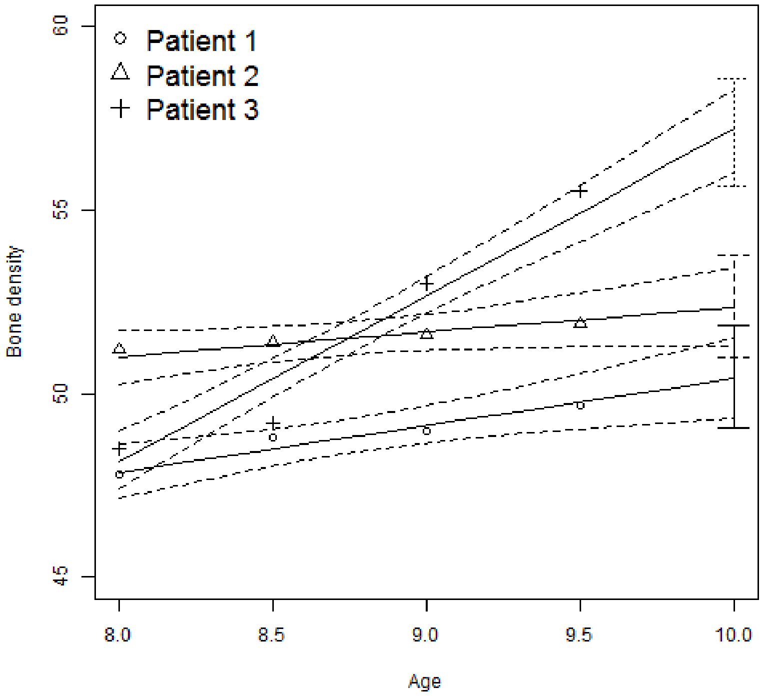
```
model_string <- textConnection("model{
  # Likelihood
   for(i in 1:n){for(j in 1:m){
     Y[i,j] ~ dnorm(alpha[i,1]+alpha[i,2]*age[j],taue)
   }}

  # Random effects
   for(i in 1:n){alpha[i,1:2] ~ dmnorm(mu[1:2],Omega[1:2,1:2])}

  # Priors
   for(j in 1:2){mu[j] ~ dnorm(0,0.0001)}
   taue ~ dgamma(0.1,0.1)
   Omega[1:2,1:2] ~ dwish(R[,],2.1)

   R[1,1]<-1/2.1
   R[1,2]<-0
   R[2,1]<-0
   R[2,2]<-1/2.1
}")

params  <- c("mu","alpha","taue","Omega")
model   <- jags.model(model_string,data = data, n.chains=n.chains,quiet=TRUE)
update(model, burn, progress.bar="none")
samples <- coda.samples(model, variable.names=params,
                        n.iter=n.iter, thin=thin, progress.bar="none")
samples <- rbind(samples[[1]],samples[[2]])
Omega   <- samples[,1:4]
a1      <- samples[,5:24]
a2      <- samples[,25:44]
mu      <- samples[,45:46]
sig     <- 1/sqrt(samples[,47])
S       <- Omega
for(i in 1:nrow(S)){
   S[i,]<-as.vector(solve(matrix(Omega[i,],2,2)))
}

r <- S[,2]/sqrt(S[,1]*S[,4])
hist(r,breaks=50,prob=TRUE,main="",xlab="Correlation between random slopes and intercepts")
```



Make predictions

This produces the estimated (posterior median) linear trend (solid line) and 95% interval (dashed lines) for three patients, plotted against their observations (points). The vertical boxplots give the posterior predictive distribution for the measurement that will be taken at age 10. This final prediction distribution accounts for both uncertainy in the random effects α_{ij} but also measurement variance σ^2.

```
these  <- c(1,11,12) # pick three subjects
na     <- 10
ages   <- seq(8,10,length=na) # Estimate the line for these ages

plot(NA,xlim=range(ages),ylim=c(45,60),xlab="Age",ylab="Bone density")
for(sub in 1:length(these)){

 # Plot the posterior of the mean alpha1+age[j]*alpha2

 i   <- these[sub]
 fit <- NULL
 for(j in 1:na){fit <- cbind(fit,a1[,i]+ages[j]*a2[,i])}
 q  <- apply(fit,2,quantile,c(0.025,0.5,0.975))
 points(age,Y[i,],pch=sub)
 lines(ages,q[1,],lty=2)
 lines(ages,q[2,],lty=1)
 lines(ages,q[3,],lty=2)

 # Plot the posterior predictive distribution at age 10

 Y10 <- a1[,i]+a2[,i]*10+rnorm(length(sig),0,sig)
 q   <- quantile(Y10,c(0.025,0.975))
 lines(c(10,10),q,lty=sub)
 lines(10+0.05*c(-1,1),rep(q[1],2),lty=sub)
 lines(10+0.05*c(-1,1),rep(q[2],2),lty=sub)
}

legend("topleft",paste("Patient",1:3),pch=1:3,cex=1.5,bty="n")
```



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