

## Linear mixed model for the jaw data

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

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

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

**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)
```

```
## Loading required package: coda
```

```
## Linked to JAGS 4.3.1
```

```
## Loaded modules: basemod,bugs
```

```
library(ggplot2)
```

```
m = 4
```

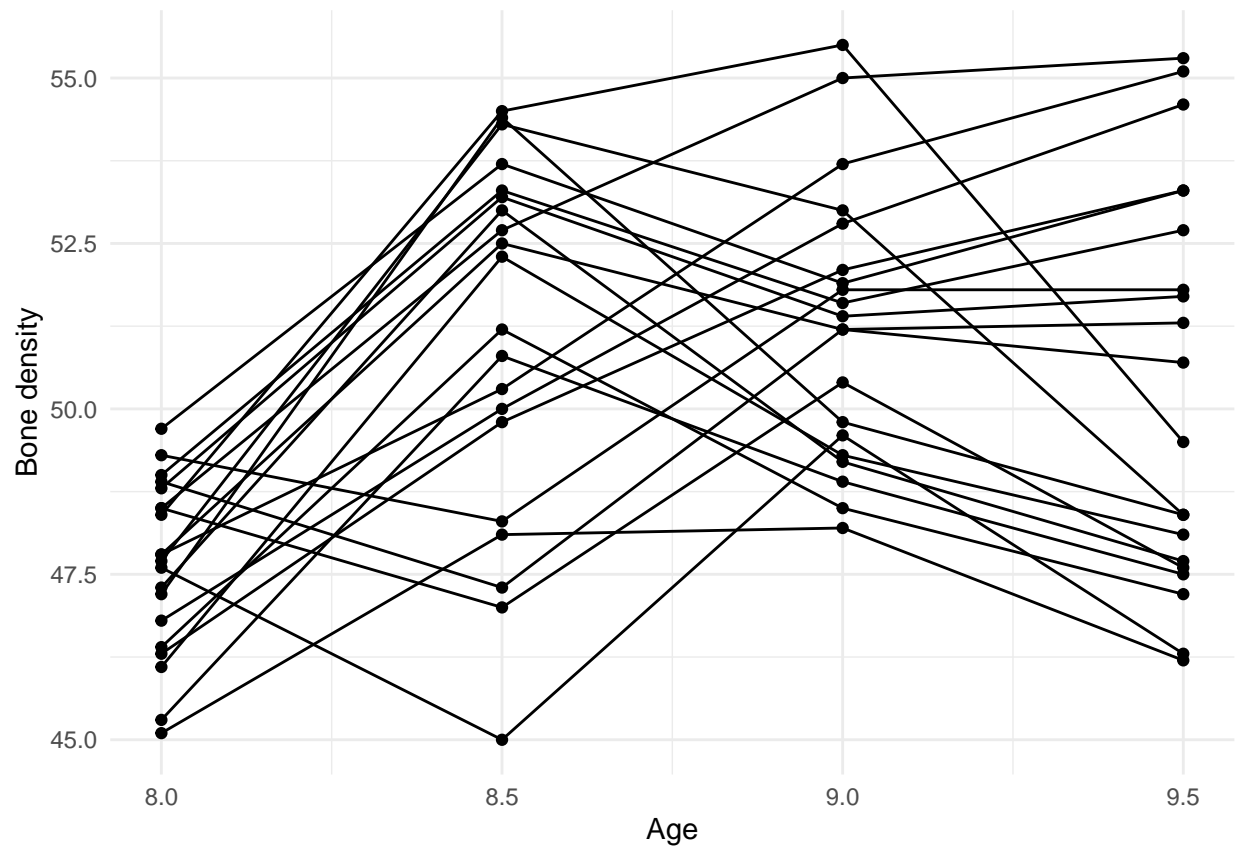
```
n = 20
```

```
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, n, m, byrow = TRUE)
```

```
# Convert the matrix to a data frame for ggplot
df = data.frame(age = rep(age, each = n),
                id = rep(1:n, times = m),
                bone_density = as.vector(t(Y)))
ggplot(df, aes(x = age, y = bone_density, group = id)) +
  geom_line() +
  geom_point() +
  labs(x = "Age", y = "Bone density") +
  theme_minimal()
```



## Prepare data for Jags

```
data      = list(Y=Y,age=age,n=n,m=m)
burn      = 10000
n.iter    = 20000
thin      = 15
n.chains  = 2
```

## Random slopes model

```

library(rjags)
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])}

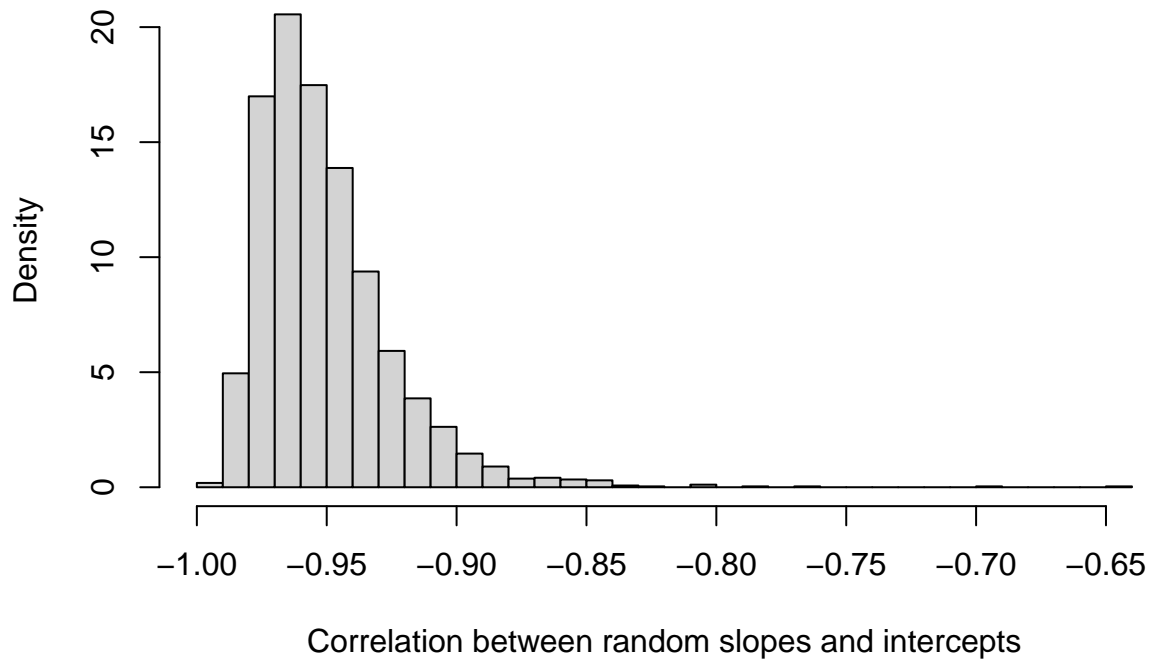
  # Priors
  for(j in 1:2){mu[j] ~ dnorm(0,0.0001)}
  taue ~ dgamma(0.1,0.1)
  Omega[1:2,1:2] ~ dwish(R[,],2.1)

  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")

```



## Predictions

This generates the estimated (posterior median) linear trend (represented by a solid line) and the 95% confidence interval (shown with dashed lines) for three patients, compared with their observed data points. The vertical boxplots display the posterior predictive distribution for the measurement expected at age 10. This final predictive distribution takes into account both the uncertainty in the random effects  $\alpha_{ij}$  and the measurement variance  $\sigma^2$ .

```
# Pick three subjects and define parameters
selected_subjects =c(1, 11, 12)
num_ages = 10
age_range =seq(8, 10, length = num_ages)

plot(NA, xlim = range(age_range), ylim = c(45, 60), xlab = "Age", ylab = "Bone density")

# Loop over selected subjects to plot the data
for (subject in selected_subjects) {

  # Calculate posterior of the mean for each age
  fit = sapply(age_range, function(age) a1[, subject] + age * a2[, subject])
  quantiles = apply(fit, 2, quantile, c(0.025, 0.5, 0.975))

  # Plot observed data points
```

```

points(age, Y[subject, ], pch = which(selected_subjects == subject))

# Plot the quantile lines
lines(age_range, quantiles[1, ], lty = 2)
lines(age_range, quantiles[2, ], lty = 1)
lines(age_range, quantiles[3, ], lty = 2)

# Posterior predictive distribution at age 10
Y10 = a1[, subject] + a2[, subject] * 10 + rnorm(length(sig), 0, sig)
q_Y10 = quantile(Y10, c(0.025, 0.975))

# Plot the posterior predictive interval at age 10
lines(c(10, 10), q_Y10, lty = which(selected_subjects == subject))
lines(10 + 0.05 * c(-1, 1), rep(q_Y10[1], 2), lty = which(selected_subjects == subject))
lines(10 + 0.05 * c(-1, 1), rep(q_Y10[2], 2), lty = which(selected_subjects == subject))
}

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

```

