One-way random effects model for the jaw data

Chapter 4.4: Random effects

Let Y_{ii} be the j^{th} measurement of jaw bone density for patient i. The one-way random effects model is

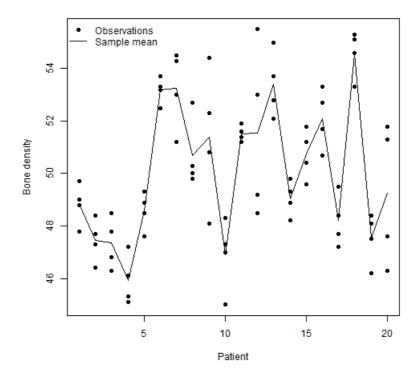
$$Y_{ii} \mid \alpha_i \sim \text{Normal}(\alpha_i, \sigma^2) \text{ where } \alpha_i \sim \text{Normal}(\mu, \tau^2).$$

The random effect α_i is the true mean for patient i, and the observations for patient i vary around α_i with variance σ^2 . In this model, the population of patient-specific means is assumed to follow a normal distribution with mean μ and variance τ^2 . The hyperparameters have uninformative prior $\mu \sim \text{Normal}(0,1000)$, $\sigma^2 \sim \text{InvGamma}(0.1,0.1)$, and $\tau^2 \sim \text{InvGamma}(0.1,0.1)$.

The objective is to borrow strength across patients to estimate the mean for each patient, a_n and to estimate the overall population mean μ .

Load and plot the data

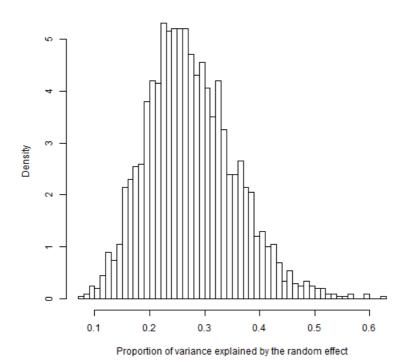
```
library(rjags)
m < -4
age < c(8.0, 8.5, 9.0, 9.5)
Y < -c(47.8, 48.8, 49.0, 49.7,
         46.4, 47.3, 47.7, 48.4,
        46.3, 46.8, 47.8, 48.5,
        45.1, 45.3, 46.1, 47.2,
        47.6, 48.5, 48.9, 49.3,
        52.5, 53.2, 53.3, 53.7,
        51.2, 53.0, 54.3, 54.5,
        49.8, 50.0, 50.3, 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(row(Y),Y,xlab="Patient",ylab="Bone density",pch=19)
lines(rowMeans(Y))
legend("topleft",c("Observations","Sample mean"),lty=c(NA,1),pch=c(19,NA),bty="n")
```



Put the data in JAGS format

(1) Fit the one-way random effects model with Gamma priors

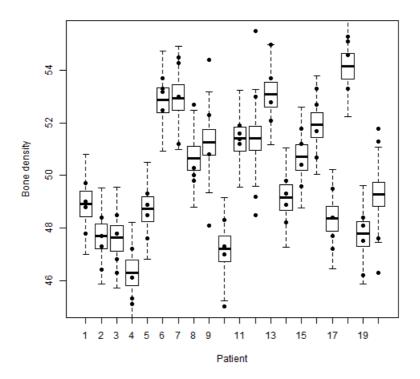
```
model_string <- textConnection("model{</pre>
  # Likelihood
   for(i in 1:n){for(j in 1:m){
     Y[i,j] ~ dnorm(alpha[i],taue)
  # Random effects
   for(i in 1:n){alpha[i] ~ dnorm(mu,taua)}
  # Priors
  mu \sim dnorm(0,0.0001)
  taue \sim dgamma(0.1,0.1)
   taua \sim dgamma(0.1,0.1)
}")
         <- c("mu", "alpha", "taue", "taua")
params
         <- jags.model(model_string, data = data,
model
                        n.chains=n.chains, quiet=TRUE)
update(model, burn, progress.bar="none")
samples1 <- coda.samples(model, variable.names=params, thin=thin,</pre>
                          n.iter=n.iter, progress.bar="none")
samples1 <- rbind(samples1[[1]],samples1[[2]])</pre>
alpha
         <- samples1[,1:n]
         <- samples1[,n+1]
mu
sigma2 <- 1/samples1[,n+2:3]</pre>
         <- sigma2[,2]/rowSums(sigma2)</pre>
hist(r,breaks=50,prob=TRUE,main="",xlab="Proportion of variance explained by the random effect")
```



Random-effect estimates

The plots the posterior of each subject's random effect, α_i , as a boxplot. The data Y_{ii} are overlain as points.

```
boxplot(alpha\sim col(alpha), ylim=range(Y), xlab="Patient", ylab="Bone density", outline=FALSE) \\ points(row(Y), Y, pch=19)
```



(2) Fit the one-way random effects model with half-Cauchy priors

```
model_string_HC <- textConnection("model{</pre>
  # Likelihood
   for(i in 1:n){for(j in 1:m){
     Y[i,j] ~ dnorm(alpha[i],taue)
  # Random effects
   for(i in 1:n){alpha[i] ~ dnorm(mu,taua)}
  # Priors
           \sim dnorm(0,0.0001)
  mu
           <- pow(sigma1,-2)
  taue
          <- pow(sigma2,-2)
  taua
  sigma1 \sim dt(0, 1, 1)T(0,)
  sigma2
           \sim dt(0, 1, 1)T(0,)
}")
model
          <- jags.model(model_string_HC, data = data,</pre>
                        n.chains=n.chains, quiet=TRUE)
update(model, burn, progress.bar="none")
samplesHC <- coda.samples(model, variable.names=params, thin=thin,</pre>
                            n.iter=n.iter, progress.bar="none")
samplesHC <- rbind(samplesHC[[1]],samplesHC[[2]])</pre>
sigma2HC <- 1/samplesHC[,n+2:3]</pre>
```

Prior sensitivity

The summaries below compare the posterior distribution of the standard deviation using InvGamma versus half-Cauchy priors. For these data the results are similar for the two priors.

```
## taua taue

## 50% 2.421446 1.467340

## 2.5% 1.757569 1.243607

## 97.5% 3.512755 1.778204
```

```
apply(sqrt(sigma2HC),2,quantile,c(0.5,0.025,0.975)) # Half-Cauchy prior
```

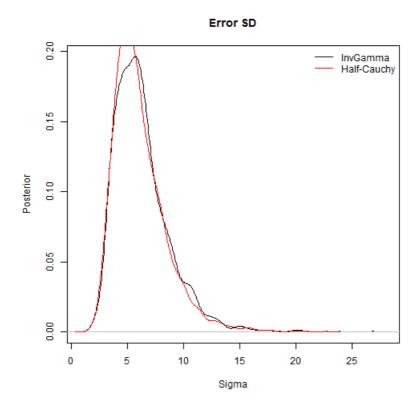
```
## taua taue

## 50% 2.374449 1.465342

## 2.5% 1.724867 1.242088

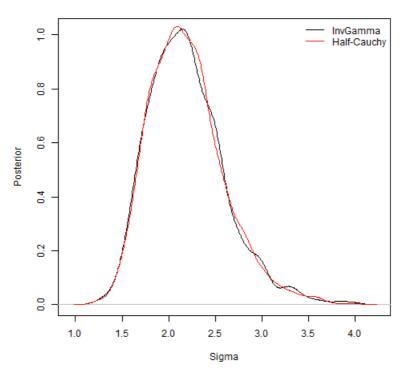
## 97.5% 3.456168 1.770958
```

```
plot(density(sigma2[,1]),xlab="Sigma",ylab="Posterior",main="Error SD")
lines(density(sigma2HC[,1]),col=2)
legend("topright",c("InvGamma","Half-Cauchy"),lty=1,col=1:2,bty="n")
```



```
plot(density(sigma2[,2]),xlab="Sigma",ylab="Posterior",main="Random effect SD")
lines(density(sigma2HC[,2]),col=2)
legend("topright",c("InvGamma","Half-Cauchy"),lty=1,col=1:2,bty="n")
```

Random effect SD



Comparison with naive model

In addition to estimating random effects, random-effect models are useful to account for correlation between observations to obtain valid uncertainty estimates for model parameters. For example, say our objective is to estimate μ . We could do this assuming all n*m=80 observations are independent. But because we ignore dependence between repeated measurements for each subject, this inference is questionable.

```
model_string0 <- textConnection("model{</pre>
  # Likelihood
   for(i in 1:n){for(j in 1:m){
     Y[i,j] \sim dnorm(mu,taue)
   }}
  # Priors
   mu \sim dnorm(0, 0.0001)
   taue \sim dgamma(0.1,0.1)
}")
          <- jags.model(model_string0,data = data,</pre>
model0
                         n.chains=2, quiet=TRUE)
update(model0, burn, progress.bar="none")
samples0 <- coda.samples(model0, variable.names=c("mu"),</pre>
                           n.iter=n.iter, thin=thin, progress.bar="none")
mu_naive <- c(samples0[[1]],samples0[[2]])</pre>
```

The posterior of μ has smaller variance under the naive model because it does not account for dependence.

```
d1 <- density(mu,from=47,to=52)
d0 <- density(mu_naive,from=47,to=52)
quantile(mu,c(0.025,0.975))</pre>
```

```
## 2.5% 97.5%
## 48.88611 51.20441
```

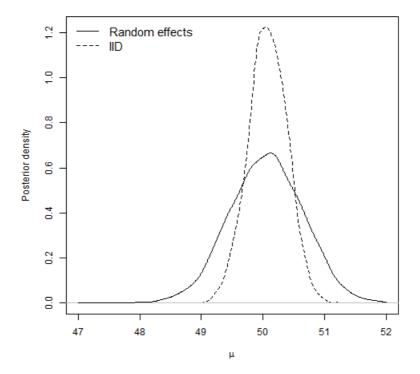
```
quantile(mu_naive,c(0.025,0.975))
```

```
## 2.5% 97.5%
## 49.45833 50.67698
```

```
var(mu)/var(mu_naive)
```

```
## [1] 3.673447
```

```
plot(d0,type="l",lty=2,xlab=expression(mu),ylab="Posterior density",main="")
lines(d1,lty=1)
legend("topleft",c("Random effects","IID"),lty=1:2,bty="n",cex=1.25)
```



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