One-way random effects model for the jaw data

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

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

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 $\tau^2 \sim \text{InvGamma}(0.1, 0.1)$.

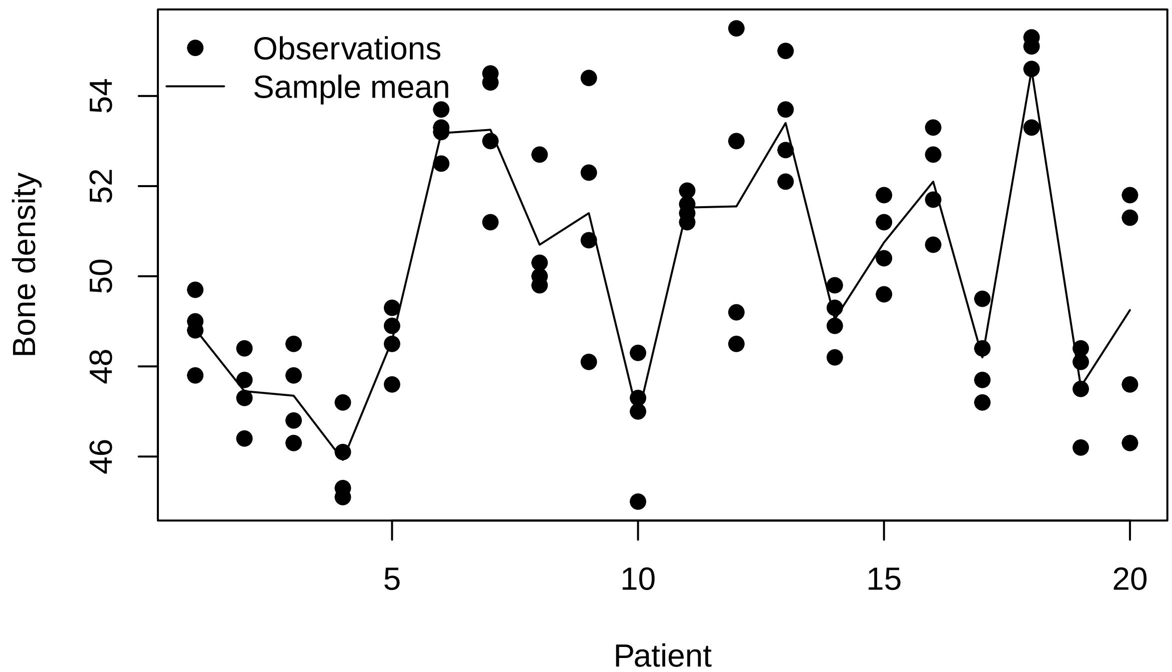
The objective is to borrow strength across patients to estimate the mean for each patient α_i and **to estimate the overall population mean** μ.

Load and plot the data

```
library(rjags)
```

```
## Loading required package: coda

## Linked to JAGS 4.3.1

## Loaded modules: basemod,bugs
```

```
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(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")
```



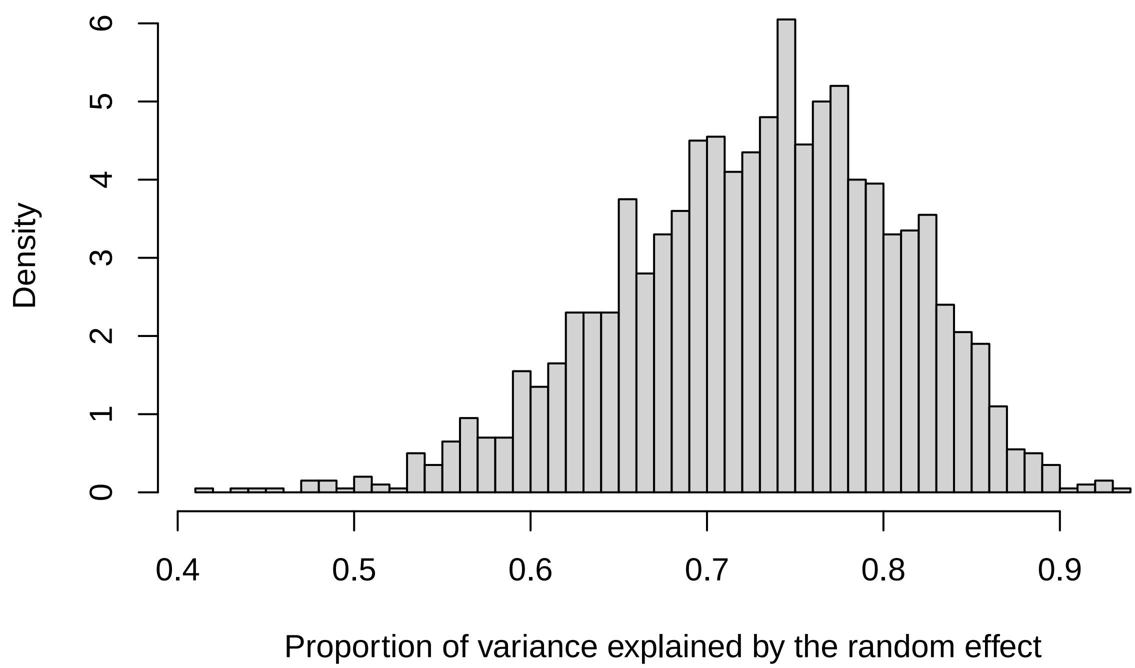
Put the data in JAGS format

```
data     <- list(Y=Y,n=n,m=m)
burn     <- 10000
n.iter   <- 20000
thin     <- 20
n.chains <- 2
```

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

```
library(rjags)
model_string <- textConnection("model{

   # 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)}
```

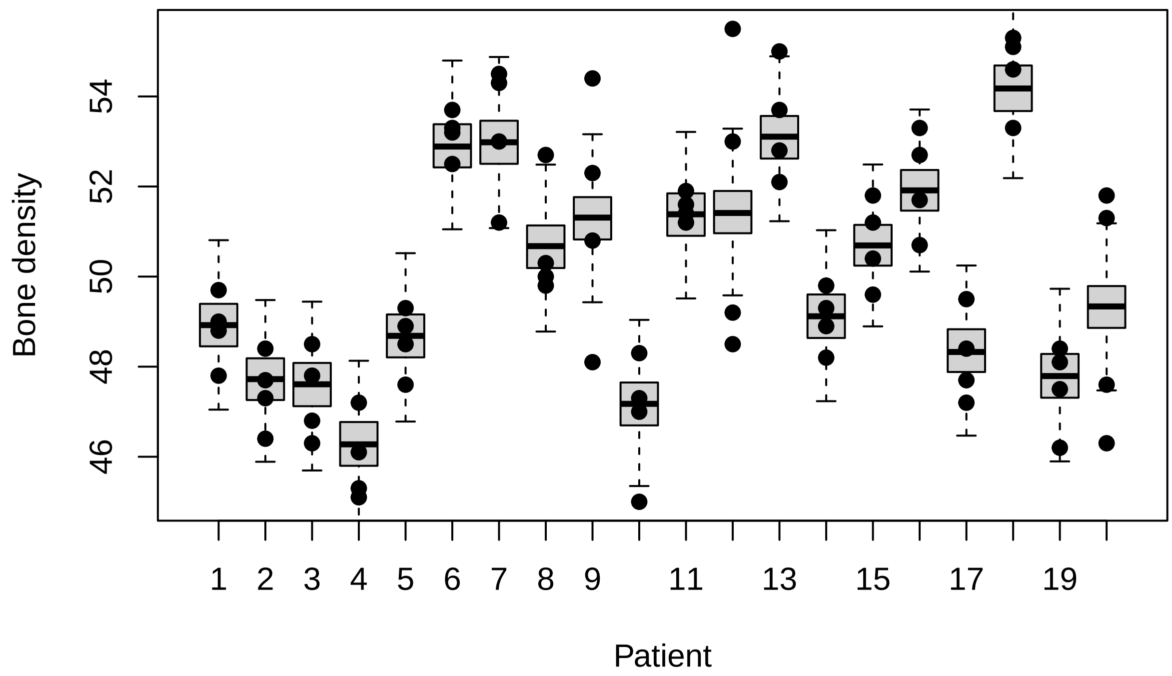
```
  # Priors
   mu   ~ dnorm(0,0.0001)
   taue ~ dgamma(0.1,0.1)
   taua ~ dgamma(0.1,0.1)
}")

params   <- c("mu","alpha","taue","taua")
model    <- jags.model(model_string, data = data,
                       n.chains=n.chains, quiet=TRUE)
update(model, burn, progress.bar="none")
samples1 <- coda.samples(model, variable.names=params, thin=thin,
                         n.iter=n.iter, progress.bar="none")

samples1 <- rbind(samples1[[1]],samples1[[2]])
alpha    <- samples1[,1:n]
mu       <- samples1[,n+1]
sigma2   <- 1/samples1[,n+2:3]
r        <- sigma2[,1]/rowSums(sigma2)
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_{ij} are overlain as points.

```r
boxplot(alpha~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

```r
model_string_HC <- textConnection("model{

   # 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       ~ dnorm(0,0.0001)
   taue     <- pow(sigma1,-2)

   taua     <- pow(sigma2,-2)

   sigma1    ~ dt(0, 1, 1)T(0,)
   sigma2    ~ dt(0, 1, 1)T(0,)
```

```r
}")

model    <- jags.model(model_string_HC, data = data,
                       n.chains=n.chains, quiet=TRUE)
update(model, burn, progress.bar="none")
samplesHC <- coda.samples(model, variable.names=params, thin=thin,
                          n.iter=n.iter, progress.bar="none")

samplesHC <- rbind(samplesHC[[1]],samplesHC[[2]])
sigma2HC <- 1/samplesHC[,n+2:3]
```

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.

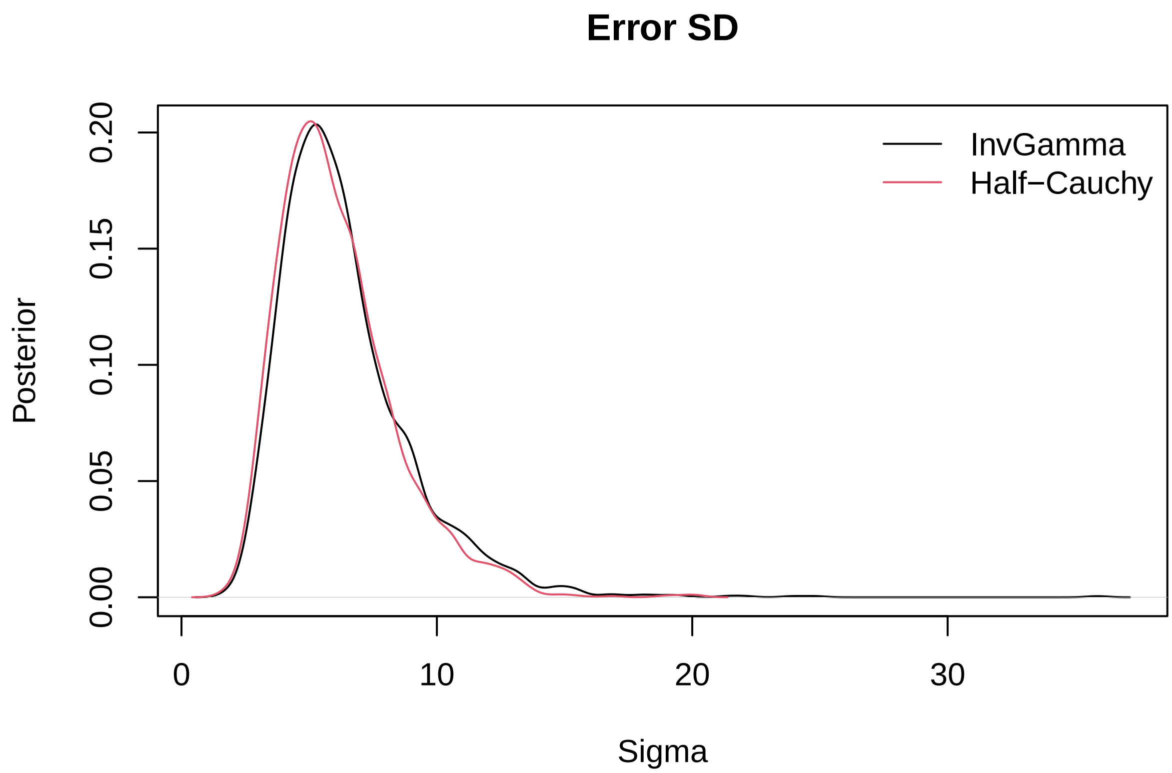
```r
apply(sqrt(sigma2),2,quantile,c(0.5,0.025,0.975))   # InvGamma prior
```

```
##            taua     taue
## 50%    2.430279 1.458925
## 2.5%   1.738470 1.249853
## 97.5% 3.572151 1.759310
```

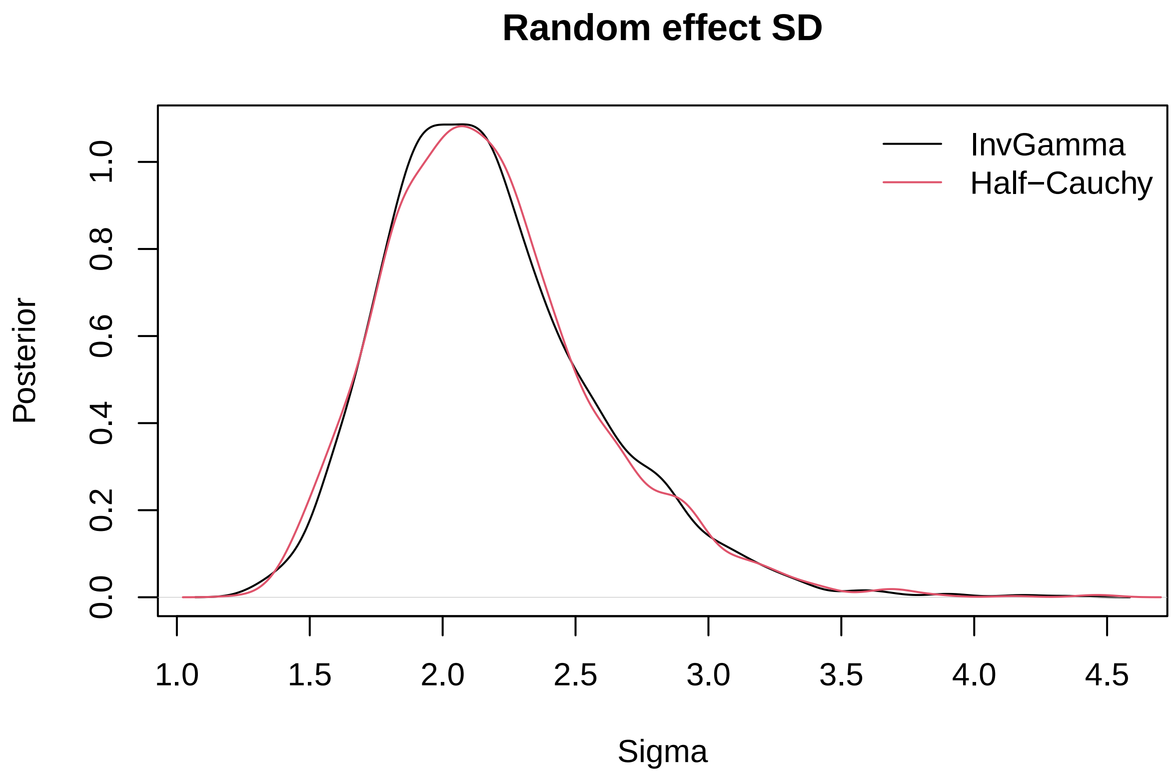
```r
apply(sqrt(sigma2HC),2,quantile,c(0.5,0.025,0.975)) # Half-Cauchy prior
```

```
##            taua     taue
## 50%    2.387119 1.457575
## 2.5%   1.715211 1.236334
## 97.5% 3.440743 1.768390
```

```r
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")
```



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{
   # Likelihood
    for(i in 1:n){for(j in 1:m){
      Y[i,j] ~ dnorm(mu,taue)
    }}

   # Priors
    mu ~ dnorm(0,0.0001)
    taue ~ dgamma(0.1,0.1)
 }")

 model0   <- jags.model(model_string0,data = data,
                        n.chains=2, quiet=TRUE)
 update(model0, burn, progress.bar="none")
 samples0 <- coda.samples(model0, variable.names=c("mu"),
                          n.iter=n.iter, thin=thin, progress.bar="none")
 mu_naive <- c(samples0[[1]],samples0[[2]])
```

Th 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))
```

```
##     2.5%    97.5%
## 48.85382 51.25702
```

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

```
##     2.5%    97.5%
## 49.45190 50.68208
```

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

```
## [1] 3.660268
```

```
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)
```