Bayesian Learning

Lab 3

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Question 1

```
options(digits=2)

rainfall <- read.table("../data/rainfall.dat", header=F)
```

Prior

$$\mu \sim N(\mu_0, \tau_0^2)$$
$$\sigma^2 \sim \text{Inv}\text{–}\chi^2(\nu_0, \sigma_0^2)$$

Likelihood

$$\mathbf{y}|\mu, \sigma^2 \sim N(\mu, \sigma^2)$$

Posterior

$$\mu|\sigma^2, \mathbf{x} \sim N(\mu_n, \tau_n^2)$$
$$\sigma^2|\mu, \mathbf{x} \sim \text{Inv}\text{–}\chi^2\left(\nu_n, \frac{\nu_0\sigma_0^2 + \sum_{i=1}^{n}(x_i - \mu)^2}{n + \nu_0}\right)$$

where

$$\mu_n = \frac{\frac{1}{\tau_0^2}}{\frac{1}{\tau_0^2} + \frac{n}{\sigma^2}}\mu_0 + \frac{\frac{n}{\sigma^2}}{\frac{1}{\tau_0^2} + \frac{n}{\sigma^2}}\bar{x}$$
$$\frac{1}{\tau_n^2} = \frac{1}{\tau_0^2} + \frac{n}{\sigma^2}$$
$$\nu_n = \nu_0 + n$$

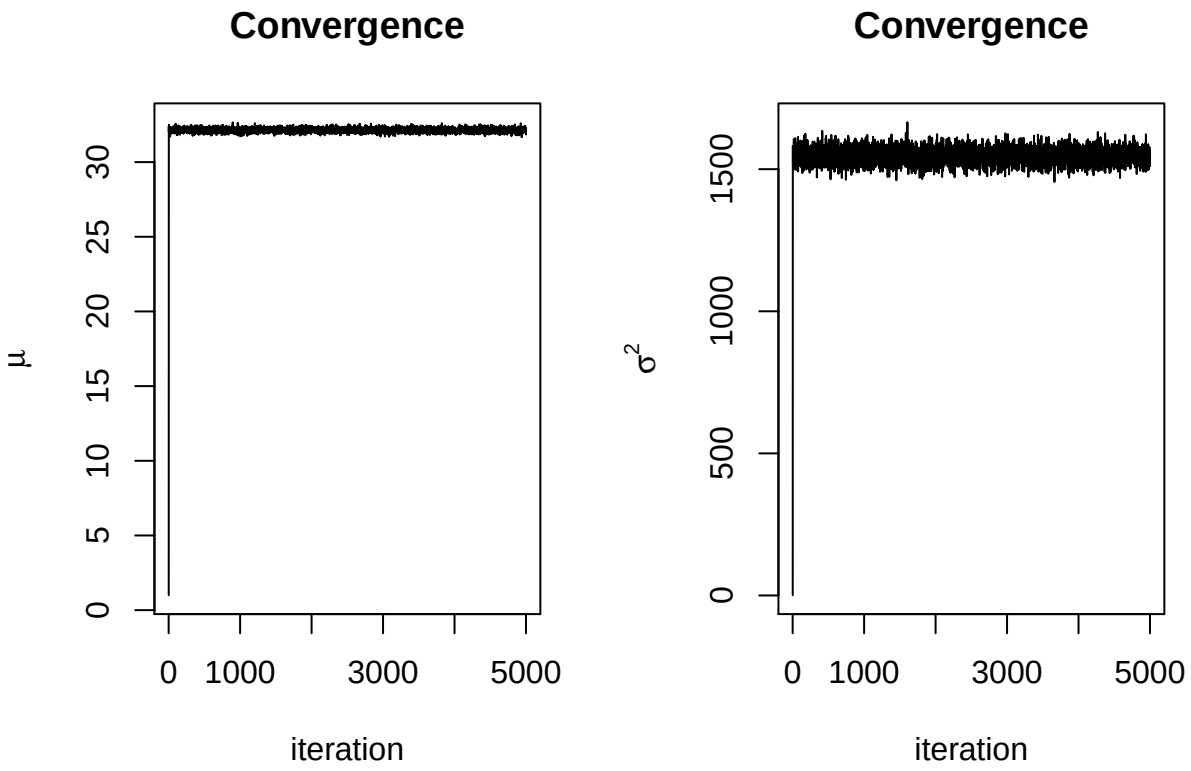
a)

```
library(geoR)

mun <- function(x, sigmasq, hyperparams){
    n <- length(x)
```

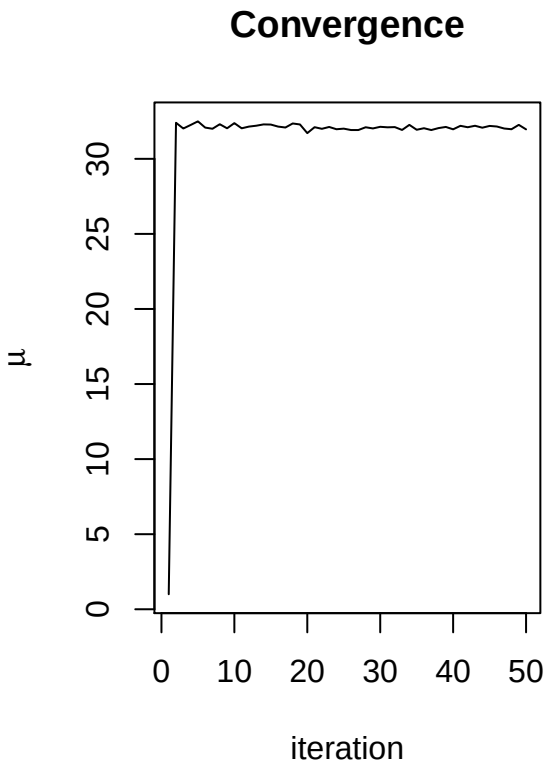
```
    denom <- ((1 / hyperparams$tausq0) + (n / sigmasq))

    pt1 <- ((1 / hyperparams$tausq0) / denom)  * hyperparams$mu0
    pt2 <- ((n / sigmasq) / denom) * mean(x)

    pt1 + pt2
}


taun <- function(x, sigmasq, hyperparams){
    hyperparams$tausq0 + (sigmasq / length(x))
    1 / hyperparams$tausq0
}

nun <- function(x, hyperparams){
    hyperparams$nu0 + length(x)
}


sigmasqn <- function(x, mu, hyperparams){
    (hyperparams$nu0 * hyperparams$sigmasq0 + sum((x - mu)^2 )) / (length(x) + hyperparams$nu0)
}


musampler <- function(x,sigmasq, hyperparams){
    mu <- mun(x, sigmasq, hyperparams)
    sigma <- sqrt(taun(x,sigmasq, hyperparams))
    rnorm(1, mu, sigma)
}

sigmasampler <- function(x, mu, hyperparams){
    scale  <- sigmasqn(x, mu, hyperparams)
    df <- nun(x, hyperparams)
    rinvchisq(1, df, scale)
}

gibbs <- function(x, iter, init, hyperparams){
    samples <- matrix(NA, ncol = 2, nrow = iter + 1)
    samples[1,] <- init

    for (i in 2:(iter+1)){
        mu <- musampler(x, samples[i-1, 2], hyperparams)
        sigma <- sigmasampler(x, mu, hyperparams)
        samples[i,] <- c(mu, sigma)
    }

    colnames(samples) <- c("mu", "sigmasq")
    samples
}
```

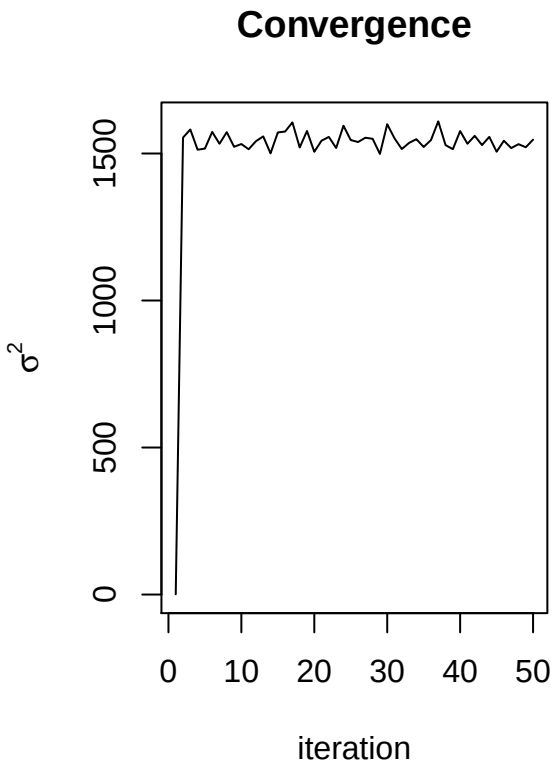
```
set.seed(123456)

hyperparams <- list(mu0=0, tausq0=50, nu0=1, sigmasq0=50)
iter <- 5000
```

```
gibbs_params <- gibbs(x=rainfall$V1, iter = iter, init = c(1,1), hyperparams)
```

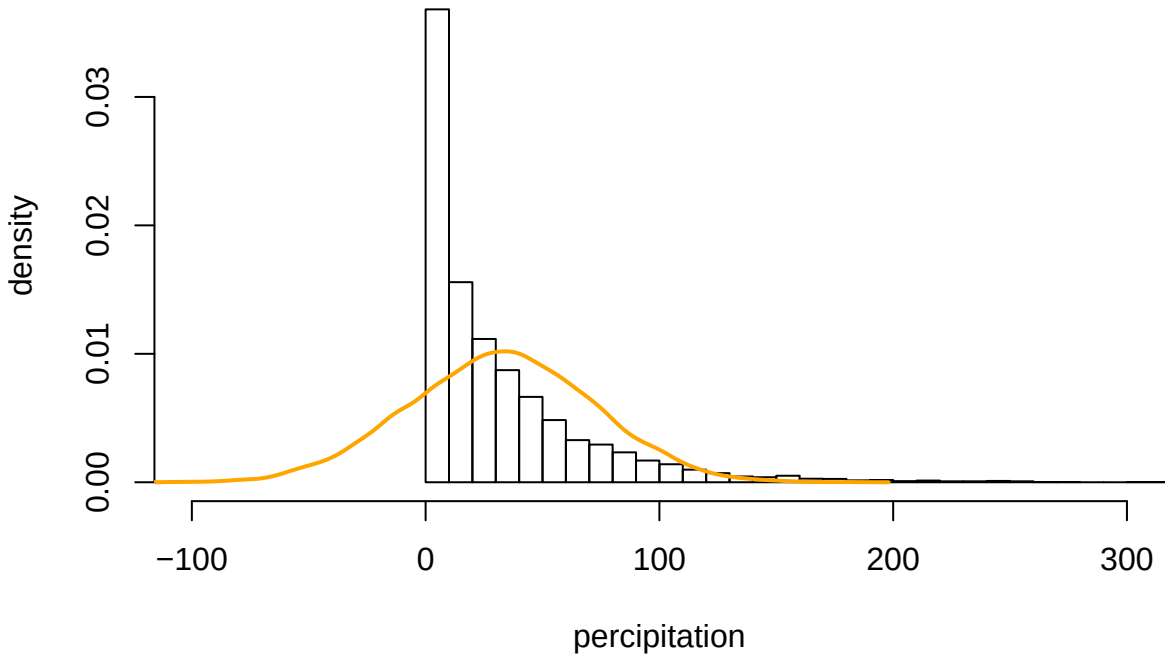


The μ converges to 32.13 which is similar to the data mean, 32.28, and σ^2 converges to 1546.15 which is similar to data variance, 1547.1.





The convergence happens after just a few iterations.



The data is obviously not normally distributed so the model is not particularly good which is seen by the blue curve.

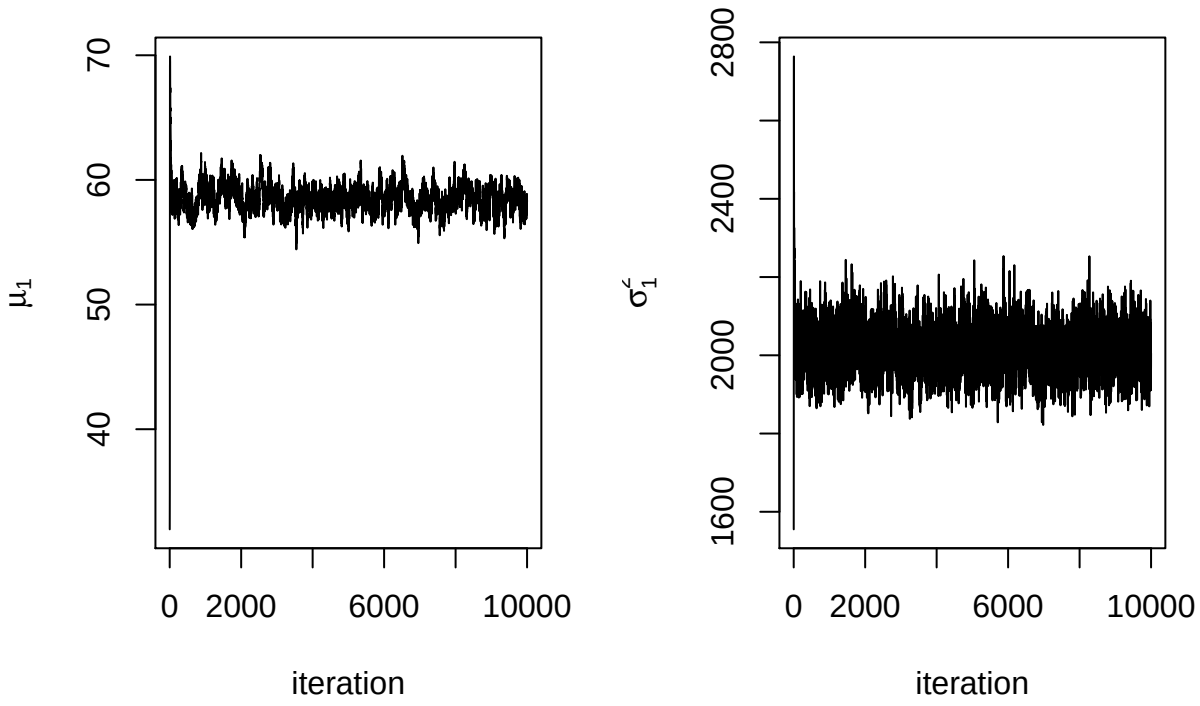
b)

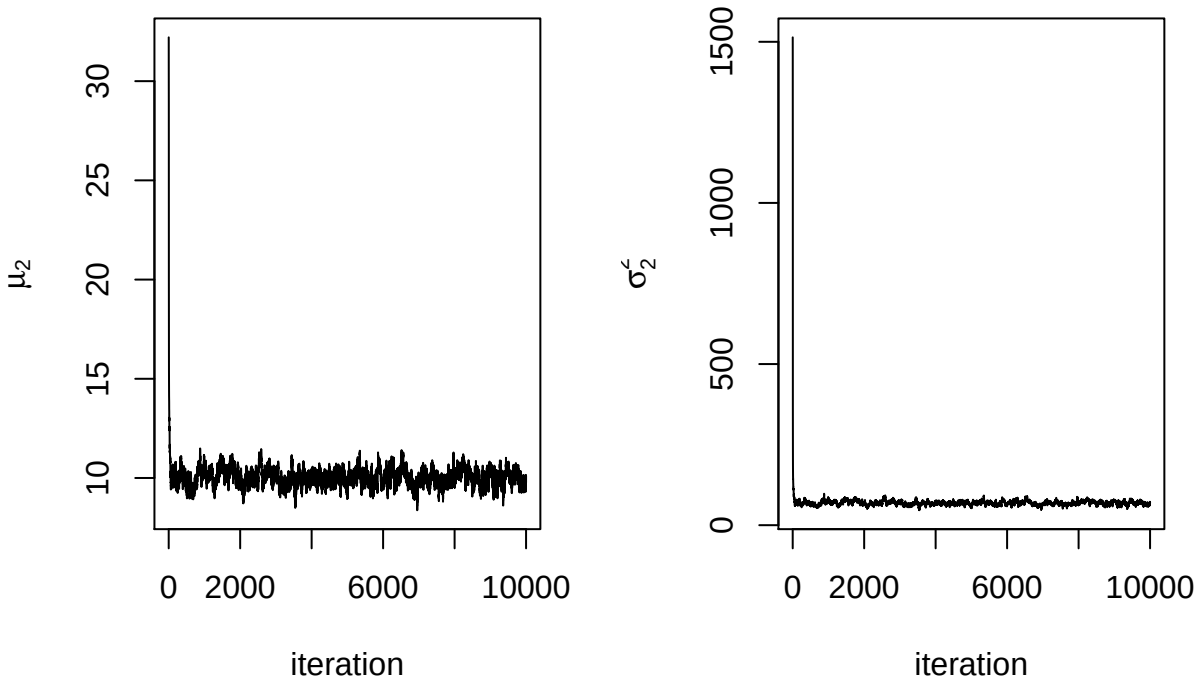
```
nn <- function(I){
    n1 <- sum(I == 1)
    n2 <- sum(I == 2)
    list(n1 = n1,n2 = n2)
}

dd <- function(x, I) {
    d1 <- x[I == 1]
    d2 <- x[I == 2]
    list(d1=d1, d2=d2)
}

pisampler <- function(x, I, hyperparams){
    n <- nn(I)
    rbeta(1, shape1 = n$n1 + hyperparams$a1 , shape2 = n$n2 + hyperparams$a2)
}

sigmasq2sampler <- function(x, I, hyperparams){
    n <- nn(I)
    d <- dd(x, I)
```

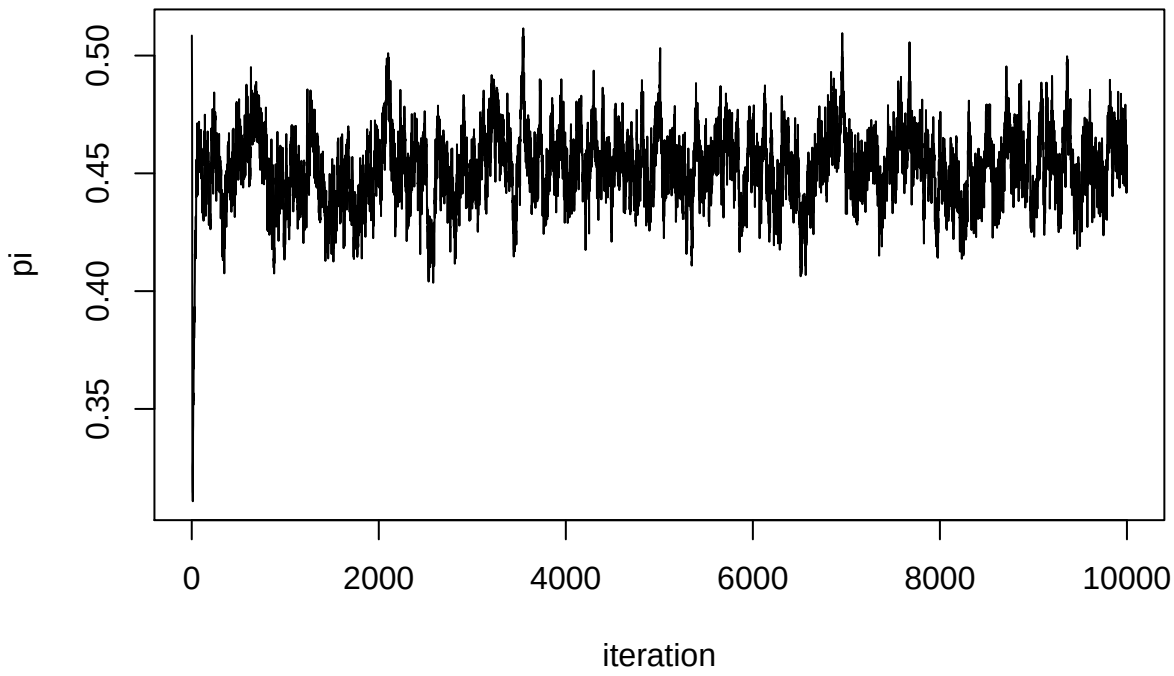
```
    vnsn1 <-  hyperparams$nu0 * hyperparams$sigmasq0 +
        (n$n1 - 1) * var(d$d1) +
        (((1 / hyperparams$tausq0) * n$n1) / ((1 / hyperparams$tausq0) + n$n1)) *
        ((mean(d$d1) - hyperparams$mu0)^2)

    vnsn2 <-  hyperparams$nu0 * hyperparams$sigmasq0 +
        (n$n2 - 1) * var(d$d2) +
        (((1 / hyperparams$tausq0) * n$n2) / ((1 / hyperparams$tausq0) + n$n2)) *
        ((mean(d$d2) - hyperparams$mu0)^2)

    vn1 <-  hyperparams$nu0 + n$n1
    vn2 <-  hyperparams$nu0 + n$n2

    sn1 <- vnsn1 / vn1
    sn2 <- vnsn2 / vn2

    sigmasq1 <- rinvchisq(1, vn1, sn1)
    sigmasq2 <- rinvchisq(1, vn2, sn2)

    c(sigmasq1, sigmasq2)
}

mu2sampler <- function(x, I, sigmasq, hyperparams){
    d <- dd(x, I)

    sigma1 <- sqrt(taun(d$d1, sigmasq[1], hyperparams))
    mu1 <- mun(d$d1, sigmasq[1], hyperparams)

    sigma2 <- sqrt(taun(d$d2, sigmasq[2], hyperparams))
    mu2 <- mun(d$d2, sigmasq[2], hyperparams)

    mu1 <- rnorm(1, mu1, sigma1)
    mu2 <- rnorm(1, mu2, sigma2)

    c(mu1, mu2)
}

Isampler <- function(x, pi, mu, sigmasq){
    nom <- (1 - pi) * dnorm(x, mu[2], sqrt(sigmasq[2]))
    denom <- pi * dnorm(x, mu[1], sqrt(sigmasq[1])) + nom
    theta <- nom / denom
    rbinom(length(x), prob = theta, size = 1) + 1 # to get them into 1 and 2
}

ysampler <- function(pi, mu, sigmasq){
    pi * rnorm(1, mu[1], sqrt(sigmasq[1])) +
        (1 - pi) * rnorm(1, mu[2], sqrt(sigmasq[2]))
}

mixedgibbs <- function(x, iter, init, hyperparams){
    params_samples <- matrix(NA, ncol = 5, nrow = iter)
    samples <- rep(NA, iter)
    I <- init
```

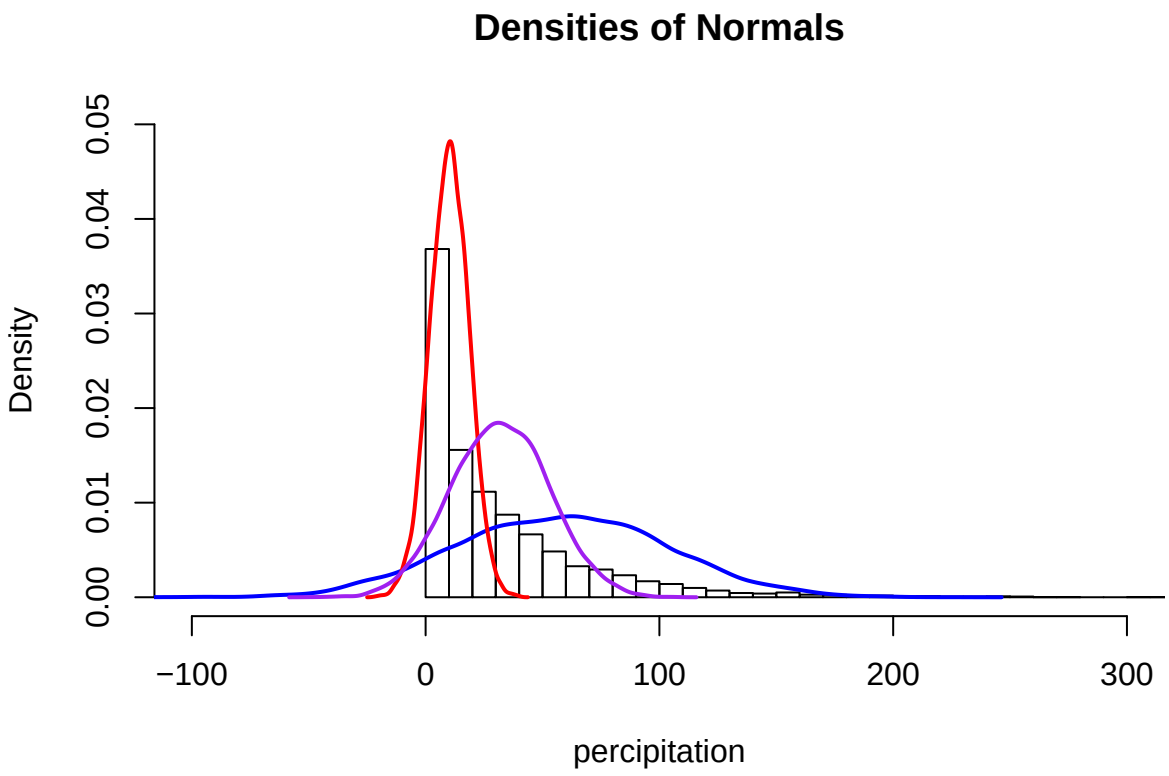
```
    for (i in 1:iter){
        pi <- pisampler(x, I, hyperparams)
        sigmasq <- sigmasq2sampler(x, I, hyperparams)
        mu <- mu2sampler(x, I, sigmasq, hyperparams)
        I <- Isampler(x, pi, mu, sigmasq)

        samples[i] <- ysampler(pi, mu, sigmasq)
        params_samples[i,] <- c(mu, sigmasq, pi)
    }

    colnames(params_samples) <- c("mu1", "mu2", "sigmasq1", "sigmasq2", "pi")
    list(samples=samples, params=params_samples)
}
```

```
set.seed(123456)

hyperparams <- list(a1=1, a2=1, mu0=1, tausq0=50, nu0=1, sigmasq0=50)
init <- sample(c(1, 2), size=length(rainfall$V1), replace=TRUE)
iter <- 10000

mixed <- mixedgibbs(rainfall$V1, iter, init, hyperparams)
mixed_params <- mixed$params
mixed_samples <- mixed$samples
```




μ2
10
15
20
25
30
0
2000
6000
10000
iteration
σ2²
0
500
1000
1500
0
2000
6000
10000
iteration


pi
0.35
0.40
0.45
0.50
0
2000
4000
6000
8000
10000
iteration

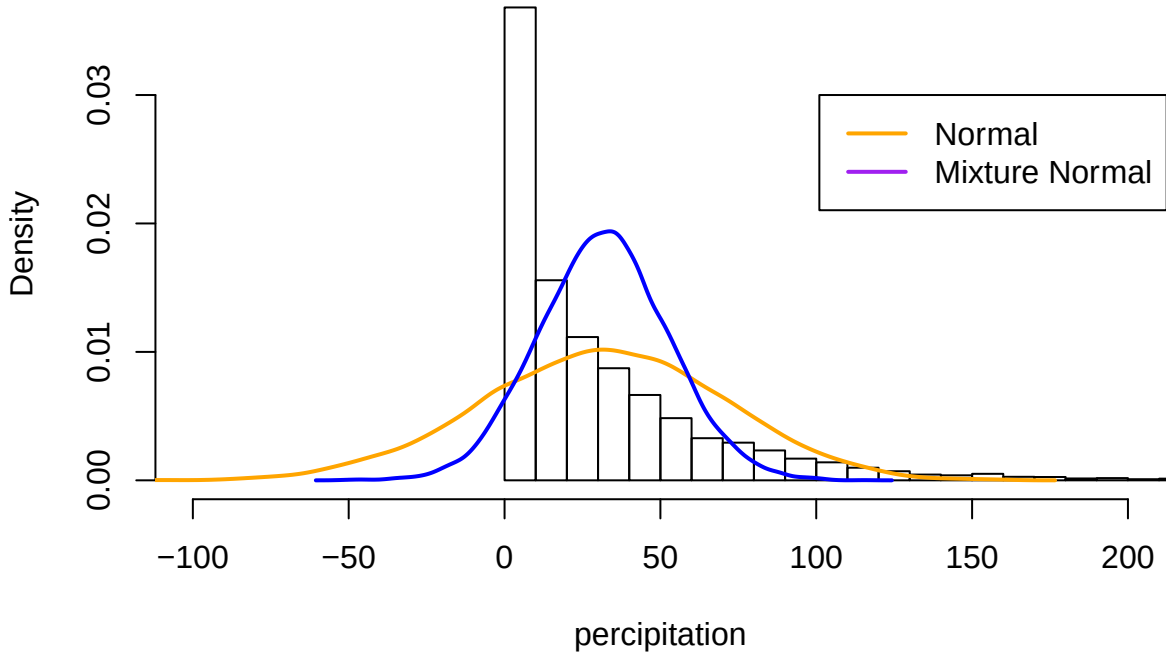


We can see that the two Gaussian distributions in the mixture model represent low values with high density, the red curve, and those with higher values with a wider distribution, the blue curve. Then the model, the purple curve, is an average of those aforementioned distributions. However, as mention before the data is not normally distributed so the final model is far from perfect.

c)

```
n <- 10000
burnins <- 1000 + 1

gibbs_params <- gibbs_params[-(1:burnins),]
mixed_params <- mixed_params[-(1:burnins),]

hist(rainfall$V1, freq=FALSE, breaks=50, xlim=c(-100, 200), main="", xlab="percipitation")

## Model A
mu <- mean(gibbs_params[, "mu"])
sigmasq <- mean(gibbs_params[, "sigmasq"])

samples <- rnorm(n, mu, sqrt(sigmasq))

lines(density(samples), lwd=2, col="orange")

## Model B
mu1 <- mean(mixed_params[, "mu1"])
```

```r
sigmasq1 <- mean(mixed_params[, "sigmasq1"])

mu2 <- mean(mixed_params[, "mu2"])
sigmasq2 <- mean(mixed_params[, "sigmasq2"])

pi <- mean(mixed_params[, "pi"])

samples <- pi * rnorm(n, mu1, sqrt(sigmasq1)) + (1 - pi) * rnorm(n, mu2, sqrt(sigmasq2))

lines(density(samples), lwd=2, col="blue")

legend(101, 0.03, lty=c(1, 1), lwd=c(2, 2), col=c("orange", "purple"),
       legend=c("Normal", "Mixture Normal"))
```



Comparing the normal model and the mixture of normals we conclude that the latter is better in this case but it would probably have been better to choose either a truncated Normal or exponential distribution as the model since we know that percipitation cannot be negative.

Question 2

```
women <- read.table("../data/WomenWork.dat", header = T)
women <- as.matrix(women)
```

a)

```
library(msm)
library(mvtnorm)

betahat <- function(XX, X, y){
  solve(XX) %*% t(X) %*% y
}

mun <- function(XX, betahat, mu0, omega0){
 solve( XX + omega0 ) %*% (XX %*% betahat - omega0 %*% mu0)
}

probitgibbs <- function(X, Y, mu0, omega0, beta0, iter){
  samples <- matrix(ncol = ncol(X), nrow = iter)
  y0 <- Y == 0
  y0n <- sum(y0)
  y1n <- sum(!y0)
  XX <- t(X) %*% X
  omegan <- XX + omega0
  u <- c(rep(1, times = length(Y)))
  beta <- beta0

  for (i in 1:iter){

    xB <- X %*% beta

    u[y0] <- rtnorm(n = y0n,mean = xB[y0], sd = 1, lower = -Inf, upper = 0)
    u[!y0]<- rtnorm(n = y1n,mean = xB[!y0], sd = 1, lower = 0, upper = Inf)

    baehat <- betahat(XX,X,u)
    myn <- mun(XX,baehat,mu0,omega0)

    beta <- as.vector(rmvnorm(1, mean = myn, sigma = 1 * solve(omegan) ))
    samples[i,] <- beta
  }
  samples
}
```

b)

```
betas <- probitgibbs(X = women[,-1], Y = women[,1],
                     mu0 = rep(0, times = ncol(women[,-1])),
                     omega0 = 100* diag(ncol(women[,-1])),
```

```
                    beta = rep(0, times = ncol(women[,-1])), iter = 10000)
probitbetas <- colMeans(betas)
```

c)

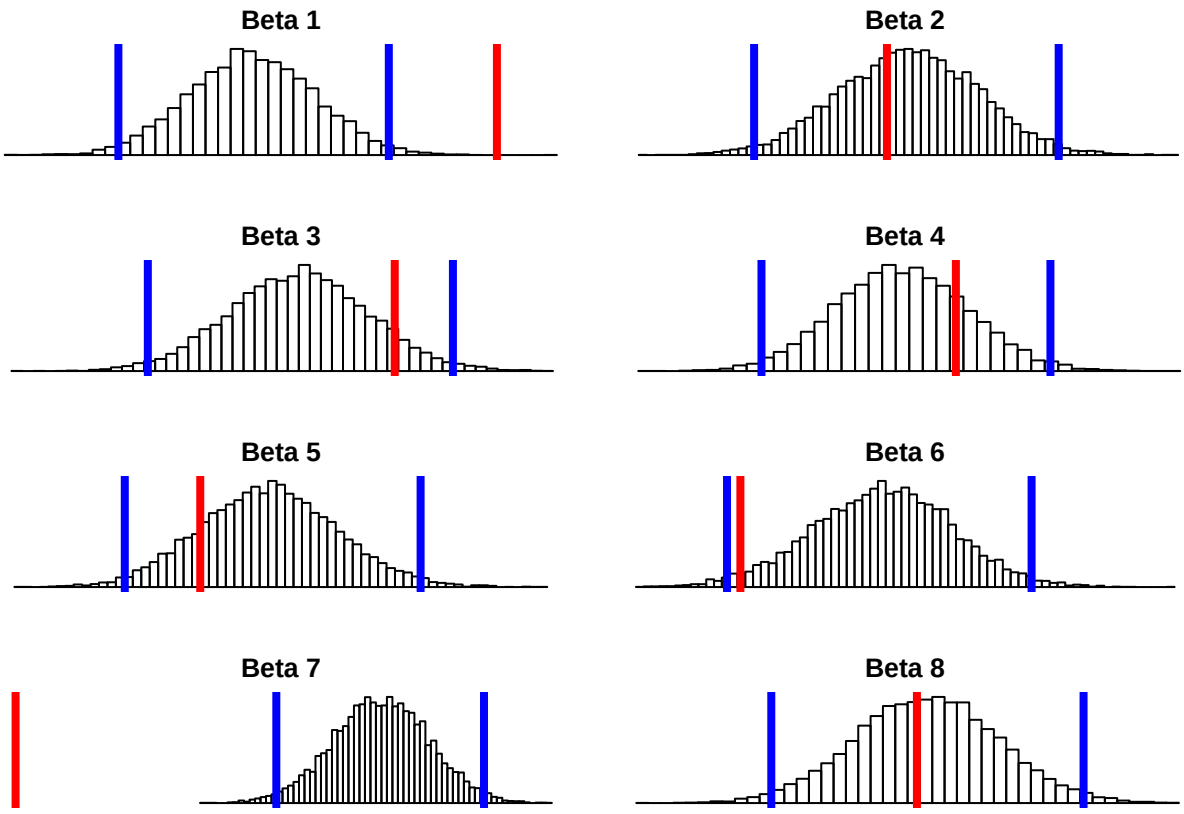
```
logprior <- function(beta, mean, sigma){
    dmvnorm(beta, mean = mean, sigma = sigma, log = TRUE)
}

loglikelihood <- function(beta, X, Y){
    linear_prediction <- t(X) %*% beta
    P <- pnorm(linear_prediction, mean = 0, sd = 1)
    probabilities <- Y * log(P) + (1 - Y)*log(1 - P)
    loglike <- sum(probabilities)

    ## if (abs(loglike) == Inf)
    ##     loglike = -20000

    loglike
}

logposterior <- function(beta, X, Y, mean, sigma){
   loglikelihood(beta, X, Y) + logprior(beta, mean, sigma)
}

tau <- 10
mu <- rep(0,8)
sigma <- tau^2 * diag(8)

womenX <- as.matrix(women[,2:ncol(women)])
womenY <- as.matrix(women[,1])

quadapprox <- optim(par = matrix(rep(0, 8), ncol = 1),
                fn = logposterior, method = "BFGS", hessian = TRUE,
                X = t(womenX), Y = womenY,
                mean = mu, sigma = sigma,
                control=list(fnscale=-1))
```

```
options(digits=3)

probitbetas
```

```
## [1] -0.00572 -0.00944  0.06510  0.08245 -0.00918 -0.03144 -0.15049 -0.00455
```

```
quadbetas <- as.vector(quadapprox$par)
quadbetas
```

```
## [1]  0.3845 -0.0121  0.1084  0.1022 -0.0902 -0.0496 -0.8157 -0.0124
```



The blue lines show the 97% credibility intervals and the red lines represent the corresponding parameter value found by normal approximation.