Freie Universität Berlin
Chair of Statistics
Location: Berlin
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Lecture: Einführung in die Bayes-Statistik
Examiner: Dr. Florian Meinfelder

# Program leave-one-out posterior predictive checking in R

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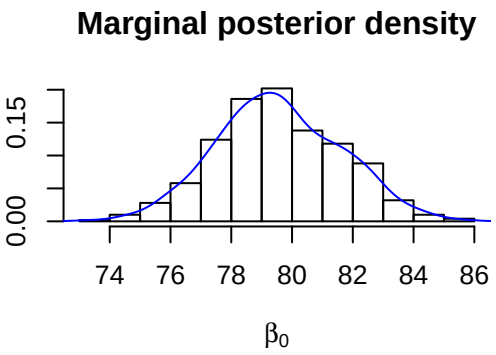
# 2 Code

```
library(mvtnorm)

plotSampling <- function(betas, sigma, traces = TRUE, density = TRUE) {
  # Get number of parameters and adjust plot frame height
  q <- ncol(betas) + 1
  frameRows <- round(q/2+0.1)

  # Traces
  if(traces == TRUE) {
    par(mfrow = c(frameRows,2))
    for(i in 1:ncol(betas)) {
      plot(betas[,i], type='l', ylab=bquote(beta[.(i-1)]), main=bquote("Trace of" ~ beta[.(i-1)]))
    }
    plot(sigma, type='l', ylab=bquote(sigma^2), main=bquote("Trace of" ~ sigma^2))
  }

  # Marginal posterior densities (remove burn in)
  if(density == TRUE) {
    # Function to draw plot
    drawHistDensity <- function(para, para_name) {
      # para      : Parameter (e.b. Beta, Sigma)
      # para_name: Title of plot

      # Estimate density for parameter values
      density <- density(para)

      # Draw histogram and add estimated density line
      hist(para, freq = FALSE, ylim = c(0,max(density$y)), xlab = para_name,
           ylab=NULL, main = "Marginal posterior density")
      lines(density, col="blue")
    }

    # Adjust frame and plot all parameters
    par(mfrow = c(frameRows,2))
    for(i in 1:ncol(betas)) {
      drawHistDensity(betas[-(1:b),i], bquote(beta[.(i-1)]))
    }
    drawHistDensity(sigma[-(1:b)], bquote(sigma))
  }
}

# The Gibbs Sampler
gibbsSampler <- function(X, Y, B, ...) {
  # Size of design matrix
  n <- nrow(X)
  p <- ncol(X)

  # Variables to store the samples in
  betas <- matrix(NA, nrow = B, ncol = p)
  sigma <- c(1, rep(NA, B))

  # Sampling
```

```
  for(i in 1:B){
    # OLS of beta
    V <- solve(t(X)%*%X)      # (X^T X)^-1
    beta_hat <- V%*%t(X)%*%Y # (X^T X)^-1 X^T Y

    # OLS of sigma
    sigma_hat <- t(Y-X%*%beta_hat)%*%(Y-X%*%beta_hat)/(n-p)

    # Sample beta from the full conditional
    betas[i,] <- rmvnorm(1,beta_hat,sigma[i]*V)

    # Sample sigma from the full conditional
    sigma[i+1] <- 1/rgamma(1,(n-p)/2,(n-p)*sigma_hat/2)
  }

  plotSampling(betas, sigma, ...)

  return(list(betas = betas, sigma = sigma))
}

crossValidation <- function(X, Y, B, ...) {
  # Size of design matrix
  n <- nrow(X)
  p <- ncol(X)

  Yhat <- rep(NA, n)
  betas <- matrix(NA, nrow = n, ncol = p)

  for(i in 1:n) {
    # Remove i-th row from data
    Xi <- X[-i,]
    Yi <- Y[-i]

    # Run gibbs sampler to get sampled parameters and plot results from first run
    if(i == 1) {
      res <- gibbsSampler(Xi, Yi, B, ...)
    } else {
      res <- gibbsSampler(Xi, Yi, B, traces = FALSE, density = FALSE)
    }

    # Calculate posterior mean from sampled betas
    betas[i,] <- apply(res$betas, 2, mean)

    # Predict value with posterior mean
    Yhat[i] <- X[i,]%*%betas[i,]
  }

  # Calculate beta estimate
  beta_cv <- colMeans(betas)

  # Calculate MSE
  mse <- sum((Y-Yhat)^2)

  return(list(betas = beta_cv, mse = mse))
}

bayesModelEvaluation <- function(models, Y, B, ...) {
  # Evaluate multiple models and return results from all models
```

```
  results <- list()
  for(i in 1:length(models)) {
    results[[i]] <- crossValidation(models[[i]], Y, B, ...)
  }
  return(results)
}

# Swiss data
dat <- swiss

# Response variable
Y <- dat$Fertility

# Design matrix
n <- nrow(dat)
X <- matrix(c(rep(1,n), dat$Education, dat$Agriculture), nrow=n)

models <- list(
  matrix(c(rep(1,n), dat$Education), nrow=n),
  matrix(c(rep(1,n), dat$Agriculture), nrow=n),
  matrix(c(rep(1,n), dat$Examination), nrow=n),
  matrix(c(rep(1,n), dat$Catholic), nrow=n),
  matrix(c(rep(1,n), dat$Education, dat$Agriculture), nrow=n),
  matrix(c(rep(1,n), dat$Education, dat$Examination), nrow=n),
  matrix(c(rep(1,n), dat$Education, dat$Catholic), nrow=n),
  matrix(c(rep(1,n), dat$Education, dat$Agriculture, dat$Examination), nrow=n),
  matrix(c(rep(1,n), dat$Education, dat$Agriculture, dat$Catholic), nrow=n),
  matrix(c(rep(1,n), dat$Education, dat$Examination, dat$Catholic), nrow=n),
  matrix(c(rep(1,n), dat$Education, dat$Agriculture, dat$Examination ,dat$Catholic), nrow=n)
)

# Number of samples
b <- 50  # Burn in
R <- 500 # Random draws to evaluate
B <- R + b

res <- bayesModelEvaluation(models, Y, B, traces = FALSE, density = TRUE)
```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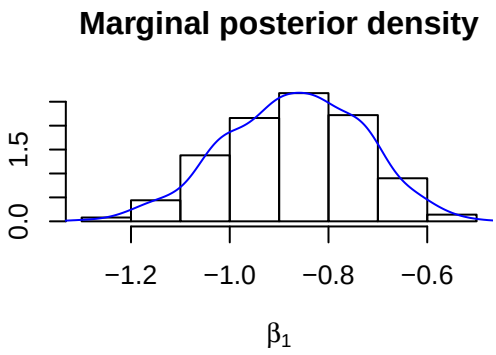
74
76
78
80
82
84
86
β0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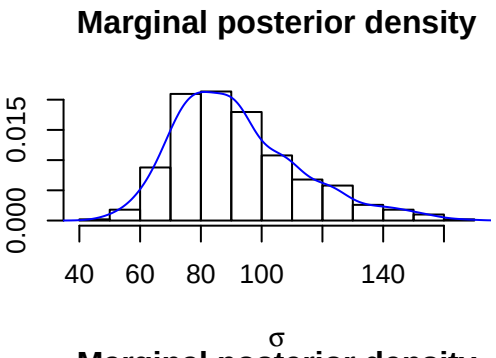
−1.2
−1.0
−0.8
−0.6
β1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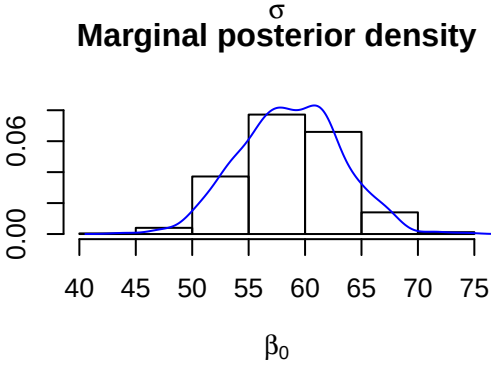
0.015
40
60
80
100
140
σ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45
50
55
60
65
70
75
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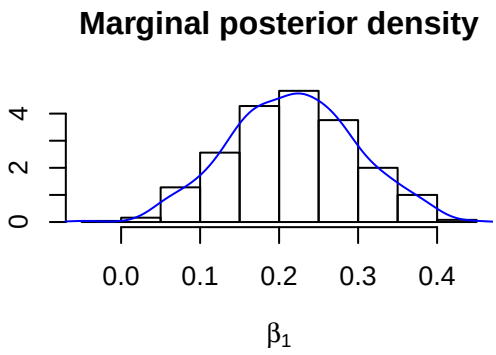
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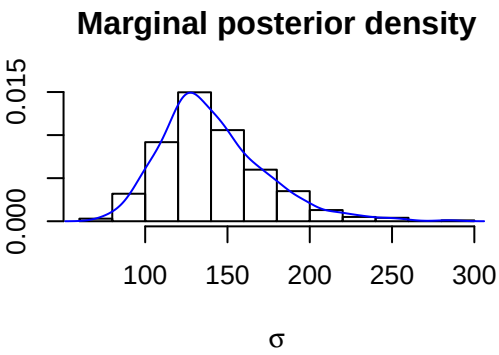
2
4
0.0
0.1
0.2
0.3
0.4
β1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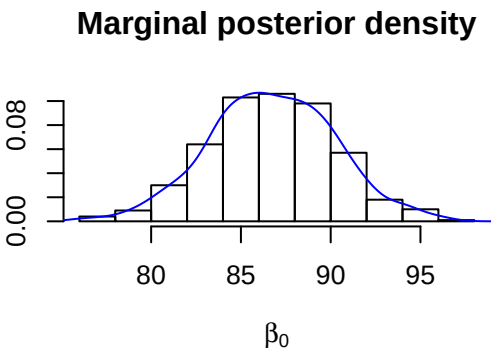
100
150
200
250
300
σ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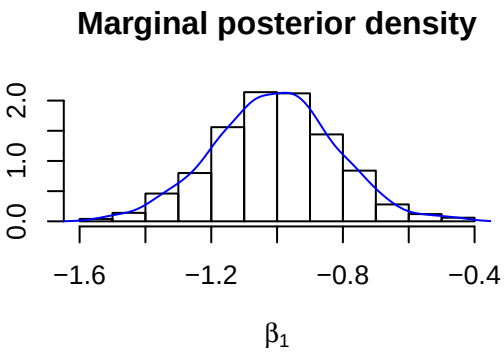
0.08
80
85
90
95
β0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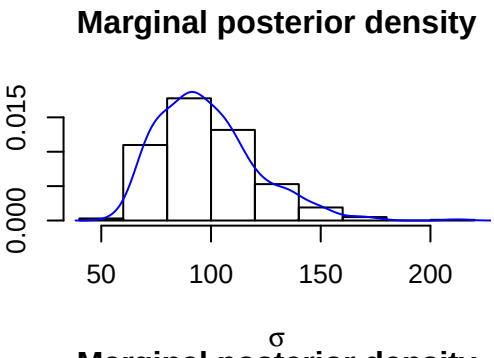
−0.8
−0.4
β1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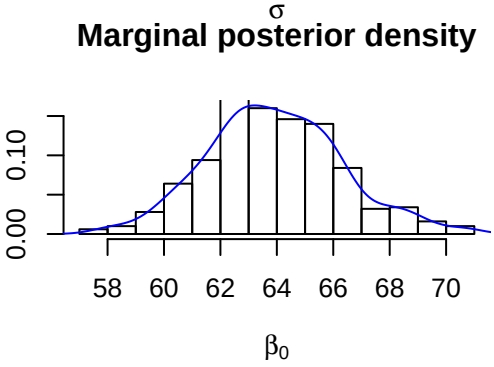
0.000
0.015
50
100
150
200
σ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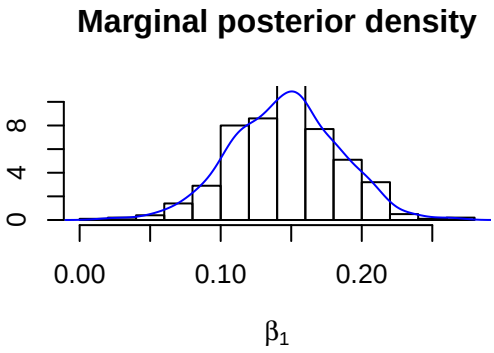
0.10
58
60
62
64
66
68
70
β0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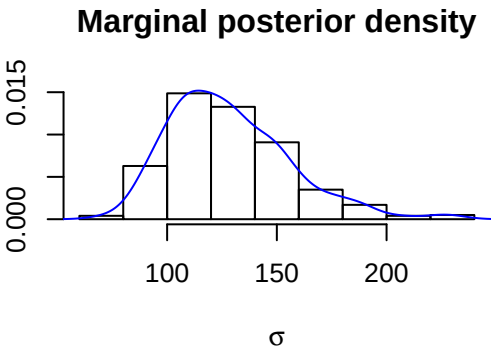
8
0.00
0.10
0.20
β1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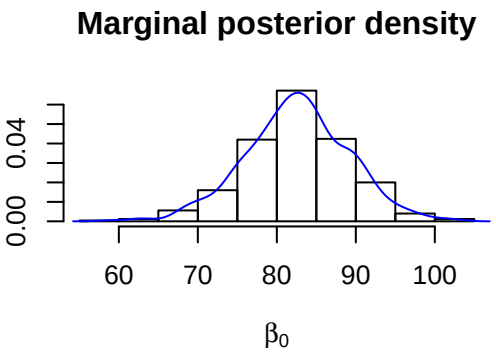
0.015
100
150
200
σ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0.04
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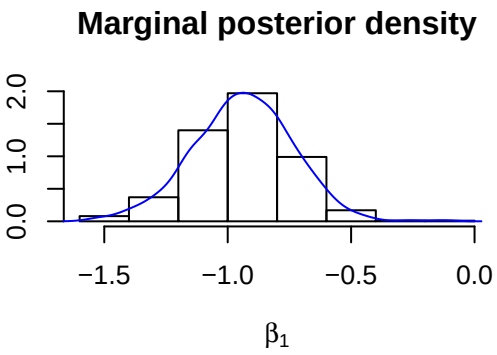
70
80
90
100
β0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−1.5
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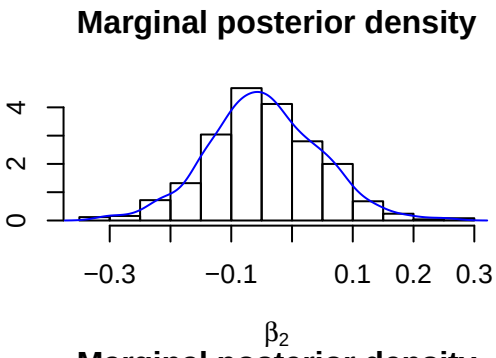
−0.5
0.0
β1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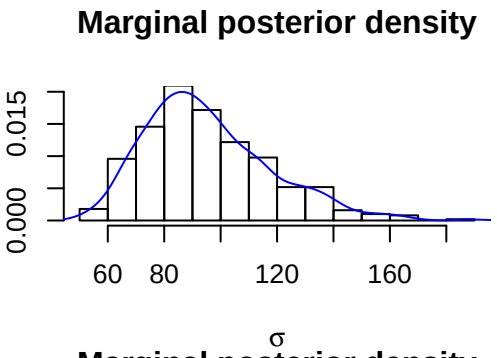
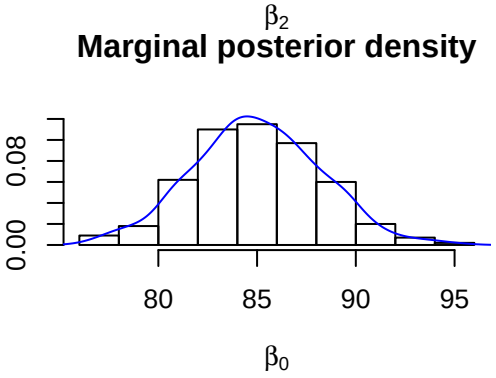
4
−0.3
−0.1
0.1
0.2
0.3
β2


Marginal posterior density
0.000
0.015
60
80
120
160
σ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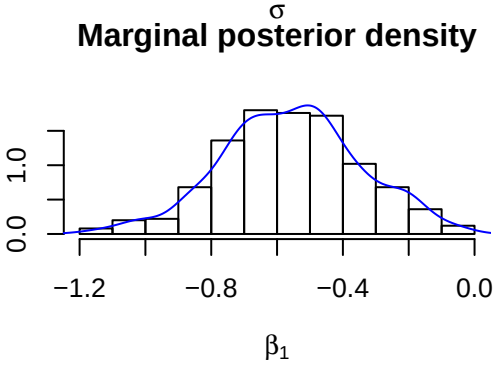
0.08
80
85
90
95
β0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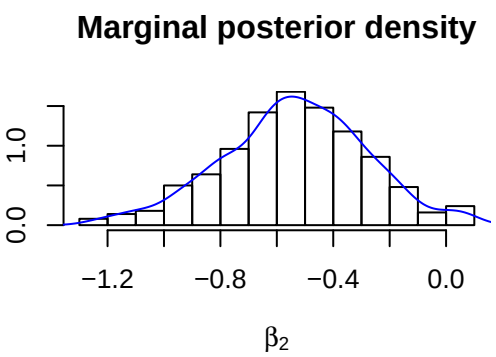
1.0
−1.2
−0.8
−0.4
0.0
β1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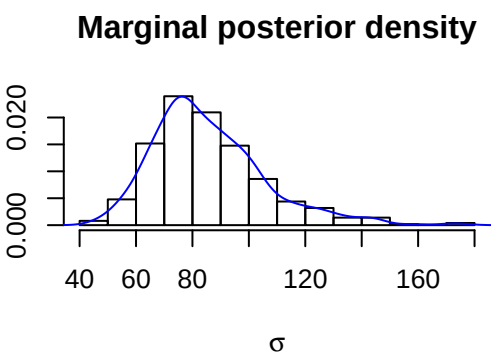
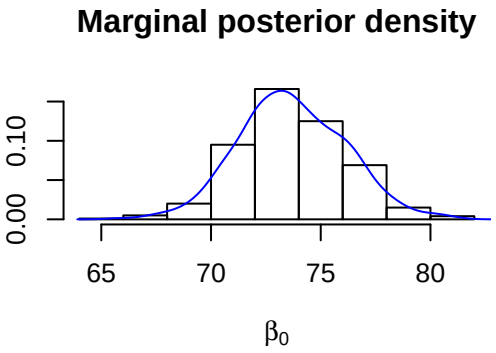
−1.2
−0.8
−0.4
0.0
β2


Marginal posterior density
0.000
0.020
40
60
80
120
160
σ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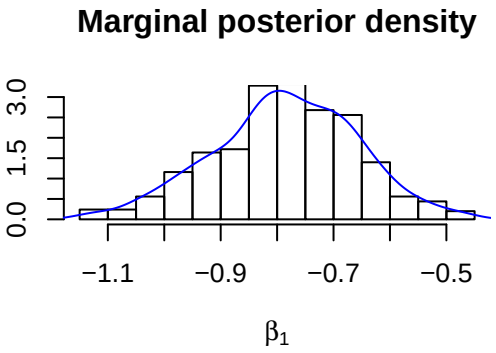
0.10
65
70
75
80
β0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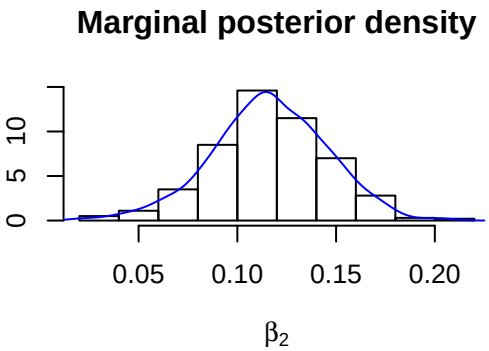
−0.7
−0.5
β1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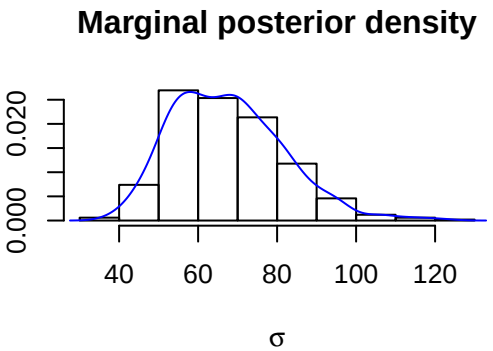
10
0.05
0.10
0.15
0.20
β2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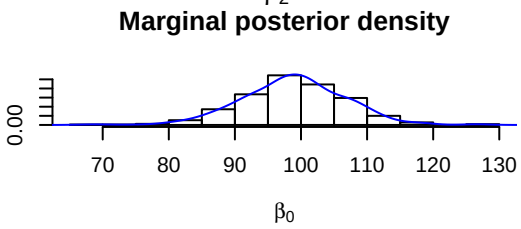
0.000
0.020
40
60
80
100
120
σ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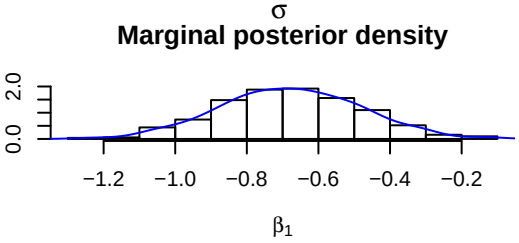
0.00
70
80
90
100
110
120
130
β0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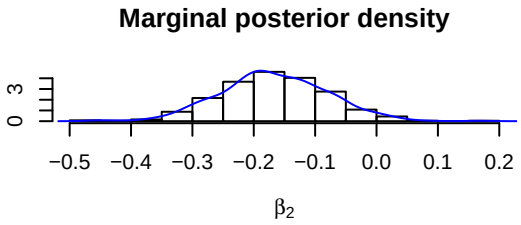
−0.6
−0.4
−0.2
β1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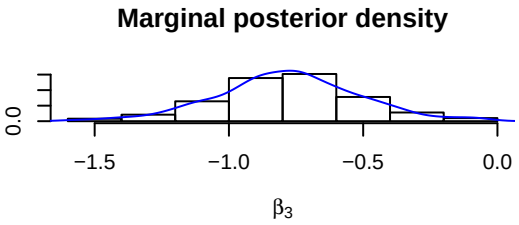
−0.1
0.0
0.1
0.2
β2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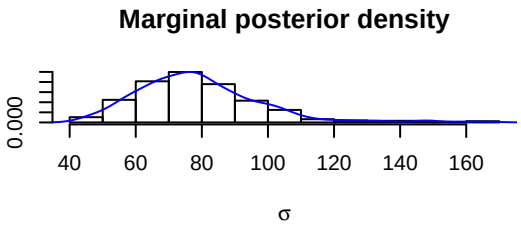
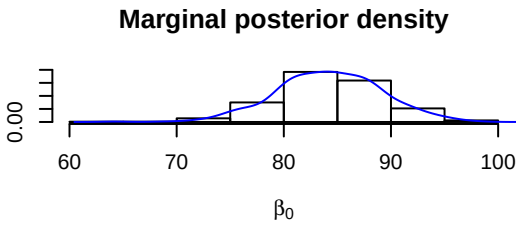
β3


Marginal posterior density
0.000
40
60
80
100
120
140
160
σ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0.00
60
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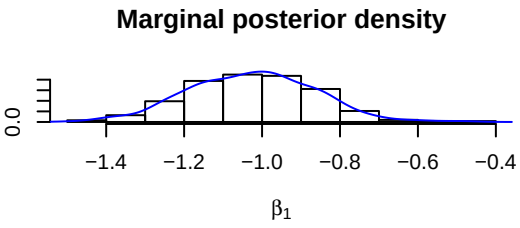
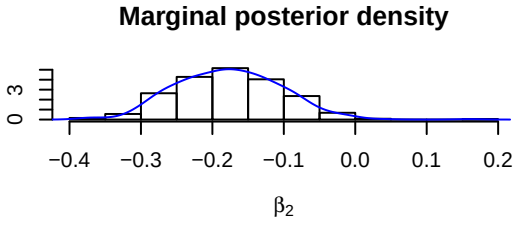
80
90
100
β0


Marginal posterior density
0.0
−1.4
−1.2
−1.0
−0.8
−0.6
−0.4
β1


Marginal posterior density
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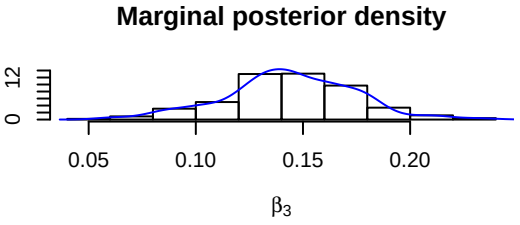
3
−0.4
−0.3
−0.2
−0.1
0.0
0.1
0.2
β2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12
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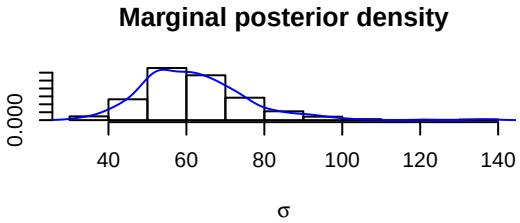
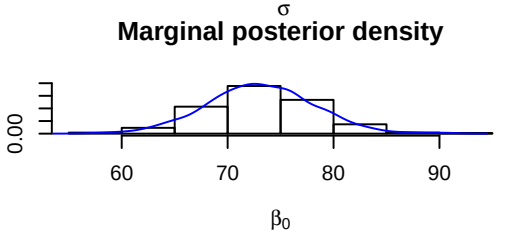
0.10
0.15
0.20
β3


Marginal posterior density
0.000
40
60
80
100
120
140
σ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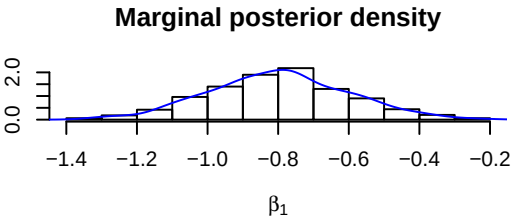
60
70
80
90
β0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−1.2
−1.0
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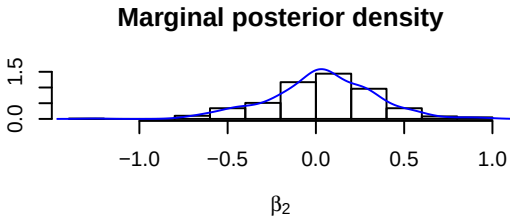
−0.6
−0.4
−0.2
β1


Marginal posterior density
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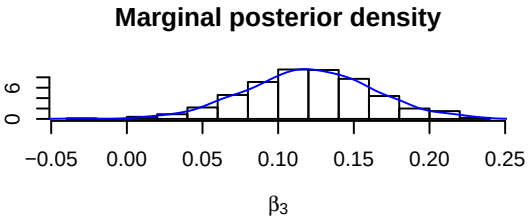
−1.0
−0.5
0.0
0.5
1.0
β2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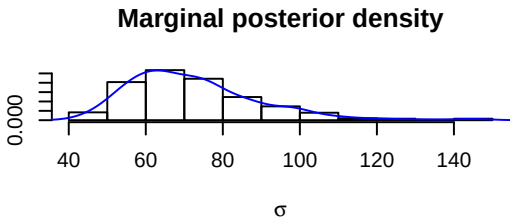
0.00
0.05
0.10
0.15
0.20
0.25
β3


Marginal posterior density
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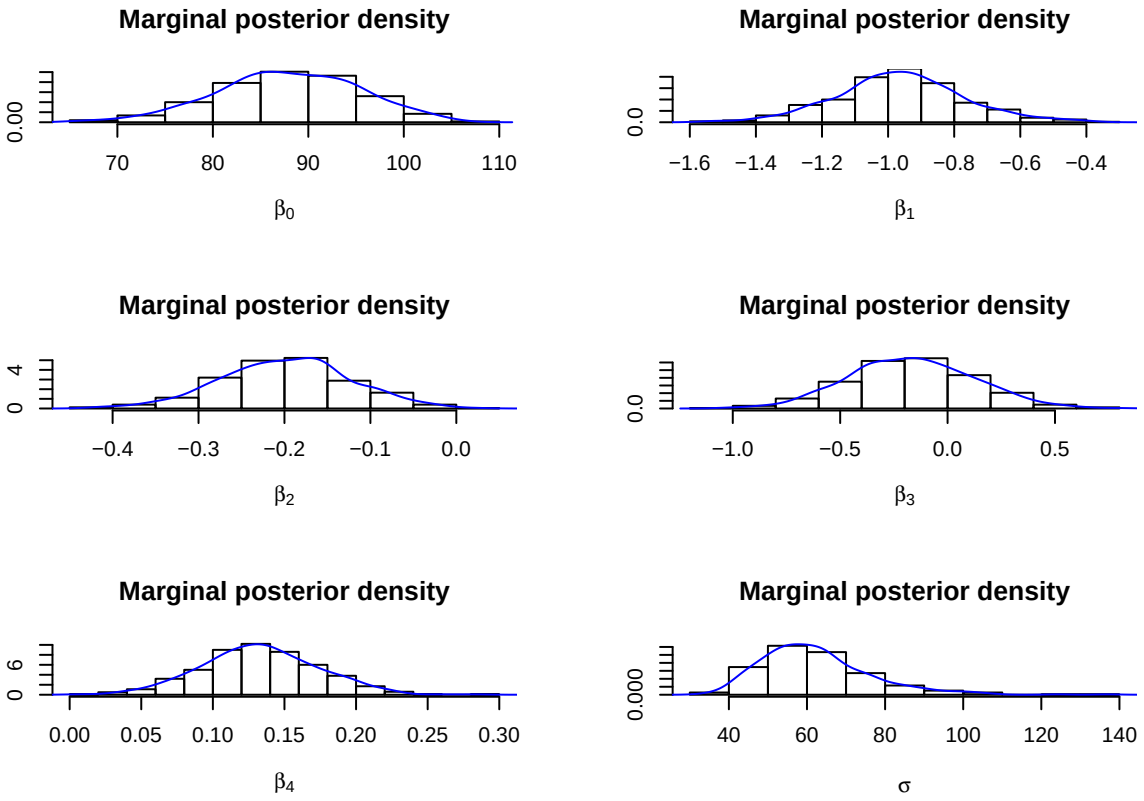
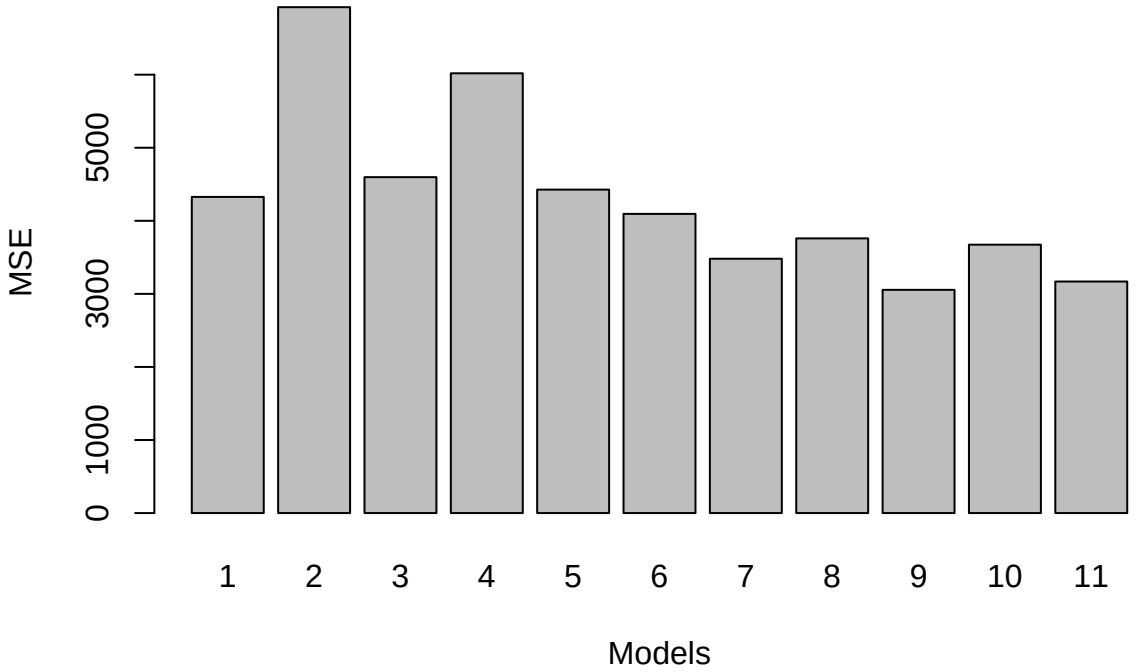
40
60
80
100
120
140
σ




```r
# Plot Mean Squared Errors
MSEs <- sapply(res, function(el) { return(el$mse) })
par(mfrow = c(1,1))
barplot(MSEs, xlab = "Models", ylab = "MSE", names.arg = seq(1,length(models)))
```




## 3 References