TDDE07 - Lab 3

Sophie Lindberg - sopli268 Arvid Edenheim - arved490 2019-05-30

${\bf 1}$ - Normal model, mixture of normal model with semi-conjugate prior

1a) - Normal model

The code for the Gibbs implementation can be seen in appendix 1.

By plotting the trajectories of the sampled Markov chains it can be seen that σ and μ converges around 39 and 32 respectively.

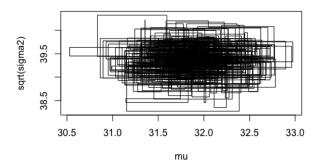


Figure 1: Analyzing the convergence

1b) - Mixture normal model

The results of the Gibbs sampling data augmentation algorithm given in Normal MixtureModel.R resulted can be seen below.

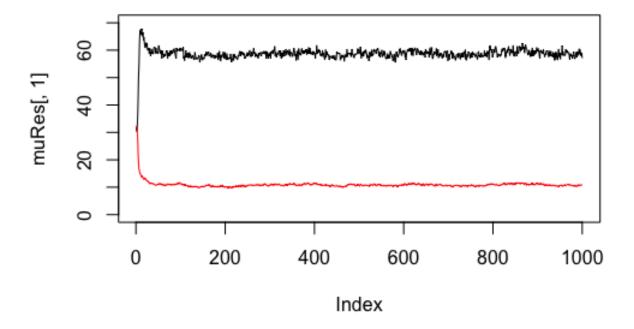


Figure 2: The convergence of mu

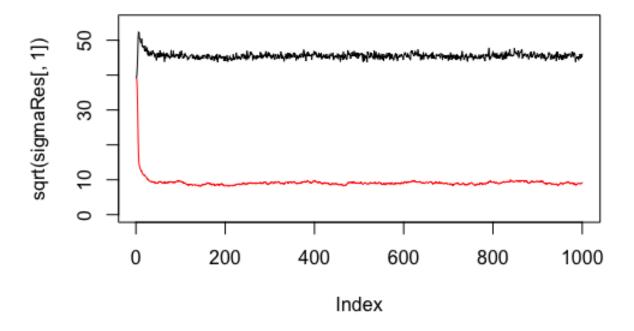


Figure 3: The convergence of sigma

Both μ and σ converged after a few samples.

1c) - Graphical comparison

The figure below shows a comparison between the samplers. The blue line represents the normal density from excercise a, and the green line represents the mixture of normals density from excercise b. Both of the models have limitations when it comes to fit the data.

Histogram of data\$x

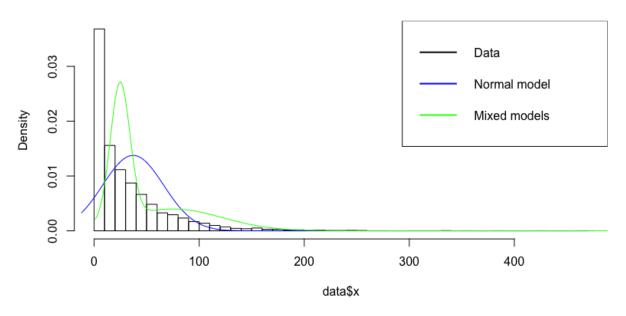


Figure 4: Graphical comparison

2 - Metropolis Random Walk for Poisson regression

2a)

The table below shows the p-values for each parameter. The p-value given for the Z-statistic can be interpreted as how likely it is that a result as extreme or more extreme than that observed would have occured under the null hypothesis. Thus, the covariates MinBidShare, Sealed, and VerifyID seams to be the most significant ones, whereas MinBlem is the least significant one.

Const	PowerSeller	VerifyID	Sealed	Minblem	MajBlem	LargNeg	LogBook	MinBidShare
4.56e-266	5.76e-01	1.96e-05	1.66e-18	3.85e-01	1.57e-02	2.09e-01	3.09e-05	9.42e-156

2b)

The logistic Poisson regression resulted in the following values for β s and σ^2 s.

					:				
	Const	PowerSeller	VerifyID	Sealed	Minblem	MajBlem	LargNeg	LogBook	MinBidShare
σ	0.4932	0.6767	1.4006	1.0888	1.0942	1.7190	1.1535	0.5236	1.0231545
$\hat{\beta}$.33285	-0.28581	0.03928	-0.14391	-0.21800	-0.19890	-0.19947	-0.15492	-0.22178

Table 1: Posterior mode and standard diviation

2c)

The result below is from 50 000 sample draws from the posterior. In order to analyze the convergence, the trajectories of β_9 are plotted in the figure below. As can be seen, the samples are converging after 6000 iterations.

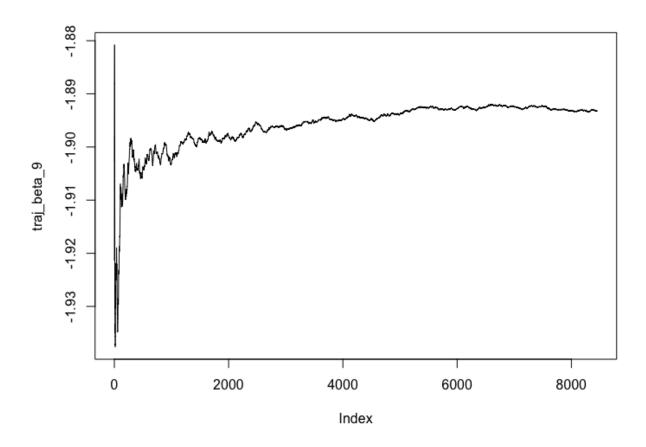


Figure 5: Convergence of sampler

Code - 1

```
data = read.table("rainfall.txt", col.names = "x")
######### A ##########
# parameter init values
mu0 <- 30
tau0 <- 1
v0 <- 0
sigma0 <- 10
n <- nrow(data)</pre>
dataMean <- mean(data$x)</pre>
vn <- v0 + n
iter <- 1000
# draw mu
drawMu <- function(prevMu, prevSigma) {</pre>
  tauSq <- 1/( (n/prevSigma) + (1/tau0^2) )</pre>
  w <- (n/prevSigma)/((n/prevSigma) + (1/tau0^2))</pre>
  mu \leftarrow w*dataMean + (1-w)*mu0
  draw <- rnorm(1, mu, sqrt(tauSq))</pre>
  return (draw)
#inv chi square
invChiSquare <- function(v, s) {</pre>
 return(v*s / rchisq(1,v))
}
# draw sigma
drawSigma <- function(mu) {</pre>
  sum <- 0
  for (i in 1:n) {
    sum <- sum + (data[i,1] - mu)^2
  s \leftarrow (v0*sigma0 + sum)/(n+v0)
  return(invChiSquare(vn, s))
mu <- c()
sigma2 <- c()
currMu <- 32
currSigma <- sigma0
for (i in 1:iter) {
  if(i \% 2 == 0) {
    currMu <- drawMu(currMu, currSigma)</pre>
  } else {
    currSigma <- drawSigma(currMu)</pre>
  mu <- c(mu, currMu)
  print(length(mu))
```

```
sigma2 <- c(sigma2, currSigma)
}
## plot trajectories of sampled mu and sigma
plot(mu, sqrt(sigma2),type='l')
# Also consider plotting the trajectories (the sampled values of mu and sigma2) over the iterations.
meanMeans = c()
meanVars = c()
for (i in 2:iter){
  # if(i\%2 == 0){
    # the trajector between the current and previous mu/sigma
    meanMeans = c(meanMeans, mean(mu[i-1:i]))
    meanVars = c(meanVars, mean(sigma2[i-1:i]))
  #}
}
plot(meanMeans, type='l', xlim=c(0,1000))
plot(sqrt(meanVars), type='l', xlim=c(0,1000))
######## C ########
densityData = density(data$x)
xGrid = seq(min(densityData$x),max(densityData$x),length = length(densityData$x))
ndens = dnorm(xGrid, mean(mu), mean(sqrt(sigma2)))
hist(data$x, 50, freq = FALSE)
lines(xGrid,
     ndens,
      col='blue')
lines(mixDens,
      col = 'green')
legend("topright",
       box.lty = 1,
       legend = c("Data",'Normal model', 'Mixed models'),
       col = c("black", 'blue', 'green'),
       lwd = 2)
```

Code - 2

```
data = read.table("rainfall.txt", col.names = "x")
library(mvtnorm)
data <- read.table("eBayNumberOfBidderData.txt", header = TRUE)</pre>
######## A #########
#The significance of a parameter is not governed by its estimated
#absolute value, but by e.g. the p-value. Use e.g. summary(fit).
fit <- glm(nBids ~ 0 + ., data, family = poisson)</pre>
#Obtain p-values
p_values <- coef(summary(fit))[,4]</pre>
coeff <- t(fit$coefficients)</pre>
plot(abs(coeff), type='h',
     lwd=2,
     xlab = "coefficient index",
     main='Significance of covariates',
     ylab='absolute value of coefficient')
X <- as.matrix(data[,2:10])</pre>
## The most significant covariate is minBidShare.
######## B ########
# Your estimated beta values should be close to the ones from glm() if
# you did it right. Double check this line:
sigmaPrior \leftarrow 100 * solve(t(X)%*%X)
logPois <- function(beta, y, X, ...) {</pre>
  # log likelihood of poisson model
  if(!is.null(dim(beta))) {
    beta <- beta[1,]</pre>
  }
  lambda <- exp(X%*%beta)</pre>
  logLik <- sum(dpois(y, lambda, log=TRUE))</pre>
  if (logLik == -Inf) {
   logLik <- -2000
   \# \ logLik \leftarrow logLik + y[i] * t(beta)%*%x[i,] - exp(\ t(beta))%*%x[i,] - log(factorial(y[i]))) 
  # log of prior
  logPrior <- dmvnorm(beta, mean = rep(0, 9), sigma = sigmaPrior, log=TRUE)
  # add
  return(logLik + logPrior)
}
```

```
OptimResults<-optim(coeff,logPois,gr=NULL, y = data$nBids,X = X, method=c("BFGS"),control=list(fnscale=
postCov <- -solve(OptimResults$hessian)</pre>
st_div <- sqrt(diag(postCov))</pre>
betaMode <- OptimResults$par</pre>
######## C #########
# Also plot the MCMC trajectories for the different betas.
# Your results will be different when you fix 2b) also.
gaussianSample <- function(theta, sigma, c) {</pre>
  val <- rmvnorm(1, theta, c*sigma)</pre>
  return (val)
RWMSampler <- function(c, it, initBeta, fn, ...) {</pre>
  accRate <- 0
  sample <- c()</pre>
  prev <- gaussianSample(initBeta, postCov, c)</pre>
  for (i in 1:it) {
    candidate <- gaussianSample(prev, postCov, c)</pre>
    alpha <- min(1, exp( fn(candidate, ...) - fn(prev, ...) ))
    u <- runif(1, 0, 1)
    if (alpha >= u) {
      # accept candidate
      prev <- candidate</pre>
      accRate <- accRate + 1
      # as matrix
      sample <- rbind(sample, prev)</pre>
    }
  }
  return (sample)
# sample with random walk metropolis
sample <- RWMSampler(1,50000,betaMode, logPois, as.vector(data$nBids), X)</pre>
hist(sample[,9])
plot(sample[,1],
     sample[,2],
     type='l',
     xlab = expression(beta[1]),
     ylab = expression(beta[2]),
     main = expression("Samples of" ~ beta[1] ~ "and" ~ beta[2])
     )
# plot trajectoroies for beta 9
traj_beta_9 = c()
for (i in 11:length(sample[,9])) {
    traj_beta_9 = c(traj_beta_1, mean(sample[i-10:i,9]))
plot(traj_beta_9, type = '1')
dev.off()
```