Group 3 R Project 2

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Abstract

The main goal of this project involves creating an MCMC sampler for a logistic regression model and then applying MCMC sampler to NFL data. Credible intervals for parameters will be created using MCMC sampler and through logistic regression model fitting.

Functions for prior, likelihood and posterior

```r
library (dplyr)
library (MASS)
library(TeachingDemos)
```

First, create functions for prior, likelihood and posterior for joint β_0, β_1 distribution including covariate variable.

Based on the assumption that β_0 and β_1 each is normally distributed $\sim N(0, 10^2)$, joint distribution could be found as

$$f(\beta_0, \beta_1) = \frac{1}{2\pi\sigma^2} e^{-\frac{1}{2\sigma^2}(\beta_0^2+\beta_1^2)}$$

.

Function for prior:

```r
prior <- function (beta0, beta1) {
  sigma_sq = 100;
  return (  1/(2*sigma_sq*pi)*exp(-(beta0^(2) + beta1^(2))/(2*sigma_sq) ) )
}
```

Model with covariate variable

$$p(x_i) = \frac{1}{1 + e^{-\beta_0 - \beta_1 x_i}}$$

The likelihood for the logistic regression model

$$L(p) \propto \prod_{i=1}^{n} p(x_i)^{y_i} (1 - p(x_i))^{1-y_i}$$

Function for likelihood:

```r
likelihood <- function (y, beta0, beta1, x) {
  return (prod((1/(1+exp (-beta0 - beta1*x)))^(y)*(1-1/(1+exp (-beta0 - beta1*x)))^(1-y)))
}
```

Posterior distribution

$$f_{\beta_0,\beta_1|Y_1,...,Y_n}(\beta_0,\beta_1|y_1,...y_n,x_1,...x_n) \propto L(p) * f(\beta_0,\beta_1)$$

Function for posterior:

```r
posterior <- function (y, beta0, beta1, x) {
  return (prior(beta0, beta1)*likelihood(y, beta0, beta1, x))
}
```

Sampler function

Create sampler function for

```r
thesampler <- function (y, x, n, niter, beta0start, beta1start, beta0proposalsd,
                        beta1proposalsd) {

  # Create empty vectors size of {niter} for storing beta0 and beta1 candidates
  beta0 = rep (0, niter)
  beta1 = rep (0, niter)

  # Initialize first elements of vectors with {beta0start} and {beta1start}
  beta0[1] = beta0start
  beta1[1] = beta1start

  # Loop through number of iterations {niter}
  for (i in 2:niter) {

    # Initialize current beta0 and beta1 with beta0 and beta1 defined on
    # the previous step
    currentbeta0 = beta0[i-1]
    currentbeta1 = beta1[i-1]

    # Use jumping distribution (here it's normal distribution) to find new beta0
    newbeta0 = currentbeta0 + rnorm (1, 0, beta0proposalsd)
    # Find ratio r
    r = posterior(y,newbeta0, currentbeta1, x)/posterior (y, currentbeta0,
                                                          currentbeta1, x)

    # Based on the ratio r decided if we update current beta0 with new value or
    # keep previous one
    if (runif (1) < r){
      beta0[i] = newbeta0}
    else{
      beta0[i] = currentbeta0}

    # Use jumping distribution (here it's normal distribution) to find new beta1
    newbeta1 = currentbeta1 + rnorm (1, 0, beta1proposalsd)
    # Find ratio r
    r = posterior(y,currentbeta0, newbeta1, x)/posterior (y, currentbeta0,
                                                          currentbeta1, x)

    # Based on the ratio r decided if we update current beta1 with new value or
    # keep previous one
    if (runif (1) < r){
      beta1[i] = newbeta1}
    else{
      beta1[i] = currentbeta1}
  }

  # Store all beta0 and beta1 in data frame
  betas <- data.frame(beta0, beta1)
  # Name columns properly
  names (betas) <- c ("beta0", "beta1")
  return (betas)
}
```

Applying to NFL data

Read NFL data and select only distance and "good" result columns

```
# Read csv file
nfl<-read.csv(file = "nfl2008_fga.csv")
# Select only required data
nfl <- dplyr::select (nfl, distance, GOOD)
```

Applying sampler function against selected NFL data. Choose Standart Deviation for jumping distributions for both β_0 and β_1 as `0.1`.

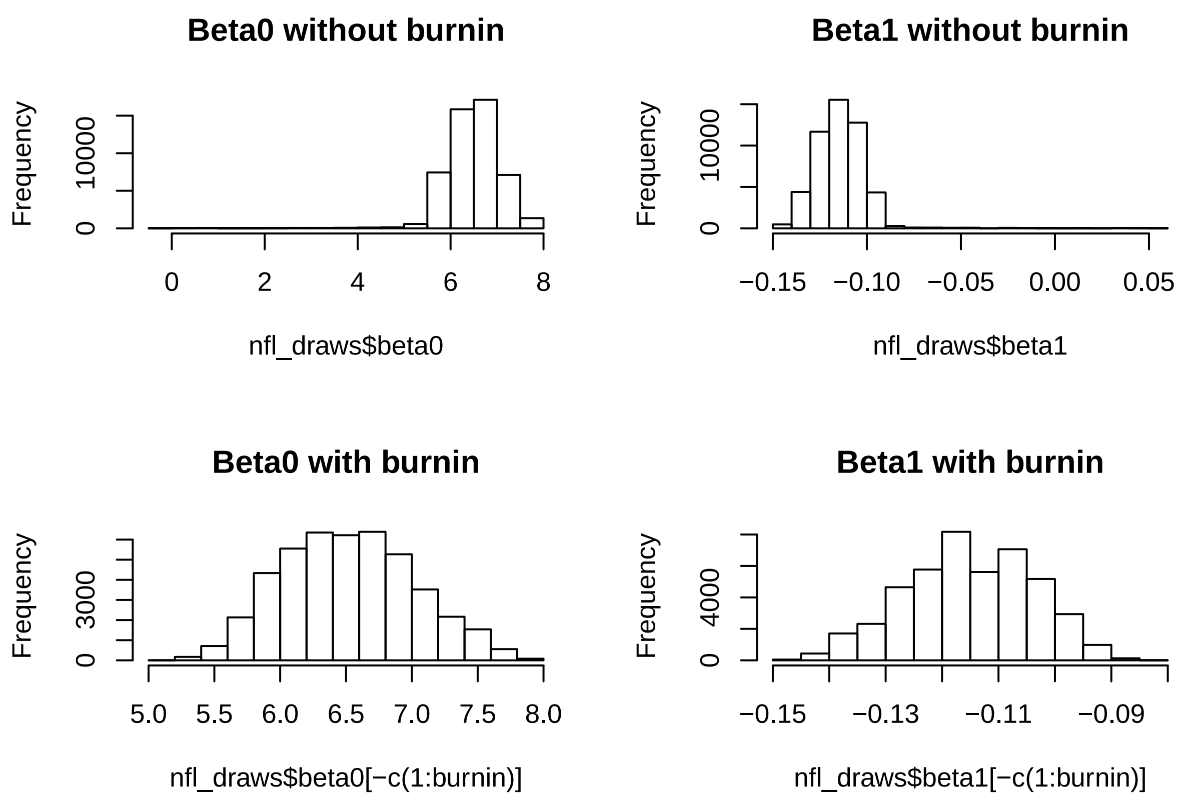
```
# Calculate number of rows in NFL data
n=nrow(nfl)
# Apply sampler function
nfl_draws <- thesampler (nfl$GOOD, nfl$distance, n, 50000, 0, 0,  0.1, 0.1 )
```

Set burnin number as a 10% from number of iterations:

```
burnin <- 5000
```

Histograms for β_0 and β_1 without and with burnin

```
# Place all historgrams on the same graph
par(mfrow=c(2,2))
hist (nfl_draws$beta0, main = "Beta0 without burnin")
hist (nfl_draws$beta1, main = "Beta1 without burnin")
hist (nfl_draws$beta0 [-c(1:burnin)], main = "Beta0 with burnin")
hist (nfl_draws$beta1 [-c(1:burnin)], main = "Beta1 with burnin")
```



Create 95% credible interval for β_0 and β_1 after using burnin

```
quantile (c (0.025, 0.975), x = nfl_draws$beta0 [-c(1:burnin)])
```

```
##     2.5%    97.5%
## 5.635876 7.526831
```

```
quantile (c (0.025, 0.975), x = nfl_draws$beta1 [-c(1:burnin)])
```

```
##       2.5%      97.5%
## -0.1379617 -0.0950601
```

Fit the model via maximum likelihood:

```
fit <- glm (GOOD ~ distance, family = binomial (link = 'logit'), data = nfl)
summary (fit)
```

```
##
## Call:
## glm(formula = GOOD ~ distance, family = binomial(link = "logit"),
##     data = nfl)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.9526   0.2039   0.3478   0.5826   1.2309
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  6.76271    0.54443  12.422   <2e-16 ***
## distance    -0.12084    0.01229  -9.836   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 817.72  on 1038  degrees of freedom
## Residual deviance: 686.93  on 1037  degrees of freedom
## AIC: 690.93
##
## Number of Fisher Scoring iterations: 6
```

```r
confint (fit)
```

```
## Waiting for profiling to be done...
```

```
##                  2.5 %      97.5 %
## (Intercept)  5.7399740  7.87764350
## distance    -0.1457751 -0.09754001
```