SDS 385: Exercise 03

September 8, 2016

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# Gradient Descent with Backtracking Line Search

#### Part A

The Wolfe Conditions are a set of two requirements for the step size  $\alpha_k$ . The purpose of these conditions is to ensure that each iteration progresses by decreasing the objective function.

(1) The first condition is called the Armijo condition. It ensures that the selected step size gives enough decrease in the objective function for each iteration.

$$f(x_k + \alpha p_k) \le f(x_k) + c_1 \alpha \nabla f_k^{\ t} p_k$$

In our case,  $x_k = \beta_k$  and  $p_k = \nabla(\beta)$ :

$$l(\beta_k) + \alpha \nabla(\beta_k) \le l(\beta_k) + c_1 \alpha \nabla(\beta_k)' \nabla(\beta_k) = l(\beta_k) + \alpha \nabla(\beta_k) \le l(\beta_k) + c_1 \alpha ||\nabla(\beta_k)||^2$$

- This is also sometimes called the 'sufficient decrease condition'.
- $c_1$  is a constant, with  $c_1 \in (0,1)$ .  $c_1$  is usually small;  $10^{-4}$  is given as an example.
- The right side of the inequality is a linear function with negative slope. The condition is met for small positive  $\alpha$  values, but we also want to make sure the  $\alpha$ s are not too small, otherwise the algorithm will take a long time to converge. A second condition is required.
- (2) The second condition is called the curvature condition. It ensures that step sizes are not too short.

$$\nabla f(x_k + \alpha_k p_k)' p_k \ge c_2 \nabla f_k' p_k$$

In our case,  $x_k = \beta_k$  and  $p_k = \nabla(\beta)$ :

$$\nabla(\beta_k + \alpha_k \nabla(\beta_k))' \nabla(\beta_k) \ge c_2 \nabla(\beta_k)$$
, with  $c_2 \in (c_1, 1)$ 

The left side of this inequality is the derivative of the left side of the previous inequality, so this condition is requiring that the slope of the left side of the inequality at  $\alpha_k$  is at least  $c_2$  times the initial slope.

The intuition here is that if the slope is very negative, we should move further in this direction, and if the slope is only slightly negative or is positive, we should not continue the line search in this direction.

The **backtracking line search** is an algorithm that makes the second condition unnecessary. The algorithm is as follows:

Choose an initial step size,  $\alpha_0$ . Set  $\alpha = \alpha_0$ . This is often set to 1, as the initial step size acts as the maximum step size; the algorithm will not take a longer step than this.

Choose a  $\rho \in (0,1)$ . I chose  $\rho = 0.5$ . The  $\rho$  value represents what  $\alpha$  is multiplied by at each iteration. (At each iteration,  $\alpha$  is updated to equal  $\alpha * \rho$ .)

Choose a constant,  $c \in (0,1)$ . This is usually very small; I set c = 0.01.

REPEAT UNTIL  $l(\beta_k - \alpha \nabla(l(\beta_k))) \le l(\beta_k) + c\alpha ||\nabla(l(\beta))||^2$ Update  $\alpha \leftarrow \rho * \alpha$ (END REPEAT)

Return  $\alpha_k = \alpha$  as the step size for this gradient descent iteration.

#### Part B

Results of the gradient descent with backtracking line search are as follows.

```
> #3. Eyeball values for accuracy & display convergence.
> beta
                     #Glm estimated beta values.
                                                        XV6
                                                                    XV7
                                                                                XV8
                                                                                            XV9
                    XV3
                                XV4
                                            XV5
 0.48701675 -7.22185053
                        1.65475615 -1.73763027 14.00484560 1.07495329 -0.07723455 0.67512313
       XV10
                   XV11
                               XV12
             0.44625631 -0.48248420
 2.59287426
> beta_hat$beta_hat #Gradient descent estimated beta values.
     0.456257036 -5.690984607 1.655931491 -3.134285791 13.753565708 1.061183504 0.003625391
 [8] 0.688046899 2.611524565 0.444316088 -0.487797615
> print(c("Algorithm converged? ",beta_hat$converged, " (1=converged, 0=did not converge)"))
[1] "Algorithm converged? "
                                         "1"
[3] " (1=converged, 0=did not converge)"
> print(beta_hat$iter)
[1] 5435
```

Figure 1: Gradient Descent Output

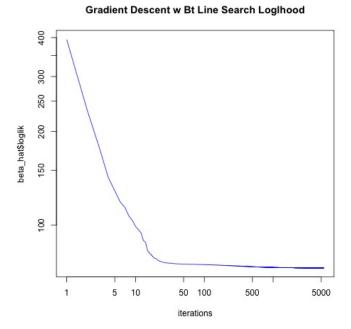


Figure 2: Gradient Descent Negative Log-Likelihood Plot

## R Code: Gradient Descent with Backtracking Line Search

```
### SDS 385 - Exercises 03 - Backtracking Line Search
   #This code implements gradient descent to estimate the
   #beta coefficients for binomial logistic regression.
   #It uses backtracking line search to calculate the step size.
   #Jennifer Starling
   #26 August 2016
   library(Matrix)
  rm(list=ls())
   #PART B:
   #Read in code.
  wdbc = read.csv('/Users/jennstarling/UTAustin/2016_Fall_SDS 385_Stats Models for
      Big Data/Course Data/wdbc.csv', header=FALSE)
   y = wdbc[,2]
   #Convert y values to 1/0's.
   Y = rep(0, length(y)); Y[y=='M']=1
  X = as.matrix(wdbc[,-c(1,2)])
   #Select features to keep, and scale features.
   scrub = which(1:ncol(X) \% 3 == 0)
   scrub = 11:30
  X = X[,-scrub]
   X <- scale(X) #Normalize design matrix features.
   X = cbind(rep(1, nrow(X)), X)
   #Set up vector of sample sizes. (All 1 for wdbc data.)
  m <- rep(1, nrow(X))</pre>
   #Binomial Negative Loglikelihood function.
       #Inputs: Design matrix X, vector of 1/0 vals Y,
          coefficient matrix beta, sample size vector m.
       #Output: Returns value of negative log-likelihood
          function for binomial logistic regression.
   logl <- function(X,Y,beta,m){</pre>
       w \leftarrow 1 / (1 + exp(-X %*% beta)) #Calculate probabilities vector w_i.
       \label{eq:loglike} \mbox{log1} \ \mbox{$\  < -$ sum(Y*log(w+1E-4) + (m-Y)*log(1-w+1E-4))$} \ \ \mbox{$\# Calculate log-likelihood.}
           #Adding constant to resolve issues with probabilities near 0 or 1.
       return(log1)
   }
45
   #Function for calculating Euclidean norm of a vector.
   norm_vec <- function(x) sqrt(sum(x^2))</pre>
   #Gradient Function:
       #Inputs: Design matrix X, vector of 1/0 vals Y,
           coefficient matrix beta, sample size vector m.
       #Output: Returns value of gradient function for binomial
         logistic regression.
   gradient <- function(X,Y,beta,m){</pre>
```

```
w \leftarrow 1 / (1 + exp(-X %*% beta)) #Calculate probabilities vector w_i.
       gradient <- array(NA,dim=length(beta)) #Initialize the gradient.</pre>
       gradient <- -apply(X*as.numeric(Y-m*w),2,sum) #Calculate the gradient.</pre>
       return(gradient)
65
   #Line Search Function
       #Inputs: X = design matrix
                 Y = vector of 1/0 response values
                 b = vector of betas
                 g = gradient for beta vector
70
                 m = sample size vector m
                 maxalpha = The maximum allowed step size.
       #Outputs: alpha = The multiple of the search direction.
   linesearch <- function(X,Y,b,gr,m,maxalpha=1){</pre>
       c <- .01
                           \#A constant, in (0,1)
       alpha <- maxalpha
                          #The max step size, ie the starting step size.
                           #The multiplier for the step size at each iteration.
       p <- .5
       #Update alpha while condition holds.
       alpha <- p*alpha
       return(alpha)
85
   }
   #Gradient Descent Algorithm:
   #Inputs:
       X: n x p design matrix.
       Y: response vector length n.
       m: vector length n.
       conv: Tolerance level for determining convergence, (length of gradient) < conv
   #
      a: Step size.
95
   #Outputs:
      beta_hat: A vector of estimated beta coefficients.
       iter: The number of iterations until convergence.
       converged: 1/0, depending on whether algorithm converged.
100
       loglik: Log-likelihood function.
   gradient_descent <- function(X,Y,m,maxiter=50000,conv=1*10^-10){
105
       #1. Initialize matrix to hold beta vector for each iteration.
       betas <- matrix(0, nrow=maxiter+1, ncol=ncol(X))</pre>
       betas[1,] \leftarrow rep(0,ncol(X)) #Initialize beta vector to 0 to start.
       #2. Initialize values for log-likelihood.
       loglik <- rep(0,maxiter)</pre>
                                   #Initialize vector to hold loglikelihood function.
110
       loglik[1] \leftarrow logl(X,Y,betas[1,],m)
       #Initialize matrix to hold gradients for each iteration.
       grad <- matrix(0,nrow=maxiter,ncol=ncol(X))</pre>
```

```
grad[1,] <- gradient(X,Y,betas[1,],m)</pre>
115
        converged <- 0
                             #Indicator for whether convergence met.
        iter <- 1
                             #Counter to track iterations for function output.
        #2. Perform gradient descent.
120
        for (i in 2:maxiter){
            #Backtracking line search to calculate step size.
            step <- linesearch(X,Y,b=betas[i-1,],gr=grad[i-1,],m,maxalpha=1)</pre>
125
            #Set new beta equal to beta - step*gradient(beta).
            betas[i,] <- betas[i-1,] - step * grad[i-1,]
            #Calculate loglikelihood for each iteration.
            loglik[i] <- logl(X,Y,betas[i,],m)</pre>
130
            #Calculate gradient for beta.
            grad[i,] <- gradient(X,Y,betas[i,],m)</pre>
            iter <- i #Track iterations.</pre>
135
            print(iter)
            #Check if convergence met: If yes, exit loop.
            if (abs(loglik[i]-loglik[i-1])/abs(loglik[i-1]+1E-3) < conv ){</pre>
140
                converged=1;
                break:
            }
       } #End gradient descent iterations.
       return(list(beta_hat=betas[i,], iter=iter, converged=converged, loglik=loglik
            [1:i]))
   }
   #Run gradient descent and view results.
   #1. Fit glm model for comparison. (No intercept: already added to X.)
   glm1 = glm(y^X-1, family='binomial') #Fits model, obtains beta values.
   beta <- glm1$coefficients
155
    #2. Call gradient descent function to estimate.
   beta_hat <- gradient_descent(X,Y,m,maxiter=10000,conv=1*10^-10)
   #3. Eyeball values for accuracy & display convergence.
160
   beta
                        #Glm estimated beta values.
   beta_hat$beta_hat
                        #Gradient descent estimated beta values.
   print(c("Algorithm converged? ",beta_hat$converged, " (1=converged, 0=did not
       converge)"))
165
   print(beta_hat$iter)
   #4. Plot log-likelihood function for convergence.
   plot(1:length(beta_hat$loglik),beta_hat$loglik,type='l',xlab='iterations',col='
       blue', log='xy',
       main='Gradient Descent w Bt Line Search Loglhood')
170
```

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```
#Save plot.
jpeg(file='/Users/jennstarling/UTAustin/2016_Fall_SDS 385_Stats Models for Big
    Data/Exercise 03 LaTeX Files/Ex03_gradwlinesearch_loglhood.jpeg')
plot(1:length(beta_hat$loglik),beta_hat$loglik,type='l',xlab='iterations',col='
    blue',log='xy',
    main='Gradient Descent w Bt Line Search Loglhood')
dev.off()
```

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# Problem 2: Quasi-Newton Method

#### Part A

#### Secant Condition Intuition

The crux of Quasi Newton's Method is to use an approximation of the Hessian matrix, to avoid the calculation overhead involved in actually computing the Hessian for each iteration. The BFGS method provides a way to approximate the Hessian which ensures that the approximation shares certain properties with the Hessian.

Specifically, we expect the Hessian to be symmetric, and to satisfy a condition called the Secant Condition.

The Secant Condition is as follows:

$$\begin{split} B_{k+1}s_k &= z_k, \text{ with } \\ s_k &= x_{k+1} - x_k, \\ z_k &= \nabla(f_{k+1}) - \nabla(f_k), \\ \mathbf{B} &= \text{the Hessian approximation.} \end{split}$$

This equation rearranges as  $B_{k+1} = \frac{z_k}{s_k} = \frac{\nabla (f_{k+1}) - \nabla (f_k)}{x_{k+1} - x_k}$ .

The intuition here is that the Hessian matrix H is the second derivative of the log-likelihood, ie the first derivative of the gradient. If we use the finite differences method to approximate the first derivative of the gradient, we get:

$$H_{k+1} \approx \frac{\nabla(l(\beta_{k+1})) - \nabla(l(\beta_k))}{\beta_{k+1} - \beta_k}$$

This is the secant condition, since our f(x) is the log-likelihood function  $l(\beta)$ , and our x is  $\beta$ . So it is logical to require a Hessian approximation to meet this same condition as the true Hessian.

The BFGS method is an equation to approximate the Hessian which ensures that the approximation is symmetric, and also meets the Secant Condition.

Also note that we are actually approximating the inverse of the Hessian instead of the Hessian itself. This technique is more efficient, so that we do not have to perform the Hessian approximation and then invert the result separately.

### Pseudo-Code for BFGS Quasi-Newton with Backtracking Line Search

The pseudo-code for Quasi-Newton with BFGS and backtracking line search:

- 1. Initialize first iteration of values (i=1).
  - (a) Set first Beta vector  $(\beta_1)$  to all zeros.
  - (b) Calculate log-likelihood ( $logl_1$ ) function using first Beta vector.
  - (c) Calculate gradient using first Beta vector  $(g_1)$ .
  - (d) Set the pxp identity matrix as the initial inverse Hessian approximation  $(B_1)$ .
- 2. Begin looping, i=2 to maxiter.
  - (a) Compute direction and step size for updating the Beta vector  $(\beta_i)$ . (p is direction,  $\alpha$  is step size.)  $p = -B_{i-1} \ g_{i-1}$  (Uses previous iteration's inverse Hessian approximation)  $\alpha = \text{linesearch}(f(\mathbf{x}) = \text{loglikelihood}, \mathbf{x} = \beta_{i-1}, \text{gradient} = g_{i-1}, \mathbf{p}, \text{maxalpha} = 1, \mathbf{c} = .01, \text{rho} = .5)$  (Perform line search according to algorithm described previously.)
  - (b) Update Beta vector as  $\beta_i = \beta_{i-1} + \alpha * p$
  - (c) Update loglikelihood function using new betas:  $logl_i = logl(X, Y, \beta_i, m)$
  - (d) Update gradient using new betas:  $g_i = gradient(X, Y, \beta_i, m)$
  - (e) Update inverse Hessian approximation B:
    - (i) First, update values required for calculation:

```
s = \alpha * p (This is s_k in article.)

z = g_i - g_{i-1} (This is y_k in article.)

rho = \frac{1}{z's} (This is \rho_k in article.)

tau = rho * (s\% * \%z') (Saving a frequently used term as its own var, for simplicity.)

I = pxp identity matrix.
```

- (ii) Second, update inverse Hessian approximation using BFGS formula:  $B_i = (I tau)\% * \%B_{i-1}\% * \%(I tau') + rho * ss'$
- (f) Check if convergence is met. If no, increment i and repeat loop. If yes, end loop.
- 3. Once loop has ended, return vector of  $\beta_i$  estimates.

### Part B

Results of the Quasi-Newton Method with backtracking line search are as follows. The algorithm converged in 40 iterations.

> #3. Eyeball values for accuracy & display convergence. #Glm estimated beta values. > beta XV4 XV6 XV7 XV8 XV9 XV3 XV5 0.48701675 -7.22185053 1.65475615 -1.73763027 14.00484560 1.07495329 -0.07723455 0.67512313 XV10 XV11 XV12 0.44625631 -0.48248420 2.59287426 > beta\_hat\$beta\_hat #Gradient descent estimated beta values. 0.4869994 -7.2217221 1.6547630 -1.7375649 14.0046594 1.0749477 -0.0772729 0.6751084 [1] [9] 2.5929000 0.4462523 -0.4824481

Figure 3: Quasi-Newton Negative Log-Likelihood Plots

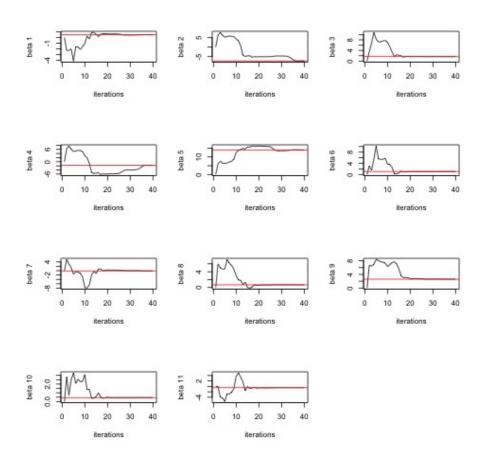


Figure 4: Quasi-Newton Betas Convergence

## Quasi-Newton Neg Loglikelihood Function

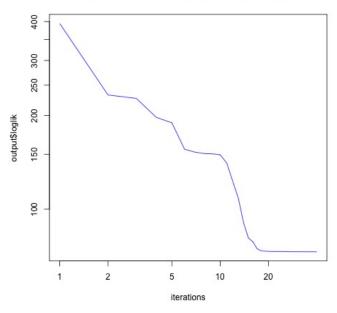


Figure 5: Quasi-Newton Negative Log-Likelihood Plot

## R Code: Quasi-Newton with Backtracking Line Search

```
### SDS 385 - Exercises 03 - Backtracking Line Search
   #This code implements gradient descent to estimate the
   #beta coefficients for binomial logistic regression.
   #It uses backtracking line search to calculate the step size.
   #Jennifer Starling
   #26 August 2016
   library(Matrix)
  rm(list=ls())
                   #Clean workspace.
   #Read in code.
   wdbc = read.csv('/Users/jennstarling/UTAustin/2016_Fall_SDS 385_Stats Models for
      Big Data/Course Data/wdbc.csv', header=FALSE)
   y = wdbc[,2]
   #Convert y values to 1/0's.
   Y = rep(0, length(y)); Y[y=='M']=1
   X = as.matrix(wdbc[,-c(1,2)])
  #Select features to keep, and scale features.
   scrub = which(1:ncol(X) \% 3 == 0)
   scrub = 11:30
   X = X[,-scrub]
   X <- scale(X) #Normalize design matrix features.
  X = cbind(rep(1, nrow(X)), X)
   #Set up vector of sample sizes. (All 1 for wdbc data.)
   m <- rep(1,nrow(X))</pre>
   #Binomial Negative Loglikelihood function.
       #Inputs: Design matrix X, vector of 1/0 vals Y,
          coefficient matrix beta, sample size vector m.
       #Output: Returns value of negative log-likelihood
       # function for binomial logistic regression.
   logl <- function(X,Y,beta,m){</pre>
       w \leftarrow 1 / (1 + exp(-X %*% beta)) #Calculate probabilities vector <math>w_i.
       log1 <- sum(Y*log(w+1E-4) + (m-Y)*log(1-w+1E-4)) #Calculate log-likelihood.
           #Adding constant to resolve issues with probabilities near 0 or 1.
       return(log1)
40
   }
   #Function for calculating Euclidean norm of a vector.
  norm_vec <- function(x) sqrt(sum(x^2))</pre>
   #Gradient Function:
       #Inputs: Design matrix X, vector of 1/0 vals Y,
          coefficient matrix beta, sample size vector m.
       #Output: Returns value of gradient function for binomial
       # logistic regression.
   gradient <- function(X,Y,beta,m){</pre>
       w \leftarrow 1 / (1 + exp(-X %*% beta)) #Calculate probabilities vector w_i.
```

```
gradient <- array(NA,dim=length(beta)) #Initialize the gradient.</pre>
        gradient <- -apply(X*as.numeric(Y-m*w),2,sum) #Calculate the gradient.</pre>
       return(gradient)
   }
    #Line Search Function
        #Inputs: X = design matrix
65
                  Y = vector \ of \ 1/0 \ response \ values
                  b = vector of betas
                  g = gradient for beta vector
                  p = direction vector
                  m = sample size vector m
70
                  maxalpha = The maximum allowed step size.
        #Outputs: alpha = The multiple of the search direction.
   linesearch <- function(X,Y,b,gr,p,m,maxalpha=1){</pre>
        c <- .01
                             \#A constant, in (0,1)
                            #The max step size, ie the starting step size.
        alpha <- maxalpha
       rho <- .5
                                 #The multiplier for the step size at each iteration.
       while ( (logl(X,Y,b + alpha*p,m)) > logl(X,Y,b,m) + c*alpha*t(gr) %*% p ) {
            alpha <- rho*alpha
       return(alpha)
   }
85
    #Quasi Newton with Backtracking Line Search Algorithm:
    #Inputs:
       X: n x p design matrix.
       Y: response vector length n.
       m: vector length n.
       conv: Tolerance level for evaluating convergence.
       a: Step size.
   #Outputs:
      beta_hat: A vector of estimated beta coefficients.
       iter: The number of iterations until convergence.
       converged: 1/0, depending on whether algorithm converged.
       loglik: Log-likelihood function.
   quasi_newton <- function(X,Y,m,maxiter=50000,conv=1*10^-10){
        converged <- 0
                             #Indicator for whether convergence met.
        #1. Initialize matrix to hold beta vector for each iteration.
105
        betas <- matrix(0,nrow=maxiter+1,ncol=ncol(X))</pre>
        betas[1,] <- rep(0,ncol(X)) #Initialize beta vector to 0 to start.
        #2. Initialize values for log-likelihood.
        loglik <- rep(0,maxiter)</pre>
                                    #Initialize vector to hold loglikelihood fctn.
110
        loglik[1] <- logl(X,Y,betas[1,],m)</pre>
        #3. Initialize matrix to hold gradients for each iteration.
        grad <- matrix(0,nrow=maxiter,ncol=ncol(X))</pre>
        grad[1,] <- gradient(X,Y,betas[1,],m)</pre>
115
```

```
#4. Initialize list of approximations of Hessian inverse, B.
            (Use identity matrix as initial value.)
        B <- list()
        B[[1]] <- diag(ncol(betas))</pre>
        #5. Perform gradient descent.
        for (i in 2:maxiter){
125
            #Compute direction and step size for beta update.
            p <- -B[[i-1]] %*% grad[i-1,]
            alpha <- linesearch(X,Y,b=betas[i-1,],gr=grad[i-1,],p,m,maxalpha=1)
            #Update beta values based on step/direction.
            betas[i,] <- betas[i-1,] + alpha*p
130
            #Calculate loglikelihood for each iteration.
            loglik[i] <- logl(X,Y,betas[i,],m)</pre>
            #Calculate gradient for new betas.
135
            grad[i,] <- gradient(X,Y,betas[i,],m)</pre>
            #Update values needed for BFGS Hessian inverse approximation.
            s <- alpha*p
            z <- grad[i,] - grad[i-1,]
            rho <- as.vector(1/(t(z) \%*\% s))
                                                   #as.vector to make rho a scalar.
            tau <- rho * s %*% t(z) #Just breaking up the formula a bit for ease.
            I <- diag(ncol(grad))</pre>
            \#BFGS formula for updating approx of H inverse.
145
            B[[i]] \leftarrow (I-tau) \% \% B[[i-1]] \% \% (I-t(tau)) + rho * s \% \% t(s)
            print(i)
            #Check if convergence met: If yes, exit loop.
150
            if (abs(loglik[i]-loglik[i-1])/abs(loglik[i-1]+1E-3) < conv ){</pre>
                converged=1;
                break;
            }
155
        } #End gradient descent iterations.
        return(list(betas=betas[1:i,],beta_hat=betas[i,], iter=i, converged=converged,
            loglik=loglik[1:i]))
160
    #Run gradient descent and view results.
    #1. Fit glm model for comparison. (No intercept: already added to X.)
   glm1 = glm(y~X-1, family='binomial') #Fits model, obtains beta values.
   beta <- glm1$coefficients
   #2. Call gradient descent function to estimate.
   output <- quasi_newton(X,Y,m,maxiter=10000,conv=1*10^-10)</pre>
   #3. Eyeball values for accuracy & display convergence.
   beta
                         #Glm estimated beta values.
   output$beta_hat #Gradient descent estimated beta values.
```

```
#Print whether the algorithm has converged, and the number of iterations.
175
   if(output$converged >0) {cat('Algorithm converged in',output$iter, 'iterations.')}
   if(output$converged<1){cat('Algorithm did not converge. Ran for max iterations.')}
   #4. Plot the convergence of the beta variables compared to glm.
   par(mfrow=c(4,3))
180
   for (j in 1:length(output$beta_hat)){
       plot(1:nrow(output$betas),output$betas[,j],type='1',xlab='iterations',ylab=
           paste('beta',j))
       abline(h=beta[j],col='red')
   }
185
   #5. Plot log-likelihood function for convergence.
   plot(1:length(output$loglik),output$loglik,type='l',xlab='iterations',col='blue',
       log='xy',
       main='Quasi-Newton Neg Loglikelihood Function')
   #6. Save plots.
   jpeg(file='/Users/jennstarling/UTAustin/2016_Fall_SDS 385_Stats Models for Big
       Data/Exercise 03 LaTeX Files/Ex03_quasinewtonloglhood.jpg')
   plot(1:length(output$loglik),output$loglik,type='l',xlab='iterations',col='blue',
       log='xy',
       main='Quasi-Newton Neg Loglikelihood Function')
   dev.off()
195
   jpeg(file='/Users/jennstarling/UTAustin/2016_Fall_SDS 385_Stats Models for Big
       Data/Exercise 03 LaTeX Files/Ex03_quasinewtonbetas.jpg')
   par(mfrow=c(4,3))
   for (j in 1:length(output$beta_hat)){
       plot(1:nrow(output$betas),output$betas[,j],type='1',xlab='iterations',ylab=
           paste('beta',j))
       abline(h=beta[j],col='red')
200
   dev.off()
```