Homework 1

Tavis Abrahamsen, Ray Bai, Syed Rhaman, Andrey Skripnikov

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1 a.) To simulate the data, we first generate a 25000×3000 matrix of random values.

```
> set.seed(12345)
> n <- 25000
> p <- 3000
> dataMat <- matrix(runif(n*p,min=-1,max=1),n,p)</pre>
```

We then perform a singular value decomposition on the above matrix.

```
> A <- svd(dataMat)
> U <- A$u
> V <- A$v
> d <- A$d</pre>
```

Note that for a matrix $X \in \mathbb{R}^{n \times p}$ $(n \ge p)$, the singular value decomposition of X is given by $X = U \Sigma V^T$ where $U \in \mathbb{R}^{n \times n}$ and $V \in \mathbb{R}^{p \times p}$ are orthogonal matrices. The matrix $\Sigma \in \mathbb{R}^{n \times p}$ is defined as

$$\Sigma = \left[\begin{array}{c} D \\ 0 \end{array} \right],$$

where $D \in \mathbb{R}^{p \times p}$ is a diagonal matrix. The diagonal entries of D are called the *singular values* of X. These values are also the square roots of the eigenvalues of X^TX . Thus, in order to generate our covariate data such that the Gram matrix, X^TX has a condition number of 1, we simply replace D with the identity matrix.

Note that in R, U is an $n \times p$ matrix of the first p left singular vectors. Since the singular values are all 1 in this case, the condition number of X^TX will be 1/1=1.

To generate data with a condition number 30, we randomly draw the singular values from a Uniform $(1,\sqrt{30})$ distribution. We then set one of the values equal to 1 and another equal to $\sqrt{30}$. Hence the condition number of the corresponding Gram matrix will be $(\sqrt{30})^2/1 = 30$.

```
> d.1 <- runif(p,min=1, max=sqrt(30))
> d.1[1] <- sqrt(30)
> d.1[p] <- 1
> X <- U%*%diag(d.1)%*%t(V)</pre>
```

Similarly, for a condition number of 500, we have

```
> d.1 <- runif(p,min=1, max=sqrt(500))
> d.1[1] <- sqrt(500)
> d.1[p] <- 1
> X <- U%*%diag(d.1)%*%t(V)</pre>
```

To generate our response data, we randomly draw the components of β .

> true.beta <- rnorm(p,0,2)</pre>

Then for each of the covariate matrices above, we generate the corresponding response data $Y_i \sim \text{Bernoulli}(p_i)$ where

$$p_i := \frac{e^{x_i^T \beta}}{1 + e^{x_i^T \beta}}, \quad i = 1, 2, \dots, 2500.$$

> prob <- exp(X%*%true.beta)/(1+exp(X%*%true.beta))
> y <- rbinom(n,1,prob)</pre>

1 b.) We chose to estimate β using the maximum likelihood estimator. This estimator is obtained by maximizing the log-likelihood function with respect to to β . Let $L(\beta)$ denote the likelihood function, then

$$L(\beta) = \prod_{i=1}^{n} \left(\frac{e^{x_i^T \beta}}{1 + e^{x_i^T \beta}} \right)^{y_i} \left(\frac{1}{1 + e^{x_i^T \beta}} \right)^{1 - y_i}.$$

The log-likelihood, $l(\beta)$ is then given by

$$l(\beta) = \sum_{i=1}^{n} \left\{ y_i \log \left(\frac{e^{x_i^T \beta}}{1 + e^{x_i^T \beta}} \right) + (1 - y_i) \log \left(\frac{1}{1 + e^{x_i^T \beta}} \right) \right\}$$
$$= \sum_{i=1}^{n} \left\{ y_i x_i^T \beta - \log \left(1 + e^{x_i^T \beta} \right) \right\}.$$

To find the MLE of β , we could maximize $l(\beta)$, or equivialently we could minimize the function $f(\beta) = -l(\beta)$. To minimize the negative log-likelihood, we use the steepest descent algorithm which is given by

$$\beta^{k+1} = \beta^k - \alpha^k \nabla (f(\beta^k)) = \beta^k + \alpha^k \nabla l(\beta^k), \quad k = 0, 1, 2, \dots$$

Notice that

$$\frac{\partial l}{\partial \beta_j} = \sum_{i=1}^n \left\{ y_i x_{ij} - \frac{e^{x_i^T \beta}}{1 + e^{x_i^T \beta}} x_{ij} \right\},\,$$

Thus,

$$\nabla l(\beta) = X^T(y - \eta(\beta)),$$

where $y^T = (y_1, y_2, \dots, y_n)^T$ and $\eta(\beta) \in \mathbb{R}^n$ with

$$\eta_i = \frac{e^{x_i^T \beta}}{1 + e^{x_i^T \beta}}, \quad i = 1, 2, \dots, n.$$

Hence, our steepest descent algorithm is

$$\beta^{k+1} = \beta^k + \alpha^k X^T (y - \eta(\beta^k)), \quad k = 0, 1, 2, \dots$$

It is worth noting that $f(\beta)$ is a convex function. To see this, consider the function

$$g(x) = -\left(ax - \log(1 + e^x)\right).$$

Indeed,

$$g''(x) = -\left(-\frac{e^x}{(1+e^x)^2}\right) = \frac{e^x}{(1+e^x)^2} > 0 \quad \forall x \in \mathbb{R},$$

and thus $f(\beta)$ has a unique global minimum.

For each condition number (1,30,500) we compare the performance of the steepest descent algorithm for three different choices of step size, α^k . The first choice is using a constant step size, i.e., $\alpha^k = s$ where s is a constant for $k = 0, 1, 2, \ldots$ The second is using a diminishing step size where $\alpha^k \to 0$ such that

$$\sum_{k=0}^{\infty} \alpha^k = \infty.$$

Lastly, we choose the step size using Armijo's rule. Here, we start with a constant s, and for $\gamma \in (0,1)$, we take $\alpha^k = s\gamma^l$ where l is the smallest non-negative integer satisfying the inequality

$$f(\beta^k) - f(\beta^k - s\gamma^l \nabla f(\beta^k)) \ge -\sigma s\gamma^l (-\nabla f(\beta^k))^T \nabla f(\beta^k)$$

for some $\sigma \in (0,1]$. In terms of the log-likelihood function, the inequality becomes

$$l(\beta^k + s\gamma^l \nabla l(\beta^k)) - l(\beta^k) \ge \sigma s\gamma^l ||\nabla l(\beta^k)||^2.$$

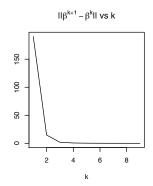
For a condition number equal to 1, and using a constant step size our steepest descent algorithm is

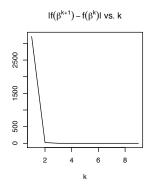
```
> comp.grad <- function(y,X,beta){</pre>
    t(X)%*%(y-(exp(X%*%beta)/(1+exp(X%*%beta))))
+ }
> log.lik <- function(y, X, beta){</pre>
    p \leftarrow \exp(X\%*\%beta)/(1+\exp(X\%*\%beta))
    sum(y*log(p)+(1-y)*log(1-p))
+ }
> alpha <- 5
> beta.old <- rep(1,p)
> delta <- .00001
> maxIter <- 1000
> d.f <- rep(0,maxIter)</pre>
> d.beta <- rep(0,maxIter)</pre>
> err.beta <- rep(0,maxIter)
> iter <- 1
> eps <- 1
> while(iter<maxIter && eps>delta ){
    beta.new <- beta.old + alpha*comp.grad(y,X,beta.old)
    eps <- abs(log.lik(y,X,beta.new)-log.lik(y,X,beta.old))</pre>
    d.f[iter] <- eps
    d.beta[iter] <- sqrt(t(beta.new-beta.old)%*%(beta.new-beta.old))</pre>
    err.beta[iter] <- sqrt(crossprod((beta.new-true.beta),(beta.new-true.beta)))</pre>
    beta.old <- beta.new
    iter <- iter+1
```

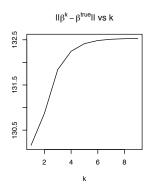
We ran our algorithm using a step size equal to 5 until the quantity $|f(\beta^{k+1}) - f(\beta^k)|$ is less than the specified tolerance of 10^{-5} . Shown below is the number of iterations the algorithm took to converge and $||\hat{\beta}_{MLE} - \beta||$, and plots of various convergence diagnostics.

```
> # Number of iterations
> iter
[1] 10
```

```
> # Error
> sqrt(t(true.beta-beta.old)%*%(true.beta-beta.old))
         [,1]
[1,] 132.5281
```



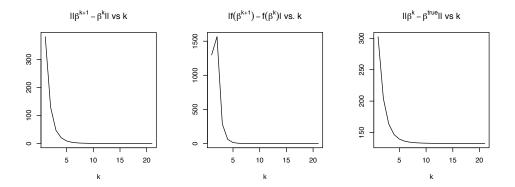




For the decreasing step size algorithm, we took $\alpha^k = \frac{10}{\sqrt{k}}$.

```
> alpha0 <- 10
> alpha <- alpha0
> beta.old <- rep(1,p)
> delta <- .00001
> maxIter <- 1000
> d.f <- rep(0,maxIter)</pre>
> d.beta <- rep(0,maxIter)</pre>
> err.beta <- rep(0,maxIter)</pre>
> iter <- 1
> eps <- 1
> while(iter<maxIter && eps>delta ){
    beta.new <- beta.old + alpha*comp.grad(y,X,beta.old)</pre>
    {\tt eps} \; \leftarrow \; {\tt abs(log.lik(y,X,beta.new)-log.lik(y,X,beta.old))}
    d.f[iter] <- eps
    d.beta[iter] <- sqrt(t(beta.new-beta.old)%*%(beta.new-beta.old))</pre>
    err.beta[iter] <- sqrt(crossprod((beta.new-true.beta),(beta.new-true.beta)))</pre>
    beta.old <- beta.new</pre>
    iter <- iter+1</pre>
    alpha <- alpha0/sqrt(iter)</pre>
+ }
> # Number of iterations
> iter
[1] 22
> # Error
> sqrt(t(true.beta-beta.old)%*%(true.beta-beta.old))
          [,1]
[1,] 132.5397
```

4

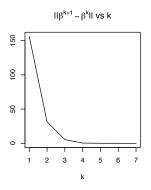


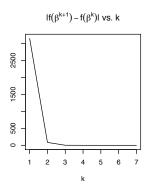
For the Armijo's rule step size we took $s=10, \gamma=0.8$ and $\sigma=0.5$.

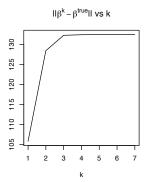
```
> s <- 10
> sigma <- .5
> gamma <- .8
> beta.old <- rep(1,p)
> delta <- .00001
> maxIter <- 1000
> d.f <- rep(0,maxIter)</pre>
> d.beta <- rep(0,maxIter)</pre>
> err.beta <- rep(0,maxIter)</pre>
> iter <- 1
> eps <- 1
> while(iter<maxIter && eps>delta ){
    check <- 0
    t <- 1
    while(check==0){
      grad.f <- comp.grad(y,X,beta.old)</pre>
      beta.new <- beta.old + s*(gamma^t)*grad.f
      a <- log.lik(y,X,beta.new)-log.lik(y,X,beta.old)</pre>
      b <- sigma*s*(gamma^t)*t(grad.f)%*%grad.f</pre>
      if(a >= b){
        check <- 1
      }
+
      else\{t \leftarrow t+1\}
    eps <- abs(log.lik(y,X,beta.new)-log.lik(y,X,beta.old))</pre>
    d.f[iter] <- eps
    d.beta[iter] <- sqrt(t(beta.new-beta.old)%*%(beta.new-beta.old))</pre>
    err.beta[iter] <- sqrt(crossprod((beta.new-true.beta),(beta.new-true.beta)))</pre>
    beta.old <- beta.new</pre>
    iter <- iter+1
+ }
> # Number of iterations
> iter
[1] 8
```

> # Error

> sqrt(t(true.beta-beta.old)%*%(true.beta-beta.old))







When the condition number is equal to 30, the constant step size algorithm would not converge when $\alpha = 5$. Instead, we had to use a step size of 0.5. The results are shown below.

> # Number of iterations

> iter

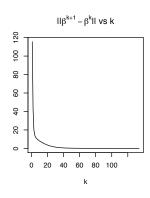
[1] 135

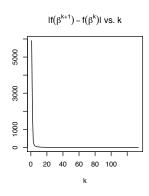
> # Error

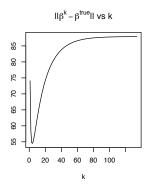
> sqrt(t(true.beta-beta.old)%*%(true.beta-beta.old))

[,1]









For the decreasing step size algorithm, $\alpha^k = 1/\sqrt{k}$.

> # Number of iterations

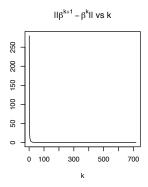
> iter

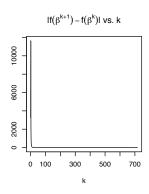
[1] 718

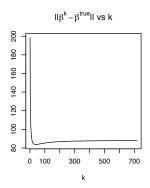
> # Error

> sqrt(t(true.beta-beta.old)%*%(true.beta-beta.old))

[,1] [1,] 87.85411







For Armijo's rule, we used the parameterization $s=2,\,\sigma=0.9$ and $\gamma=0.5.$

> # Number of iterations

> iter

[1] 110

> # Error

> sqrt(t(true.beta-beta.old)%*%(true.beta-beta.old))

[1,] 87.90057

